## Miloje M. Rakočević

## HARMONY OF GENETIC CODE Previous works

## Volume 2

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## Previous Note

This book contains my works published in the period 2005-2017 on my website (also in some Preprints portals). The concept of "harmony" in the title refers to the determination of the genetic code by golden mean, generalized golden mean and harmonic mean. Some parts of the contents, in the meantime are published in some of the official journals, but most are not, and this was the reason for my decision to publish all papers here in their entirety. [Now, 2017.12.13, I store this Proceedings of my works in "OSF Preprints" for the purpose of wider availability to the scientific public.]

Belgrade, 13.12.2017
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## 1.

## On the Completeness of Genetic Code: Part I

In the chapter is presented the chemically meaningful splitting of codons after pyrimidine and purine distinctions; such a splitting that is accompanied by the balance of number of atoms in the set of 61 amino acid molecules. In doing so, the increase or decrease of number of atoms occurs in the quantities of decimal units, what can be understood as analogous filling of the orbitals within atoms.

Comment: New facts in connection to the paper, published in JTB, Volume 229 (2004) 221-234

# ON THE COMPLETENESS OF GENETIC CODE: SOME NEW EXAMPLES 

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#### Abstract

In the paper is presented the chemically meaningful splitting of codons after pyrimidine / purine distinctions; such a splitting that is accompanied by the balance of number of atoms in the set of 61 amino acid molecules. In doing so, the increase / decrease of number of atoms occurs in the quantities of decimal units, what can be understood as analogous filling of the orbitals within atoms.


In a previous work (Rakočević, 2004) we put forward the hypothesis that the Genetic Code (GC) was complete even in prebiotic conditions. As evidence indicated the unity of the physicochemical properties of amino acids (AAs) and arithmetical regularities of the number of atoms and nucleons within genetic code constituents (Figure 1 in relation to Table 1.1). In this paper, however, we present a few new examples of this unity. In addition, as the physicochemical properties of the amino acids are taken the distinctions corresponding to the codons; distinctions according pyrimidine / purine type ( $\mathrm{Py} / \mathrm{Pu}$ ) of nucleotides and/or binding of nucleotides with two/three hydrogen bonds.

In Table 1.2, under (a) and (b), we have the situation that we have already presented (Rakočević, 2004 Table 3a; here: Fig. 1). Now we show that indicated $\mathrm{Py} / \mathrm{Pu}$ splitting corresponds to the 8th, 9th and 10th case in a specific arithmetical system (Table 1.1).

In Tables 2-6 are listed examples of chemicaly meaningful distinctions. ${ }^{1}$ Immediately it is obvious an analogy with the filling of orbitals in an atom: the splittings are accompanied by increasing / decreasing of the quantities of number of atoms for one, two or more units of the number-decades.

The conclusion imposes itself. Such strict regularity would not be able to occur if it were true (as most researchers thought) that it is so in the GC, in the act of the origin of life, when were only 7 to 8 AAs; and later, apparently, that number increased during the "evolution" of genetic code. However, after our opinion, it can evolve only the life, but not his code. If it did that, then it would not be a possibility for the existence of one and such a code.

[^0](a) The atom number balances within Table of genetic code


The number of atoms within AAs (side chains). First column
Figure 1. "The number of atoms within AAs (side chains). First column (I-III) designates the type of the base in first-third position of corresponding codons. The letters U, C, A, G are related to four columns in Genetic Code Table. Within two inner and two outer rows as well as within two first and two second columns there are $(8 \times 33),[(9 \times 33) \pm 1]$, and $(10 \times 33)$ of atoms, respectively" (Rakočević, 2004).

| 27 | 162 | 1782 | 17982 | 999 | 81 | 891 | 8991 | 999 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 26 | 156 | 1716 | 17316 | 962 | 78 | 858 | 8658 | 962 |
| 25 | 150 | 1650 | 16650 | 925 | 75 | 825 | 8325 | 925 |
| $\ldots$. |  |  |  |  | $\ldots$ |  |  |  |
| 13 | 78 | 858 | 8658 | 481 | 39 | 429 | 4329 | 481 |
| 12 | 72 | 792 | 7992 | 444 | 36 | 396 | 3996 | 444 |
| 11 | 66 | 726 | 7326 | 407 | 33 | 363 | 3663 | 407 |
| 10 | 60 | 660 | 6660 | 407 | 30 | 330 | 3330 | 407 |
| 09 | 54 | 594 | 5994 | 333 | 27 | 297 | 2997 | 333 |
| 08 | 48 | 528 | 5328 | 296 | 24 | 264 | 2664 | 333 |
| $\ldots$ |  |  |  |  | $\ldots$ |  |  |  |
| 03 | 18 | 198 | 1998 | 111 | 9 | 99 | 999 | 111 |
| 02 | 12 | 132 | 1332 | 074 | 6 | 66 | 666 | 074 |
| 01 | 6 | 66 | 666 | 037 | 3 | 33 | 333 | 037 |

Tab. 1.1. The multiples of numbers 6,66 and 666 and of their halves 3,33 and 333 , respectively. Here one must notice that this relationship is an example of „the symmetry in the simplest case" (Marcus, 1989). Notice also that 8th, 9th and 10th case corresponds with the number of atoms in GC, as it is presented in Figure 1 and Table 1.2.

| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) | UCU(S) | UAU(Y) | UGU(C) |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) | UUC (F) | UCC(S) | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) | UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) | UUG (L) | UCG(S) | UAG(ct) | UGG(W) |
| CUU (L) | CCU(P) | CAU (H) | CGU(R) | CUU (L) | CCU(P) | $\mathrm{CAU}(\mathrm{H})$ | CGU(R) |
| CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) | CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | CAG(Q) | CGG(R) | CUG (L) | CCG(P) | CAG(Q) | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | ACU(T) | AAU(N) | AGU(S) |
| AUC (I) | ACC(T) | AAC(N) | AGC(S) | AUC (I) | ACC(T) | AAC(N) | AGC(S) |
| AUA ( I ) | ACA(T) | AAA(K) | AGA(R) | AUA (I) | ACA(T) | $\mathrm{AAA}(\mathrm{K})$ | AGA(R) |
| AUG (M) | ACG(T) | AAG(K) | AGG(R) | AUG (M) | ACG(T) | AAG(K) | AGG(R) |
| GUU(V) | GCU(A) | GAU(D) | GGU(G) | GUU(V) | GCU(A) | GAU(D) | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) | GGA(G) |
| GUG(V) | GCG(A) | GAG(E) | GGG(G) | GUG(V) | GCG(A) | GAG(E) | GGG(G) |
| (c) $=\mathbf{3 4 0 / 2 5 4}$ |  |  |  | $(\mathrm{d})=\mathbf{3 5 0 / 2 4 4}$ |  |  |  |
| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) | UCU(S) | UAU(Y) | UGU(C) |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) | UUC (F) | UCC(S) | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) | UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) | UUG (L) | UCG(S) | UAG(ct) | UGG(W) |
| CUU (L) | $\mathrm{CCU}(\mathrm{P})$ | $\mathrm{CAU}(\mathrm{H})$ | CGU(R) | CUU (L) | $\mathrm{CCU}(\mathrm{P})$ | $\mathrm{CAU}(\mathrm{H})$ | CGU(R) |
| CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) | CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | CAG(Q) | CGG(R) | CUG (L) | CCG(P) | CAG(Q) | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | $\mathrm{ACU}(\mathrm{T})$ | AAU(N) | AGU(S) |
| AUC (I) | ACC(T) | $\mathrm{AAC}(\mathrm{N})$ | AGC(S) | AUC (I) | ACC(T) | $\mathrm{AAC}(\mathrm{N})$ | AGC(S) |
| AUA (I) | $\mathrm{ACA}(\mathrm{T})$ | AAA(K) | AGA(R) | AUA (I) | ACA(T) | $\mathrm{AAA}(\mathrm{K})$ | AGA(R) |
| AUG (M) | ACG(T) | $\mathrm{AAG}(\mathrm{K})$ | AGG(R) | AUG (M) | ACG(T) | $\mathrm{AAG}(\mathrm{K})$ | AGG(R) |
| GUU(V) | GCU(A) | GAU(D) | GGU(G) | GUU(V) | GCU(A) | GAU(D) | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) | GGA(G) |
| GUG(V) | GCG(A) | GAG(E) | GGG(G) | GUG(V) | GCG(A) | GAG(E) | $\mathrm{GGG}(\mathrm{G})$ |
| (a) $=296 / 298(297 \pm 1) ;[(33 \times 9) \pm 1]$ |  |  |  | (b) $=330 / 264$; [33 x (9 $\pm 1)$ ] |  |  |  |

Tab. 1.2. The splitting into pyrimidine/purine codons as in Figure 1 with two results more (340 and 350)


Tab. 2. The splitting under (a) gives the same resut (pattern) as in Table 1.2 under (b). After the quantity 330 follow the quantities 320 and 310 ; the 320 in two and 310 in three synonymous situations.

| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) | UCU(S) | UAU(Y) | UGU(C) |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) | UUC (F) | UCC(S) | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) | UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) | UUG (L) | UCG(S) | UAG(ct) | UGG(W) |
| CUU (L) | $\mathrm{CCU}(\mathrm{P})$ | CAU(H) | CGU(R) | CUU (L) | $\mathrm{CCU}(\mathrm{P})$ | CAU(H) | CGU(R) |
| CUC (L) | $\mathrm{CCC}(\mathrm{P})$ | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) | CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | CAG(Q) | CGG(R) | CUG (L) | CCG(P) | CAG(Q) | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | ACU(T) | AAU(N) | AGU(S) |
| AUC (I) | ACC(T) | $\mathrm{AAC}(\mathrm{N})$ | AGC(S) | AUC (I) | ACC(T) | $\mathrm{AAC}(\mathrm{N})$ | AGC(S) |
| AUA (I) | ACA(T) | AAA(K) | AGA(R) | AUA (I) | ACA(T) | $\mathrm{AAA}(\mathrm{K})$ | AGA(R) |
| AUG (M) | ACG(T) | AAG(K) | AGG(R) | AUG (M) | ACG(T) | $\mathrm{AAG}(\mathrm{K})$ | AGG(R) |
| GUU(V) | GCU(A) | GAU(D) | GGU(G) | GUU(V) | GCU(A) | GAU(D) | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) | GGA(G) |
| GUG(V) | GCG(A) | GAG(E) | GGG(G) | GUG(V) | GCG(A) | GAG(E) | GGG(G) |
|  | (c) $=2$ | 70/324 |  |  | (d) $=$ | 60/334 |  |
| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) | UCU(S) | UAU(Y) | UGU(C) |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) | UUC (F) | UCC(S) | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) | UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) | UUG (L) | UCG(S) | UAG(ct) | UGG(W) |
| CUU (L) | CCU(P) | $\mathrm{CAU}(\mathrm{H})$ | CGU(R) | CUU (L) | $\mathrm{CCU}(\mathrm{P})$ | $\mathrm{CAU}(\mathrm{H})$ | CGU(R) |
| CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) | CUC (L) | $\mathrm{CCC}(\mathrm{P})$ | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | $\mathrm{CAG}(\mathrm{Q})$ | CGG(R) | CUG (L) | CCG(P) | CAG(Q) | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | $\mathrm{ACU}(\mathrm{T})$ | $\mathrm{AAU}(\mathrm{N})$ | AGU(S) |
| AUC (I) | ACC(T) | AAC(N) | AGC(S) | AUC (I) | ACC(T) | AAC(N) | AGC(S) |
| AUA (I) | ACA(T) | AAA(K) | AGA(R) | AUA (I) | ACA(T) | AAA(K) | AGA(R) |
| AUG (M) | ACG(T) | AAG(K) | AGG(R) | AUG (M) | ACG(T) | AAG(K) | AGG(R) |
| GUU(V) | GCU(A) | GAU(D) | GGU(G) | GUU(V) | GCU(A) | GAU(D) | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) | GGA(G) |
| GUG(V) | GCG(A) | GAG(E) | GGG(G) | GUG(V) | GCG(A) | GAG(E) | GGG(G) |
| (a) $=\mathbf{2 9 0 / 2 9 4}$ |  |  |  | (b) $=\mathbf{2 8 0 / 3 1 4}$ |  |  |  |

Tab. 3. The further splitting: after the quantity 310 follow the quantities $300,290,280,270$ and 260. Notice that the case under (b) is very specific: all AAs within dark toned areas are nonpolar, while in light tones - polar. By this the square balance is $4 \pm 0$. On the other hand, in intermedial area the square balance is $4 \pm 1$ : within three squares on the left are nonpolar AAs (LIMA), while within five on the right - polar (DERYS). (For details see in: Rakočević, 2014.)

| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) | UCU(S) | UAU(Y) | UGU(C) |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) | UUC (F) | UCC(S) | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) | UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) | UUG (L) | UCG(S) | UAG(ct) | UGG(W) |
| CUU (L) | $\operatorname{CCU}(\mathrm{P})$ | CAU(H) | CGU(R) | CUU (L) | $\mathrm{CCU}(\mathrm{P})$ | CAU(H) | CGU(R) |
| CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) | CUC (L) | $\mathrm{CCC}(\mathrm{P})$ | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | CAG(Q) | CGG(R) | CUG (L) | CCG(P) | CAG(Q) | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | $\mathrm{ACU}(\mathrm{T})$ | AAU(N) | AGU(S) |
| AUC (I) | ACC(T) | AAC(N) | AGC(S) | AUC (I) | ACC(T) | AAC(N) | AGC(S) |
| AUA (I) | ACA(T) | AAA(K) | AGA(R) | AUA (I) | ACA(T) | $\mathrm{AAA}(\mathrm{K})$ | AGA(R) |
| AUG (M) | ACG(T) | AAG(K) | AGG(R) | AUG (M) | ACG(T) | $\mathrm{AAG}(\mathrm{K})$ | AGG(R) |
| GUU(V) | GCU(A) | GAU(D) | GGU(G) | GUU(V) | GCU(A) | GAU(D) | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) | GGA(G) |
| GUG(V) | GCG(A) | GAG(E) | GGG(G) | GUG(V) | GCG(A) | GAG(E) | GGG(G) |
|  | (a) $=$ | 58/336 |  |  | (b) $==$ | 248/346 |  |
| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) | UCU(S) | UAU(Y) | UGU(C) |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) | UUC (F) | UCC(S) | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) | UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) | UUG (L) | UCG(S) | UAG(ct) | UGG(W) |
| CUU (L) | $\mathrm{CCU}(\mathrm{P})$ | $\mathrm{CAU}(\mathrm{H})$ | CGU(R) | CUU (L) | CCU(P) | CAU(H) | CGU(R) |
| CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) | CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | CAG(Q) | CGG(R) | CUG (L) | CCG(P) | $\mathrm{CAG}(\mathrm{Q})$ | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | ACU(T) | AAU(N) | AGU(S) |
| AUC (I) | $\mathrm{ACC}(\mathrm{T})$ | $\mathrm{AAC}(\mathrm{N})$ | $\operatorname{AGC}(\mathrm{S})$ | AUC (I) | $\mathrm{ACC}(\mathrm{T})$ | AAC(N) | AGC(S) |
| AUA (I) | ACA(T) | AAA(K) | AGA(R) | AUA (I) | ACA(T) | $\mathrm{AAA}(\mathrm{K})$ | AGA(R) |
| AUG (M) | ACG(T) | AAG(K) | AGG(R) | AUG (M) | $\operatorname{ACG}(\mathrm{T})$ | AAG(K) | AGG(R) |
| GUU(V) | GCU(A) | GAU(D) | GGU(G) | GUU(V) | GCU(A) | GAU(D) | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) | GGA(G) |
| GUG(V) | GCG(A) | GAG(E) | GGG(G) | GUG(V) | GCG(A) | GAG(E) | GGG(G) |
| (a) $=\mathbf{2 8 8} / 306$ |  |  |  | (b) $=278 / 306$ |  |  |  |

Tab. 4. After the quantity 298 in Table 1.2 follow the quantities 288, 278, 268, 258 and 248.

| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) | UCU(S) | UAU(Y) | UGU(C) |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) | UUC (F) | UCC(S) | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) | UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) | UUG (L) | UCG(S) | UAG(ct) | UGG(W) |
| CUU (L) | CCU(P) | $\mathrm{CAU}(\mathrm{H})$ | CGU(R) | CUU (L) | $\mathrm{CCU}(\mathrm{P})$ | CAU(H) | CGU(R) |
| CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) | CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | CAG(Q) | CGG(R) | CUG (L) | CCG(P) | CAG(Q) | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | $\mathrm{ACU}(\mathrm{T})$ | $\mathrm{AAU}(\mathrm{N})$ | AGU(S) |
| AUC (I) | ACC(T) | AAC(N) | AGC(S) | AUC (I) | ACC(T) | AAC(N) | AGC(S) |
| AUA (I) | ACA(T) | AAA(K) | AGA(R) | AUA (I) | ACA(T) | AAA(K) | AGA(R) |
| AUG (M) | ACG(T) | AAG(K) | AGG(R) | AUG (M) | ACG(T) | AAG(K) | AGG(R) |
| GUU(V) | $\operatorname{GCU}(\mathrm{A})$ | GAU(D) | GGU(G) | GUU(V) | GCU(A) | GAU(D) | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) | GGA(G) |
| GUG(V) | GCG(A) | GAG(E) | GGG(G) | GUG(V) | GCG(A) | GAG(E) | GGG(G) |
| (c) $=\mathbf{3 1 8 / 2 7 6}$ |  |  |  | $(\mathrm{d})=328 / 266$ |  |  |  |
| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F)UUC (F)UUA (L)UUG (L) | UCU(S) <br> UCC(S) <br> UCA(S) <br> UCG(S) | UAU(Y) <br> UAC(Y) <br> UAA(ct) <br> UAG(ct) | UGU(C) <br> UGC(C) <br> UGA(ct) <br> UGG(W) |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) |  |  |  |  |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |  |  |  |  |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) |  |  |  |  |
| CUU (L) | CCU(P) | $\mathrm{CAU}(\mathrm{H})$ | CGU(R) | $\begin{aligned} & \hline \text { CUU (L) } \\ & \text { CUC (L) } \\ & \text { CUA (L) } \\ & \text { CUG (L) } \\ & \hline \end{aligned}$ | CCU(P) | $\mathrm{CAU}(\mathrm{H})$ | CGU(R) |
| CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) |  | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) |  | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | $\operatorname{CAG}(\mathrm{Q})$ | CGG(R) |  | CCG(P) | CAG(Q) | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | $\mathrm{ACU}(\mathrm{T})$ <br> $\mathrm{ACC}(\mathrm{T})$ | AAU(N) | AGU(S) |
| AUC (I) | ACC(T) | AAC(N) | AGC(S) | AUC (I) |  | AAC(N) | AGC(S) |
| AUA (I) | ACA(T) | AAA(K) | AGA(R) | AUA (I) | $\mathrm{ACA}(\mathrm{~T})$ | AAA(K) | AGA(R) |
| AUG (M) | ACG(T) | AAG(K) | AGG(R) | AUG (M) |  | AAG(K) | AGG(R) |
| GUU(V) | $\mathrm{GCU}(\mathrm{A})$ | GAU(D) | GGU(G) | GUU(V) | GCU(A) |  | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G)GGA(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) |  |
| GUG(V) | GCG(A) | GAG(E) | GGG(G) | GUG(V) | GCG(A) | GAG(E) | GGG(G) |
| (c) $=308 / 286$ |  |  |  |  | (d) $=308 / 286$ |  |  |
| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) UUC (F) UUA (L) UUG (L) | $\begin{aligned} & \hline \mathrm{UCU}(\mathrm{~S}) \\ & \mathrm{UCC}(\mathrm{~S}) \\ & \mathrm{UCA}(\mathrm{~S}) \\ & \mathrm{UCG}(\mathrm{~S}) \end{aligned}$ | UAU(Y) | UGU(C) |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) |  |  | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |  |  | UAA (ct) | UGA(ct) UGG(W) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) |  |  | UAG(ct) |  |
| CUU (L) | CCU(P) | CAU(H) | CGU(R) | CUU (L) | $\begin{aligned} & \text { CCU(P) } \\ & \text { CCC(P) } \end{aligned}$ | CAU(H) | CGU(R) |
| CUC (L) | $\mathrm{CCC}(\mathrm{P})$ | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) | CUC (L) |  | $\mathrm{CAC}(\mathrm{H})$ | $\begin{aligned} & \text { CGC(R) } \\ & \text { CGA(R) } \end{aligned}$ |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | $\begin{aligned} & \text { CCA(P) } \\ & \text { CCG(P) } \end{aligned}$ | CAA(Q) |  |
| CUG (L) | CCG(P) | CAG(Q) | CGG(R) | CUG (L) |  | $\mathrm{CAG}(\mathrm{Q})$ | $\begin{aligned} & \text { CGA(R) } \\ & \text { CGG(R) } \end{aligned}$ |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | $\mathrm{ACU}(\mathrm{T})$ | AAU(N) | AGU(S) |
| AUC (I) | ACC(T) | AAC(N) | AGC(S) | AUC (I) | $\begin{aligned} & \mathrm{ACC}(\mathrm{~T}) \\ & \mathrm{ACA}(\mathrm{~T}) \end{aligned}$ | $\begin{aligned} & \text { AAC(N) } \\ & \text { AAA(K) } \end{aligned}$ | $\begin{aligned} & \text { AGC(S) } \\ & \text { AGA(R) } \end{aligned}$ |
| AUA (I) | ACA(T) | AAA(K) | AGA(R) | AUA ( I ) |  |  |  |
| AUG (M) | ACG(T) | AAG(K) | AGG(R) | AUG (M) | $\begin{aligned} & \mathrm{ACA}(\mathrm{~T}) \\ & \mathrm{ACG}(\mathrm{~T}) \end{aligned}$ | $\begin{aligned} & \text { AAA(K) } \\ & \text { AAG(K) } \end{aligned}$ | $\mathrm{AGG}(\mathrm{R})$ |
| GUU(V) |  GCU(A) <br> GCC(A) GAU(D) <br> GAC(D)  <br> GCA(A) GAA(E) <br> GCG(A) GAG(E) |  | GGU(G) | GUU(V) | $\begin{aligned} & \mathrm{GCU}(\mathrm{~A}) \\ & \mathrm{GCC}(\mathrm{~A}) \\ & \mathrm{GCA}(\mathrm{~A}) \\ & \mathrm{GCG}(\mathrm{~A}) \\ & \hline \end{aligned}$ | $\begin{aligned} & \hline \text { GAU(D) } \\ & \text { GAC(D) } \\ & \text { GAA(E) } \\ & \text { GAG(E) } \end{aligned}$ | $\begin{aligned} & \hline \text { GGU(G) } \\ & \text { GGC(G) } \\ & \text { GGA(G) } \\ & \text { GGG(G) } \\ & \hline \end{aligned}$ |
| GUC(V) |  |  | GGC(G) | GUC(V) |  |  |  |
| GUA(V) |  |  | GGA(G) | GUA(V) |  |  |  |
| GUG(V) |  |  | GGG(G) | GUG(V) |  |  |  |
| (a) $=298 / 296$ |  |  |  |  | (b) $==298 / 296$ |  |  |

Tab. 5. After the quantity 298 in Table 1.2 follow the quantities 308, 318 and 328.

| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) | UCU(S) | UAU(Y) | UGU(C) |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) | UUC (F) | UCC(S) | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) | UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) | UUG (L) | UCG(S) | UAG(ct) | UGG(W) |
| CUU (L) | CCU(P) | $\mathrm{CAU}(\mathrm{H})$ | CGU(R) | CUU (L) | CCU(P) | $\mathrm{CAU}(\mathrm{H})$ | CGU(R) |
| CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) | CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | $\mathrm{CAG}(\mathrm{Q})$ | CGG(R) | CUG (L) | CCG(P) | CAG(Q) | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | ACU(T) | AAU(N) | AGU(S) |
| AUC (I) | $\mathrm{ACC}(\mathrm{T})$ | $\mathrm{AAC}(\mathrm{N})$ | AGC(S) | AUC (I) | ACC(T) | $\mathrm{AAC}(\mathrm{N})$ | AGC(S) |
| AUA (I) | $\mathrm{ACA}(\mathrm{T})$ | $\mathrm{AAA}(\mathrm{K})$ | AGA(R) | AUA (I) | ACA(T) | AAA(K) | AGA(R) |
| AUG (M) | $\mathrm{ACG}(\mathrm{T})$ | AAG(K) | AGG(R) | AUG (M) | ACG(T) | AAG(K) | AGG(R) |
| GUU(V) | GCU(A) | GAU(D) | GGU(G) | GUU(V) | GCU(A) | GAU(D) | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) | GGA(G) |
| GUG(V) | GCG(A) | GAG(E) | GGG(G) | GUG(V) | GCG(A) | GAG(E) | GGG(G) |
| (c) $=368 / 226$ |  |  |  | $(\mathrm{d})=398 / 196$ |  |  |  |

Tab.6. After the quantity 328 in previous Table 5, follow the quantities $338,348,358,368$; then 378,388 and 398.

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## 2.

## On the Completeness of Genetic Code: Part II

As in first part of this work, in this second part we present the chemically meaningful splitting of codons after pyrimidine and purine distinctions; the splitting which is also in relation to Rumer nucleotide doublet Table.

# ON THE COMPLETENESS OF GENETIC CODE: PART II 

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#### Abstract

As in first part of this work, in this second part we present the chemically meaningful splitting of codons after pyrimidine / purine distinctions; the splitting which is also in relation to Rumer nucleotide doublet Table.

Starting from our hypothesis of prebiotic completeness of the genetic code (Rakočević, 2004), we have presented several new examples of that completeness, in Part I of this work (Rakočević, 2014). Now, in this part (Part II) we present the relationships between the nucleotide triplets table (TT) and nucleotide doublets Table (DT) through the said completeness.

As first step we show the Rumer's Table of 16 nucleotide doublets and the Modified Rumer's Table (Tables $1 \& 2$ in relation to Tables $3 \& 4$ ) (Rakočević, 2014a). By this, the presented balances of the number of nucleons as well as atoms within amino acid side chains are valid for the set of 23 AAs. In a new Table (Table 5), however, we show the relationships only through the balances of the number of atoms, but in the set of 61 amino acid molecules.


The conclusion is the same as in Part I.

| 01. G | GG (6) | 02. F | UU (4) | 03. L |
| :---: | :---: | :---: | :---: | :---: |
| 04. P | CC (6) | 05. N | AA (4) | 06. K |
| 07. R | CG (6) | 08.1 | AU (4) | 09. M |
| 10. A | GC (6) | 11. Y | UA (4) | 12. St. |
| 13. T | AC (5) | 14. H | CA (5) | 15. Q |
| 16. V | GU (5) | 17. C | UG (5) | 18. W |
| 19. S | UC (5) | 20. D | GA (5) | 21. E |
| 22. L | CU (5) | 23. S | AG (5) | 24. R |

Table 1. Rumer's Table of nucleotide doublets

| 01. $\mathbf{G}$ | GG (6) | 02. F | UU (4) | 03. $\mathbf{~}$ |
| :--- | :--- | :--- | :--- | :--- |
| 04. $\mathbf{P}$ | CC (6) | 05. N | AA (4) | 06. K |
| 07. A | GC (6) | 08. $\mathbf{Y}$ | UA (4) | 09. St. |
| 10. R | CG (6) | 11. I | AU (4) | 12. M |
| 13. V | GU (5) | 14. C | UG (5) | 15. $\mathbf{W}$ |
| 16. T | AC (5) | 17. . | CA (5) | 18. Q |
| 19. L | CU (5) | 20. S | AG (5) | 21. R |
| 22. S | UC (5) | 23. D | GA (5) | 24. E |

Table 2. The modified Rumer's Table: four quadruplets, each with $1^{\text {st }}, 2^{\text {nd }}, 3^{\text {rd }}, 4^{\text {th }}$ doublet.


Table 3. Distributions of AAs after nucleotide doublets presented in Table 2: Four squares with more dark tones (outer) contain four first doublets from Table 2 and four less dark tones (inner) contain four second doublets. In amino acids, within their side chains (in the set of 23 AAs) at outer/inner areas there are 369/369 nucleons and 61/61 atoms, respectively. All AAs in outer area are nonpolar whereas those in inner area are polar, measured by cloister energy. [Cloister energy as in Swanson, 1984.]

| 1st | 2nd letter |  |  |  |  | 3rd |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | U | C | A | G |  |  |
| U | UUU | UCU | UAU | UGU |  | $U$ |
|  | 'UuC F | UCC | UAC Y | UGC | C | C |
|  | UUA | UCA | UAA | UGA | CT | A |
|  | UUG`, & UCG & UAG CT & UGG & W & G \\ \hline \multirow{5}{*}{C} & \multirow[t]{5}{*}{\begin{tabular}{l} CUU \\ CUC \\ CUA L \\ CUG \end{tabular}} & \multirow[t]{5}{*}{\[ \begin{aligned} & \text { CCU } \\ & \text { CCG } \\ & \text { CCA } \\ & \text { CCG } \end{aligned} \]} & CAU & CGU & & \(U\) \\ \hline & & & CAC H & CGC & & C \\ \hline & & & CAA & CGA & R & A \\ \hline & & & CAG & CGG & & G \\ \hline & & & \(\because, ~ Q\) & & & \\ \hline \multirow{4}{*}{A} & AUU & ACU & AAU, & AGU & & \(U\) \\ \hline & AUC & ACC & AAC `N | AGC | S | C |  |  |
|  | AUA | ACA $T$ | AAA | AGA |  | A |
|  | AUG M | ACG | AAG K | AGGG | R | G |
| G | GUU | GCU | GAU | GGU |  | $U$ |
|  | GUC v | GCC | GAC | GGC' |  | C |
|  | GUA V | GCA A | GAA | GGA |  | A |
|  | GUG | GCG | GAG | GGG |  | G |

Table 4. Distributions of AAs after nucleotide doublets presented in Table 2: Four squares with more dark tones contain four third doublets from Table 2 and four with less dark tones contain four fourth doublets; two and two doublets on the right, and two and two on the left. In amino acids (within their side chains), in right/left areas there are 369/369-33 nucleons and 59/58 atoms, respectively. All AAs on the right together with D \& E from the left are polar and other on the left are nonpolar. Because the balance is realized in relation to diagonal and not in relation to the type of nucleotide doublets (third or fourth) it follows that positions $3 \& 4$ in DT are not invariant, but only positions $1 \& 2$ as it is shown in Table 3.

| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) | UCU(S) | UAU(Y) | UGU(C) |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) | UUC (F) | UCC(S) | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) | UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) | UUG (L) | UCG(S) | UAG(ct) | UGG(W) |
| CUU (L) | CCU(P) | CAU(H) | CGU(R) | CUU (L) | CCU(P) | CAU(H) | CGU(R) |
| CUC (L) | $\mathrm{CCC}(\mathrm{P})$ | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) | CUC (L) | CCC(P) | CAC(H) | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | CAG(Q) | CGG(R) | CUG (L) | CCG(P) | CAG(Q) | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | ACU(T) | AAU(N) | AGU(S) |
| AUC (I) | ACC(T) | AAC(N) | AGC(S) | AUC (I) | ACC(T) | AAC(N) | AGC(S) |
| AUA (I) | ACA(T) | AAA(K) | AGA(R) | AUA (I) | ACA(T) | AAA(K) | AGA(R) |
| AUG (M) | ACG(T) | AAG(K) | AGG(R) | AUG (M) | ACG(T) | AAG(K) | AGG(R) |
| GUU(V) | GCU(A) | GAU(D) | GGU(G) | GUU(V) | GCU(A) | GAU(D) | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) | GGA(G) |
| GUG(V) | GCG(A) | GAG(E) | GGG(G) | GUG(V) | GCG(A) | GAG(E) | GGG(G) |
| $(\mathrm{c})=330 /$ | 4 (blue | dark) vs | d+light) | $(\mathrm{d})=296$ | 8 (red+d | k) vs (b | ++light) |
| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) | UCU(S) | UAU(Y) | UGU(C) |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) | UUC (F) | UCC(S) | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) | UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) | UUG (L) | UCG(S) | UAG(ct) | UGG(W) |
| CUU (L) | CCU(P) | CAU(H) | CGU(R) | CUU (L) | $\mathrm{CCU}(\mathrm{P})$ | CAU(H) | CGU(R) |
| CUC (L) | $\mathrm{CCC}(\mathrm{P})$ | CAC(H) | CGC(R) | CUC (L) | CCC(P) | CAC(H) | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | CAG(Q) | CGG(R) | CUG (L) | CCG(P) | CAG(Q) | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | $\mathrm{ACU}(\mathrm{T})$ | AAU(N) | AGU(S) |
| AUC (I) | ACC(T) | AAC(N) | AGC(S) | AUC (I) | ACC(T) | AAC(N) | AGC(S) |
| AUA (I) | ACA(T) | AAA(K) | AGA(R) | AUA (I) | ACA(T) | AAA(K) | AGA(R) |
| AUG (M) | ACG(T) | AAG(K) | AGG(R) | AUG (M) | ACG(T) | AAG(K) | AGG(R) |
| GUU(V) | GCU(A) | GAU(D) | GGU(G) | GUU(V) | GCU(A) | GAU(D) | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) | GGA(G) |
| GUG(V) | GCG(A) | GAG(E) | GGG(G) | GUG(V) | GCG(A) | GAG(E) | GGG(G) |
| (a) $=\mathbf{2 8 0 / 3 1 4}$ (red+blue) vs (light) |  |  |  | (b) $=298 / 296$ (red+dark) vs (blue+light) |  |  |  |

Table 5. Distributions of AAs after nucleotide doublets presented in Tables 2, 3 and 4: The (a) as Table 3 here, and as Table 3, under (b) in Part I (Rakočević, 2014b). In (b) at red squares (four first doublets in Table 2) there are 126 atoms; in four squares with dark tones (four forth doublets in Table 2) 172 atoms $(126+172=298=297+1)[(9 \times 33)+1]$. In (b) at blue squares (four second doublets in Table 2) there are 154 atoms; in four light squares (four third doublets in Table 2) there are 142 atoms $(154+142=296$ $=297-1)$ [( $9 \times 33$ ) -1]. In (c) there are 154 atoms at blue squares, plus 176 atoms in four squares on the right (with dark tones) equals 330 atoms [ $(9+1) \times 33]$; on the other hand, 126 atoms at the red squares, plus 138 atoms in four light squares on the left equals 264 atoms [( $9-1$ ) x 33]. In (d) there are 126 atoms at red squares, plus 170 atoms in four squares above (with dark tones) equals $296=297-1$ atoms [( $9 \times 33$ ) $-1]$; on the other hand, 154 atoms at the blue squares, plus 144 atoms in four light squares down equals $298=297+1)$ atoms [ $(9 \times 33)+1]$. (By all these balances one must notice that number patterns $296 / 298$ and 264 / 330 correspond with the same patterns in Table 1.2, within Part I of this work (Rakočević, 2014b).)

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## 3.

## On the Completeness of Genetic Code: Part III

In this third part of the work about the completeness of the genetic code, we present new examples that show that the codon splitting after pyrimidine and purine nucleotides distinctions are followed by specific arithmetical balances of the number of atoms in the amino acid molecules side chains.

# ON THE COMPLETENESS OF GENETIC CODE: PART III 

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#### Abstract

In this third part of the work about the completeness of the genetic code, we present new examples that show that the codon splitting after pyrimidine / purine nucleotides distinctions are followed by specific arithmetical balances of the number of atoms in the amino acid molecules side chains.


The codon splitting in Table 1, under (a), designates a distinction of YYN and RRN codons in dark areas versus YRN and RYN in light areas. ${ }^{1}$ The same distinctions we have also under (b), but with further nuance-splitting: YYY, RYY, RYR, YRY, YRR, RRY, RRR.

| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) | UCU(S) | UAU(Y) | UGU(C) |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) | UUC (F) | UCC(S) | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) | UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) | UUG (L) | UCG(S) | UAG(ct) | UGG(W) |
| CUU (L) | CCU(P) | CAU(H) | CGU(R) | CUU (L) | CCU(P) | $\mathrm{CAU}(\mathrm{H})$ | CGU(R) |
| CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) | CUC (L) | CCC(P) | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | $\mathrm{CAG}(\mathrm{Q})$ | CGG(R) | CUG (L) | CCG(P) | CAG(Q) | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | ACU(T) | AAU(N) | AGU(S) |
| AUC (I) | ACC(T) | AAC(N) | AGC(S) | AUC (I) | ACC(T) | $\mathrm{AAC}(\mathrm{N})$ | AGC(S) |
| AUA (I) | $\mathrm{ACA}(\mathrm{T})$ | AAA(K) | AGA(R) | AUA (I) | $\mathbf{A C A}(\mathbf{T})$ | AAA(K) | AGA(R) |
| AUG (M) | ACG(T) | $\mathrm{AAG}(\mathrm{K})$ | AGG(R) | AUG (M) | ACG(T) | AAG(K) | AGG(R) |
| GUU(V) | $\mathrm{GCU}(\mathrm{A})$ | GAU(D) | GGU(G) | GUU(V) | $\mathrm{GCU}(\mathrm{A})$ | GAU(D) | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) | GGA(G) |
| GUG(V) | GCG(A) | GAG(E) | GGG(G) | GUG(V) | GCG(A) | GAG(E) | GGG(G) |
| (a) $=286 / 308(296-10 / 298+10)$ |  |  |  | (b) $=122+164 / 166+142(296+10 / 298-10)$ |  |  |  |

Table 1. Distributions of AAs (within four quadruplets of GCT) after nucleotide doublets presented in Table 2 in Part II (Rakočevič, 2015).

| ( $\mathrm{a}_{1}$ ) | $\left(a_{2}\right) 158+128=296-10$ | ( $\mathrm{b}_{1}$ ) | $\left(\mathrm{b}_{2}\right)$ |
| :---: | :---: | :---: | :---: |
| $54+20+52+32=158$ | $170+138=298+10$ | YYY $80+Y Y R 78=158$ | YYY 80+ YRY $96=176$ |
| $30+28+44+68=170$ | $\left(a_{3}\right)$ YYN 158; RRN 128 | RRR $86+$ RRY $42=128$ | RYY 70+RRR $86=156$ (20) |
| $50+40+32+16=138$ | RYN 138; YRN 170 | YRY $96+$ YRR $74=170$ | YYR 78+RYR $68=146$ (10) |
| $46+44+34+04=128$ |  | RYY 70 + RYR $68=138$ | RRY 42+YRR 74= 116 (30) |

Survey 1. Atom number balances within amino acid side chains, which follow splitting in Table 1.

[^1]The codon splitting in Table 2, under (a), designates a further codons distinction, valid for first and second doublets in four doublet-quadruplets, presented in Table 2, in Part II. The same distinctions we have also under (b), but valid for third and fourth doublets in four doubletquadruplets, presented in Table 2, in Part II of this work.

| UUU (F) | UCU(S) | UAU(Y) | UGU(C) | UUU (F) | UCU(S) | UAU(Y) | UGU(C) |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| UUC (F) | UCC(S) | UAC(Y) | UGC(C) | UUC (F) | UCC(S) | UAC(Y) | UGC(C) |
| UUA (L) | UCA(S) | UAA(ct) | UGA(ct) | UUA (L) | UCA(S) | UAA(ct) | UGA(ct) |
| UUG (L) | UCG(S) | UAG(ct) | UGG(W) | UUG (L) | UCG(S) | UAG(ct) | UGG(W) |
| CUU (L) | $\operatorname{CCU}(\mathrm{P})$ | CAU (H) | CGU(R) | CUU (L) | CCU(P) | $\mathrm{CAU}(\mathrm{H})$ | CGU (R) |
| CUC (L) | $\operatorname{CCC}(\mathrm{P})$ | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) | CUC (L) | $\mathrm{CCC}(\mathrm{P})$ | $\mathrm{CAC}(\mathrm{H})$ | CGC(R) |
| CUA (L) | CCA(P) | CAA(Q) | CGA(R) | CUA (L) | CCA(P) | CAA(Q) | CGA(R) |
| CUG (L) | CCG(P) | CAG(Q) | CGG(R) | CUG (L) | CCG(P) | CAG(Q) | CGG(R) |
| AUU (I) | ACU(T) | AAU(N) | AGU(S) | AUU (I) | ACU(T) | AAU(N) | AGU(S) |
| AUC (I) | $\mathrm{ACC}(\mathrm{T})$ | AAC(N) | AGC(S) | AUC (I) | ACC(T) | AAC( N ) | AGC(S) |
| AUA (I) | ACA(T) | AAA(K) | AGA(R) | AUA (I) | ACA(T) | $\mathrm{AAA}(\mathrm{K})$ | AGA(R) |
| AUG (M) | ACG(T) | AAG(K) | AGG(R) | AUG (M) | ACG(T) | AAG(K) | AGG(R) |
| GUU(V) | GCU(A) | GAU(D) | GGU(G) | GUU(V) | GCU(A) | GAU(D) | GGU(G) |
| GUC(V) | GCC(A) | GAC(D) | GGC(G) | GUC(V) | GCC(A) | GAC(D) | GGC(G) |
| GUA(V) | GCA(A) | GAA(E) | GGA(G) | GUA(V) | GCA(A) | GAA(E) | GGA(G) |
| GUG(V) | GCG(A) | GAG(E) | $\mathrm{GGG}(\mathrm{G})$ | GUG(V) | GCG(A) | GAG(E) | GGG(G) |
| (a) $=(60+66 / 70+84)$ |  |  |  | $(b)=(74+68 / 84+88)$ |  |  |  |
| 126/154 |  |  |  | 142/172 |  |  |  |

Table 2. Distributions of AAs within eight (a), plus eight (b) squares of GCT, after nucleotide doublets presented in Table 2 in Part II of this work. The Table under (a) corresponds with Table 3, and Table under (b) with Table 4 in Part II of this work.

| $\left(\mathrm{a}_{1}\right)=(60+66 / 70+84)$ [126/154]; | $\left(\mathrm{b}_{1}\right)=(74+68 / 84+88)[(142 / 172) ;$ | $\begin{aligned} \left(\mathrm{a}_{2}\right) 60 & =10 \times 6 \\ 66 & =11 \times 6 \end{aligned}$ |
| :---: | :---: | :---: |
| $(1$ NY $60+$ II NY $70=130)(140-10)$ | (III NY $74+$ IV NY $84=158)(157+1)$ | $70=10 \times 7$ |
| (I NR 66 + II NR $84=150)(140+10)$ | (III NR 68 + IV NR $88=156$ ) (157-1) | $84=12 \times 7$ |
| I NY $60+$ I NR $66=126$ | III NY $74+$ III NR $68=142$ |  |
| I NR $66+11$ NY $70=136$ | III NR 68 + IV NY $84=152$ |  |
| I NY $60+$ II NR $84=144$ | III NY $74+$ IV NR $88=162$ | ( $\mathrm{b}_{2}$ ) |
| II NY $70+$ II NR $84=154$ | IV NY $84+$ IV NR $88=172$ | 142+154 = 296 |
|  |  | $152+144=296$ |
|  |  | $162+136=298$ |
|  |  | $172+126=298$ |

Survey 2. Atom number balances within amino acid side chains, which follow splitting in Table 2.

## REFERENCE

Rakočević, M. M. (2015) On the Completeness of Genetic Code: Part II, viXra:1501.0117.

## 4.

## On the Completeness of Genetic Code: Part IV

In this fourth part of the work about the completeness of the genetic code, we present further connections and relations between nucleotide doublets and triplets within Genetic Code Table.

# ON THE COMPLETENESS OF GENETIC CODE: PART IV 

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#### Abstract

In this fourth part of the work about the completeness of the genetic code, we present further connections and relations between nucleotide doublets and triplets within Genetic Code Table.


In Table 1 are designated nucleotide doublets from modified Rumer's Table (Part II): with brown color four $1^{\text {st }}$, blue color with four $2^{\text {nd }}$, dark tones with four $3^{\text {rd }}$ and light tones with four $4^{\text {th }}$ doublets. These four areas correspond with four classes of AAs, presented through chemically meaningful pairs (right side of Table 2).

| 1st | 2nd letter |  |  |  |  |  |  | 3rd |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | U | C |  | A |  | C |  |  |
| U | UUU | UCU |  | UAU |  | UGU |  | U |
|  | UUC F | UCC |  | UAC | Y | UGC | C | C |
|  | UUA | UCA | S | UAA |  | UGA | CT | A |
|  | UUG L | UCG |  | UAG | CT | UGG | W | G |
| C | CUU | CCU |  | CAU |  | CGU |  | U |
|  | CUC | CCC |  | CAC | H | CGC |  | C |
|  | CUA L | CCA | P | CAA |  | CGA | R | A |
|  | CUG | CCG |  | CAG | 0 | CGG |  | G |
| A | AUU | ACU |  | AAU |  | AGU |  | U |
|  | AUC | ACC |  | AAC | N | AGC | S | C |
|  | AUA M | ACA | T | AAA |  | AGA |  | A |
|  | AUG | ACG |  | AAG | K | AGG | R | G |
| G | GUU | GCU |  | GAU |  | GGU |  | $U$ |
|  | GUC v | GCC |  | GAC |  | GGC |  | C |
|  | GUA $V$ | GCA | A | GAA |  | GGA | G | A |
|  | GUG | GCG |  | GAG | E | GGG |  | $G$ |

Table 1. Distributions of AAs within four times four codon quadruplets of GCT in connection with nucleotide doublets, presented in Table 2 in Part II (Rakočevič, 2015).

At left side of Table 2 has presented the splitting into four classes of AAs: one-codon, twocodon, three-codon and four-codon amino acids (AAs), respectively; at right side, as in Table 1.

As it is self-evident from Table 2 two splittings are followed by a specific balance (near to be 2:1) in both cases: [2 $\mathrm{x}(80 \pm 0)]:[1 \times(80-1)]$.


Table 2. Distributions of AAs; on the left: after the number of coding codons; on the right: after the splitting into four times of four nucleotide doublets (Table 1) and in relation to number of atoms within amino acid side chains.

In addition there are other partial balances, such as these: $(20+41+27+34=122$ and $(09+45+23+40=117)$ versus $(20+27+45+40=122+10$ and $(41+34+09+23=117-10)$. Also the balances and relationships, presented in Table 3 and in Surveys 1, 2 and 3.

| 3,4 | small | 1,2 | large |
| :---: | :---: | :---: | :---: |
| 1 | F | M | W |
| L | C | W | L |
| V | G | F | V |
| S |  | L |  |
| P | P | S | T |
| T | H | Y | K |
| A | N | H | Q |
| G |  | Q |  |
| R | A | N | L |
|  | ct | K | Y |
|  | S | D | R |
|  |  | E |  |
|  | M | R | 1 |
|  | S | C | R |
|  | D |  | E |
| 61 | 61 | 86 | 86 |
| 18 | 18 | 74 | 74 |
| 79 | 79 | 160 | 160 |

Table 3. The comparison of left and right side of Table 2. Here are on the left the amino acids (AAs) encoded by 3 or 4 codons and smaller AAs within amino acid pairs, presented on the right side of Table 2 . On the other hand, here, on the right are AAs encoded by 1 or 2 codons and larger AAs within the said amino acid pairs.

| ILVTR (61) = FCHNMSD (61) |  |
| :---: | :---: |
| ILVTR (61) + FCHNMSD (61) $=122$ | FCG WLV PHN TKQ (122) |
| LVT (31) + FCHN (38) $=69$ | FCLVHNT (69) + GWPKQ (53) = 122 |
| IR (30) + MSD (23) = 53 |  |

Survey 1. The results of comparison of the first and the second column on the left side of Table 3.

| MFSYHNDEC (86) = VTLYIRE (86) |  |
| :--- | :--- |
| MFSYHNDEC (86) + VTLYIRE (86) = 122 + 50 | ILVTR (61) = FCHNMSD (61) [Survey 1, first row] |
| YE (25) + YE (25) = 50 | VTLIR (61) = MFSHNDC (61) [Survey 2, last row] |
| MFSHNDC (61) + VTLIR (61) = 122 |  |

Survey 2. The results of comparison of the first and the second column on the right side of Table 3.

| $61+86=147$ | 147 | 137 | 127 | $\mathbf{1 1 7}$ | 107 | 97 | 87 |
| :--- | ---: | :--- | :--- | :--- | :--- | :--- | :---: |
| $18+74=92$ | 92 | 102 | 112 | $\mathbf{1 2 2}$ | 132 | 142 | 152 |

Survey 3. The "intermediated" results of final atom number sums, given in Table 3 (first and second column); within the fifth column is the real result from right side of Table 2 (up/down summarizing); all other results appear to be our prediction - in future one will find such splitting in GCT.

*     *         * 

All presented balances and relationships go in favor of our hypothesis that the genetic code still in prebiotic conditions was complete.

## REFERENCE

Rakočević, M. M. (2015) On the Completeness of Genetic Code: Part II, viXra:1501.0117.

## 5.

## On the Completeness of Genetic Code: Part V

In this fifth part of the work on the completeness of the genetic code, we present further connections and relations between nucleotide doublets and triplets within Genetic Code Table; in all cases through balances of atom number, nucleon number and isotope number.

# ON THE COMPLETENESS OF GENETIC CODE: PART V 

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#### Abstract

In this fifth part of the work on the completeness of the genetic code, we present further connections and relations between nucleotide doublets and triplets within Genetic Code Table; in all cases through balances of atom number, nucleon number and isotope number.


Starting from Tables 1, 2 and 3 in the previous part of this work (Part IV), in this fifth part, except of correspondence between nucleotide Doublets Table (DT) and nucleotide Triplets Table (TT), we show that the pyrimidine / purine distinctions are followed by the balances of the number of particles - atoms and nucleons, as well as the number of isotopes (nuclides).

| 1st | 2nd letter |  |  |  |  |  | 3rd |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | U | C | A |  | G |  |  |
| U | UUU | UCU | UAU |  | UGU |  | $U$ |
|  | UUQ F | U | UA $\overline{\mathbf{C}}$ | Y | UGG | C | C |
|  | UUA | UCA S | UAA |  | UGA | CT | A |
|  | UQUG | U $\overline{\mathbf{C}} \mathrm{G}$ | UA $\underline{\mathbf{G}}$ | CT | U $\underline{\mathbf{G}} \mathrm{G}$ | W | G |
| C | CUU | CCU | CAU |  | CGU |  | U |
|  | $\underline{\text { CuC }}$ | CCC | $\underline{\underline{C}} \mathrm{C} A C$ | H | C $\mathrm{G}^{\text {C }}$ |  | C |
|  | $\overline{\underline{C}}$ UA | $\underline{\text { che }}$ CA | $\underline{\underline{C}} \mathrm{C} A$ |  | $\mathrm{C} \underline{\underline{\mathbf{G}} \mathrm{A}}$ | R | A |
|  | $\underline{\underline{\mathbf{C}} \mathrm{UG}}$ | $\underline{\text { C CG }}$ | $\underline{\underline{\mathbf{C}}} \mathrm{AG}$ | Q | C $\underline{\mathbf{G}} \mathrm{G}$ |  | G |
| A | AUU | $\underline{\text { ACU }}$ | $\underline{\text { A } A U}$ |  | AGU |  | U |
|  | AU它 I | $\underline{\text { asc }}$ | $\underline{\text { a }}$ AC | N | $\mathrm{AG}^{\underline{\mathbf{C}}}$ | S | C |
|  | AUA M | A ${ }^{\text {Cla }}$ | $\underline{\text { a }}$ AA |  | AGE |  | A |
|  | AUG ${ }^{\text {M }}$ | A ${ }^{\text {cheg }}$ | $\underline{\text { A }}$ AG | K | $\mathrm{AG}^{\mathbf{G}}$ | R | G |
| G | GUU | GCU | GAU |  | GGU |  | U |
|  | G $\underline{\underline{U}} \mathrm{C}$ | $\underline{\mathbf{G}} \mathrm{CC}$ | GA $\overline{\mathbf{C}}$ | D | GGE | G | C |
|  | GUEA | GCA A | GAA | E | G $\underline{\underline{\mathbf{G}} \text { A }}$ | G | A |
|  | GUVG | GCG | GA $\underline{\underline{\mathbf{G}}}$ |  | $\mathrm{G} \underline{\underline{\mathbf{G}}} \mathrm{G}$ |  | G |

The Pairs: going from pyrimidine to purine coding AAs
I. (F-W, L-C, V-G) / II. (P-T, H-K, Q-N)
III. (L-A, Y-ct, S-T) / IV. (S-R, I-M, D-E)

Table 1.1. Distributions of AAs in GCT, in correspondence with pyrimidine / purine distinctions within nucleotide doublets and triplets (I)

| 1st | 2nd letter |  |  |  | 3 rd |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  | U | C | A | G |  |
| U | UUU | UCU | UAE | UGU | U |
|  | U $\underline{\underline{U} C}$ F | U $\underline{\underline{C}}$ | UA $\overline{\mathbf{C}} \quad \mathbf{Y}$ | UGG C | C |
|  | UUA | UCA S | UAA | UGA CT | A |
|  | UVUG L | U $\underline{\underline{\mathbf{C}}}$ | UA $\underline{\underline{\mathbf{G}}} \mathrm{CT}$ | UGGG W | G |
| C | CUU | $\underline{\mathrm{CCU}}$ | $\underline{\text { CAU }}$ | CGU | U |
|  | $\underline{\text { c }}$ UC | $\underline{\underline{\mathrm{C}} \mathrm{CC}}$ | $\underline{\text { C }}$ - | CGC | C |
|  | $\underline{\text { CuA }}$ L | CCA P | $\underline{C}$ | CGA R | A |
|  | $\underline{\underline{C} U G}$ | $\underline{\underline{\mathbf{C}} \mathrm{CG}}$ | $\underline{\underline{C} A G ~} \quad$ Q |  | G |
| A | AUU | $\underline{\text { ACU }}$ | $\underline{\text { A } A U}$ | AGU | U |
|  | AU亨 I | $\underline{\text { A }}$ CC | $\underline{\underline{\mathbf{a}} A C} \mathbf{N}$ | AG $\underline{\mathbf{C}} \quad \mathbf{S}$ | C |
|  | AUA M | $\underline{\text { A }}$ CA T | $\underline{\text { a }}$ AA | AG플 | A |
|  | AUG ${ }^{\text {M }}$ | $\underline{\text { A }}$ CG | $\underline{\underline{\text { a }} \text { AG }}$ K | $\mathrm{AG} \underline{\underline{\mathbf{G}}} \mathbf{R}$ | G |
| G | GUU | $\underline{\mathrm{G} C U}$ | GA | GGU | U |
|  | G $\underline{\mathbf{U}} \mathrm{C}$ V | $\underline{\mathbf{G} C C}$ | GA $\overline{\mathbf{C}}$ D | G $\underline{\underline{G} C}$ | C |
|  | G $\underline{\underline{U}} \mathrm{~A}$ | $\underline{\underline{\mathbf{G}} \mathrm{CA}} \mathbf{A}$ | GAA | G鳥A | A |
|  | G $\underline{\underline{U} G}$ | GCG | GA $\underline{\mathbf{G}}$ | G $\underline{\underline{G} G}$ | G |

The Pairs: going from pyrimidine to purine coding AAs
I. (F-W, L-C, V-G) / II. (P-T, H-K, Q-N)
III. (L-A, Y-ct, S-T) ${ }^{1} /$ IV. (S-R, I-M, D-E)

Table 1.2. Distributions of AAs in GCT, in correspondence with pyrimidine / purine distinctions within nucleotide doublets and triplets (II)

In Table 1.1, in the squares with the dark tones are nucleotide doublets UU, GG, GU and UG, all four in first positions within four quadruplets of modified Rumer's Table (as it is shown in Table 2 of Part II of this work). On the other hand, in the squares with light tones are nucleotide doublets CC, AA, AC and CA, all four in second positions within four quadruplets of modified Rumer's Table.

In Table 1.2, in the squares with the dark tones are nucleotide doublets CU, AG, GC and UA, all four in third positions within four quadruplets of modified Rumer's Table (as it is shown in Table 2 of Part II of this work). On the other hand, in the squares with light tones are nucleotide doublets UC, GA, AU and CG, all four in fourth positions within four quadruplets of modified Rumer's Table.

As a very interesting fact, there is a distinction in Table 2.1, in relation to Table 2 in Part IV. As we had complete balance of the number of atoms (in two different classifications) in Table 2

[^2]of Part IV, we got it here also in Table 2.1; there were 160/79 both times, and here it is 125/114 also both times, in both classifications (on the left / on the right).

| 1 | 2 | 3 | 4 | 6 | Pyr | idine |  | urine |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $\mathrm{M}_{11} \quad \mathrm{~F}_{14}$ $W_{18} Y_{15}$ $\mathrm{H}_{11}$ Q11 No8 $\mathrm{K}_{15}$ D07 $\mathrm{E}_{10}$ C05 |  | $\mathrm{I}_{13}$ | $V_{10}$ <br> P08 <br> T08 <br> A04 <br> G01 | $\begin{aligned} & \mathrm{L}_{13} \\ & \mathrm{~L}_{13} \\ & \mathrm{~S}_{05} \\ & \mathrm{~S}_{05} \\ & \mathrm{R}_{17} \\ & \mathrm{R}_{17} \end{aligned}$ | $\mathrm{F}_{14}$ $\mathrm{~L}_{13}$ $\mathrm{~V}_{10}$ |  | 24 | $W_{18}$ <br> C05 <br> Go1 |
|  |  |  |  |  |  |  |  |
|  |  | $\begin{aligned} & \mathrm{P}_{08} \\ & \mathrm{H}_{11} \\ & \mathrm{Q}_{11} \end{aligned}$ |  |  |  | 31 | $\begin{aligned} & \mathrm{T}_{08} \\ & \mathrm{~K}_{15} \\ & \mathrm{~N}_{08} \end{aligned}$ |
|  |  | $L_{13}$ $Y_{15}$ $S_{05}$ |  |  |  | 21 | A04 ct $R_{17}$ |
|  |  | $\begin{aligned} & I_{13} \\ & S_{05} \\ & D_{07} \end{aligned}$ |  |  |  | 38 | $\begin{aligned} & \mathbf{M}_{11} \\ & \mathbf{R}_{17} \\ & \mathrm{E}_{10} \end{aligned}$ |
| $\begin{gathered} 29 \quad 96 \\ 125 \\ \hline \end{gathered}$ |  |  | 13 | 31 | 70 |  |  |  |  |
|  |  |  | 114 |  |  | 125 | 114 |  |
|  |  | 125-114 | = 11 |  | Cross | 126 | 113 |  |
| $\begin{aligned} & 50+29 \\ & 75+85 \end{aligned}$ |  |  | = 79 |  | Black | 50 | 85 | (125+10) |
|  |  |  | $=160$ |  | - Red | 75 | 29 | (114-10) |

Table 2.1. Distributions of AAs after the number of coding codons (on the left) and after the splitting into four times of four nucleotide doublets (on the right) (cf. Table 1.1 and Table 1.2).

The pairing process in Table 2.1 is directed from pyrimidine to purine as it is a reality in GCT (cf. Table 1.1 and 1.2). By this, one must notice that the pairs in red color have a vice versa status in relation to the pairs within Table 2 in Part IV; also in relation to the pairs in Tables 2.2, 2.3 and 2.4 in this part of the work. The point is that there are two possibilities; first, the classification by the size of the molecule, and the second one, by direction: the first member of the pair is encoded by a pyrimidine, and the second by a purine nucleotide, as it is shown in Tables 1.1 and 1.2.


Table 2.2. Distributions of AAs; on the left: after the number of coding codons; on the right: after the splitting into four times of four nucleotide doublets (Table 1.1 and Table 1.2) and in relation to number of nucleons within amino acid side chains.[Nucleon number in first nuclide, as in Shcherbak, 1994.]

In Table 2.2 it is shown that the above said distinctions of AAs are followed by balances of the number of nucleons in the side chains of amino acids. Immediately it is obvious an analogy with the filling of orbitals in an atom: 1053 vs 0530 and 390 vs 913 . By this, the patterns 530 and

[^3]1443 correspond with perfect numbers, as determinants of genetic code (Rakočević, 1997, p. 60 and www.rakocevcode.rs).


Table 2.3. Everything is the same as in the previous table (Table 2.2), except that here is the total number of nucleons within AA side chains, in all nuclides (as in Table 7, in Rakočević, 2004, p. 228). [Example of calculation for serine: $(3 \times \mathrm{H})+(1 \times \mathrm{C})+(1 \times \mathrm{O})=(3 \times 1)+(3 \times 2)+(1 \times 12)+(1 \times 13)+(1 \times 16)+$ $(1 \times 17)+(1 \times 18)=85$.]

[^4]Analogue with Table 2.2 is Table 2.3, all is the same, except that in Table 2.3 in the question is total number of nucleons, calculated in the manner shown in the legend of Table 2.3.

| 1 | 2 | 3 | 4 | Small |  | Large |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $\begin{aligned} & M_{24} \\ & W_{36} \end{aligned}$ | $F_{28}$ <br> L26 <br> $S_{11}$ <br> $Y_{31}$ <br> $\mathrm{H}_{22}$ <br> Q23 <br> $\mathrm{N}_{17}$ <br> $\mathrm{K}_{30}$ <br> $\mathrm{D}_{16}$ <br> $\mathrm{E}_{22}$ <br> $\mathrm{R}_{34}$ <br> $\mathrm{C}_{12}$ | $\mathrm{l}_{26}$ | $\begin{aligned} & \mathrm{L}_{26} \\ & \mathrm{~V}_{20} \\ & \mathrm{~S}_{11} \\ & \mathrm{P}_{16} \\ & \mathrm{~T}_{17} \\ & \mathrm{~A}_{08} \\ & \mathrm{G}_{02} \\ & \mathrm{R}_{34} \end{aligned}$ | $F_{28}$ <br> $\mathrm{C}_{12}$ <br> $\mathrm{G}_{02}$ |  | 82 | $\begin{aligned} & W_{36} \\ & L_{26} \\ & V_{20} \end{aligned}$ |
|  |  |  |  |  |  |  |  |
|  |  |  |  | $\begin{aligned} & \mathrm{P}_{16} \\ & \mathrm{H}_{22} \\ & \mathrm{~N}_{17} \end{aligned}$ |  | 70 | T 17 <br> $K_{30}$ <br> Q23 |
|  |  |  |  |  |  |  |  |
|  |  |  |  | A08 ct $\mathrm{S}_{11}$ |  | 91 | $L_{26}$ <br> $Y_{31}$ <br> $R_{34}$ |
|  |  |  |  |  |  |  |  |
|  |  |  |  | $\begin{aligned} & \mathrm{M}_{24} \\ & \mathrm{~S}_{11} \\ & \mathrm{D}_{16} \end{aligned}$ |  | 82 | $\mathrm{I}_{26}$ <br> $R_{34}$ <br> $\mathrm{E}_{22}$ |
| 60 | 272 |  | 134 | 167 |  |  |  |
| 332 |  | 160 |  |  |  | 325 |  |
| 492 |  |  |  | 492 |  |  |  |
| $332-160=2 \times 86$ |  |  |  | 325-167 = $2 \times 79$ |  |  |  |

Table 2.4. Distributions of AAs as in previous tables, but here in relation to isotope number. The patterns ( $2 \times 86$ ) and $(2 \times 79)$ as in Tab. 3.1: atom number versus isotope number, what means the self-similarity through the same quantities of AAs.

In Table 2.4 all is the same as in the preceding two tables, except that here in the question is the number of isotopes. For example, for glycine it has been indicated that in the side chain it has two isotopes, because its side chain consists only of one hydrogen atom, having two natural isotopes: protium and deuterium.

Tables 3.1 and 3.2 follow from Table 3 in Part IV, in the manner that is explained in their legends.

| 3,4 | small | 1,2 | large |
| :---: | :---: | :---: | :---: |
| $\left.\right\|_{13}$ | $\mathrm{F}_{14}$ | M11 | $\mathbf{W}_{11}$ |
| L13 | C05 | $\mathbf{W}_{11}$ | L 11 |
| $\mathrm{V}_{10}$ | $\mathrm{G}_{01}$ | $\mathrm{F}_{11}$ | V11 |
| S05 |  | $L_{11}$ |  |
| P08 | P08 | $\mathrm{S}_{11}$ | T11 |
| T08 | $\mathrm{H}_{11}$ | Y 11 | $\mathbf{K}_{11}$ |
| A04 | N08 | $\mathrm{H}_{11}$ | $\mathbf{Q}_{11}$ |
| G01 |  | $\mathbf{Q}_{11}$ |  |
| R17 | A11 | $\mathrm{N}_{11}$ | L11 |
|  | ct | K 11 | $Y_{11}$ |
|  | $\mathrm{S}_{11}$ | $\mathrm{D}_{11}$ | $\mathbf{R}_{11}$ |
|  |  | $\mathrm{E}_{11}$ |  |
|  | $M_{11}$ | $\mathbf{R}_{11}$ | $\mathrm{I}_{11}$ |
|  | $\mathrm{S}_{11}$ | $\mathrm{C}_{11}$ | $\mathrm{R}_{11}$ |
|  | $\mathrm{D}_{11}$ |  | $\mathrm{E}_{11}$ |
| 61 | 61 | 86 | 86 |
| 18 | 18 | 74 | 74 |
| 79 | $\underline{79}$ | 160 | 160 |

Table 3.1. The Table is the same as Table 3 in Part IV, except the color and underlining. The underlined patterns ( $2 \times 86$ ) and ( $2 \times 79$ ) appear to be determinants of the number of isotopes, as it is shown in Table 2.4. The comparison of left and right side of Table 2.4 (analogously as in Table 3 of Part IV): on the left are the amino acids encoded by 3 or 4 codons and smaller AAs within amino acid pairs, presented on the right side of Table 2.4. On the other hand, on the right side are AAs encoded by 1 or 2 codons and larger AAs within the said amino acid pairs. [Cf. the quantities 61-61 with the quantities $71-71$ in Table 3.2.]


Table 3.2. The comparison of left and right side of Table 2.1. On the left are the amino acids encoded by 1 or 2 codons and smaller AAs within amino acid pairs, presented on the right side of Table 2.1. On the other hand, on the right side are AAs encoded by 3 or 4 , or 6 codons and larger AAs within the said amino acid pairs. [Cf. the quantities 71-71 with the quantities 61-61 in Table 3.1.]

All presented facts are such that ones reaffirm the other and vice versa. All together, they favor the recognition that the chemical reactions that determine the GC are not only the reactions in a "test tube", but these reactions are associated with a specific balance of the number of particles (atoms, nucleons and isotopes). Presented facts also support the hypothesis that the genetic code was a complete code from very begining, in prebiotic times and conditions. ${ }^{7}$ On the other hand, the knowledge that "the chemistry of living" is actually a harmonized chemistry requires great care in medicine, agriculture and natural environment; all that because genetic code must be reflected in the proteins and cells.

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[^5]
## 6.

## On the Completeness of Genetic Code: Part VI

In this sixth part of the work on the completeness of the genetic code, we present further relationships within Rumer Table and modified Rumer Table of nucleotide doublets within genetic code.

# ON THE COMPLETENESS OF GENETIC CODE: PART VI 

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#### Abstract

In this sixth part of the work on the completeness of the genetic code, we present further relationships within Rumer Table and modified Rumer Table of nucleotide doublets within genetic code.


In Table 1 are given nucleotide doublets within modified Rumer's Table; all is the same as in a previous Table (Table II/2) ${ }^{1}$, except it is indicated here the splitting into odd and even rows of the Table. With that indication it becomes immediately obvious that the quantities of atom number correspond to the quantities obtained in splitting presented in Part V. In fact, there (Table V/2.1) were obtained results (125/114) and (135/104), and here the preceding result (115/124), which is once more confirmation of analogy of filling of atomic orbitals. In addition, the indicated balances (the changes in the number of atoms for 00,01 and 10) establish modification of Rumer's Table, because such balances cannot be obtained in original Rumer's Table (cf. Table II/1 with Table II/2).

| 01. G | GG (6) | 02. F | UU (4) | 03. L | 先 |
| :---: | :---: | :---: | :---: | :---: | :---: |
| 04. P | CC (6) | 05. N | AA (4) | 06. K |  |
| 07. A | GC (6) | 08. Y | UA (4) | 09. St. | \% |
| 10. R | CG (6) | 11.1 | AU (4) | 12. M | 昜 |
| 13. V | GU (5) | 14. C | UG (5) | 15. W | in |
| 16. T | AC (5) | 17. H | CA (5) | 18. Q | $\stackrel{\square}{*}$ |
| 19.L | CU (5) | 20. S | AG (5) | 21. R | - |
| 22. S | UC (5) | 23. D | GA (5) | 24. E | $\bigcirc$ |
| 28 |  | 39 |  | 48 |  |
| 38 | (10) | 39 | (00) | 47 | (01) |
| 66 |  | 78 |  | 60+3 |  |

Table 1. The modified Rumer's Table: the balances of the number of atoms in amino acids (their side chains), corresponding with two octets of nucleotide doublets.

[^6]It is interesting that the three sums of the number of atoms in three columns of AAs in Table $1(66,78$ and $60+35)$ are in correspondence with the three sums that get in the determination of the binary tree of GC with golden mean (cf. Figure 1 in Rakočević, 1998 and Table 3 in this Part of the work). And this is an example more of the similarity and self-similarity of quantities in genetic code.

| 114 | $\begin{gathered} 30 \\ 116 \end{gathered}$ | 119 | $\begin{gathered} \hline 89 \\ 108 \end{gathered}$ | 125 |
| :---: | :---: | :---: | :---: | :---: |
| Gly | GG (6) | Phe | UU (4) | Leu |
| Pro | CC (6) | Asn | AA (4) | Lys |
| Arg | CG (6) | lle | AU (4) | Met |
| Ala | GC (6) | Tyr | UA (4) | Stop |
| (35) | (40) | (43) | (36) | (38) |
| Thr | AC (5) | His | CA (5) | Gln |
| Val | GU (5) | Cys | UG (5) | Trp |
| Ser | UC (5) | Asp | GA (5) | Glu |
| Leu | CU (5) | Ser | AG (5) | Arg |
| (40) | (37) | (30) | (39) | (45) |
| 125 | $\begin{gathered} 36 \\ 106 \end{gathered}$ | 120 | $\begin{gathered} 84 \\ 118 \end{gathered}$ | 114 |
|  | 330-66 | $330 \pm 00$ |  |  |

Table 2. The Rumer's Table of nucleotide doublets: the key quantities in the set of 23 AAs (black) and in the set of 61 AAs (blue color). Cf. the results $330-66$ and $330 \pm 00$ with the same results in Figure I/1 and Table I/1.1.

The comparing Table 1 and Table 2 shows that the modification of Rumer Table does not apply to splitting into top and bottom part of the Table. Table 2 is the original Rumer's Table, with the quantities which are identical in the modified table.

Amino acid quantities, as number of all atoms in the amino acid side chains, in Table 2, are calculated as follows. Upper left column: Gly $01+$ Pro $08+\operatorname{Arg} 17+$ Ala $04=\mathbf{3 0}$; upper middle and right column: [(Phe $14+$ Asn $08+$ Ile $13+$ Tyr 15) $=49+01]+[($ Leu $13+$ Lys $15+$ Met $11)=49-10)]=\mathbf{8 9}(30+89=119)$; Lower left column: Thr $08+$ Val $10+$ Ser $05+$ Leu $13=$ 36; lower middle and right column: [(His $11+$ Cys $05+$ Asp $07+$ Ser 05$)=28 \times 1]+[(G l n 11+$ $\operatorname{Trp} 18+\operatorname{Glu} 10+\operatorname{Arg} 17)=28 \times 2)]=\mathbf{8 4}(36+84=120) .{ }^{2}$


Scheme 2. Survey 2.1. Atom number balance directed by Golden mean route on the binary-code tree (I).

Table 3. Atom number balance directed by Golden mean on the binary code tree (after: Rakočević, 1998, p. 289). Notice that on the two zigzag lines there are $102 \pm 1$ atoms.

[^7]Analogously are calculated the quantities as the number of all atoms in the nucleotide doublets (116/108 versus $106 / 118) .^{3}$. Finally, it remains to show the balance of atomic quantities of the AAs along two diagonals: $30+84=\mathbf{1 1 4}$ versus $89+36=\mathbf{1 2 5}$. It is expected that the reader will see that the pattern $114 / 125$ appears also in Table V/2.1, although in a completely different arrangement of AAs.

Amino acid quantities, as number of hydrogen atoms in amino acid whole molecules, in Table 2, are calculated as follows. Upper left column: Gly $05+$ Pro $09+\operatorname{Arg} 14+$ Ala $07=35$ (the number in parentheses); upper middle column: Phe $11+$ Asn $08+$ Ile $13+$ Tyr 11) $=43$ (the number in parentheses); upper right column Leu $13+$ Lys $14+$ Met $11=38$ (the number in parentheses) $[35+43+38=\mathbf{1 1 6}]$; Lower left column: Thr $09+$ Val $11+$ Ser $07+$ Leu $13=40$; lower middle column: His $09+$ Cys $07+$ Asp $07+$ Ser 07 ) $=30$; lower right column: Gln $10+$ $\operatorname{Trp} 12+$ Glu $09+\operatorname{Arg} 14=45(40+30+45=\mathbf{1 1 5}) .{ }^{4}$

Analogously are calculated the quantities as the number of all hydrogen atoms in the nucleotide doublets. (Above: $40+36=76$; down: $37+39=76$ ). ${ }^{5}$

In Table 3 the first seven amino acids, on the left, are 'golden' amino acids, while on the right are their complements; below are three amino acid pairs as non-complements. Within seven 'golden' amino acids (side chains) there are 60 atoms; within their seven pairing complements there are $[60+(1 \mathrm{x} 6)]$ atoms, and within six non-complements there are $[60+(1 \times 6)]+(2 \mathrm{x} 6)$ of atoms. [Notice that the differences are $1 \times 6,2 \times 6$ and $3 \times 6$.]

$$
* * *
$$

The above presented examples of balances, correspondences, interrelationships, similarity and self-similarity, with everything stated in the previous parts of this work, also make a contribution to understanding the completeness of the genetic code.

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[^8]
## 7.

## On the Completeness of Genetic Code: Part VII

In this seventh part of the work on the completeness of the genetic code, we present further relationships of different variants of Genetic Code Table and modified Rumer's Table of nucleotide doublets within genetic code.

# ON THE COMPLETENESS OF GENETIC CODE: PART VII 

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#### Abstract

In this seventh part of the work on the completeness of the genetic code, we present further relationships of different variants of Genetic Code Table and modified Rumer Table of nucleotide doublets within genetic code.


In previous six parts of this work ${ }^{1}$ we have listed more examples of splittings and distinctions within genetic code, from which is obvious an analogy with the filling of orbitals in an atom: the classifications of AAs and codons within nucleotides triplet table (TT) ${ }^{2}$ as well as nucleotides doublet table (DT) ${ }^{3}$ are accompanied by increasing / decreasing (for one, two or more) of the specific quantities of number of atoms, or nucleons; all this in a strict relation to a specific and unique arithmetical system, consisting of the multiples of numbers 6-66-666 and their halves 3-33-333. ${ }^{4}$

In the first part of this paper we presented (Figure I/1) the multiples of the middle member of the lower sequence (number 33) in position of modular zero (in modulo 9) and its neighbors: ( 8 x $33=284),(9 \times 33=297),(10 \times 33=330)^{5}$ and showed that the number of atoms in the GC constituents in key distinctions (Py / Pu; 2 or 3 hydrogen bonds) corresponds with these numbering patterns. In this seventh part of the work on the completness of GC we will give some new examples. [For now we can not know why 6-66-666 sequence appears as a determinant of GC. A possible reason is the fact that the number 6 is the first perfect number, and we have already proved that perfect and friendly numbers are really determinants of GC (see: Figures 1.1 and 1.2 here, and: MMR, Genetic code as a unique system, p. 60, on my web site).]

In all presented cases, we follow the completeness of the genetic code, expressed through the unity and balance of physical and chemical properties of molecules (from one side) and arithmetical regularities, manifested in the number of atoms and nucleons (from the other side). By this we find, in the GCT, three sets of amino acids: 20 AAs (Table 1.1), 23 AAs (Table 2.1) and 61 AAs (Table 3.1).

[^9]| 1st lett. | 2nd letter |  |  |  |  |  |  |  | 3rd lett. |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | U |  | C |  | A |  | G |  |  |
| U | 00. UUU |  | 08. UCU | S | 32. UAU | Y | 40. UGU | C | $U$ |
|  | 01. UUC | F | 09. UCC |  | 33. UAC |  | 41. UGC | $\begin{aligned} & \text { CT } \\ & \mathbf{W} \end{aligned}$ | C |
|  | 02. UUA |  | 10. UCA |  | 34. UAA |  | 42. UGA |  | A |
|  | 03. UUG | L | 11. UCG |  | 35. UAG | CT | 43. UGG |  | G |
| C | 04. CUU | L | 12. CCU | P | 36. CAU | H | 44. CGU | R | $U$ |
|  | 05. CUC |  | 13. CCC |  | 37. CAC |  | 45. CGC |  | C |
|  | 06. CUA |  | 14. CCA |  | 38. CAA |  | 46. CGA |  | A |
|  | 07. CUG |  | 15. CCG |  | 39. CAG | Q | 47. CGG |  | G |
| A | 16. AUU | I | 24. ACU | T | 48. AAU | N | 56. AGU | S | $U$ |
|  | 17. AUC |  | 25. ACC |  | 49. AAC |  | 57. AGC |  | C |
|  | 18. AUA | M | 26. ACA |  | 50. AAA |  | 58. AGA |  | A |
|  | 19. AUG | M | 27. ACG |  | 51. AAG | K | 59. AGG | R | G |
| G | 20. GUU | V | 28. GCU | A | 52. GAU | D | 60. GGU | G | $U$ |
|  | 21. GUC |  | 29. GCC |  | 53. GAC |  | 61. GGC |  | C |
|  | 22. GUA |  | 30. GCA |  | 54. GAA | E | 62. GGA |  | A |
|  | 23. GUG |  | 31. GCG |  | 55. GAG | E | 63. GGG |  | G |

Figure 1.1. The GCT corresponds with 6-bit binary-code tree (Rakočević, 1998, Biosystems, 46, pp. 283291). In such a case, the key distinctions ( $\mathrm{Py} / \mathrm{Pu}$ ) are determined with the first four perfect numbers. So, the first distinction is with the natural numbers $0-3$ whose sum is 6 (first perfect number); the second one $0-7$ with the sum 28 (second perfect number); and the third distinction with the sequence $0-31$ which numbers give the sum of 496 (third perfect number); finally, the cycling sequence 0-63-0 (from the beginning to the end and vice versa) gives a sum of 8128 (fourth perfect number).

$$
\begin{aligned}
& \text { /00-07/08-15/16-23/24-31//32-39/40-47/48-55/56-63/ } \\
& 28{ }_{64}{ }^{92}{ }_{64}{ }^{156} \quad 644^{220} 4^{284} 4_{64}^{348} 4_{64}^{412} 476 \\
& / 00-07 / 00-15 / 00-23 / 00-31 / / 00-39 / 00-47 / 00-55 / 00-63 / \\
& \begin{array}{llllllll}
28 & 120 & 276 & 496 & 780 & 1128 & 1540 & 2016
\end{array} \\
& \begin{array}{lllllll}
92 & 156 & 220 & 284 & 348 & 412 & 476
\end{array}
\end{aligned}
$$

Table 3. The eight octets within 6-bit binary-code tree (Rakočević, 1998) as well as within GCT are determined with the first pair of friendly numbers ( 220 \& 284) and third perfect number (496). For details see the text, especially Remarks 1 \& 2 .

Figure 1.2. The eight octets within 6-bit binary-code tree (Rakočević, 1998) as well as within GCT have determined with the first pair of friendly numbers (220 \& 284) and third perfect number (496). (After arXiv:q-bio/0703011v2 [q-bio.OT])

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Table 7
The AAs sequence taken from GCT as well as from binary-code tree of Genetic Code (Rakočević, 1998a)

| Conf. N | 12 | 22 | 20 | 20 | 08 | 12 | 24 | 38 | 16 | 66 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Isot. N | 28 | 26 | 26 | 24 | 20 | 31 | 22 | 23 | 17 | 30 |
| PN | 49 | 33 | 33 | 41 | 25 | 57 | 43 | 39 | 31 | 41 |
| NN-1 | 91 | 57 | 57 | 75 | 43 | 107 | 81 | 72 | 58 | 72 |
| NN-T | 196 | 127 | 127 | 231 | 96 | 247 | 173 | 173 | 142 | 159 |
| M. Mass | 165.19 | 131.18 | 131.18 | 149.21 | 117.15 | 181.19 | 155.16 | 146.15 | 132.12 | 146.19 |
| AN | 14 | 13 | 13 | 11 | 10 | 15 | 11 | 11 | 08 | 15 |


|  | $\begin{aligned} & + \\ & \mathrm{F} \\ & \mathrm{~S} \end{aligned}$ | + | - |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | L | I | M | V | Y | H | Q | N | K |
|  |  | P | T | A | C | W | R | G | E | D |
|  |  | - | - | + | + | - |  | - | - |  |
| AN | 05 | 08 | 08 | 04 | 05 | 18 | 17 | 01 | 10 | 07 |
| M. Mass | 105.09 | 115.13 | 119.12 | 089.09 | 121.16 | 204.23 | 174.20 | 075.07 | 147.13 | 133.10 |
| NN-T | 85 | 90 | 116 | 34 | 169 | 278 | 217 | 03 | 192 | 161 |
| NN-1 | 31 | 41 | 45 | 15 | 47 | 130 | 100 | 01 | 73 | 59 |
| PN | 17 | 23 | 25 | 09 | 25 | 69 | 55 | 01 | 39 | 31 |
| Isot. N | 11 | 16 | 17 | 08 | 12 | 36 | 34 | 02 | 22 | 16 |
| Conf. N | 09 | 02 | 08 | 03 | 21 | 24 | 66 | 04 | 20 | 10 |

After AAs encoded by middle "U" codons come AAs encoded by middle "A" codons; then follow AAs encoded by middle "G" and "C" in a cyclic organized system. The system can be seeing also as a sequence of the pairs (F-S, L-P, etc.). The data are as follows: The sign " + " and " - " for nonpolar and polar AAs, respectively (after hydropathy index); AN-the number of atoms within AA side chain; M Mass-the molecule mass of AA molecule; NN-T-the total nucleon number within AA side chain [example of calculation for serine: $(3 \times \mathrm{H})+(1 \times \mathrm{C})+(1 \times \mathrm{O})=(3 \times 1)+(3 \times 2)$ $+(1 \times 12)+(1 \times 13)+(1 \times 16)+(1 \times 17)+(1 \times 18)=85$ ]; NN-1- the nucleon number within first nuclide [example for serine: $(3 \times 1)+(1 \times 12)$ $+(1 \times 16)=31$ ]; PN-the number of protons [example for serine: $(3 \times 1)+(1 \times 6)+(1 \times 8)=17$ ]; Isot. $N$-the number of isotopes (nuclides) [example for serine: $(3 \times 2) \mathrm{H}+(1 \times 2) \mathrm{C}+(1 \times 3) \mathrm{O}=11$ ]; Conf. N -the number of conformations, as in Popov (1989, Table 8 , p. 88$)$. (Note: nucleon number and proton number for proline is calculated as in Shcherbak, 1994, and as in Dlyasin, 1998: one H atom from side chain, must be, in calculation, associated with the AA "head", because the same AA "head" must be referent system for all 20 canonical AAs).

Table 1.1. The amino acids sequences taken from GCT for two and two columns, after hydrogen bonds between nucleotides (UA versus CG). [All references for Part VII in this article.]

Explanation of Table 1.1: After AAs encoded by middle "U'" codons come AAs encoded by middle "A" codons; then follow AAs encoded by middle " $G$ " and ' $C$ " in a cyclic organized system. (The cyclization itself is also tested through symmetry: first 10 versus second 10 AAs (Table 1.2.) ${ }^{6}$ The system can be seeing also as a sequence of the pairs (F-S, L-P, etc.). The data are as follows: The sign " + " and " - ," for nonpolar and polar AAs, respectively (after hydropathy index); AN-the number of atoms within AA side chain; M. Mass-the molecule mass of AA molecule; NN-T-the total nucleon number within AA side chain [example of calculation for serine: $(3 \times H)+(1 \times C)+(1 \times \mathrm{O})=(3 \times 1)+(3 \times 2)+(1 \times 12)$ $+(1 \times 13)+(1 \times 16)+(1 \times 17)+(1 \times 18)=85] ; \mathrm{NN}-1-$ the nucleon number within first nuclide [example for serine: $(3 \times 1)+(1 \times 12)+(1 \times 16)=31$ ]; PN—the number of protons [example for serine: $(3 \times 1)+(1 \times 6)+(1 \times 8)=17$ ]; Isot. N-the number of isotopes (nuclides) [example for serine: (3 x 2) H $+(1 \times 2) \mathrm{C}+(1 \times 3) \mathrm{O}=11$ ]; Conf. N -the number of conformations, as in Popov (1989, Table 8, p. 88). (Note: nucleon number and proton number for proline is calculated as in Shcherbak, 1994, and as in

[^10]Dlyasin, 1998: one H atom from side chain, must be, in calculation, associated with the AA "head", because the same AA "head'" must be referent system for all 20 canonical AAs.)

## Table 8

The results of calculations from data given in Table 7

|  | AN | M. Mass | NN-T | NN-1 | PN | Isot. $N$ | Conf. N |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Odd | $102-1$ | $1369-1$ | $15 \underline{1} 3$ | $627-1$ | $343-1$ | $210-1$ | $203+1$ |
| Even | $102+1$ | $1369+1$ | $15 \underline{\underline{3}}$ | $628+1$ | $343+1$ | $211+1$ | $202-1$ |

All designations as in Table 7. The sums are given for AAs pairs in odd (bold) as well as in even positions within the system in Table 7. For example, within five AAs pairs [(F-S), (I-T), (V-C), (H-Y), (N-E)], existing in odd positions, there are 10 AAs molecules with molecules mass of 1368 units and with atom number of 101 atoms, etc., as it is presented in this table. The balances are self-evident.

Table 1.2. The results of calculations for the parameters given in Table 1.1.


Table 2.1. The standard Genetic Code Table (GCT): 64 codons and 23 amino acids; the arrangement by second letter (U, C, A, G: 16 times each in middle position within codons). Position hierarchy: II - I - III as II (16) - I (4) - III (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

| 2nd | 1st letter |  |  |  | 3rd |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | U | C | A | G |  |  |
| U | $\begin{array}{ll} \hline \text { UUU } & \\ \text { UUC } & \mathbf{F} \\ \text { UUA } & \\ \text { UUG } & \mathbf{L} \end{array}$ | $\begin{array}{\|ll\|} \hline \text { CUU } & \\ \text { CUC } & \\ \text { CUA } & \mathbf{L} \\ \text { CUG } & \\ \hline \end{array}$ | AUU  <br> AUC $\mathbf{I}$ <br> AUA  <br> AUG $\mathbf{M}$ | GUU  <br> GUC  <br> GUA  <br> GUG  | $\begin{aligned} & U \\ & C \\ & A \\ & G \end{aligned}$ | 74 |
| C | UCU <br> UCC <br> UCA $S$ <br> UCG | CCU <br> CCC <br> CCA $\mathbf{P}$ <br> CCG |  ACU <br> ACC  <br> ACA $\mathbf{T}$ <br> ACG  | GCU GCC GCA A GCG | $\begin{aligned} & U \\ & C \\ & A \\ & G \end{aligned}$ | 25 |
| A |   <br> UAU  <br> UAC $\mathbf{Y}$ <br> UAA CT <br> UAG  | $\begin{array}{\|lc\|} \hline \text { CAU } & \\ \text { CAC } & \mathbf{H} \\ \text { CAA } & \\ \text { CAG } & \mathbf{Q} \\ \hline \end{array}$ | AAU  <br> AAC $\mathbf{N}$ <br> AAA  <br> AAG $\mathbf{K}$ | GAU  <br> GAC $\mathbf{D}$ <br> GAA  <br> GAG $\mathbf{E}$ | $\begin{aligned} & U \\ & C \\ & A \\ & G \end{aligned}$ | 77 |
| G |   <br> UGU $\mathbf{C}$ <br> UGC CT <br> UGA $\mathbf{W}$ <br> UGG  | CGU  <br> CGC  <br> CGA $\mathbf{R}$ <br> CGG  | AGU  <br> AGC $\mathbf{S}$ <br> AGA  <br> AGG $\mathbf{R}$ | GGU  <br> GGC  <br> GGA $\mathbf{G}$ <br> GGG  | $\begin{aligned} & U \\ & C \\ & A \\ & G \end{aligned}$ | 63 |
|  | 70 | 60 | 77 | 32 |  |  |
| $(70+32=\mathbf{1 0 2})(60+77=\mathbf{1 3 7}) /(74+63=\mathbf{1 3 7})(25+77=\mathbf{1 0 2})$ |  |  |  |  |  |  |

Table 2.2. The second variant of standard GCT with the set of 23 amino acids; the arrangement is given by first letter (U, C, A, G: 16 times each in first position within codons). Position hierarchy: I-II - III as I (16) - II (4) - III (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

| 157 | $\mathbf{1 4 7}$ | $\mathbf{1 3 7}$ | 127 | $\mathbf{1 1 7}$ | 107 | 97 | 87 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 82 | $\mathbf{9 2}$ | $\mathbf{1 0 2}$ | 112 | $\mathbf{1 2 2}$ | 132 | 142 | 152 |
|  |  |  |  |  |  |  |  |
|  | Tab. IV/3 | Tab. VII/2.2 |  | Tab. IV/2 | Tab. IV/2 |  |  |

Survey 1. The atom number patterns within the set of 23 AAs (Cf. Survey IV/ 3.)


Table 3.1. The first variant of standard GCT with 61 amino acids and 16 nucleotides in second position of codons; the arrangement by second letter (U, C, A, G: 16 times each in middle position within codons). Position hierarchy: II - I - III as II (16) - I (4) - III (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

| $\mathbf{2 6 6}$ | 276 | 286 | $\mathbf{2 9 6}$ | $\mathbf{3 0 6}$ | 316 | 326 | $\ldots$ |
| :---: | :--- | :---: | :---: | :---: | :--- | :--- | :--- |
| $\mathbf{3 2 8}$ | 318 | 308 | $\mathbf{2 9 8}$ | $\mathbf{2 8 8}$ | 278 | 268 | $\ldots$ |
| $(\text { Tab. VII/3.1) })^{7}$ |  |  | $(\text { Tab. } \mathrm{I} / 1.2)^{8}$ | $(\text { Tab. } \mathrm{VII} / 3.2)^{9}$ |  |  |  |

Survey 2. The atom number patterns within the set of 61 AAs (I)

[^11]| $\mathbf{2 6 6}$ | 276 | 286 | $\mathbf{2 9 0}$ | 306 | 316 | 326 | $\ldots$ |
| :--- | :---: | :---: | :---: | :---: | :---: | :--- | :--- |
| 328 | 318 | 308 | 304 | 288 | 278 | 268 | $\ldots$ |
|  | $($ Tab. VII/4.3) |  | (Tab. VII/3.5) $^{10}$ | $(\text { Tab. VII/3.2) })^{11}$ |  |  |  |

Survey 3. The atom number patterns within the set of 61 AAs (II)

| 3rd | 2nd letter |  |  |  |  |  |  |  | 1st | a | b |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | U |  | C |  | A |  | G |  |  |  |  |
| U | UUU | F | UCU | S | UAU | Y | UGU | C | U |  | 288 |
|  | CUU | L | CCU | P | CAU | H | CGU | R | C |  |  |
|  | AUU | I | ACU | T | AAU | N | AGU | S | A | 144 |  |
|  | GUU | V | GCU | A | GAU | D | GGU | G | G |  |  |
|  |  | 50 |  | 25 |  | 41 |  | 28 |  |  |  |
| C | UUC | F | UCC | S | UAC | Y | UGC | C | $U$ | 144 |  |
|  | CUC | L | CCC | P | CAC | H | CGC | R | C |  |  |
|  | AUC | I | ACC | T | AAC | N | AGC | S | A |  |  |
|  | GUC | V | GCC | A | GAC | D | GGC | G | $G$ |  |  |
|  |  | 50 |  | 25 |  | 41 |  | 28 |  |  |  |
| A | UUA | L | UCA | S | UAA | * | UGA | * | U |  | 306 |
|  | CUA | L | CCA | P | CAA | Q | CGA | R | C |  |  |
|  | AUA | I | ACA | T | AAA | K | AGA | R | A | 145 |  |
|  | GUA | V | GCA | A | GAA | E | GGA | G | G |  |  |
|  |  | 49 |  | 25 |  | 36 |  | 35 |  |  |  |
| G | UUG | L | UCG | S | UAG | * | UGG | W | U | 161 |  |
|  | CUG | L | CCG | P | CAG | Q | CGG | R | C |  |  |
|  | AUG | M | ACG | T | AAG | K | AGG | R | A |  |  |
|  | GUG | v | GCG | A | GAG | E | GGG | G | $G$ |  |  |
|  |  | 47 |  | 25 |  | 36 |  | 53 |  |  |  |
|  |  | 196 |  | 100 |  | 154 | 144 |  |  |  |  |
|  | 296 (306-10) |  |  |  | 298 (288+10) |  |  |  |  |  |  |
|  | $297 \pm 1$ |  |  |  |  |  |  |  |  |  |  |

Table 3.2. The second variant of standard GCT with 61 amino acids and 16 nucleotides in second position of codons; the arrangement by second letter (U, C, A, G: 16 times each in middle position within codons). Position hierarchy: II - III - I as II (16) - III (4) - I (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

[^12]

Table 3.3. The first variant of standard GCT with 61 amino acids and 16 nucleotides in first position of codons; the arrangement by first letter ( $\mathrm{U}, \mathrm{C}, \mathrm{A}, \mathrm{G}: 16$ times each in first position within codons). Position hierarchy: I - II - III as I (16) - II (4) - III (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).


Table 3.4. The second variant of standard GCT with 61 amino acids and 16 nucleotides in first position of codons; the arrangement by first letter (U, C, A, G: 16 times each in first position within codons). Position hierarchy: I - III - II as I (16) - III (4) - II (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

| 1st | 3rd letter |  |  |  | 2nd |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | U | C | A | G |  |  |  |  |
| U | UUU $\mathbf{F}$ <br> UCU $\mathbf{S}$ <br> UAU $\mathbf{Y}$ <br> UGU $\mathbf{C}$ <br>  39 | UUC $\mathbf{F}$ <br> UCC $\mathbf{S}$ <br> UAC $\mathbf{Y}$ <br> UGC $\mathbf{C}$ <br>  $\mathbf{3 9}$ | UUA  <br> L  <br> UCA S <br> UAA $*$ <br> UGA $*$ <br>  18 | UUG L <br> UCG $\mathbf{S}$ <br> UAG $*$ <br> UGG $\mathbf{W}$ <br>  $\mathbf{3 6}$ | $\begin{aligned} & U \\ & C \\ & A \\ & G \end{aligned}$ | 132 | 328 |  |
| C |   <br> CUU $\mathbf{L}$ <br> CCU $\mathbf{P}$ <br> CAU $\mathbf{H}$ <br> CGU $\mathbf{R}$ <br>  49 | CUC $\mathbf{L}$ <br> CCC $\mathbf{P}$ <br> CAC $\mathbf{H}$ <br> CGC $\mathbf{R}$ <br>  49 |   <br> CUA $\mathbf{L}$ <br> CCA $\mathbf{P}$ <br> CAA $\mathbf{Q}$ <br> CGA $\mathbf{R}$ <br>  49 |   <br> CUG $\mathbf{L}$ <br> CCG $\mathbf{P}$ <br> CAG $\mathbf{Q}$ <br> CGG $\mathbf{R}$ <br>  49 | $\begin{aligned} & U \\ & C \\ & A \\ & G \end{aligned}$ | 196 |  |  |
| A | AUU $\mathbf{I}$ <br> ACU $\mathbf{T}$ <br> AAU $\mathbf{N}$ <br> AGU $\mathbf{S}$ <br>  $\mathbf{3 4}$ | AUC $\mathbf{I}$ <br> ACC $\mathbf{T}$ <br> AAC $\mathbf{N}$ <br> AGC $\mathbf{S}$ <br>  $\mathbf{3 4}$ |  AUA <br> ACA $\mathbf{I}$ <br> AAA $\mathbf{K}$ <br> AGA $\mathbf{R}$ <br>  $\mathbf{5 3}$ |   <br> AUG $\mathbf{M}$ <br> ACG $\mathbf{T}$ <br> AAG $\mathbf{K}$ <br> AGG $\mathbf{R}$ <br>  $\mathbf{5 1}$ | $\begin{aligned} & U \\ & C \\ & A \\ & G \end{aligned}$ | 172 | 266 |  |
| G |   <br> GUU $\mathbf{V}$ <br> GCU A <br> GAU $\mathbf{D}$ <br> GGU G <br>  $\mathbf{2 2}$ | GUC $\mathbf{V}$ <br> GCC $\mathbf{A}$ <br> GAC $\mathbf{D}$ <br> GGC $\mathbf{G}$ <br>  $\mathbf{2 2}$ | GUA $\mathbf{V}$ <br> GCA A <br> GAA $\mathbf{E}$ <br> GGA $\mathbf{G}$ <br>  $\mathbf{2 5}$ | GUG $\mathbf{V}$ <br> GCG $\mathbf{A}$ <br> GAG $\mathbf{E}$ <br> GGG $\mathbf{G}$ <br>  $\mathbf{2 5}$ | $\begin{aligned} & U \\ & C \\ & A \\ & G \end{aligned}$ | 94 |  |  |
|  | 144 | 144 | 145 | 161 |  |  |  |  |
|  | 288 |  |  | 306 |  |  |  |  |

Table 3.5. The first variant of standard GCT with 61 amino acids and 16 nucleotides in third position of codons; the arrangement by third letter (U, C, A, G: 16 times each in third position within codons). Position hierarchy: III - I - II as III (16) - I (4) - II (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

| 2nd | 3rd letter |  |  |  | 1st |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | U | C | A | G |  |  |  |
| U | UUU F | UUC F | UUA L | UUG L | U | 196 | 296 |
|  | CUU L | CUC L | CUA L | CUG L | C |  |  |
|  | AUU I | AUC I | AUA I | AUG M | A |  |  |
|  | GUU V | GUC v | GUA V | GUG V | G |  |  |
|  | 50 | 50 | 49 | 47 |  |  |  |
| C | UCU $\mathbf{S}$ | UCC S | UCA S | UCG L | U | 100 |  |
|  | CCU $\mathbf{P}$ | CCC P | CCA P | CCG P | C |  |  |
|  | ACU T | ACC T | ACA T | ACG T | A |  |  |
|  | GCU A | GCC A | GCA A | GCG A | G |  |  |
|  | 25 | 25 | 25 | 25 |  |  |  |
| A | UAU $\mathbf{Y}$ | UAC $\mathbf{Y}$ | UAA CT | UAG CT | $U$ | 154 | 298 |
|  | CAU H | CAC H | CAA $\mathbf{Q}$ | CAG $\mathbf{Q}$ | C |  |  |
|  | AAU $\mathbf{N}$ | AAC $\mathbf{N}$ | AAA $\quad \mathbf{R}$ | AAG K | A |  |  |
|  | GAU D | GAC D | GAA E | GAG E | G |  |  |
|  | 41 | 41 | 36 | 36 |  |  |  |
| G | UGU C | UGC C | UGA CT | UGG W | $U$ | 144 |  |
|  | CGU R | CGC R | CGA R | CGG R | C |  |  |
|  | AGU $\mathbf{S}$ | AGC $\mathbf{S}$ | AGA R | AGG R | A |  |  |
|  | GGU G | GGC G | GGA G | GGG G | $G$ |  |  |
|  | 28 | 28 | 35 | - 53 |  |  |  |
|  | 144 | 144 | 145 | 161 |  |  |  |
|  |  | 288 |  | 306 |  |  |  |

Table 3.6. The second variant of standard GCT with 61 amino acids and 16 nucleotides in third position of codons; the arrangement by third letter (U, C, A, G: 16 times each in third position within codons). Position hierarchy: III - II - II as III (16) - II (4) - I (1).

| I-II |  |  | I-II |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| GG | GGGG |  | UU | FFLL |  |  | $\begin{aligned} & \text { స̀ } \\ & \stackrel{\rightharpoonup}{\circ} \\ & \text { ì } \end{aligned}$ | $\underset{\sim}{\infty}$ |
| GU | VVVV | 44 | UG | CC*W | 82 | 126 |  |  |
| CC | $\begin{aligned} & \text { PPPP } \\ & \text { TTTT } \end{aligned}$ | 64 | AA | NNKK | 90 | 154 |  |  |
| AC |  |  | CA | HHQQ |  |  |  |  |
| GC | AAAA LLLL | 68 | UA | YY** | 74 | 142 |  | $\stackrel{ \pm}{m}$ |
| CU |  |  | AG | SSRR | 74 | 142 |  |  |
| CG | $\begin{array}{\|l} \hline \text { RRRR } \\ \text { SSSS } \\ \hline \end{array}$ | 88 | AU | IIIM | 84 | 172 |  |  |
| UC |  |  | GA | DDEE |  |  |  |  |
| 264 |  |  |  | 330 |  |  |  |  |

Table 4.1. The nucleotide doublets as in Table II/2: positions I \& II in the codon. (Cf. Fig. I/1.)

| I-III |  |  | I-III |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| GG | VAEG |  | UU | FSYC |  |  | $\begin{aligned} & \text { ep } \\ & \text { II } \\ & \stackrel{+}{0} \\ & \stackrel{e}{n} \end{aligned}$ |
| GU | VADG | 47 | UG | LS*W | 75 | 122 |  |
| CC | LPHR <br> ITNS | 83 | AA | ITKR | 102 | 185 |  |
| AC |  |  | CA | LPQR |  |  |  |
| GC | $\begin{aligned} & \hline \text { VADG } \\ & \text { LPHR } \end{aligned}$ | 71 | UA | LS** | 69 | 140 | $\begin{gathered} \underset{\sim}{\infty} \\ \underset{\sim}{\\|} \\ \underset{\sim}{1} \\ \underset{\sim}{\infty} \end{gathered}$ |
| CU |  |  | AG | MTKR | 69 | 140 |  |
| CG | $\begin{aligned} & \hline \text { LPQR } \\ & \text { FSYC } \\ & \hline \end{aligned}$ | 88 | AU | LS** | 59 | 147 |  |
| UC |  |  | GA | MTKR |  |  |  |
| $288+1=$ |  | 289 | $306-1=$ |  | 305 |  |  |

Table 4.2. The nucleotide doublets taken from positions I \& III in the codon. The atom number pattern 289/305 corresponds (making a balance) to the atom number 290/304 in Table 3.1; also to the atom number 290-10 / 304 + 10 in Table 4.1. On the other hand, the atom number pattern 287/307 corresponds to the atom number 288/306 in Table 3.2.

| II-III |  |  | II-III |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| GG | WRRG CRSG | 81 | UU | $\begin{aligned} & \hline \text { FLIV } \\ & \text { LLMV } \end{aligned}$ | 97 | 178 | $\begin{aligned} & \text { en } \\ & \text { II } \\ & \stackrel{1}{1} \\ & \stackrel{\sim}{e} \end{aligned}$ |
| GU |  |  | UG |  |  |  |  |
| CC | SPTAYHND | 66 | AA | $\begin{aligned} & \text { QKE } \\ & \text { SPTA } \end{aligned}$ | 61 | 127 |  |
| AC |  |  | CA |  |  |  |  |
| GC | CRSG | 53 | UA | LLIV | 85 | 138 | $\begin{aligned} & \text { ò } \\ & \underset{\sim}{11} \\ & \underset{\sim}{\infty} \\ & \underset{\sim}{\infty} \end{aligned}$ |
| CU | SPTA |  | AG | QKE |  |  |  |
| CG | SPTA | 75 | AU | YHND | 76 | 151 |  |
| UC | FLIV |  | GA | RRG |  |  |  |
| 276-1 |  |  | $318+1$ |  |  |  |  |

Table 4.3. The nucleotide doublets taken from positions II \& III in the codon. The atom number pattern 289/305 corresponds (making a balance) to the same atom number pattern 289/305 in Table 4.2. On the other hand, the atom number pattern 276/318 corresponds to the same pattern in Survey 2.

Presented facts support the hypothesis that the genetic code was a complete code from very begining, from prebiotic times and conditions. On the other hand, such a complet code must be expressed into genotype and phenotype, ${ }^{12}$ and that is the reason why all the presented relationships in the genetic code one needs to know.

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[^13]
## 8.

## Notes about Genetic Code, Note 1: Four Diversity Types of Protein Amino Acids

In this Note is presented the existence of four diversity types of protein amino acids (AAs). Fist type with two AAs (G; P); second with four AAs (A, L; V, I); third with six AAs (F, Y, H, W; C, M); and fourth type with eight AAs (S, T, D, E; N, Q; K, R).

# NOTES ABOUT GENETIC CODE, NOTE 1: FOUR DIVERSITY TYPES OF PROTEIN AMINO ACIDS 

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#### Abstract

For the first time, in this Note is presented the existence of four diversity types of protein amino acids (AAs). Fist type with two AAs (G; P); second with four AAs (A, L; V, I); third with six AAs (F, Y, H, W; C, M); and fourth type with eight AAs (S, T, D, E; N, Q; K, R).


## 1 INTRODUCTION

With this note we begin a series of notes on some new insights about the relations between the constituents of the genetic code, with a system-chemical interpretation; a system in terms of Mendeleev: for him it was a system of atoms, and here it comes a complete system of molecules, a system that is able to make something: to produce and maintain the life.

## 2 RESULTS AND DISCUSSION

For the first time, in this Note is presented the existence of four diversity types of protein amino acids (AAs). Fist type with two AAs ( $\mathrm{G} ; \mathrm{P}$ ); second with four AAs (A, L; V, I); third with six AAs (F, Y, H, W; C, M); and fourth type with eight AAs (S, T, D, E; N, Q; K,
R). All 20 AAs as a realization of a pattern of first four even natural numbers in decimal numbering system $(2+4+6+8)^{1}$; the 20 AAs as a full system, in accordance with both Crick hypotheses (Crick, 1966, 1968; Rakočević, 2009a,b). So, in this research we find that there are four diversity types ${ }^{2}$ of protein amino acids (Figure 1):

1. Without a "standard" hydrocarbon side chain (G, P);
2. With hydrocarbon side chain (L, A, I, V);
3. With aromatic ring, and/or with a hetero atom in side chain (F, Y, H, W; C, M);
4. The rest of eight AAs (S, T, D, E; N, Q; K, R) with the same (or near to the same) functional groups within "head" and "body". (A scientific puzzle: the side chain is a "body" or a "head"?)
[Remark 1: If 20 AAs $(2+4+6+8)$ make a whole (and full) system, then sulfur is also a "hetero" atom!]

The presented strict regularities, through a connection between particles number (number of atoms as well as of amino acid molecules) and physico-chemical properties ${ }^{3}$ give a satisfaction to the ideas according to which the genetic code is a complete, unique and unifying system (Rumer, 1966; Swanson, 1984; Doolittle, 1985;

[^14]Damjanović, 1998; Dlyasin, 1998; Qiu, Zhu 2000; Yang, 2004; Negadi, 2009,a,b); and/or a complete system from the begining, from prebiotic times (Sukhodolec, 1981, 1985; Rakočević, 2004b).


Figure 1. A modified "Gauss algorithm" Table - third and fourth row replaced their positions. (About algorithm see in: arXiv:q-bio/0610044v1 [q-bio.OT]) ("Genetic code as a harmonic system")

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## APPENDIX 1. Mendeleev's first work on the periodic system



## 9.

## Notes About Genetic Code, Note 2: the Relations Between Four Diversity Types of Protein Amino Acids

This Note follows from Note 1, submitted on 2016-12-08 and it shows further distinctions and splittings within four diversity types of protein amino acids (AAs). First type as in Note 1 (G, P) and second one, also as in Note 1 (A, L; V, I). Within third type there is a chemicaly directed splitting into $4+2$ AAs [(F, Y, H, W) $+(\mathrm{C}$, M)]. Forth type consists of two halves in form of $4+4$ AAs; four AAs with nitrogen, and four without: [(N, Q; K, R) + (S, T, D, E)]. All these distinctions are followed through specific arithmetical regularities.

# NOTES ABOUT GENETIC CODE, NOTE 2: THE RELATIONS BETWEEN FOUR DIVERSITY TYPES OF PROTEIN AMINO ACIDS 

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#### Abstract

This Note follows from Note 1 and it shows further distinctions and splittings within four diversity types of protein amino acids (AAs). First type as in Note 1 $(\mathrm{G}, \mathrm{P})$ and second one, also as in Note $1(\mathrm{~A}, \mathrm{~L} ; \mathrm{V}, \mathrm{I})$. Within third type there is a chemicaly directed splitting into $4+2$ AAs $[(F, Y, H, W)+(C, M)]$. Forth type consists of two halves in form of $4+4$ AAs; four AAs with nitrogen, and four without: $[(\mathrm{N}, \mathrm{Q} ; \mathrm{K}, \mathrm{R})+(\mathrm{S}, \mathrm{T}, \mathrm{D}, \mathrm{E})]$. All these distinctions are followed by specific arithmetical regularities.


In a previous Note (Note 1, Version 2) we presented the existence of four diversity types of protein amino acids (AAs). Fist type with two AAs (G; P); second one with four AAs (A, L; V, I); third with six (F, Y, H, W; C, M), and fourth type with eight AAs (S, T, D, E; N, Q; K, R) (Figure 1). In this Note we show further distinctions and splittings within four diversity types. First type as in Note 1 (G, P), second one also as in Note 1 ( $\mathrm{A}, \mathrm{L} ; \mathrm{V}, \mathrm{I}$ ). Within third type there is a chemicaly directed splitting into $4+2$ AAs $[(\mathrm{F}, \mathrm{Y}, \mathrm{H}, \mathrm{W})+(\mathrm{C}, \mathrm{M})]$. Forth type consists of two halves in form of $4+4 \mathrm{AAs}$; four AAs with nitrogen, and four without nitrogen: $[(\mathrm{N}, \mathrm{Q} ; \mathrm{K}, \mathrm{R})+(\mathrm{S}, \mathrm{T}, \mathrm{D}$,
E)]. All these distinctions are followed by specific arithmetical regularities. As we see from Figure 2, the chemistry as well as arithmetic show that there are two ( $\mathrm{G}, \mathrm{P}$ ) and two ( $\mathrm{C}, \mathrm{M}$ ) "nonstandard" AAs. First two (G, P) are "non-standard" through their whole side chains, whereas the second two (C, M) through their functional groups within side chain.


Figure 1. As Figure 1 in Note 1: a modified "Gauss algorithm" Table - third and fourth row replaced their positions. (About algorithm see in: arXiv:qbio/0610044v1 [q-bio.OT]) ("Genetic code as a harmonic system")

| S T <br> D E | $\begin{array}{ll}\text { L } & \mathrm{A} \\ \mathrm{I} & \mathrm{V}\end{array}$ | G P |  |
| :---: | :---: | :---: | :---: |
| $\begin{array}{ll}\mathrm{N} & \mathrm{Q} \\ \mathrm{K} & \mathrm{R}\end{array}$ | $\begin{array}{ll}\text { F } & \text { Y } \\ \text { H } & \text { W }\end{array}$ | C M |  |
| 30 | 40 | 09 | 079 |
| 51 | 58 | 16 | 125 |
| 81 | 98 | 025 |  |

Figure 2. This Figure follows from Figure 1. The AAs are presented in a manner which demonstrates the existence of $4 \times 4$ chemically classified AAs, plus $2 \times 2$ "non-standard" AAs. Notice that for atom number within side chains of four "non-standard" AAs a specific arithmetical rule is valid; the same rule as for nucleon number in Shcherbak's system, for nucleon number in eight four-codon AAs (G, P; A, V, L; S, T, R) (Shcherbak, 1994, p. 475: "... the sums demonstrate the squares of the first three Pythagorean numbers").

Remark 1: Nucleon number within whole molecules of 8 four-codon AAs: $\left(3^{2} \times 037\right)+\left(4^{2} \times 037\right)=\left(5^{2} \times 037\right)^{1}$.

Remark 2: Atom number within side chains of 4 "non-standard" AAs: $\left(3^{2} \times 001\right)+\left(4^{2} \times 001\right)=\left(5^{2} \times 001\right)$.

Remark 3: In the set of 8 four-codon AAs the distinction occurs in this way: the 8 different side chains plus 8 times the same functional amino acid group (aaFG). On the other side, in the set of 4 "nonstandard" AAs the distinction occurs in a different way: atom

[^15]number within side chains of two non-sulfur AAs plus atom number within side chains of two sulfur AAs.

In conclusion we can say that all presented regularities give the satisfaction to two things, to my general hypothesis on the genetic code and to an earlier conclusion; to the hypothesis that the genetic code was complete from the beginning (from the prebiotic area!); and the conclusion, according to which, at least in the genetic code, Aristotle's thesis about the unity of form and essence appears to be valid (Rakočević, 2004) ${ }^{2}$.

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[^16]
## ADDITIONAL COMMENTS

This Note, as "Note 2", together with Note 1 (viXra:1612.0127, submitted on 2016-1208 07:01:10) corresponds with the paper "Genetic Code: Four Diversity Types of Protein Amino Acids", published in arXiv (arXiv:1107.1998v2 [q-bio.OT]). Also, the key ideas about four diversity types of protein amino acids are given in the paper: Rakočević, M.M. (2011) Genetic code as a coherent system. Neuroquantology, 9 (4), 821-841;

These key ideas are as follows:
The first type includes two amino acids (G, P), both without standard hydrocarbon side chains; the second one four amino acids, as two pairs [(A, L), (V, I)], all with standard hydrocarbon side chains; the third type comprises the six amino acids, as three pairs [(F, $\mathrm{Y}),(\mathrm{H}, \mathrm{W}),(\mathrm{C}, \mathrm{M})$, two aromatic, two hetero aromatic and two "hetero" non-aromatic (all six without functional group in side chain, that is in "body", from the amino acid "head"); finally, the fourth type consists of eight amino acids, as four pairs [(S, T), (D, E), (N, Q), (K, R)], all with a functional group which also exists in amino acid functional group, that is "head" (wholly presented amino acid functional group: $\mathrm{H} 2 \mathrm{~N}-\mathrm{I} . \mathrm{CH}-\mathrm{COOH}$; separately: $\mathrm{OH}, \mathrm{COOH}, \mathrm{CONH} 2, \mathrm{NH} 2$ ). The insight into existence of four types of diversity was possible only after an insight into the existence of some very new arithmetical regularities, which were so far unknown. Also, as for showing these four types was necessary to reveal the relationships between several key harmonic structures of the genetic code, which we presented in our previous works).

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## 10.

## Enigmas of the Genetic Code, Enigma 1: A Hidden Arithmetical Algorithm

In a certain way, this enigma is standing in relation to so-called Gaussian arithmetical algorithm, valid for the genetic code (Rakocevic, 2006). However, the difference is, among other things, that there (in the article on the Gaussian algorithm), I said and showed all openly - what is the enigma [classes of AAs $(2 \times 2)$, or $(4 \times 5)$, or $(2 \times 4)$ with $11,21,31,41,-, 61,71$, 81, 91 of atoms within their side chains, respectively]; and here the hidden algorithm is hidden twice: once by the very Nature, the other way from myself. I make here, namely, only a hint of the solution. Certainly, in coming a few weeks (or months), I will present the solution, if someone else, in meantime, offers (or doesn't offer) the solution. [The solution of Enigma 1 is covered in Addendum 2, Equations (1) and Figure 1.]

# ENIGMAS OF THE GENETIC CODE, ENIGMA 1: A HIDDEN ARITHMETICAL ALGORITHM (Version 1) 

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#### Abstract

In a certain way, this enigma is standing in relation to so-called Gaussian arithmetical algorithm, valid for the genetic code (Rakočević, 2006) ${ }^{1}$. However, the difference is, among other things, that there (in the article on the Gaussian algorithm) I said and showed all openly - what is the enigma [classes of AAs ( 2 x 2 ), or ( $4 \times 5$ ), or ( $2 \times 4$ ) with $11,21,31,41,-, 61,71,81,91$ of atoms within their side chains, respectively]; and here the hidden algorithm is hidden twice: once by the very Nature, the other way from myself. I make here, namely, only a hint of the solution. Certainly, in coming a few weeks (or months), I will present the solution, if someone else, in meantime, offers (or doesn't offer) the solution.


## The Problem

Find the key number X (Starting result); At the starting result X add $\mathrm{X}-10$ (First new result);

[^17]At the first new result add X-9 (Second new result); At the second new result add X-8 (Third new result).

Four results (Starting, plus three new results) correspond to the number of atoms in the four classes of protein amino acids ( $4 \times 5=$ 20 canonical amino acids in the genetic code).

The sum of the four results (Y) corresponds to the total number of atoms in 20 protein amino acids (within their side chains).

The sum of three addings, $\mathrm{Z}=[(\mathrm{X}-10)+(\mathrm{X}-9)+(\mathrm{X}-8)]$, corresponds to one quarter ${ }^{2}$ of the total number of atoms $(\mathrm{Y} / 4)$.

To solve this problem (Table 1) one must know about four diversity types of protein amino acids in the forms as we presented in our two Notes (Note 1 and Note 2) at our web-site (www.rakocevcode.rs).

## Comment

The solutions of this enigma give the satisfaction to our hypothesis that the genetic code was complete from the very beginning and that it represents a unique system in which the positions of each amino acid is strictly determined, and that with several different aspects (Rakočević, 2004).

[^18]

Table 1. The number of atoms within side chains of four classes of amino acids $\left(a_{1}-a_{5}, b_{1}-b_{5}, c_{1}-c_{5}, d_{1}-d_{5}\right)$ corresponds to the four results ( $a, b, c, d$ ) and to solutions of presented enigma, i.e. problem (X,Y,Z).

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## 11.

## Enigmas of the Genetic Code, Enigma 2: A Second Hidden Arithmetical Algorithm

This second Enigma is standing in relation to Enigma 1 in our previous communication. It is relating to total number of atoms (204) in side chains of 20 protein amino acids, within standard genetic code. [The solution of Enigma 2 is covered in Chapter 16, Table 3.]

# ENIGMAS OF THE GENETIC CODE, ENIGMA 2: A SECOND HIDDEN ARITHMETICAL ALGORITHM (Version 1) 

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#### Abstract

This second enigma is standing in relation to enigma 1 in our previous communication. It is relating to total number of atoms (204) in side chains of 20 protein amino acids, within standard genetic code.


## INTRODUCTORY NOTES

1. From the aspect of symmetry, the relation between the numbers 2 and 5 appears to be special (Table 1). Namely, in the binary numbering system, the pair $2-5$ is the first possible pair with both symmetry - direct (vertical) and indirect (horizontal):

010

$$
\begin{equation*}
010 / 101 \tag{1}
\end{equation*}
$$

101
2. It is known that the balances of atom number and/or nucleon number in amino acid molecules (within genetic code) are determined by the differences for $00,01,10$ and/or 11 , writing in decimal numbering system [see about that in our works; for example, References in Note 1 (version 2) in our site (www.rakocevcode.rs)].
3. The question is whether the standpoints of point 1 and point 2 may be related? The answer to this question incorporates arithmetic system presented in Table 2.

## THE PROBLEM

Find such an arrangement of amino acids $(5 \times 4)$ that the number of atoms (in the side amino acid chains), in five rows (Table 3), corresponds to $10^{\text {th }}$ event within the system in Table 2. (Hint: In a series of even natural numbers just $10^{\text {th }}$ case is the number 20.)

## COMMENT

The solutions of this enigma give the satisfaction to our hypothesis that the genetic code was complete from the very beginning and that it represents a unique (full and whole) system in which the position of each amino acid is strictly determined, and that with several different aspects (Rakočević, 2004).


Table 1. The pairs of numbers (from the sequence of natural numbers) that have mutual symmetry [see binary number presentation (1)].

| 00 | 02 | 04 | 06 | 08 | 10 | 12 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 11 | 13 | 15 | 17 | 19 | 21 | 23 |
| 22 | 24 | 26 | 28 | 30 | 32 | 34 |
| 11 | 16 | 21 | 26 | 31 | 36 | 41 |
| 00 | 05 | 10 | 15 | 20 | 25 | 30 |
| 44 | 60 | 76 | 92 | 108 | 124 | 140 |
|  | 12 | 14 | 16 | 18 | 20 | 22 |
|  | 23 | 25 | 27 | 29 | 31 | 33 |
|  | 34 | 36 | 38 | 40 | 42 | 44 |
|  | 41 | 46 | 51 | 56 | 61 | 66 |
|  | 30 | 35 | 40 | 45 | 50 | 55 |
|  | 140 | 156 | 172 | 188 | 204 | 220 |
|  | 22 | 24 | 26 | 28 | 30 | 32 |
|  | 33 | 35 | 37 | 39 | 41 | 43 |
|  | 44 | 46 | 48 | 50 | 52 | 54 |
|  | 66 | 71 | 76 | 81 | 86 | 91 |
|  | 55 | 60 | 65 | 70 | 75 | 80 |
|  | 220 | 236 | 252 | 268 | $\underline{284}$ | $\underline{\underline{300}}$ |
|  | 32 | 34 | 36 | 38 | 40 | 42 |
|  | 43 | 45 | 47 | 49 | 51 | 53 |
|  | 54 | 56 | 58 | 60 | 62 | 64 |
|  | 91 | 96 | 101 | 106 | 111 | 116 |
|  | 80 | 85 | 90 | 95 | 100 | 105 |
|  | 300 | 316 | 332 | 348 | 364 | 380 |
|  | .. |  |  |  |  |  |

Table 2. A specific arithmetical system. Start with 00-11-22-11-00, and then adding the number 2 in the first three cases, and number 5 in the last two cases. As a result we have $10^{\text {th }}$ event, correspondent with number of atoms within $4 \times 5$ amino acids as it is shown in Table 3. (Notice, that the pair 220-284 is the first pair of friendly numbers; cf. Figures A. 1 and A. 2 in Appendix A.)


Table 3. The number of atoms within side chains of five rows of amino acids $\left(a_{1}-a_{4}, b_{1}-b_{4}, \ldots, e_{1}-e_{4}\right)$ corresponds to the five results in $10^{\text {th }}$ case of an arithmetical system presented in Table 2.

## REFERENCES

Rakočević, M. M. (1998) The genetic code as a Golden mean determined system, Biosystems 46, 283-291.
Rakočević, M. M. (2004) A harmonic structure of the genetic code, J. Theor. Biol. 229, 221-234.

## APPENDIX A

The six-bit binary code tree of the genetic code (Rakočević, 1998) in Figure A. 1 and its determination with third perfect number (496) as well as first pair of friendly numbers $(220,284)$ in Figure A.2.


Figure A.1. The six-bit binary code tree of the genetic code (Rakočević, 1998)


Figure A.2. The determination of six-bit binary code tree (Figure A.1) with third perfect number (496) and with first pair of friendly numbers $(220,284)$.

## 12.

## Enigmas of the Genetic Code, Enigma 3: A Third Hidden Arithmetical Algorithm

This third enigma is standing in relation to enigmas $1 \& 2$, given in our previous two communications. It is relating to total number of atoms (239) in side chains of 23 protein amino acids, within standard genetic code. By this three amino acids (L, S, R) are included twice each. [The solution of Enigma 3 is covered in Chapter 16, Table 3 and illustrations that follow.]

# ENIGMAS OF THE GENETIC CODE, ENIGMA 3: A THIRD HIDDEN ARITHMETICAL ALGORITHM (Version 1) 

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#### Abstract

This third enigma is standing in relation to enigmas $1 \& 2$, given in our previous two communications. It is relating to total number of atoms (239) in side chains of 23 protein amino acids, within standard genetic code. By this three amino acids (L, S, R) are included twice each.


## INTRODUCTORY NOTE

It is known that the balances of atom number and/or nucleon number in amino acid molecules (within genetic code) are determined by the differences for $00,01,10$ and/or 11 , writing in decimal numbering system [see about that in our works; for example, References in Note 1 (version 2) in our site (www.rakocevcode.rs)].

## THE PROBLEM

1. Find a new arithmetical algorithm for a connection between 10 and 11 (Table 1), such an arrangement which corresponds to an adequate amino acid arrangement (Table 2).
2. The problem (question) is: which chemical law (which regularity) dictates the arrangement, given in Table 2.

|  | c' | $\mathrm{b}^{\prime}$ | a |  | b | c | d | e | f |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1 | 10 |  |  |  |  |  |  |  |  |  |
| 2 | $\underline{-10}=09-\left(\begin{array}{c}11 \\ -01)\end{array} \mathrm{c}^{(11} \stackrel{-23}{=}\right.$ |  |  |  |  |  |  |  |  |  |
| 3 |  |  |  |  |  |  |  |  |  |  |
| 4 |  |  | 01 |  |  |  |  |  | -45 | (35) |
| 5 | $(-02-10=$ |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |
| 1 | $\begin{array}{ll}20 & -15\end{array}$ |  |  |  |  |  |  |  |  |  |
| 2 |  |  |  |  |  |  |  |  |  |  |
| 3 | $\underline{01}=08-(09)-12$ |  |  |  |  |  |  |  |  |  |
| 4 |  |  |  |  |  |  |  |  | -27 | (28) |
| 5 | (08) - $10=-02$ |  |  |  |  |  |  |  |  |  |
| 6 |  |  |  |  |  |  |  |  |  |  |
| 1 |  |  | 30 |  |  |  |  |  |  |  |
| 2 |  |  |  |  |  |  |  |  |  |  |
| 3 |  |  |  |  |  |  |  |  |  |  |
| 4 |  |  |  |  |  |  |  |  |  |  |
| 5 | (18) - 10 |  |  |  |  |  |  |  |  |  |
| 6 |  |  |  |  |  | -02 |  |  |  |  |
| 1 |  |  | 40 |  |  |  |  |  |  |  |
| 2 | $\underline{23}=06$ |  | 11 |  |  | 01 |  |  |  |  |
| 3 |  |  | (29) | - | 14 | $=$ |  | (07) | $\underline{09}$ | (14) |
| 4 |  |  |  |  |  |  |  |  |  |  |
| 5 |  |  |  | - | 10 | $=$ | 18 |  |  |  |
| 6 |  |  |  |  |  | 08 | , |  |  |  |
| 1 |  |  | 50 |  |  |  |  |  |  |  |
| 2 | $\underline{34}=05-\left(\begin{array}{l}11 \\ (39)\end{array}-15 \stackrel{09}{=} 24\right.$ |  |  |  |  |  |  |  |  |  |
| 3 |  |  |  |  |  |  |  |  |  |  |
| 4 |  |  |  |  |  |  |  |  | $\underline{27}$ | (07) |
| 5 | (38) - $10 \underset{18}{=}$ |  |  |  |  |  |  |  |  |  |
| 6 |  |  |  |  |  |  |  |  |  |  |
| 1 |  |  | 60 |  |  |  |  |  |  |  |
| 2 | $\underline{45}=04-\begin{gathered}11 \\ (49)\end{gathered} \mathrm{C}^{(16} \stackrel{17}{=} 33$ |  |  |  |  |  |  |  |  |  |
| 3 |  |  |  |  |  |  |  |  |  |  |
| 4 |  |  | 01 |  |  |  |  |  | 45 | (00) |
| 5 | (48) $-10 \begin{gathered}= \\ \\ \\ \\ \\ \end{gathered}$ |  |  |  |  |  |  |  |  |  |
| 6 |  |  |  |  |  |  |  |  |  |  |

Table 1 (1). From a start of 10-11 follows a specific arithmetical arrangement, which $6^{\text {th }}$ event is a zeroth one at the same time.

|  | c' |  | $\mathrm{b}^{\prime}$ | a |  |  |  | c |  | e | f |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $\begin{aligned} & 1 \\ & 2 \\ & 3 \\ & 4 \\ & 5 \\ & 6 \end{aligned}$ |  |  |  | 60 11 $(49)$ 01 $(48)$ |  |  |  | $\begin{gathered} 17 \\ = \\ = \\ 28 \end{gathered}$ |  | (11) |  |  |
| $\begin{aligned} & \hline 1 \\ & 2 \\ & 3 \\ & 4 \\ & 5 \\ & 6 \end{aligned}$ |  |  |  | 70 11 $(59)$ 01 $(58)$ |  |  |  | $\begin{gathered} 25 \\ = \\ = \\ 38 \end{gathered}$ |  | (13) | 63 | (-07) |
| $\begin{aligned} & 1 \\ & 2 \\ & 3 \\ & 4 \\ & 5 \\ & 6 \end{aligned}$ |  |  |  | 80 11 $(69)$ 01 $(68)$ |  |  |  | $\begin{aligned} & 33 \\ & = \\ & = \\ & 48 \end{aligned}$ |  | 15) | 81 |  |
| $\begin{aligned} & 1 \\ & 2 \\ & 3 \\ & 4 \\ & 5 \\ & 5 \\ & \hline \end{aligned}$ |  |  | 01 | 90 11 $(79)$ 01 $(78)$ |  |  |  | $\begin{aligned} & 41 \\ & = \\ & = \\ & 58 \end{aligned}$ |  | (17) | 99 | (-21) |
| $\begin{aligned} & 1 \\ & 2 \\ & 3 \\ & 4 \\ & 5 \\ & 6 \end{aligned}$ |  |  | 00 | $\begin{gathered} 100 \\ 11 \\ (89) \\ 01 \\ (88) \end{gathered}$ |  |  |  | $\begin{gathered} 49 \\ = \\ = \\ 68 \end{gathered}$ |  | (19) | 117 | (-28) |
| $\begin{aligned} & \hline 1 \\ & 2 \\ & 3 \\ & 4 \\ & 5 \\ & 6 \\ & \hline \end{aligned}$ |  |  | 01 | $\begin{gathered} \hline 110 \\ 11 \\ (99) \\ 01 \\ (98) \end{gathered}$ |  |  |  | $\begin{aligned} & 41 \\ & = \\ & = \\ & 78 \end{aligned}$ |  | (21) | 135 | (-35) |

Table 1 (2). All quantities, appeared in sixth event, one can find in a specific amino acid arrangement (Table 2).

| $\begin{aligned} & \text { GGU } \\ & \text { GGC } \\ & \text { GGA } \\ & \text { GGG } \end{aligned}$ | G |  | L | $\begin{aligned} & \text { AAU } \\ & \text { AAC } \end{aligned}$ | N | $\begin{gathered} - \\ \overline{-} \\ \text { AUG } \end{gathered}$ | M | 33 |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $\begin{aligned} & \text { GCU } \\ & \text { GCC } \\ & \text { GCA } \\ & \text { GCG } \end{aligned}$ | A | $\begin{array}{\|l\|} \hline \text { CUU } \\ \text { CUC } \\ \text { CUA } \\ \text { CUG } \end{array}$ | L | $\begin{gathered} \text { GAU } \\ \text { GAC } \\ - \end{gathered}$ | D | $\begin{gathered} \text { UUU } \\ \text { UUC } \\ - \end{gathered}$ | F | 38 | 5 |
| $\begin{aligned} & \text { GUU } \\ & \text { GUC } \\ & \text { GUA } \\ & \text { GUG } \end{aligned}$ | V | $\begin{aligned} & \overline{\mathrm{AAA}} \\ & \mathrm{AAG} \end{aligned}$ | K | $\begin{gathered} \text { AGU } \\ \text { AGC } \end{gathered}$ | S | $\begin{gathered} \text { UAU } \\ \text { UAC } \\ - \end{gathered}$ | Y | 45 | 7 |
| $\begin{aligned} & \text { CCU } \\ & \text { CCC } \\ & \text { CCA } \\ & \text { CCG } \end{aligned}$ | P | $\begin{aligned} & \text { CGU } \\ & \text { CGC } \\ & \text { CGA } \\ & \text { CGG } \end{aligned}$ | R | UCU UCC UCA UCG | S | $\begin{gathered} - \\ \text { UGG } \end{gathered}$ | w | 48 | 3 |
| $\begin{aligned} & \text { AUU } \\ & \text { AUC } \\ & \text { AUA } \end{aligned}$ | I | $\overline{\overline{A G A}}$ | R | $\begin{aligned} & \hline \text { ACU } \\ & \text { ACC } \\ & \text { ACA } \\ & \text { ACG } \end{aligned}$ | T | $\begin{gathered} \hline \mathrm{CAU} \\ \mathrm{CAC} \\ - \\ - \end{gathered}$ | H | 49 | 1 |
|  |  | $\overline{-}$ | Q | $\begin{gathered} \text { UGU } \\ \text { UGC } \\ - \end{gathered}$ | C |  |  | 16 |  |
|  |  | $\overline{-}$ |  |  |  |  |  | 10 |  |

Table 2. A specific amino acid arrangement, correspondent with a specific arithmetical algorithm, given in Table 1, and related to other harmonic structures of the genetic code (Rakočević, 1998, 2004).

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## ADDITIONAL COMMENTS

All my work on the genetic code, published here in viXra, contain a common law - the analogy with quantum physics, the "packaging" of energy in the atom and / or filling out the orbitals by electrons. I will give here only two examples. In Note 2, in Figure 1, shown is the filling of decimal positions in the decimal numeral system (doublets $079 / 179$ and $025 / 125$ ), with the change of the unit, in one of the positions, analog to the filling of atomic orbitals with one by one of electrons. Another example is an analogy with the quantum of energy in the atom; there are quanta of energy, and here a "quantity" of number of molecules, atoms, nucleons, or other particles. Thus, the quantum of "79" is found again, and twice, in Table 2 of the paper "On the completeness of genetic code", Part IV. (The first case is: amino acids encoded with four or three codons: LVSPTAGR $+\mathrm{I}=79$ atoms; and for the second case we refer the reader to view directly in the said Table.) However, we also find the quantum of "125" ["On the completeness of genetic code", Part V, Table 2. (The first case: the amino acids encoded by the two or one codons: FYHQNKDEC + MW $=125$ atoms; and for the second case we also refer the reader to directly view in the said Table).]

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## 13.

## Golden and Harmonic Mean in the Genetic Code (Shorter Version)

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Life Sciences Biochemistry, Biophysics, and Structural Biology
In previous two works [1], [2] we have shown the determination of genetic code by golden and harmonic mean within standard Genetic Code Table, i.e. nucleotide triplet table, whereas in this paper we show the same determination through a specific connection between two tables - of nucleotide doublets Table and triplets Table, over polarity of amino acids, measured by Cloister energy. [This is the version of the article published in Proceedings of the 2nd International Conference "Theoretical Approaches to BioInformation Systems" (TABIS.2013), September 17-22, 2013, Belgrade, Serbia.]

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Biochemistry, biophysics, cdl text preprint cdl.cos, life sciences, cloister energy, genetic code, golden mean.

# Golden and Harmonic Mean in the Genetic Code 

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#### Abstract

In previous two works [1], [2] we have shown the determination of genetic code by golden and harmonic mean within standard Genetic Code Table (GCT), i.e. nucleotide triplet table, whereas in this paper we show the same determination through a specific connection between two tables - of nucleotide doublets Table (DT) and triplets Table (TT), over polarity of amino acids, measured by Cloister energy.


## 1. Introduction

In a previous work we have shown that golden mean is a characteristic determinant of the genetic code (GC), regarding on the codons binary tree, 0-63 [1]. In a second one we showed a splitting of Genetic Code Table (GCT) into three equal and significant parts, using the harmonic mean $[\mathrm{H}(\mathrm{a}, \mathrm{b})=2 \mathrm{ab} /(\mathrm{a}+\mathrm{b}) ; a=63, b=31.5])$ [2]. In this paper, however, we will show that a specific unity of golden mean and harmonic mean appears to be the determinant of Rumer's Table of 16 nucleotide doublets [3] (Tables $1 \& 2$ in relation to Tables $3 \& 4$ ).

| 01. G | GG (6) | 02. F | UU (4) | 03. L | 01. G | GG (6) | 02. F | UU (4) | 03. L |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 04. P | CC (6) | 05. N | AA (4) | 06. K | 04. P | CC (6) | 05. N | AA (4) | 06. K |
| 07. R | CG (6) | 08.1 | AU (4) | 09. M | 07. A | GC (6) | 08. Y | UA (4) | 09. St. |
| 10. A | GC (6) | 11. Y | UA (4) | 12. St. | 10. R | CG (6) | 11.1 | AU (4) | 12. M |
| 13. ${ }^{\text {16 }}$ | AC (5) | 14. H | CA (5) | 15. Q | 13. V | GU (5) | 14. C | UG (5) | 15. W |
| 16. V | GU (5) | 17. C | UG (5) | 18. W | 16. T | AC (5) | 17. H | CA (5) | 18. Q |
| 19. S | UC (5) | 20. D | GA (5) | 21. E | 19.L | CU (5) | 20. S | AG (5) | 21. R |
| 22. L | CU (5) | 23. S | AG (5) | 24. R | 22. S | UC (5) | 23. D | GA (5) | 24. E |

Table 1. Rumer's Table of nucleotide doublets
Table 2. The modified Rumer's Table
As we have shown, golden mean "falls" between the 38th and 39th codon (38. CAA, 39. CAG), which code for glutamine (Q), a more complex of only two amide amino acids (AAs); two codons, adjacent to the codons (40.UGU, 41.UGC), which code for one of the only two sulfur AAs, cysteine (C). This "harmonization" of diversity is increased by the harmonic mean, in position 42 on the sequence $0-63$. The harmonization extends further to "stop" codon (42.UGA) and to codon (43.UGG) that codes for the most complex AA, tryptophan (W). (The "42" as ending position on the "Golden route" - with Fibonacci numbers - on the Farey tree, corresponding with six-bit GC binary tree [1].)

On the other side, the splitting of GCT into three parts through harmonic mean [2] makes that AAs are distinguished on the basis of the validity of the evident regularities of key factors, such as polarity, hydrophobicity and enzyme-mediated AAs classification (with parameter values as in Table 2.1 in Rakočević, 2013).

## 2. A new rearrangement of nucleotide doublet Table

With a minimal modification of Rumer's nucleotide doublets Table (DT) follows the next result: if at the beginning of first sub-system, ${ }^{1}$ with $6 / 4$ hydrogen bonds, are GG/UU doublets, chemical reasons require GU/UG doublets at the beginning of the second sub-system, with $5 / 5$ hydrogen bonds, instead of AC/CA as it is in Table 1. From the same reasons, we have the changes: $\mathrm{CG} / \mathrm{GC} \& \mathrm{UC} / \mathrm{CU}$ on the left and AU/UA \& GA/AG on the right. With the four first doublets we have four outer squares, i.e. codon families ( $\mathrm{n}_{1}=\mathrm{GG}, \mathrm{UU}, \mathrm{GU}, \mathrm{UG}$ ) in nucleotide triplets Table (TT) which code for nonpolar AAs; the four second doublets give four inner codon families ( $\mathrm{n}_{2}=\mathrm{CC}, \mathrm{AA}, \mathrm{AC}, \mathrm{CA}$ ), which code for polar AAs (Table 3). ${ }^{2}$ With the four third ( $n_{3}=\mathrm{GC}, \mathrm{CU} ; \mathrm{UA}, \mathrm{AG}$ ) and four fourth ( $\mathrm{n}_{4}=\mathrm{CG}, \mathrm{UC} ; A U, G A$ ) doublets are chosen eight intermediate codon families, the first three code for nonpolar AAs [(CU,AU,GC) $\rightarrow$ (L, I, M, A)] and the second five for polar AAs [(UC,UA,CG, AG, GA) $\rightarrow(S, Y, R, D, E)]$ (Table 4). As we see the polar/nonpolar distribution of squares in Table 3 is realized as $4 \pm 0$ and in Table 4 as $4 \pm 1$. By this, the polarity/nonpolarity is taken after cloister energy as in Ref. [4]. ${ }^{3}$

| 1st | 2nd letter |  |  |  |  |  | 3rd |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | U | C | A |  | G |  |  |
| U | UUU | UCU | UAU |  | UGU |  | $U$ |
|  | UUC F | UCC | UAC | Y | UGC | C | C |
|  | UUA | UCA S | UAA |  | UGA | CT | A |
|  | UUG L | UCG | UAG | CT | UGG | W | G |
| C | CUU | CCU | CAU |  | CGU |  | $U$ |
|  | CUC | CCC | CAC | H | CGC |  | $C$ |
|  | CUA L | CCA $\mathbf{P}$ | CAA |  | CGA | R | A |
|  | CUG | CCG | CAG | Q | CGG |  | G |
| A | AUU | ACU | AAU |  | AGU |  | $U$ |
|  | AUC I | ACC T | AAC | N | AGC | S | C |
|  | AUA M | ACA 1 | AAA |  | AGA |  | A |
|  | AUG | ACG | AAG | K | AGG | R | G |
| G | GUU | GCU | GAU |  | GGU |  | $U$ |
|  | GUC v | GCC A | GAC |  | GGC | G | C |
|  | GUA | GCA A | GAA |  | GGA | G | A |
|  | GUG | GCG | GAG | E | GGG |  | G |

Table 3. Distributions of AAs after nucleotide doublets presented in Table 2: Four squares with dark tones (outer) contain four first doublets from Table 2 and four light (inner) contain four second doublets. In amino acids (within their side chains) at outer/inner areas there are 369/369 nucleons and 61/61 atoms, respectively. All AAs in outer area are nonpolar whereas those in inner area are polar, measured by cloister energy.

[^19]| 1st | 2nd letter |  |  |  | 3rd |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  | U | C | A | G |  |
| U | , UUU | UCU | UAU | UGU | $U$ |
|  | UUC F | UCC | UAC Y | UGC C | $C$ |
|  | UUA | UCA S | UAA | UGA CT | A |
|  | UUG `冫 & UCG & UAG CT & UGG W & \(G\) \\ \hline \multirow{5}{*}{C} & CUU & `CU | CAU | CGU | $U$ |  |
|  | CUC | CCC | CAC H | CGC | $C$ |
|  | CUA | CCA`,\(~ \mathbf{P}\) & CAA & CGA R & A \\ \hline & CUG & CCG & CAG \(\mathbf{Q}\) & CGG & \(G\) \\ \hline & & & \(\because\) & & \\ \hline \multirow{4}{*}{A} & AUU & ACU & AȦU & AGU & \(U\) \\ \hline & AUC & ACC T & AAC`, N | AGC | C |  |
|  | AUA M | ACA 1 | AAA | AGA | A |
|  | AUG M | ACG | AAG K | AGG R | $G$ |
| G | GUU | GCU | GAU D | GGU | $U$ |
|  | GUC V | GCC | GAC D | GGC, , | $C$ |
|  | GUA | GCA A | GAA | GGA $\because$, | A |
|  | GUG | GCG | GAG | GGG $\quad$, | $G$ |

Table 4. Distributions of AAs after nucleotide doublets presented in Table 2: Four squares with dark tones contain four third doublets from Table 2 and four light contain four fourth doublets; two and two doublets on the right, and two and two on the left. In amino acids (within their side chains), in right/left areas there are 369/369-33 nucleons and 59/58 atoms, respectively. All AAs on the right together with D \& E from the left are polar and other on the left are nonpolar. Because the balance is realized in relation to diagonal and not in relation to the type of nucleotide doublets (third or fourth) it follows that positions $3 \& 4$ in DT are not invariant, but only positions $1 \& 2$ as it is shown in Table 3 .

## 3. Particles number balances through polarity

Distinctions through polarity, presented in Tables $3 \& 4$, are followed by the balance of the number of nucleons and atoms. Irrespectively of the Table of nucleotide doublets, V. shCherbak showed [Ref. 10, Fig. 10, p. 173] that it makes sense to display the Table of nucleotide triplets (TT) exactly as here in Tables $3 \& 4$ : four squares at the corners and four squares in the center as in Table 3; then, eight squares in middle, i.e. in "between" positions, as in Table 4. After shCherbak's view, the balance of the number of nucleons is the next: AAs in four squares in the corners of TT as well as AAs in four squares in the center of TT have 369 nucleons $[(\mathrm{F} 91+\mathrm{L} 57+\mathrm{V} 43+\mathrm{G} 01+\mathrm{W} 130+\mathrm{C} 47=369) ;(\mathrm{P} 41+\mathrm{T} 45+\mathrm{K} 72+\mathrm{N} 58+$ $\mathrm{Q} 72+\mathrm{H} 81=369)$ ].

To this $s h C h e r b a k$ 's insight, we now add: the same quantity give the AAs in right site of TT; the right site in relation to the diagonal $\mathrm{F}-\mathrm{G}^{4}$ in $\mathrm{TT}(\mathrm{S} 31+\mathrm{Y} 107+\mathrm{R} 100+\mathrm{S} 31+\mathrm{R} 100=369)$. On the left side of the diagonal there are 336 nucleons (L57+I57+M75+A15+D59+E73=336), what means 33 nucleons less, in relation to 369 . With this emergence of difference of " 33 " on the scene appears a specific self-similarity because the number 33 is an important determinant of the number of atoms in the rows and columns of GCT, i.e. of TT. ${ }^{5}$

[^20]To this self-similarity determination by nucleon number we now also add the selfsimilarity determination by atom number: AAs in four squares in the corners as well as in the center of TT have 61 atoms in amino acid side chains [(F14+L13+V10+G01+W18+C05=61); $(\mathrm{P} 08+\mathrm{T} 08+\mathrm{K} 15+\mathrm{N} 08+\mathrm{Q} 11+\mathrm{H} 11=61)]$. In relation to the diagonal $\mathrm{F}-\mathrm{G}$, in TT, there are 58 and 59 atoms, respectively; on the left: $\mathrm{L} 13+\mathrm{I} 13+\mathrm{M} 11+\mathrm{A} 04+\mathrm{D} 07+\mathrm{E} 10=58$, and on the right: $\mathrm{S} 05+\mathrm{Y} 15+\mathrm{R} 17+\mathrm{S} 05+\mathrm{R} 17=59$. These quantities (58 and 59) are the same as the quantities of hydrogen atoms in Sukhodolets' system (what is a further self-similarity): 58 in two inner and 59 hydrogen atoms in two outer rows [Ref. 11, Tab. 7, p. 830], [12]. (Notice that $58+59=$ 117 is total number of hydrogen atoms in 20 canonical AAs of GC, within their side chains, what is the self-similarity once more.)

## 4. Determination through "golden whole"

The splitting of GCT (i.e. TT) into 4 outer, 4 inner and 8 intermediate squares, corresponding to responsible nucleotide doublets, leads us to the following conclusion. Within the set of all $n$-gons, where $n$ is even number, the case $n=4$ is only and one case where harmonic mean of "golden whole" $\left(n^{2}-n\right)^{6}$ and its half [ $\left(n^{2}-n\right) / 2$ ] equals $2 n$, and $n^{2}-n=\mathbf{3} n$. So, in this case we have that the ratio $\mathbf{2 : 3}$ appears to be the harmonic mean within the harmonic mean, and, by this, the sequence $\mathrm{n}_{1}-\left(\mathrm{n}_{3}\right.$ or $\left.\mathrm{n}_{4}\right)-\mathrm{n}_{2}$ corresponds with the Cantorian triadic set. Moreover, such a harmonic mean appears to be corresponding with the number of "small squares" within intermediate space in form of only one "ring" as it follows: [(2 + 2) + $(4 \times \underline{0})=4] ;[(\mathbf{4}+\mathbf{4})+(\mathbf{8} \times \underline{\mathbf{1}})=\mathbf{1 6}] ;[(6+6)+(12 \times \underline{2})=36] ;[(8+8)+(16 \times \underline{3})=64]$ etc. As it is self-evident, the symmetrical "out - middle- in" arrangement (1:1:1 of rings) is not possible for $n \neq 4$, neither for $n$-gons nor for $n$-letter alphabets. At the same time here is a selfsimilarity expressed through the number of "small squares" in the sequence $\mathrm{n}_{1}-\left(\mathrm{n}_{3}\right.$ or $\left.\mathrm{n}_{4}\right)-\mathrm{n}_{2}$ and the number of codons within them: four squares per $n_{1}, n_{2}, n_{3}, n_{4}$, each square per four codons. Moreover, there is a self-similarity between golden and harmonic mean versus 4letter alphabet: $\mathbf{1} n$ as 1 square ( 1 nucleotide doublet), $\mathbf{2} n$ as harmonic mean (in the sense above said), $3 n$ as golden whole and $\mathbf{4} n$ as the sum $n_{1}+n_{2}+n_{3}+n_{4}$; all these versus 1 letter of alphabet (as letter minimum), $\underline{2}$ letters as word root (nucleotide doublet), $\underline{3}$ letters as 3 -letter word (codon) and 4 letters as letter maximum within alphabet. ${ }^{7}$

## 5. Concluding remark

With the title of the paper is given a working hypothesis that the golden mean (GM) and harmonic mean (HM) are determinants of the genetic code. The findings presented by four illustrations show that this hypothesis is confirmed. However, unlike the previous access to

[^21]the same determination, it refers not only the analysis of the nucleotide triplet Table, but rather refers to the two tables - Table of doublets (DT) and Table of triplets (TT). In fact, it is precisely presented that these tables are unique in terms of determination just over GM and HM.

It is expected that all these uniqueness correspond to the same, or similar uniqueness, found by other authors ([16], [17], [18], [19]), what in future researches should be checked.

However, presented facts are such that ones reaffirm the other and vice versa. All together, they favor the recognition that the chemical reactions that determine the GC are not only the reactions in a "test tube", but these reactions are associated with a specific balance of the number of particles (atoms and nucleons); balance, determinated by unique arithmetic and algebraic regularities and expressed in the form of specific (nonfractal) self-similarity ("a harmonized chemistry"). From this it follows further that presented facts also support the hypothesis that the genetic code was from very begining, in prebiotic times and conditions, a complete code [10], [15]. On the other hand, the knowledge that "the chemistry of living" is actually a harmonized chemistry requires great care in medicine, agriculture and natural environment, taking into account the fact that this harmonization is strictly immanent to the living as such, mediated by genetic code as such.

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## 14.

## Golden and Harmonic Mean in the Genetic Code (Expanded Version)

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Life Sciences Biology
In previous two works (Rakočević, 1998; 2013), we have shown the determination of genetic code by golden and harmonic mean within standard Genetic Code Table, i.e. nucleotide triplet table, whereas in this paper we show the same determination through a specific connection between two tables - of nucleotide doublets Table and triplets Table, over polarity of amino acids, measured by Cloister energy in general, and by hydropathy and polar requirement, partialy. [This is the expanded version of the article published in Proceedings of the 2nd International Conference "Theoretical Approaches to BioInformation Systems" (TABIS.2013), September 17-22, 2013, Belgrade, Serbia. That first version is also stored, as Version 1, in OSF Preprints.]

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Cloister energy genetic code, golden mean, harmonic mean, hydropathy, mendeleev system, polar requirement, protein amino acids.

# Golden and Harmonic Mean in the Genetic Code 

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#### Abstract

In previous two works (Rakočević, 1998; 2013), we have shown the determination of genetic code by golden and harmonic mean within standard Genetic Code Table, i.e. nucleotide triplet table, whereas in this paper we show the same determination through a specific connection between two tables - of nucleotide doublets Table and triplets Table, over polarity of amino acids, measured by Cloister energy in general, and by hydropathy and polar requirement, partialy. [This is the expanded version of the article published in Proceedings of the 2nd International Conference "Theoretical Approaches to BioInformation Systems" (TABIS.2013), September 17-22, 2013, Belgrade, Serbia. That first version is also stored, as Version 1, in OSF Preprints.]


Key words: Cloister Energy; Hydropathy; Polar requirement; Golden mean; Harmonic Mean; Genetic Code; Protein amino acids; Mendeleev system.

## 1. Introduction

In a previous work we have shown that golden mean is a characteristic determinant of the genetic code (GC), regarding on the codons binary tree, 0-63 (Rakočević, 1998). In a second one we showed a splitting of Genetic Code Table (GCT) into three equal and significant parts, using the harmonic mean $[\mathrm{H}(\mathrm{a}, \mathrm{b})=2 \mathrm{ab} /(\mathrm{a}+\mathrm{b}) ; a=63, b=31.5]$ ) (Rakočević, 2013). In this paper, however, we will show that a specific unity of golden mean and harmonic mean appears to be the determinant of Rumer's Table of 16 nucleotide doublets (Rumer, 1966) (Tables $1 \& 2$ in relation to Tables $3 \& 4$ ).

| 01. G | GG (6) | 02. F | UU (4) | 03. L |
| :--- | :--- | :---: | :---: | :---: |
| 04. P | CC (6) | 05. N | AA (4) | 06. K |
| 07. R | CG (6) | 08. I | AU (4) | 09. M |
| 10. A | GC (6) | 11. Y | UA (4) | 12. St. |
| 13. T | AC (5) | 14. H | CA (5) | 15. Q |
| 16. V | GU (5) | 17. C | UG (5) | 18. W |
| 19. S | UC (5) | 20. D | GA (5) | 21. E |
| 22. L | CU (5) | 23. S | AG (5) | 24. R |


| 01. G | GG (6) | 02. F | UU (4) | 03. L |
| :---: | :---: | :---: | :---: | :---: |
| 04. P | CC (6) | 05. N | AA (4) | 06. K |
| 07. A | GC (6) | 08. Y | UA (4) | 09. St. |
| 10. R | CG (6) | 11. 1 | AU (4) | 12. M |
| 13. V | GU (5) | 14. C | UG (5) | 15. W |
| 16. T | AC (5) | 17. H | CA (5) | 18. Q |
| 19.L | CU (5) | 20. S | AG (5) | 21. $R$ |
| 22. S | UC (5) | 23. D | GA (5) | 24. E |

Table 2. The modified Rumer's Table
As we have shown, golden mean "falls" between the 38th and 39th codon (38. CAA, 39. CAG), which code for glutamine ( Q ), a more complex of only two amide amino acids (AAs); two codons, adjacent to the codons (40.UGU, 41.UGC), which code for one of the only two sulfur AAs, cysteine (C). This "harmonization" of diversity is increased by the harmonic mean, in position 42 on the sequence $0-63$. The harmonization extends further to "stop" codon (42.UGA) and to codon (43.UGG) that codes for the most complex AA, tryptophan (W). [The "42" as ending position on the "Golden route" - with Fibonacci numbers - on the Farey tree, corresponding with six-bit GC binary tree (Rakočević, 1998).]

On the other side, the splitting of GCT into three parts through harmonic mean (Rakočević, 2013) makes that AAs are distinguished on the basis of the validity of the evident regularities of key factors, such as polarity, hydrophobicity and enzyme-mediated AAs classification (with parameter values as in Table 5) ( Table 2.1 in Rakočević, 2013).

## 2. A new rearrangement of nucleotide doublet Table

With a minimal modification of Rumer's nucleotide doublets Table (DT) follows the next result: if at the beginning of first sub-system, ${ }^{1}$ with $6 / 4$ hydrogen bonds, are GG/UU doublets, chemical reasons require GU/UG doublets at the beginning of the second sub-system, with $5 / 5$ hydrogen bonds, instead of AC/CA. From the same reasons, we have the changes: CG/GC \& $\mathrm{UC} / \mathrm{CU}$ on the left and AU/UA \& GA/AG on the right. With the four first doublets we have four outer squares, i.e. codon families ( $\mathrm{n}_{1}=\{\mathrm{GG}, \mathrm{UU}, \mathrm{GU}, \mathrm{UG}\}$ ) in nucleotide triplets Table (TT) which code for nonpolar AAs; the four second doublets give four inner codon families $\left(n_{2}=\{C C, A A, A C, C A\}\right)$, which code for polar AAs (Table 3). ${ }^{2}$ With the four third $\left(n_{3}=\{G C\right.$, CU; UA, AG $\}$ ) and four fourth ( $\mathrm{n}_{4}=\{\mathrm{CG}, \mathrm{UC} ; \mathrm{AU}, \mathrm{GA}\}$ ) doublets are chosen eight intermediate codon families, the first three code for nonpolar AAs [(CU, AU, GC) $\rightarrow(\mathrm{L}, \mathrm{I}, \mathrm{M}$, A)] and the second five for polar AAs [(UC,UA,CG, AG, GA) $\rightarrow(\mathrm{S}, \mathrm{Y}, \mathrm{R}, \mathrm{D}, \mathrm{E})]$ (Table 4). As we see the polar/nonpolar distribution of squares in Table 3 is realized as $4 \pm 0$ and in Table 4 as $4 \pm 1$. By this, the polarity/nonpolarity is taken after cloister energy ${ }^{3}$ (Table 5 ) as in $R$. Swanson's article (Swanson, 1984). ${ }^{4}$

| 1st | 2nd letter |  |  |  |  |  | 3rd |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | U | C | A |  | G |  |  |
| U | UUU | UCU | UAU |  | UGU |  | $U$ |
|  | UUC F | UCC | UAC | Y | UGC | C | C |
|  | UUA | UCA S | UAA |  | UGA | CT | $A$ |
|  | UUG L | UCG | UAG | CT | UGG | W | G |
| C | CUU | CCU | CAU |  | CGU |  | $U$ |
|  | CUC | CCC | CAC | H | CGC |  | C |
|  | CUA L | CCA $\mathbf{P}$ | CAA |  | CGA | R | A |
|  | CUG | CCG | CAG | Q | CGG |  | G |
| A | AUU | ACU | AAU |  | AGU |  | $U$ |
|  | AUC | ACC | AAC | N | AGC | S | C |
|  | AUA M | ACA ${ }^{\text {T }}$ | AAA |  | AGA |  | A |
|  | AUG | ACG | AAG | K | AGG | R | $G$ |
| G | GUU | GCU | GAU |  | GGU |  | $U$ |
|  | GUC v | GCC A | GAC |  | GGC |  | C |
|  | GUA | GCA A | GAA |  | GGA | G | $A$ |
|  | GUG | GCG | GAG | E | GGG |  | ${ }_{G}$ |

Table 3. Distributions of AAs after nucleotide doublets presented in Table 2. Four squares with dark tones (outer) contain four first doublets from Table 2 and four light (inner) contain four second doublets. In amino acids (within their side chains) at outer/inner areas there are $369 / 369$ nucleons and $61 / 61$ atoms, respectively. All AAs in outer area are nonpolar whereas those in inner area are polar, measured by cloister energy, except histidine that is neutral, but it is polar from the aspect of hydropathy.

[^22]| 1st | 2nd letter |  |  |  | 3rd |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  | U | C | A | G |  |
| U | UUU | UCU | UAU | UGU | $U$ |
|  | CUC F | UCC | UAC Y | UGC C | C |
|  | UUA | UCA S | UAA | UGA CT | A |
|  | UUG ` '冫' & UCG & UAG CT & UGG W & \(G\) \\ \hline \multirow{5}{*}{C} & CUU & ©CU & CAU & CGU & \(U\) \\ \hline & \multirow{3}{*}{L} & CCC & CAC H & CGC & C \\ \hline & & CCA` ${ }^{\text {P }}$ | CAA | CGA R | A |  |
|  |  | CCG | CAG $\mathbf{Q}$ | CGG | $G$ |
|  |  |  | $\because$ Q |  |  |
| A | AUU | ACU | AȦU | AGU | $U$ |
|  | AUC | ACC | AAC , N | AGC | C |
|  | AUA m | ACA | AAA | AGA | A |
|  | AUG M | ACG | AAG K `& AGG & \(G\) \\ \hline \multirow{4}{*}{G} & GUU & GCU & GAU & GGU & \(U\) \\ \hline & GUC v & GCC & GAC & GG', , & C \\ \hline & GUA & GCA A & GAA & GGA` | A |  |
|  | GUG | GCG | GAG E | GGG | G |

Table 4. Distributions of AAs after nucleotide doublets presented in Table 2. Four squares with dark tones contain four third doublets from Table 2 and four light contain four fourth doublets; two and two doublets on the right, and two and two on the left. In amino acids (within their side chains), in right/left areas there are 369/369-33 nucleons and 59/58 atoms, respectively. All AAs on the right together with D \& E from the left are polar and other on the left are nonpolar. Because the balance is realized in relation to diagonal and not in relation to the type of nucleotide doublets (third or fourth) it follows that positions $3 \& 4$ in DT are not invariant, but only positions $1 \& 2$ as it is shown in Table 3.

## 3. Particles number balances through polarity

Distinctions through polarity, presented in Tables $3 \& 4$, are followed by the balance of the number of nucleons and atoms. Irrespectively of the Table of nucleotide doublets, V. shCherbak showed (Shcherbak, 2008, Fig. 10, p. 173] that it makes sense to display the Table of nucleotide triplets (TT) exactly as in Tables $3 \& 4$ : four squares at the corners and four squares in the center as in Table 3; then, eight squares in middle, i.e. in "between" positions, as in Table 4. After $s h$ Cherbak's view, the balance of the number of nucleons is the next: AAs in four squares in the corners of TT as well as AAs in four squares in the center of TT have 369 nucleons [(F-91 + L-57 + V-43 + G-01 + W-130 + C-47 $=369)$; (P-41 + T-45 + K-72 + $\mathrm{N}-58+\mathrm{Q}-72+\mathrm{H}-81=369)]$.

To this $s h$ Cherbak's insight, we now add: the same quantity give the AAs in right site of TT; the right site in relation to the diagonal $\mathrm{F}-\mathrm{G}^{5}$ in TT $(\mathrm{S} 31+\mathrm{Y} 107+\mathrm{R} 100+\mathrm{S} 31+\mathrm{R} 100=369)$. On the left side of the diagonal there are 336 nucleons (L57+I57+M75+A15+D59+E73=336), what means 33 nucleons less, in relation to 369 . With this emergence of difference of "33" on

[^23]the scene appears a specific self-similarity ${ }^{6}$ because the number 33 is an important determinant of the number of atoms in the rows and columns of GCT, i.e. of TT. ${ }^{7}$

To this self-similarity determination by nucleon number we now also add the selfsimilarity determination by atom number: AAs in four squares in the corners as well as in the center of TT have 61 atoms in amino acid side chains $[(\mathrm{F} 14+\mathrm{L} 13+\mathrm{V} 10+\mathrm{G} 01+\mathrm{W} 18+\mathrm{C} 05=61)$; $(\mathrm{P} 08+\mathrm{T} 08+\mathrm{K} 15+\mathrm{N} 08+\mathrm{Q} 11+\mathrm{H} 11=61)]$. In relation to the diagonal $\mathrm{F}-\mathrm{G}$, in TT , there are 58 and 59 atoms, respectively; on the left: $\mathrm{L} 13+\mathrm{I} 13+\mathrm{M} 11+\mathrm{A} 04+\mathrm{D} 07+\mathrm{E} 10=58$, and on the right: $\mathrm{S} 05+\mathrm{Y} 15+\mathrm{R} 17+\mathrm{S} 05+\mathrm{R} 17=59$. These quantities ( 58 and 59) are the same as the quantities of hydrogen atoms in Sukhodolets' system (what is a further self-similarity): 58 in two inner and 59 hydrogen atoms in two outer rows (Rakočević, 2011, Tab. 7, p. 830; Sukhodolets, 1985). (Notice that $58+59=117$ is total number of hydrogen atoms in 20 canonical AAs of GC, within their side chain, what is the self-similarity once more.)

| h | + | + | + | + | + | + | + | + | - | + |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | 0.825 | 0.943 | 0.680 | 0.043 | 0.251 | 0.738 | 0.943 | 0.880 | 0.000 | 0.878 |
| CE | - | - | - | + | + | - | - | + | + | - |
|  | -0.52 | -0.54 | -0.73 | +0.71 | +0.91 | -0.57 | -0.56 | +0.42 | +0.87 | -0.25 |
| HP | + | + | + | - | - | + | + | - | - | + |
|  | +4.2 | +3.8 | +2.5 | -3.5 | -3.5 | +1.9 | +4.5 | -1.3 | -4.5 | -0.9 |
| I | $\mathrm{V}_{10}$ | $\mathrm{~L}_{13}$ | $\mathrm{C}_{05}$ | $\mathrm{E}_{10}$ | $\mathrm{Q}_{11}$ | $\mathrm{M}_{11}$ | $\mathrm{I}_{13}$ | $\mathrm{Y}_{15}$ | $\mathrm{R}_{17}$ | $\mathrm{~W}_{18}$ |
| II | $\mathrm{G}_{01}$ | $\mathrm{~A}_{04}$ | $\mathrm{~S}_{05}$ | $\mathrm{D}_{07}$ | $\mathrm{~N}_{08}$ | $\mathrm{~T}_{08}$ | $\mathrm{P}_{08}$ | $\mathrm{H}_{11}$ | $\mathrm{~F}_{14}$ | $\mathrm{~K}_{15}$ |
| HP | -0.4 | +1.8 | -0.8 | -3.5 | -3.5 | -0.7 | -1.6 | -3.2 | +2.8 | -3.9 |
|  | - | - | - | - | - | - | - | - | + | - |
| CEE | -0.16 | -0.09 | +0.24 | +0.69 | +0.52 | +0.27 | +0.46 | $\pm 0.00$ | -0.56 | +1.46 |
|  | + | + | + | - | - | + | + | - | - | + |
| h | 0.501 | 0.616 | 0.359 | 0.028 | 0.236 | 0.450 | 0.711 | 0.165 | $\mathbf{1 . 0 0 0}$ | 0.283 |

Table 5. Two classes of amino acids handled by two classes of enzymes aminoacyl-tRNA synthetases. The ordering after class II; the pairing after (Rakočević, 1998, Survey 2.2, p. 289). Class I contains larger amino acids (larger within the pairs), all handled by class I of enzymes. Class II contains smaller amino acids, all handled by class II of synthetases. Within the rows the given values for the parameters are the following: hydrophobicity (h) on a natural scale (0-1) as in Blac and Mould, 2004, and in Chechetkin and Lobzin, 2011; cloister energy, CE (Swanson, 1984) and hidropathy index, HP (Kyte and Doolittle, 1982). The designations " + " and " - " above/below for the number record - more/less within the amino acid pair, respectively. Within the set of " 23 " AAs, on odd/even pairs, there are $114 / 125$ atoms (with the difference of 11 atoms ), exactly as in Table A.4, in Appendix A, what means a self-similarity [(VG $+\mathrm{CS}_{2}+\mathrm{QN}+\mathrm{IP}+$ $\left.\left.\mathrm{R}_{2} \mathrm{~F}=114\right) ;\left(\mathrm{L}_{2} \mathrm{~A}+\mathrm{ED}+\mathrm{MT}+\mathrm{YH}+\mathrm{WK}=125\right)\right]$. On the other hand, within first five above there are 62 atoms (Leucine two times in the sum) and within second five 91 of atoms (Arginine two times in the sum);

[^24]below: 30/56 respectively (Serine two times in the sum); then, with a crossing, there is a balance: $62+56=$ $119-1$ and $30+91=120+1$, what is a change for $\pm 1$ in relation to result 119/120 in Tables A. 1, A. 2 and A. 3 in Appendix A. Regarding to the set of 20 AAs, instead 114/125 there are $92 / 112$ atoms respectively, what also means a balance: $102 \pm 10$.

| $\left\lvert\, \begin{array}{llllllll}G & 01 & \mathrm{~S} & 05 & \mathrm{Y} & 15 & \mathrm{~W} & 18 \\ A & 04 & \mathrm{D} & 07 & \mathrm{M} & 11 & \mathrm{R} & 17\end{array}\right.$ | Table 6. The Mendeleevian type of arrangement o AAs molecules (MAM) which follows from fou |
| :---: | :---: |
| C 05 T 08 E 10 F 14 | W, H), (R, K, Q, N, E, D, T, S)] (Ref. 14, Figs 2 |
| N 08 Q $11 \times 10 \mathrm{l}$ \| 13 | Within first two and last two columns: $1 \times 68$ and |
| $\begin{array}{lllllllllll}\text { P } & 08 & \text { H } & 11 & \text { L } & 13 & \text { K } & 15\end{array}$ | 68 atoms, respectively. Within two inner and two columns: $102 \pm 1$ of atoms. All amino acid sequ |
| $\begin{array}{llll}26 & 42 & 59 & 77\end{array}$ | atoms; all but one, in which $\mathrm{Q}-11$ precedes V - |
| $16 \quad 17 \quad 18$ | ause different stereochemical types |
| $26+42=68 \times 1$ | reochemical type [analogous to the Mendeleev |
| $59+77=68 \times 2$ | ation in which heavier tellurium (127.6) |
| 42-59 + $77=89 \times 2$ | stereochemical types of AAs see in Rakočević and Jokić, 1996.) |


| G 75.07 | S 105.09 | Y 181.19 | W 204.23 | Tab. 7. The same arrangement of AAs as in MAM in Table 6, each AA with its molecule mass. From the aspect of self-similarity it makes sense a comparison this Table (a structure of Mendeleevian type, SMT) with "a specific harmonic structure of genetic code" (SHS) [Ref. 13, Tab. 2, p. 223], especially through amino So, within two odd columns in SHS the sum is $1258.43 \approx 1258$ ( $34 \times 37$ ) and in two even 1479.61 $\approx 1480(40 \times 37)$. On the other hand within two inner columns here in SMT the sum is $1332.25 \approx$ 1332 ( $36 \times 37$ ) and in two outer columns $1405.66 \approx 1406$ (38 x 37). |
| :---: | :---: | :---: | :---: | :---: |
| A 88.09 | D 133.10 | M 149.21 | R 174.20 |  |
| C 121.16 | T 119.12 | E 147.13 | F 165.19 |  |
| N 132.12 | Q 146.15 | V 117.15 | \| 131.18 |  |
| P 115.13 | H 155.16 | L 131.07 | K 146.19 |  |
| 532.57 | 658.62 | 725.86 | 820.99 |  |
| 1258. | 1258 | $(34 \times 37)$ |  |  |
|  | 222 |  |  |  |
| 1479.6 | $\approx 1480$ | $0 \times 37)$ |  |  |
|  | . 04 ~ 2738 | (74 | 7) (2×372) |  |

## 4. Determination through 'golden whole"

The splitting of GCT (i.e. TT) into 4 outer, 4 inner and 8 intermediate squares, corresponding to responsible nucleotide doublets, leads us to the following conclusion. Within the set of all $n$-gons, where $n$ is even number, the case $n=4$ is only and one case where harmonic mean of "golden whole" $\left(n^{2}-n\right)^{8}$ and its half $\left[\left(n^{2}-n\right) / 2\right]$ equals $2 n$, and $n^{2}-n=3 n$.

[^25]So, in this case we have that the ratio $2: 3$ appears to be the harmonic mean within the harmonic mean, and, by this, the sequence " $\mathrm{n}_{1}-\left(\mathrm{n}_{3}\right.$ or $\left.\mathrm{n}_{4}\right)-\mathrm{n}_{2}$ " corresponds with the Cantorian triadic set. Moreover, such a harmonic mean appears to be corresponding with the number of "small squares" within intermediate space in form of only one "ring" as it follows: $[(2+2)+(4 \times \underline{0})=4] ;[(\mathbf{4}+\mathbf{4})+(\mathbf{8} \times \underline{\mathbf{1}})=\mathbf{1 6}] ;[(6+6)+(12 \times \underline{2})=36] ;[(8+8)+(16 \times \underline{3})=$ $64]$ etc. As it is self-evident, the symmetrical "out - middle- in" arrangement (1:1:1 of rings) is not possible for $n \neq 4$, neither for $n$-gons nor for $n$-letter alphabets.

At the same time here is a self-similarity expressed through the number of "small squares" in the sequence " $n_{1}-\left(n_{3}\right.$ or $\left.n_{4}\right)-n_{2}$ " and the number of codons within them: four squares per $\mathrm{n}_{1}, \mathrm{n}_{2}, \mathrm{n}_{3}, \mathrm{n}_{4}$, each square per four codons. Moreover, there is a self-similarity between golden and harmonic mean versus 4 -letter alphabet: $1 n$ as 1 square ( 1 nucleotide doublet), $2 n$ as harmonic mean (in the sense said above.), $3 n$ as golden whole and $4 n$ as the sum $n_{1}+n_{2}+n_{3}+$ $n_{4}$; all these versus 1 letter of alphabet (as letter minimum), 2 letters as word root (nucleotide doublet), 3 letters as 3 -letter word (codon) and 4 letters as letter maximum within alphabet. ${ }^{9}$

## 5. A possible testing of polarity

Regularities presented above require a testing of polarity parameters, primarily the cloister energy, as follows. In previous papers we have come to a structure of system of the twenty canonical amino acids, which structure is of a Mendeleevian type (Mendeleevian Arrangement of Molecules, MAM): sequences of molecules in rows are given by the number of their atoms (Table 6 in relation to Table 7). ${ }^{10}$ We start from four diversity types of AAs, first time presented in (Kyte and Doolittle, 1982): [I (G-P), II (A-L, V-I), III (C-M, F-Y, WH ), IV (R-K, Q-N, E-D, T-S) ${ }^{11}$ and through some strict symmetry relations we came to Table 6 [Ref. 14, Figs $2 \& 3$ ]. The number of atoms per columns ( $26,42,59,77$ ) is identical with quantities which follow from a strict arithmetical arrangement - by rows and columns of natural number series (Mendeleevian Arrangement of Numbers, MAN): $1^{\text {st }}$ row: 01, 02, $03, \ldots, \underline{11} ; 2^{\text {nd }}$ row: $\mathbf{1 2}, 13,14, \ldots, \underline{22} ; 3^{\text {rd }}$ row: $\mathbf{2 3}, 24,25, \ldots, \underline{33} ; \ldots ; 9^{\text {th }}$ row: $\mathbf{8 9}, 90,91, \ldots$, 99 [Ref. 14, Table 4]. But, as a noteworthy is the fact that all these quantities also follow from a unique algorithm, presented here in Figure 1. If we take this algorithm as an input algorithm, then from it follows an output algorithm (Figure 2). (Both algorithms as initial ones, IA.) And now, a fascinate result: all essential quantities from output algorithm appear to be key determinants of a display of AAs through their polarity, measured by cloister energy (Figure 3). Unexpectedly, the self-similarity between two disparate systems?!

[^26]| x |  |  |
| :---: | :---: | :---: |
| $x+(x-10)$ |  |  |
| $x+(x-10)+(x-10)+1$ |  |  |
| $x+[(x-10)+(x-10)+1]+(x-10)+2$ |  |  |
| (1) $x$ | 26 |  |
| (2) $2 x-10$ | 42 |  |
| (3) $3 x-19$ | 59 |  |
| (4) $4 x-27$ | 77 |  |
| * |  |  |
| $2(x+(2 x-10))=(3 x-19)+(4 x-27)$ |  |  |
| $x=26$ |  |  |

Figure 1. Algorithm of Atom Number Uniqueness (ANU), expressed in Mendeleevian arrangement of AAs molecules (MAM) in Table 6.

| $26+42+59+77=204$ | $68+68+68$ | ABP |
| :---: | :---: | :---: |
| $(1 \times 68)+(2 \times 68)$ | $\begin{aligned} & 69+68+\underset{(-10)}{69}+\underset{(-10)}{67} \end{aligned}$ |  |
| $16+17+18=204: 4$ | $89+58+57$ | $\begin{aligned} & 57+32=89 \\ & 58+31=89 \end{aligned}$ |
| $26+89+89=204$ | 32 | $\begin{array}{ll} -26 & 26 \\ (89)(89) \end{array}$ |

Figure 2. Algorithm of Balance through Polarity (ABP): all quantities are in relations to results presented in Table 6 and Figure 3. [One cam notice that reciprocal value of number 89 is unique because it corresponds to Fibonacci series $(1: 89=0.011235 \ldots$..]


Figure 3.1. Distributions of AAs after polarity, expressed by cloister energy (Swanson, 1984) in relation to quantities presented on the right in Figure 2. Between all presented quantities notice also these characteristic: $31+11=42$ (42 versus 32); then: $32+15=47$ ( 47 versus 57 ) (57 versus 67) and so on. All other explanations in the text.

| G 01 | 05 S | G 01 |  | 05 S |
| :---: | :---: | :---: | :---: | :---: |
| A 04 | 07 D | A 04 |  | 07 D |
| C 05 | 08 N | C 05 | 31 (67) 36 | 08 N |
| V 10 | 08 T | V 10 |  | 08 T |
| M 11 | $08 \mathbf{P}$ | M 11 |  | 08 P |
| H 11 | 10 E | H 11 |  | 10 E |
| L 13 | 11 Q | L 13 |  | 11 Q |
| \| 13 | 15 Y | \| 13 | (69) (68) | 15 Y |
| F 14 | 15 K | F 14 | (137) | 15 K |
| W 18 | 17 R | W 18 |  | 17 R |
| 44 56 | $\begin{array}{r} \text { 91) } 47 \\ \text { 113) } 57 \\ \hline \end{array}$ | (102 $\pm 1$ ) |  |  |
|  | 2 $\pm 2$ |  |  |  |

Figure 3.2. Distributions of AAs after polarity, expressed by cloister energy (Swanson, 1984) in relation to odd/even positions (on the left) and to distribution into first ten, second five and third five AAs (on the right).


Figure 4.1. The amino acid ordering is the same as in Figure 3.2, except that histidine "plays" as polar and proline as non-polar amino acid. [(Cf. this Figure with Figure A. 5 in Appendix A; also the pattern 92/112 with the same pattern in legend of Table 5.) (Notice that $107=117-10$, where number 117 represents mumber of hydrogen atoms in 20 protein AAs, within their side chains. On the other hand, $97=87+10$, where number 87 represents mumber of non-hydrogen atoms in 20 protein AAs, within their side chains) (187/197 in whole amino acid molecules, respectively).]

| G 01 |  | S | G 01 |  | 05 S |
| :---: | :---: | :---: | :---: | :---: | :---: |
| A 04 |  | D | A 04 |  | 07 D |
| C 05 | 08 | N | C 05 | 28 (66) 38 | 08 N |
| P 08 | 08 |  | P 08 |  | 08 T |
| V 10 | 10 | E | V 10 |  | 10 E |
| M 11 |  |  |  |  |  |
| 느 13 | 15 | K | M 11 |  | 11 Q |
| I 13 | 17 | R | L 13 |  | 11 H |
| F 14 | 11 | H | I 13 | (69) | 15 Y |
| W 18 | 15 | Y | F 14 | (138) | 15 K |
| $\begin{gathered} 43 \text { (92) } 49(102+1) \\ 54(112) 58(102-1) \end{gathered}$ |  |  | W 18 |  | 17 |
|  |  |  |  |  |
| $\begin{array}{ll}97 & 107\end{array}$ |  |  |  | [(102 $\pm 01)(102 \pm 10)]$ |  |  |
| 187197 |  | 187 non-H \& 197 H , in whole molecules |  |  |  |
| (87 + 10 / $117-10)$; (87/117 atoms in side chains: non-H/H) |  |  |  |  |  |

Figure 4.2. The exchange of $\mathrm{HY} / \mathrm{KR}$ in relation to Figure 4.1, so that the aromatics are at the bottom. But it does not changes any essential fact in the arrangement. Self-similarity in relation to hydrogen and non-hydrogen atom $s$ as in legend of Figure 4.1.

| G 01 | 08 N | G 01 |  | 08 N |
| :---: | :---: | :---: | :---: | :---: |
| A 04 | 08 P | A 04 |  | 08 P |
| S 05 | 08 T | S 05 | 22 (66) 44 | 08 T |
| C 05 | 10 V | C 05 |  | 10 V |
| D 07 | 10 E | D 07 |  | 10 E |
| Q 11 | 14 F |  | $(102 \pm 1)$ |  |
| M 11 | 15 Y | Q 11 |  | 14 F |
| H 11 | 15 K | M 11 |  | 15 Y |
| 느 13 | 17 R | H 11 | (59) (79) | 15 K |
| I 13 | 18 W | L 13 | (138) | 17 R |
|  | $58 \text { (102) }$ | \| 13 |  | 18 W |
| 81 | 23 |  |  |  |

Figure 5. The amino acid arrangement in relation to atom number in molecule: first five AAs on the left, second five on the right, third five on the left and fourth five on the right.

| G 01 | 09 | 08 N |
| :---: | :---: | :---: |
| A 04 | 12 | 08 P |
| S 05 | 13 | 08 T |
| C 05 | 15 | 10 V |
| D 07 | 17 | 10 E |
| 13/09 | 39/27 | 26/18 |
| 04 | 12 | 08 |
| Q 11 | 25 | 14 F |
| M 11 | $\underline{26}$ | 15 Y |
| H 11 | 26 | 15 K |
| L 13 | 30 | 17 R |
| I 13 | 31 | 18 W |
| 24/35 | 56/82 | 32/47 |
| 11 | $\begin{aligned} & 13 \\ & 13 \end{aligned}$ | 15 |
| $\begin{aligned} & 39+82=121 \\ & 27+56=83 \\ & \hline \end{aligned}$ |  |  |

Figure 6. The amino acid arrangement as in Figure 5 with further balances.

In relation to input algorithm in Figure 1, the next reason is important: If instead of ( $x$ 10) were $(x-y)$, then for the different values for $y$ we gain the different values of $x$. However, only for $y=10$ it gives the quantities, which have been found in the genetic code. This supports the hypotheses after that just decimal numbering system is a key determinant of the genetic code [Ref. 19, p. 153: "The genetic code turns out to be a syntactic structure of
arithmetic, the result of unique summations that have been carried out by some primordial abacus at least three and half billion years ago. The decimal place-value numerical system with a zero conception was used for that arithmetic."], [Ref. 14, p. 831: "It is self-evident that only at the six-bit binary tree the determination with the generalized golden mean is going through module 9 , that is through the decimal numbering system. On the other hand, because two golden mean values are calculated from the quadratic equation by square root of the number five (which represents half of the decimal scale of 10 digits) it is reason why decimal numbering system is - the only "golden" numbering system"].

In relation to aromatic $\mathrm{Y}-\mathrm{H}$ "loop", i.e. line, at Figure 3, disclosed is a display of a qualitative self-similarity (and quantitative at the same time), expressed through the hierarchy of number of carbon atoms in side chains of aliphatic AAs. So, all aliphatic AAs under the line ( $\mathrm{L}, \mathrm{I}, \mathrm{K}, \mathrm{R}$ ) have four carbon atoms in the side chain each, whereas above come $\mathrm{M}, \mathrm{V}, \mathrm{Q}$, $\mathrm{E}, \underline{\mathrm{P}}$, each with the three carbon atoms; follow $\underline{\mathrm{P}}, \mathrm{T}, \mathrm{N}, \mathrm{D}$, all with two, then $\mathrm{C}, \mathrm{A}, \mathrm{S}$ with one, and $G$ with zero of carbon atoms. ${ }^{12}$

The display of aromatic AAs was realized also in accordance with the principle of selfsimilarity. More nonpolar AAs, F \& W, go together with the nonpolar, L \& I. The selfsimilarity itself is expressed through possession of the same structural motif: "the branching within four carbon atoms." On the other hand more polar Y, which has the same motif of branching as F , exists in the neighborhood of the set of two four-atomic AAs, K-R; two, of which ( R ) has a quasi-branching in which the central carbon atom, instead with the three carbon, linked to three nitrogen atoms. Ambivalent H, which also has a quasi-branching motif - the central carbon atom is bonded with two carbon and one nitrogen atom - is located in the neighborhood of molecules with three carbon atoms in the side chain.

### 5.1. Relationships between parameters

With the quantities from output algorithm (Figure 2 in relation to Figure 3) are also determined the relationships between key parameters which refer to the polarity. So, if we assign two corner "stones" of the system on left site of Figure 3, G \& W, together with the central one $(\mathrm{H})$, we became the scale of polar AAs after the values of their hydropathy index: G-S, D, N, P, T, E, Q, H-Y, K, R-W (Kyte and Doolittle, 1982) (cf. Box B.1). On the other hand, the "promotion" of tyrosine ( Y ) and proline ( P ) in "partial-nonpolar" amino acids follows from the polar requirement as well as "natural scale" of hydrophobicity of AAs (Box B.2). From the said it must follow a new rearrangement with Histidine (H) as polar and Proline (P) as nonpolar amino acid (Figure 4.1) with new balances and new self-similarities (cf. Figure 4.1 with Table A. 5 in Appendix A).

As we see, this testing shows that the key parameter of polarity of amino acid molecule is just cloister energy, in relation to other relevant parameters such as hydropathy index and "polar requirement"; also in relation to the natural scale ( $0-1$ ) of hydrophobicity. By this, the presented interactions between these parameters correspond to the specific arithmetical

[^27]algorithms, related to golden and harmonic mean and to unique arithmetical and algebraic regularities. All this, and altogether, said us that physicochemical reactions within genetic code are mediated by a harmonizing system, in which amino acid molecules as well as nucleotides belong. Moreover, after our prediction future researches will show that the arithmetic regularities found in the genetic code by other authors (Sukhodolets, 1985; Dragovich, 2011; Mišić, 2011; Négadi, 2011; Castro-Chavez, 2011) also appear to be, mutatis mutandis, in relation to the findings shown here as harmonizing GC system, two initial algorithms as well as the Mendeleevian Arrangement of Molecules (MAM) and Mendeleevian Arrangement of Numbers (MAN).

## 6. Concluding remarks

6.1. The key point in this research is the classification of AAs into four diversity types (as it is shown in the first paragraph of Section 5), with the first two classes in which AAs have (in the side chain) carbon and/or hydrogen, while the other two classes have elements of higher order ( N or O , or NO, or S ). From this classification follows a strict system of Mendeleevian type (Tables $6 \& 7$ ), and from this system two formal algorithms (Figs $1 \& 2$ ), with quantities through which are connected all the important parameters of amino acid polarity (cloister energy, hydropathy index, polar requirement and hydrophobicity "natural scale") (Figs 3.1, 3.2, 4, 5 \& 6).
6.2. The approach to the research was achieved through minimal modification of Rumer's DT, and TT is viewed as a set of $61+3$ codons and 20, 23 and 61 amino acid molecules at the same time, with respect to their sequence number, in terms of Mendeleevian arrangements of "numbers", with ascending/descending hierarchy within the rows and columns as it is shown in illustrations within the main text as well as in Appendix A.
6.3. The strict connection of GCT and Codon ring from one site, and the Mutation ring from the other site, as shown in the figures and tables in Appendix B (cybernetic said: a very clear negative feedback) suggests two possible trends in further researches, when it comes to the biological aspects of the results presented in this paper; one theoretical and one practical trend. As a theoretical matter, it is necessary to understand Darwinian selection so that it has been, per se, limited by the said negative feedback. Practical uses however could be multilateral, of which we present only a minimum. Starting from the presented relations within Mutation ring it could be made some "golden" simulations in order to realize new protein syntheses where be obtain such proteins which would be "measure" of real life and which would have been useful, at least in the form of precursors, for adequate food additives, for the production of new types of drugs and the similar things.
6.4. This state of affairs in the genetic code caused a proposal for further researches, according to which must not be allowed any "modification" of organisms and organic materials by „ordinary" laboratory chemistry because it is expected that all of these relationships, contained in the GC, must inevitably be mapped on real proteins and real living processes.
6.5. With the title of the paper is given a working hypothesis that the golden mean (GM) and harmonic mean (HM) are determinants of the genetic code. The findings presented by significant number of illustrations show that this hypothesis is confirmed. However, unlike the previous access to the same determination, it refers not only the analysis of the nucleotide triplet Table, but rather refers to the two tables - Table of doublets (DT) and Table of triplets (TT). In fact, it is precisely presented that these tables are unique in terms of determination just over GM and HM.
6.6. Presented facts are such that ones reaffirm the other and vice versa. All together, they favor the recognition that the chemical reactions that determine the GC are not only "reactions in a tube", but these reactions are associated with a specific balance of the number of particles (atoms and nucleons); balance, determinated by unique arithmetic and algebraic regularities and expressed in the form of specific - nonfractal - selfsimilarity ("a harmonized chemistry"). From this it follows further that presented facts also support the hypothesis that the genetic code was from very begining, in prebiotic times and conditions, a complete code (Sukhodolets, 1985; Rakočević, 2004). On the other hand, the knowledge that "the chemistry of living" is actually a harmonized chemistry requires great care in medicine, agriculture and natural environment, taking into account the fact that this harmonization is strictly immanent to the living as such, mediated by genetic code as such.

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## Appendix A

## Position non-fractal selfsimilarities

Here we present orderings of AAs in DT and TT and calculated number of atoms in odd and even positions. Self-similarities over the number of atoms in sets of AAs ${ }^{13}$ are immediately apparent: (139/100), (129/110), (119/120), (109/130), (108/131); (115/124), (125/114), (126/113), (116/123), (117/122), (127/112), (137/102). ${ }^{14}$

| 6,4 / 5,5 hb | Polarity (a) |
| :---: | :---: |
| $\underline{\mathbf{G}} 01 \quad 10 \underline{\underline{V}} 13$ | ${ }^{01} \underline{\mathbf{G}} 0108 \underline{\mathbf{P}} 04$ |
| F 14 05 C 14 | 02 F 1408 N 05 |
| $03 \underline{\underline{L}} 1318 \underline{\mathbf{W}} 15$ | ${ }^{03} \mathbf{L} \underline{L} 1315$ K 06 |
| P 0808 | ${ }_{07} \mathrm{~A} 04{ }^{15}$ Y 08 |
| $05 \mathbf{N} 0811$ | $17 \mathrm{R}{ }_{10}$ |
| $06 \mathrm{~K}^{15} \quad 11 \overline{\mathrm{Q}}_{18}$ | ${ }_{11}$ I 1308 T 16 |
| $07 \mathbf{A} 04 \quad 13 \underline{\underline{L}} 19$ | 12 M 1111 |
| 08 Y 1505 S 20 | ${ }^{13} \underline{\mathrm{~V}} 10{ }^{105} \mathbf{S} 20$ |
| 09 * 17 R 21 | ${ }_{14} \mathrm{C} 0517 \mathrm{R}{ }^{21}$ |
| $10 \underline{\mathbf{R}} 17$ 05 S 22 | ${ }^{15} \underline{\mathrm{~W}} 1805 \mathrm{~S}^{22}$ |
| 11\| $1307 \underline{\text { D }} 23$ | 17 H 1107 |
| 12 M $11 \quad 10$ E 24 | 19 L 1310 |
| Odd / Even arrangement |  |
| 54 (130) 76 (141) | 68 (143) 75 |
| 65 (109) 44 (98) | 45 (96) 51 (119) |
| 119 |  |

Table A.1.1. The ordering after Table 2. On the left as in original Table 2 after the number of hydrogen bonds. On the right the same ordering but with a separation into polar and nonpolar AAs, measured by cloister energy.

[^28]| 6,4 / 5,5 hb | Polarity (b) |
| :---: | :---: |
| $01 \underline{\mathbf{G}} 01 \quad 10 \underline{\mathbf{V}} 13$ | ${ }^{01} \underline{\text { G }} 0108 \underline{\mathbf{N}} 05$ |
| $02 \mathrm{~F} 14 \quad 05$ C 14 | 02 F 1415 K 06 |
| $03 \underline{\underline{L}} 1318 \underline{\underline{W}} 15$ |  |
| P 0808 T 16 | 04 P 0817 R 10 |
| $05 \underline{\mathbf{N}} 0811 \underline{\underline{\text { H }} 17}$ | ${ }^{07} \boldsymbol{A} 0408 \underline{\mathbf{T}}^{16}$ |
| K 15 11 Q 18 | 09 * $11 \mathrm{H}^{17}$ |
| $07 \underline{\mathbf{A}} 04 \quad 13 \underline{\underline{L}} 19$ | ${ }_{11}$ \\| $1311 \underline{Q}^{18}$ |
| 08 Y $15 \quad 05 \mathrm{~S} 20$ | 12 M $1105 \mathrm{~S}_{20}$ |
| 09 * 17 R 21 | ${ }_{13}$ V 1017 |
| $10 \underline{\underline{R}} 17 \quad 05$ S 22 | ${ }_{14} \mathbf{C} 0505{ }^{22}$ |
| 11] 1307 (—23 | $1807 \underline{D}^{23}$ |
| 12 M $11 \quad 10 \bar{E}_{24}$ | 19 L $1310 \bar{E}^{24}$ |
| Odd / Even arrangement |  |
| 54 (130) 76 (141) | 47 (113) 66 (129) |
| 65 (109) 44 (98) | 63 (126) 63 (110) |
| 119/120 | 110/129 |

Table A.1.2. The ordering after Table 2. On the left as in original Table 2 after the number of hydrogen bonds. On the right the same ordering but with a separation into polar and nonpolar AAs, measured by cloister energy.

| 6,4 / 5,5 hb |  |  |
| :---: | :---: | :---: |
| ${ }^{01} \mathbf{G} 01$ |  | $10 \underline{V}^{13}$ |
| 02F 14 |  | 05 C 14 |
| ${ }_{03} \mathbf{L} 13$ |  | 18 W ${ }_{15}$ |
| ${ }_{04} \overline{\mathrm{P}} 08$ | 59/63 | 08 T 16 |
| ${ }_{05} \mathbf{N} 08$ | (122) | $11 \mathrm{H}^{17}$ |
| 06 K 15 |  | 11 Q 18 |
| 07 A 04 | (116/123) | $13 \underline{\underline{L}} 19$ |
| ${ }_{08} \overline{\mathrm{Y}} 15$ |  | 05 S 20 |
| 09* |  | 17 R 21 |
| ${ }_{10} \underline{\text { R }} 17$ | 60/57 | 05 S 22 |
| ${ }_{11}$ \| 13 | (117) | 07 D 23 |
| ${ }_{12}$ M 11 |  | $10{ }^{\text {E }} 24$ |
| Odd / Even arrangement 54 (130) 76 (141) |  |  |
|  |  |  |
| 65 (109) 44 (98) |  |  |

Table A.2. The ordering after Table 2: left site of Table A.1.2 with further balances.


Table A.3.1. The ordering after Table 2: the right site of Table A.1.1 with further balances.

| Polarity (b) |  |  |
| :---: | :---: | :---: |
| $\begin{array}{\|ll} \frac{\mathbf{G}}{\mathbf{F}} & 01 \\ \boldsymbol{F} & 14 \\ \underline{L} & 13 \\ \mathrm{P} & 08 \\ \frac{\mathbf{A}}{\star} & 04 \end{array}$ | $\underset{(114)}{40 / 74}$ | $\begin{aligned} & 08 \\ & 15 \end{aligned}$ |
|  |  |  |
|  |  | 15 Y |
|  |  | 17 R |
|  | (95/144) | 08 |
|  |  | 11 H |
| 13 |  | 11 |
| M 11 |  | 05 S |
| V 10 | 70/55 | 17 R |
| $\underline{\text { C }} 05$ | (125) | 05 S |
| W 18 |  | 07 D |
| $\underline{\underline{L}} 13$ |  | 10 E |
| Odd / Even arrangement |  |  |
| 47 (113) 66 (129) |  |  |
| $\begin{gathered} 63(126) 63(110) \\ 110 / 129 \end{gathered}$ |  |  |

Table A.3.2. The ordering after Table 2: the right site of Table A.1.2. with further balances.

| ${ }^{01}$ F 14 |  | 13 L 02 |
| :---: | :---: | :---: |
| 03 L 13 |  | 13 \| 04 |
| ${ }^{05}$ M 11 |  | 10 V 06 |
| 07 S 05 | 66 / 48 | 08 P 08 |
| 09 T 08 | (114) | $04 \underline{A}^{10}$ |
| $11 \overline{\mathrm{Y}} 15$ |  | * 12 |
| ${ }^{13} \mathrm{H} 11$ | (113/126\} | $11 Q^{14}$ |
| 15 N 08 |  | 15 K 16 |
| 17 D 07 | 65 / 60 | 10 E 18 |
| ${ }_{19} \mathrm{C} 05$ | (125) | 18 W 20 |
| ${ }^{21}$ R 17 |  | $05 \mathrm{~S}^{22}$ |
| 23 R 17 |  | $01 \mathbf{G}^{24}$ |
| $\underline{68}$ | (129) | 61 (124) |
| 63 | (110) | 47 (115) |
| 131 |  | 108 |

Table A.4. The ordering in GCT, within the set of „ 23 " AAs.

| ${ }^{01} \mathrm{~F} 14$ |  | $13 \underline{\underline{L}}{ }^{02}$ |
| :---: | :---: | :---: |
| 03 \| 13 |  | $11 \mathrm{M}^{04}$ |
| ${ }^{05}$ V 10 | 49 / 52 | $05 \mathrm{~S}^{06}$ |
| 07 P 08 | (102-1) | 08 T 08 |
| ${ }^{09} \mathbf{A} 04$ |  | $15 \underline{Y}^{10}$ |
| ${ }^{11} \mathrm{H} 11$ | (102 $\pm 2$ ) | $11 \mathrm{Q}^{12}$ |
| ${ }^{13} \mathrm{~N} 08$ |  | $15 \mathbf{K}^{14}$ |
| 15 D 07 | 48/55 | 10 E 16 |
| ${ }^{17}$ C 05 | (102+1) | $18 \mathrm{~W}^{18}$ |
| 19 R 17 |  | 01 G 20 |
| Odd 41 | (107) | 66 (122) |
| Even 56 | (97) | $41 \quad$ (82) |
| 97 |  | 107 |

Table A.5. The ordering in GCT, within the the set of 20 AAs. Notice the balances through self-similarities of atom number patterns: 97/107 within columns and odd/even positions, $102 \pm 1$ in up/down halves, $102 \pm 2$ through the crossing of two and two column halves; also the pattern $82 / 122$ in relation to the pattern 92/112 in Table 5.

## Appendix B

## Relations between GCT, codon ring, and mutation ring

Here we present Swanson's Mutation ring (Swanson, 1984) ${ }^{15}$ (Mutation ring I), and our modification of the same ring (Mutation ring II) (Rakočević, 1997). In the modification we showed additional relationships, for example the relations to Space-3 and Space-4 within Boolean GC cube ${ }^{16}$ as well as to essential/nonessential AAs. In addition to the amino acid similarity, presented in (Swanson, 1984), we can now see that the similarity corresponds also to four diversity types of AAs (which types we stated, in the form of amino acid pairs, in the first paragraph of Section 5); and this similarity can be very visible through an expression of amino acid pairs in adequate positioned brackets: (P-G), $\underline{\mathbf{A}}\{(\mathrm{S}-\mathrm{T})[\mathbf{C}(\mathrm{V}-\mathrm{I}) \mathbf{M}]\} \underline{\mathbf{L}}, \mathrm{F}-\mathrm{Y}, \mathrm{W}-\mathrm{H}, \mathrm{R}-$ $\mathrm{K}, \mathrm{Q}-\mathrm{N}, \mathrm{D}-\mathrm{E}$ ). However, as a special, noteworthy fact, is that the mutation ring (as an image and likeness of real proteins) clearly marked division between the polar and non-polar (bold underlined), and partially nonpolar AAs (underlined) (Table B.1).


Figure B.1. Mutation ring I


Figure B.2. Mutation ring II

Explanation of Figure B.1: "Mutation ring. As the codon ring expresses the minimum change relation among codons, so the mutation ring expresses the minimum change relation among the amino acids. The mutation ring shows the broader relationships among the amino acids, as well as the detailed ordering. For this the ring is quartered into the four groups, and for each group the average values of energy and volume are entered. ... The patterns represent progressions in the physical properties of the

[^29]amino acids. Dark tones are for large residues, light for small. Coarse, checkered or blotchy textures signify external residues, and smooth, delicate or even-textured patterns designate internal" [Ref. 21, Fig. 3, p. 191].

Explanation of Figure B.2: "Everything is the same as on Mutation Ring I, only the S.T.-Q.K. line is shifted by one step on both ends in relation to Mutation Ring I; and P.E.-M.L. line is shifted only on one (the other) end. The squares designate the amino acids from Space-4 and triangles designate the amino acids from Space-3. The empty squares and empty triangles designate the nonessential amino acids, otherwise they designate the essential amino acids; the dots designate the semi-essential amino acids. The lines strictly separate non-essential from essential amino acids; then the lines strictly separate the Space-3 amino acids from Space-4 amino acids. There are the two exceptions: C is fullstrayed; R is semi-strayed. One should note that the complementarity principle is applied as follows: outer-inner: non-essential amino acids from Space-4 are complementary with the essential amino acids from Space-3, etc." [Ref. 11, Fig. 6, p. 28].

Additional explanations of physical facts: Six bold underlined AAs in Table B. 1 are nonpolar in all four parameters (Cloister energy, Hydropathy, Hydrophobicity and Polar requirement). ${ }^{17}$ Partial nonpolarity of G, A, P and T follows from next facts: A \& G have border positions in hydropathy index, whereas A \& T in polar requirement. On the other hand, proline $(\mathrm{P})$ is polar in two parameters (Cloister energy and Hydropathy), whereas in other two (Hydrophobicity and Polar requirement) is not (cf. Tables B. 1 and B.2).

Additional explanations of chemical facts: Six bold underlined AAs in Table B. 1 are nonpolar also from chemical aspects. So, phenylalanine possesses the extremely non-polar benzene ring; valine, leucine and isoleucine have more non-polar methylene and/or methyl groups; two sulfur AAs are the only two AAs that have (within molecule) an atom from the third period of Periodic system of elements (sulfur atom) where the polarity of atoms is much smaller than of atoms in the second period. Partial nonpolarity of G, A, P and T also follows from chemical facts. So glycine is nonpolar through nonpolar hydrogen atom, but polar through direct contact with amino acid functional group (amino acid "head"); similar is with alanine because it possesses only one methyl group. Proline is nonpolar through three methylene groups but polar through a binding of side chain with amino group in amino acid "head". Finely, threonine (T) is one and only amino acid within the set of 16 AAs of alanine stereochemical type (Rakočević, 1997), with the screen $\mathrm{H}-\mathrm{C}-\mathrm{CH}_{3}$ between amino acid "head" and "body" (instead H-C-H) where a $\mathrm{CH}_{3}$ group is more nonpolar than a H atom. (A possible explanation for serine "deviation" in Mutation ring is that it is a member within the pair S-T, only two aliphatic AAs with OH functional group.)

[^30]|  | III | IV | I | II |
| :--- | :---: | :---: | :--- | :---: |
| GCT | Y,H,Q,N,K,D,E | C,W,R,S,R,G | F,L,L,I,M,V | S, P, T, A |
| CR | K, N, D, E, Q | H,Y,W,C,R,P,S,L,F | L, V, I, M, | T, A, G, S |
| MR-I | E, D, N, Q, K | H, R, W, Y, $\underline{\mathbf{F}}$ | $\underline{\mathbf{L}}, \underline{\mathbf{M}}, \underline{\mathbf{I}}, \underline{\mathbf{V}}, \underline{\mathbf{C}}$ | $\underline{\text { T, S, }, \underline{A}, \underline{\mathrm{G}}, \underline{\mathrm{P}}}$ |
| MR-II | E, D, N, Q | K,H,R, $\underline{\mathrm{W}}, \underline{\mathrm{Y}, \underline{\mathbf{T}}, \underline{\mathbf{L}}}$ | $\underline{\mathbf{M}}, \underline{\mathbf{I}}, \underline{\mathbf{V}}, \underline{\mathbf{C}}, \underline{\mathrm{T}}$ | S, $\underline{\text { A }, \underline{\mathrm{G}}, \underline{\mathrm{P}}}$ |
|  | OUTER | LARGE | INNER | SMALL |

Table B.1. Relations between Genetic Code Table, Codon ring and Mutation ring
Explanation of Table B.1: Roman numbers at the top refer to the columns in the standard Genetic Code Table (GCT). In next three rows there are presentations of AAs into four groups as it is designated below. Codon ring (CR) and Mutation ring (MR-I) as in [Ref. 21, Figs $1 \& 3$, respectively]. The modified Mutation ring (MR-II) as in Ref. 11, Fig. 6.

|  | I | II |  | III / IV |  |  |
| :--- | :---: | :---: | :---: | :---: | :---: | :---: |
| GCT | F,L,L,I,M,V | S, P, T, A | Y,H,Q,N,K,D,E / C,W,R,S,R,G |  |  |  |
| DR-I | F,M,L,I,V | C, P, A, T | S,G,D,N | E,Q,K,R | Y,H,W |  |
|  | large nonpolar | small nonpolar | small polar | large polar | 1.m.polar |  |
| DR-II | I, V, L, F, C, M, A | G T, W, S, Y, P | H, E, Q, D, N, K, R |  |  |  |
|  | Cluster III |  | Cluster II |  | Cluster I |  |

Table B.2. Relations between Genetic Code Table and two Doolittle's amino acid rings
Explanation of Table B.2: Roman numbers at the top refer to the columns in the standard Genetic Code Table (GCT). In next rows there are two Doolittle's amino acid rings: DR-I as in (Weaver, 1985) and DR-II as in (Kyte and Doolittle, 1982); 1.m.polar = large moderately polar. The correspondence with Mutation ring in Table B. 1 is self-evident.

Box B.1. Polarity of amino acids (plus vs minus and vice versa)
Cloister energy (Swanson, 1984):
$\mathrm{K}+1.46 ; \mathrm{Q}+0.91 ; \mathrm{R}+0.87 ; \mathrm{E}+0.71 ; \mathrm{D}+0.69 ; \mathrm{N}+0.52 ; \mathrm{P}+0.46 ; \mathrm{Y}+0.42 ; \mathrm{T}+0.27 ; \mathrm{S}+0.24 ; \mathbf{H} \pm \mathbf{0 . 0 0}$
$\mathbf{H} \pm \mathbf{0 . 0 0} ; \mathrm{A}-0.09$; G-0.16; W -0.25; V -0.52; L -0.54; I -0.56; F -0.56; M -0.57; C -0.73;

Hydropathy index (Kyte and Doolittle, 1982):
R -4.5; K -3.9; D -3.5; E -3.5; N -3.5; Q -3.5; H -3.2; P -1.6; Y -1.3; W -0.9; S -0.8; T -0.7; G -0.4
$\mathbf{A}+\mathbf{1 . 8} ; \mathrm{M}+1.9 ; \mathrm{C}+2.5 ; \mathrm{F}+2.8 ; \mathrm{L}+3.8 ; \mathrm{V}+4.2 ; \mathrm{I}+4.5$

Box B.2. Polarity of amino acids (first ten more and second ten less polar)
Hydrophobicity natural scale ((Blac and Mould, 2004), (Chechetkin and Lobzin, 2011)):
R 0.000; D 0.028; E 0.043; H 0.165; N 0.236; Q 0.251; K 0.283; S 0.359; T 0.450; G 0.501
A 0.616; C 0.680; P 0.711; M 0.738; V 0.825; W 0.878; Y 0.880; L 0.943; I 0.943; F 1.000

Polar requirement ((Woese et al., 1966), (Konopel'chenko and Rumer, 1975)):
D 13.0; E 12.5; K 10.1; N 10.0; R 9.1; Q 8.6; H 8.4; G 7.9; S 7.5; A 7.0
T 6.6; P 6.6; V 5.6; Y 5.4; M 5.3; W 5.2; F 5.0; L 4.9; I 4.9; C 4.8

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## 15.

## Analogies of Genetic and Chemical Code

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Starting from the previously established hypothesis on the existence of the coherence of the chemical and genetic code, new facts and new insights on the existence of essential analogies between the genetic and chemical code are presented, whereby the chemical code is derived from the original Mendeleev work on the periodic system of chemical elements. When, namely, all elements are scheduled into adequate groups of Periodic system of chemical elements, in accordance to Mendeleev original manuscript tables, then are revealed some very specific mathematical and chemical regularities; among others, Periodic system appears to be a code - the chemical code - in an entity analogy with the terrestrial genetic code. These regularities correspond to the mathematical regularities within the genetic code. Between others relations, it appears also a correspondence between the distribution of codons in the Genetic Code Table and the distribution of chemical elements in the Periodic system with respect to their even/odd parity and stability/instability of the isotopes.

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# ANALOGIES OF GENETIC AND CHEMICAL CODE 

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#### Abstract

Starting from the previously established hypothesis on the existence of "the coherence of the chemical and genetic code" (Rakočević, 1991), new facts and new insights on the existence of essential analogies between the genetic and chemical code are presented, whereby the chemical code is derived from the original Mendeleev's work on the periodic system of chemical elements. When, namely, the 14 lanthanides are scheduled into 14 groups of Periodic system of chemical elements (PSE) (Rakočević, 1991), in accordance to Mendeleev's original manuscript tables, then are revealed some very specific mathematical and chemical regularities within the PSE; among others, PSE appears to be a code - the chemical code - in an entity analogy with the terrestrial genetic code. These regularities correspond to the mathematical regularities within the genetic code. Between others relations, it appears also a correspondance between the distribution of codons in the Genetic Code Table and the distribution of chemical elements in the PSE with respect to their even/odd parity and stability/instability of the isotopes. Based on the significant mathematical expressions it is showed a new essence of coding formalism in natural code as such: it cannot be reduced only to two alphabets (which are consequences, and not the cause); a natural code is such an essence that can be represented by an appropriate mathematical expression, which contains a sequence from the series of natural numbers within itself. From this follows that both are natural codes, the Genetic code as well as the Periodic system of chemical elements (PSE).


Keywords. Genetic code; periodic system of chemical elements; chemical code; lanthanides; protein amino acids; stereochemical types of amino acids; diversity types of amino acids; molecular diversity; golden mean; generalized golden mean.

## 1. Preliminaries

### 1.1. Analogies with quantum physics

V. Shcherbak showed that a specific classification of the protein amino acids (AAs), "canonical" amino acids within the genetic code (GC), reveals some arithmetical regularities and stated that "the physical nature of such a phenomenon is so far not clear" (Shcherbak, 1993). There is a similar statement of A. Verkhovod in his work on the same subject and published a few months later: "The nature of these mechanisms is presently unknown" (Verkhovod, 1994). In the second part of his rsearches Shcherbak (1994) "seeks to identify a trend of possible physical interpretation of the new code properties", and reveals that in the question are "analogies with quantum physics." By this, the Shcherbak's classification refers to the splitting into four-codon and non-four-codon AAs, based on the original work of Rumer (Rumer, 1966) (Table A. 1 in Appendix A). If so, then there are analogies in the next sense: $01 \times 111$ of electrons in the half-filled state of the atom orbitals, or $01 \times 222$ in the full-filled state, according to Hund's rule, versus $10 \times 111$ nucleons in 15 side chains as well as in 15 "heads", i.e. amino acid functional groups (after Shcherbak: "standard boxes") of 15 non-four-codon AAs, what equals
$10 \times 222$ in 15 whole molecules; at the same time there are $01 \times 333$ nucleons in 8 side chains of 8 four-codon AAs (for details see: Shcherbak, 1994). ${ }^{1}$

Considering that $01 \times 333$ can be "read" as $01 \times \underline{\mathbf{3}}^{\wedge} 2 \mathrm{PQ}$, then we find that in 8 "heads" of 8 four-codon AAs there are $01 \times \underline{4}^{\wedge} 2 \mathrm{PQ}$, or in total $01 \times \underline{\mathbf{5}}^{\wedge} 2 \mathrm{PQ}$ of nucleons, what is again an analogy with quantum physics, as well as with two Mendeleev principles at the same time (see Remarks 1-3).

Remark 1. Whether it is a move for one electron in filling of the orbital, or for a single numbering unit in filling the positions in the number record of the number of nucleons, both have correspondence with two key Mendelevian principles: with the principle of continuity and the principle of minimum change. In addition to this, it should be noted that this is a special case of a minimum change - a change for a unit; ${ }^{2}$ and there is also an analogy with the changes on the Gray code model of the genetic code, ${ }^{3}$ as well as on the GC binary tree that follows from the Gray Code. ${ }^{4}$

Remark 2. The uniqueness of the number 037 in the Shcherbak's pattern "Prime Quantum 037" (PQ) follows from the uniqueness of a specific sequence, generated from the series of natural numbers: ( $13_{4}$, $\left.25_{7}, 37_{10}, 49_{13}, \ldots\right)^{5}$, for which two Mendeleev's principles also are valid. [The validity through the sequence $1,2,3,4$, etc., in front position, and through the sequence $3,5,7,9$, etc., in ending position.]

Remark 3. The chemical and formal bond between four-codon and non-four-codon amino acids is described in the next Section. However, one specific formal-mathematical relation, in a certain way hidden, ${ }^{6}$ we present here: ( $\mathbf{1} 0 \times 3^{\wedge} \underline{\mathbf{1}} \mathrm{PQ}$ ) nucleons within 15 side chains of 15 non-four-codon AAs versus ( $0 \underline{1} \times 3^{\wedge} \underline{\mathbf{2}} \mathrm{PQ}$ ) nucleons within 8 side chains of 8 four-codon AAs. It should be noted here that the " 15 " encoded entities are actually 16 encoded entities because the $16^{\text {th }}$ entity joins a "stop" signal. In this case, the ratio of four-codon and non-four-codon situations is in a strictly symmetrical manner of view, 8: $16=1: 2$ (cf. Survey 1 and Table A.1).

As far as Verkhovod's work is concerned, he showed that the number of nucleons in the 23 amino acid molecules in the standard GCT directly corresponds with the sequence of the series of natural numbers (in decimal numbering system) in a specific way, through the "game" of the visible and invisible image in the "mirror": 456/789 and 987/654. Namely, in amino acid side chains, within $\left(1^{\text {th }}+4^{\text {th }}\right)$ rows, as well as within $\left(2^{\text {nd }}+3^{\text {rd }}\right)$ columns there are 654 nucleons in both

[^31]area; vice versa, within $\left(1^{\text {th }}+4^{\text {th }}\right)$ columns, as well as within $\left(2^{\text {nd }}+3^{\text {rd }}\right)$ rows there are 789 nucleons in each of two area (Figure 2 in Verkhovod, 1994).

### 1.2. Agreement-disagreement principle

As we can see in above presented classification of AAs appears a specific unity of chemistry and mathematical formalism, which in this paper will be analyzed in details, starting from both works, Rumer's and Shcherbak's. In his first work on the genetic code, Rumer (1966) shows that four variations of nucleotide doublet CG (CC, GG, CG, GC) with 6 hydrogen bonds (higher rank!) encode four-codon AAs (higher rank!), while four variations of UA (UU, AA, UA, AU), each with 4 hydrogen bonds (lower rank!) encode non-four-codon AAs (also lower rank!). However, the situation is more "complicated" in the coding with nucleotide doublets that have 5 hydrogen bonds each. There is a characteristic "crossing", but also in relation to a strict chemical distinction. Thus, nucleotide doublets that in the second position possess a more complex nucleotide (CA \& UG), i.e. the nucleotides of higher rank, encode non-four-codon AAs, what is per se a situation of lower rank. On the other hand, nucleotide doublets that in the second position possess a less complex nucleotide (AC \& GU), i.e. the nucleotides of lower rank, encode four-codon AAs, what is the situation of higher rank. Finally, pyrimidine doublets (UC \& CU) (lower rank!) encode four-codon AAs (higher rank!), while purine doubles (GA \& AG) (higher rank!) encode non- four-codon AAs (lower rank!).

As we see, the state of things is such that the disagreement in the number of hydrogen bonds ( $6 \& 4$ ) is accompanied by an agreement in the rank of the complexity of the molecules and / or the complexity of the coding process; vice versa, the agreement in the number of hydrogen bonds $(5 \& 5)$ is accompanied by disagreement in the ranking. In a certain way, here we indeed have an analogy with quantum physics, more precisely with Heisenberg's uncertainty principle (in the form of an agreement/disagreement principle).

### 1.3. Some other mathematical formalisms

Independently of Shchrbak and Verkhovod, other authors, during the last decades, have also presented other different arrangements in which chemical distinctions are accompanied by some kinds of mathematical formalism. So, R. Swanson has shown that the genetic code can be reduced into a strict mathematical-formal model, determined with the "Gray code binary symbols for numbers $0-63$ ", and also reduced into the "Codon path cube" in which "all 64 codons are displayed", and where "the three edges of the cubes represent the three positions in a codon" (Swanson, 1984). By this, in both cases the principles of minimum change and continuity are valid, the same principles which are valid for the arrangement of chemical elements in the periodic system of D.I. Mendeleev.
R. Swanson, however, showed another more important thing. The "Codon ring" in the form of a Gray code model, which we have in GC (input!) and the "Mutation ring" of the amino acids, which is the result of the evolution of proteins in the terrestrial organisms (output!) are more than very similar - mutatis mutandis they are the same. With this insight, she rightly states that these findings "provides a new standpoint for addressing questions of selection vs random drift in the evolution of the code." The additional reason for this reexamination is the fact that in both rings (Codon and Mutation ring) AAs are classified into small/large and inner/outer, in terms of their
position in proteins, with directly visible certainty/uncertainty of these positions, which is again an analogy with quantum physics, i.e. with Heisenberg's uncertainty principle.

Using the same rules ${ }^{7}$ that were applyed to the generation of the Gray Code model of GC, it was possible to obtain a six-bit binary tree of GC, and show that the GC is determined by the Golden mean (Rakočević, 1998b). On the other hand, if the splitting of the amino acids into two (by enzymes aminoacyl-tRNA synthetases handled) groups, instead in the standard Genetic Code Table (GCT) (Wetzel, 1995), is made in Codon path cube, the significant regularities are noted the separating of two classes of AAs with only one exception (Rakočević, 1997a) (see Table B. 1 in Appendix B).

Remark 4. The six-bit binary tree is specific, in addition to everything else, in following: only at such a binary tree the sums of numbers within two inner branches (two octets) corresponds to the first pair of friendly numbers $(220+284=504)$; and each two adjacent branches give the same sum (504); all together, a kind of logical square is realized: (0) $220+284=504$; (1) $156+348=504$; (2) $92+412=$ 504; (3) $28+476=504$. On the other hand, the sum of the numbers of the first quartet is 6 , the first octet 28; the sum of numbers on the left half (which coincides with the first half of the GCT), from 0 to 31, is 496, which in turn is the realization of the first three perfect numbers ( $6,28,496$ ). If, however, we count all numbers $0-63$, then go back (cyclic!), where 0 (zero) becomes to be 127 , then the sum of all numbers within the sequence $0-127$ equals 8128 , which is actually the fourth perfect number. After these insights, it is clearer the analogy between the binary records of 64 codons in the genetic code and 64 hexagrams in the Chinese book I Ching, at least three thousand years old; the records, on the six-bit binary-code tree in both cases (Stent, 1969; Schoenberger, 1951; Rakočević, 1994) (www.rakocevcode.rs).

A year later, after R. Swanson's published work, an article more about specific mathematical formalism, accompanied by the chemical distinctions of AAs according to the number of hydrogen atoms in their molecules has been published (Sukhodolets, 1985). Such a distinction corresponds with the characteristic sequence from a series of natural numbers: 5, (6), 7, 8, 9, 10, $11,12,13,14$ of hydrogen atoms (Appendix C).

On all the said and some other similar investigations of mathematical regularities of the GC one can see the following works: (Sukhodolets, 1985; Leunissen and De Jong, 1986; Koruga, 1992; Madox, 1992, 1994; Shcherbak, 1993-2008; Damjanović, 1998-2006; Qiu and Zhu, 2000; Yang, 2004; Dragovich, 2006-2012; Negadi, 2009-2014; Castro-Chavez, 2010, 2011; Mišić, 2011; Petoukhov, 2014; 2016; Wohlin, 2015; Rakočević, 1988-2014).

## 2. New insights

### 2.1. The problem of lanthanides arrangement in the PSE

The reason why it has not been previously noted the possible analogies between mathematics of the GC and mathematics of the PSE, lies in the fact that all 14 lanthanides are placed in the third group of PSE, i.e. at the same position where is the Lanthanum. However, this is in disagreement with Mendeleev's approach that every element in the PSE should have its own

[^32]position. Namely, the book of B.M. Kedrov (Kedrov, 1977, p. 188, Table 16) contains a variant of Mendeleev's Periodic Table, in which Mendeleev did not formally indicated the groups, but it is evident that each element occupies one position. In that Table, lanthanum is located in the third group, Cerium in the fourth group and so consequently all other 13 elements, although two elements ( $\mathrm{Pm} \& \mathrm{Lu}$ ) were not known in Mendeleev's time. (Some Mendeleev's manuscript Tables can be seen in the author website, www.rakocevcode. rs. $)^{8}$

This problem with lanthanides positions in the PSE is still actual, because recently IUPAC (International Union of Pure and Applied Chemistry) has launched a new research project which should determine whether lanthanum with atomic number 57, or the last lanthanide, Lutetium with atomic number 71, should be written in the formal Table of PSE (see Appendix D).

Following Mendeleev's methodology, it was possible to show that the 14 lanthanides require exposition into 14 groups of the PSE. Then together with zeroth group, there are 15 groups (Rakočević, 1991) (see Table 1 in this paper). If we have such an arrangement, then it is easy to recognize not only arithmetical but also some algebraic regularities in the PSE. In a previous work (Rakočević, 1991) we proposed a hypothesis that the PSE of the short period groups corresponds to the Boolean cube as well as the PSE of the long period groups to the Boolean hypercube ${ }^{9}$ the role of the $16^{\text {th }}$ group in such a case (in a cyclic ordering) plays either zeroth group or the first one. In fact we mainly pay attention to this chemical code, because it is an analog of the genetic code. ${ }^{10}$ [Mendeleev also entered the elements of the first group - copper, silver and gold - twice, at the beginning and at the end of the PSE (Kedrov, 1977, p. 128, photocopy XII).] ${ }^{11}$

### 2.2. Specific arithmetical patterns

Table 1 (in relation to Survey 2) shows that for $\left[(\mathrm{s} \& \mathrm{p})\right.$, d, f] elements, ${ }^{12}$ to the stability/instability border in PSE (to the Po-84), we have 8 times the pattern 5-3-1; then 2 times the pattern 0-3-1 and 4 times the pattern 0-0-1. All together 9-4-1 elements: 9 elements 8 times; 4

[^33]elements 2 times and 1 element 4 times; the patterns $9-4-1$ and 8-4-2 as unique and very specific mathematical expressions (Eq. 1).

Table 1. Periodic system of chemical elements with 14 lanthanides in 14 groups (Table 4.2 in: Rakočević, 1991, or Table 18 in: Rakočević, 1997b).


$$
\begin{align*}
\left(1^{2}+2^{2}+3^{2}\right. & =1+4+9) /\left(2^{1}+2^{2}+2^{3}=2+4+8\right) \\
\sum_{n=1}^{3} n^{2} & =14 \quad \sum_{n=1}^{3} 2^{n}=14 \quad \ldots \ldots . . . \tag{1}
\end{align*}
$$

$$
\begin{array}{cc}
\left(1^{1}+2^{1}+3^{1}=1+2+3\right) /\left(1^{1}+1^{2}+1^{3}=1+1+1\right) \\
\sum_{n=1}^{3} n^{1}=6 & \sum_{n=1}^{3} 1^{n}=3 \tag{2}
\end{array}
$$

|  | $\begin{aligned} & \left(\mathrm{m}^{1}, \mathrm{~m}^{2}, \mathrm{~m}^{3}\right) ; \\ & \left(\mathrm{n}^{1}, \mathrm{n}^{2}, \mathrm{n}^{3}, \ldots, \mathrm{n}^{6}\right) \end{aligned}$ | $\begin{aligned} & (\mathrm{m}=4) \\ & (\mathrm{n}=2) \end{aligned}$ | $\ldots \ldots \ldots . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . ~(3) ~$ <br> $[" m "$ as GC alphabet; "n" as binary alphabet (0, <br> $1), ~ v a l i d ~ f o r ~ t h e ~ g e n e t i c ~ c o d e ~ b i n a r y ~ t r e e . ~$ |
| :---: | :---: | :---: | :---: |
| 3. | $\mathrm{m}^{\mathrm{n}}=\mathrm{n}^{\mathrm{m}}=16$ | $(\mathrm{n}=2)$ | ["m^n" as number of doublets in Surv. $1 ;$ " $\mathrm{n}^{\wedge} \mathrm{m}$ " as number of four-codon families (16) in Table 5 as well as on the genetic code binary tree.] |

Table 2. Periodic system of chemical elements with 6 groups


The expression in Eq. (1) ${ }^{14}$ is related to the number of chemical elements in Table 1. On the other hand, the expression (2) is related to triads, diads, monads, respectively, in Table 2 and

[^34]Table 3 (in relation to Table 4). In addition one can notice that in reality to the Eq. (1) precedes Eq. (2) as a previous step in exponentiation, valid for the first three natural numbers. The expression in Eq. (3) shows the relationships within the genetic code (cf. Survey 1 and Table 5). As a special case is the set $\left\{\mathrm{m}^{1}, \mathrm{~m}^{2}, \mathrm{~m}^{3}\right\}$ in an indirect correspondence with the set $\left\{2^{1}+2^{2}+2^{3}\right\}$ in Eq. (1) what means the correspondence among genetic code and chemical code. [Eq. (1) corresponds with Table 1; Eq. (2) with Table 2 and Tables 3 \& 4; Eq. (3) with Survey 1 and Table 5.]

Remark 5. Table 1 is essentially a periodic system of short periods. As in the original works of Mendeleev, it can develop into a periodic system of long periods when it per se has a satus of a blockPSE ${ }^{15}$ as a set of adjacent groups: s-block, p-block, d-block and $\mathbf{f}$-block (Rakočević, 1991, Table 4.3 or Rakočević, 1997b, Table 19) (www.rakocevcode.rs). Otherwise, the term "Block Periodic System" as well as "Block Periodic Table" appears to have been first used by Charles Janet, which is understandable (footnote 8), because talking about blocks makes sense only if lanthanides are distributed into 14 groups. Nevertheless, all three of our 1991 Tables where just hypothetical, as it was also the hypothesis that it makes sense to consider PSE as a chemical code. However, now with this new insights into the correspondence with the genetic code, the one confirms the other: without of the PSE Tables of this kind it is not possible to understand the essence of Genetic code, and vice versa - without the insights into the correspondence with the GC we would not have any insight into the existence of a chemical code, which with the genetic code make up a unity, based at the same time on an analogous formalism as well as on a chemical essence.

In Table 2 we actually have the correspondence with the mathematical expression in Eq. (2): 1 set of monads, 1 set of diads, 1 set of triads; at the same time: within the set of monads the isotope number relationships are realized through the singlets of chemical elements; within diads through doublets, and within triads through triplets.

From the $1^{\text {st }}$ to the $8^{\text {th }}$ group, with sub-groups a, b, c, in the PSE (Table 1) are realized the elements correspondingly with the first member of the first mathematical expression in Eq. (1), in the form of $(5+3+1=9)$ elements: 5 intransitive elements ( $s$ or $p), 3$ first transitive elements ( $d$ ) and 1 second transitive element $(f)$. In the final (eighth) case, the zeroth group has the status of $8^{\text {th }}$ group, with 5 intransitive elements. [The group of noble gases has zeroth group status in terms of chemical reactivity, and the status of eighth group in terms of filling the orbitals by electrons.] After the eighth group (with sub-groups b, c) are realized the elements into the ninth and tenth group, corresponding to the second member of the mathematical expression in Eq. (1), in the form of $(3+1)$ : 3 first transitive elements ( $d$ ) and 1 second transitive element $(f)$. Finally, after tenth group, followed the groups: XI, XII, XIII and XIV, each group with one "second transitive" element $(f)$ correspondent with the third member of the mathematical expression, given in Eq. (1). [Notice that the first three periods are single, each with a single row; fourth and fifth are double, each with two rows and sixth period is threefold - it has three rows.]

Within Table 2 all isotopes (indicated in the brackets) are naturally occurring (stable plus unstable primordial). The exception is Polonium with the number of 'end nuclides', as a result of

[^35]radioactive decay of its isotopes existing in the nature in trace amounts, or synthesized: $\mathrm{Pb}-204$, $\mathrm{Pb}-205, \mathrm{~Pb}-206, \mathrm{Bi}-208, \mathrm{Bi}-209$. [This six-groups-PSE one can cf. with the first Mendeleev's Table of PSE, with 6 groups, March 13, 1869, in: Kedrov, 1977, p. 128, photocopy II; also in: Mendelejeff, 1869, reprinted in 1970.]

Let us notice that the arrangement in Table 1 corresponds to the PSE, constituted of 14 groups and 6 periods, and the arrangement in Table 2 corresponds to the PSE constituted of 6 groups and 14 periods. These two PSEs are in correspondance with each other: odd elements are in odd groups, and even element in even groups - in both systems. (Cf. Tables 4.1 \& 4.2 in: Rakočević, 1991, or Tables 18 \& 20 in: Rakočević, 1997b.) (The Reference: Rakočević, 1997b one can see in website: www.rakocevcode.rs)

### 2.3. Quantum like relationships within nucleotides arrangements

The expressions in Eq. (1-3) show the essence of coding / encoding in a natural code; it cannot be reduced only into two alphabets (which are consequences and not the cause). A natural code is such an essence that can be represented by an appropriate mathematical expression, which contains within itself a sequence from the series of natural numbers. From this follows that both, the Genetic code as well as the Periodic system of chemical elements (PSE) are natural codes.

Bearing all this in mind, the expression $\mathrm{N}=\mathrm{n}^{\mathrm{k}}$, valid for the genetic code, is "readable" in the following way: $\mathrm{n}=4 ; \mathrm{k}=3$, where 4 is the number of letters within the GC alphabet, 3 is the number of letters within a word, 2 is the root of the word, and 1 is the number of letters within one letter; altogether, $1,2,3,4$, as the sequence of the natural numbers; finely, N is the number of codons, which encode "letters" from another alphabet, i.e. molecules of AAs. As we see, both Mendeleevian principles are valid, which could not be the case, for example, for $\mathrm{n}=5$, when, in the case of validity of Mendeleevian principles, we have uncertainty about the root of the word is it of two or three letters?

The expressions in Eq. (3) show multiple relationships of nucleotide doublets and AAs in Survey 1. But in order to understand these relationships, it is necessary to analyze the relationships between nucleotide doublets arrangement in Survey 1 and arrangement in the original Rumer's Table (Table A. 1); also in order for better understand the sense of our new insight. By comparing two Tables, we find that both in the upper part contain nucleotides with 6 and 4 hydrogen bonds, respectively, that encode AAs, which have 119 atoms in their side chains. In the lower part there are nucleotide doublets with 5 and 5 hydrogen bonds, which encode AAs, which have 120 atoms in their side chains. It can therefore be said that here, in up/down direction, exists a balance with the difference for $\pm 1$ atom. However, significant differences exist from the aspect of the left/right organization (cf. Survey 1 and Survey A.1).

Remark 6. The number of atoms in the four molecules that build messenger RNA, corresponding to the GCT, is: $\mathrm{U}=12, \mathrm{C}=13, \mathrm{~A}=15, \mathrm{G}=16$; in doublets: $\mathrm{UG}=28 \times 1$ and $\mathrm{CA}=28 \times 1$. When the nucleotide form is taken, then the number of atoms is: $\mathrm{U}=34, \mathrm{C}=35, \mathrm{~A}=37, \mathrm{G}=38$; in doublets: $\mathrm{UG}=$ $36 \times 2$ and CA = $36 \times 2$. [Cf. (Rakočević, 1997a); (Rakočević, 1997b: Solutions 25-29, pp. 62-63; www.rakocevcode.rs)]. The question arises: is this a curiosity and a coincidence, or is it a certain natural-
code essence when the sums of the number of atoms per doublets correlate with the square of the first perfect number (6) and the first degree of the second perfect number (28)?

In the Rumer's Table (Table A.1) on the left side are nucleotide doubles that encode fourcodon AAs and on the right side ones that encode non-four-codon AAs. In our Table (Survey 1), however, the nucleotides are mixed; from both types, some of them are on the left and some on the right in original Rumer's Table. Nevertheless, when it looks more carefully, then it can be seen that this is a strictly symmetrical arrangement, a type of mirror symmetry. To more complex "geometric figures" (higher rank!), on the left, correspond less complex "figures" (lower rank!) on the right side: [(UC-CU-GU / CC-GG) // (AU-UA / CA-GA-AG)]; and vice versa: [(UU-AA / UG) // (AC / GC-CG)]. But that what is particularly interesting, and in some way very surprising, is the fact that all this "geometry" is accompanied by a "quantum" change for 1 unit in the second position of the decimal number record of the number of atoms: $1 \underline{1} 0$ versus $1 \underline{\mathbf{2}} 0$ and $1 \underline{2} 9$ versus 119. (For details see Surveys A. 1 and A.2).

There is also an additional question - what is the sense of the existence of a link between the left and the right side of the Rumer's Table; the link, expressed through the mirror symmetry and the quantization, presented in Surveys 1 and Surveys A.1, A.2, A.3? The possible respond is: in all here presented arrangements on the scene is a nuance principle in polarity of the amino acid molecules. [For the same reason, some AAs in GCT as well as in the "doublet-triplet" arrangement have been duplicated.] ${ }^{16}$


[^36]The generation of the 16 nucleotide doublets from four-letter genetic code alphabet, according to the expression $\mathrm{m}^{\wedge} \mathrm{n}(\mathrm{m}=4 ; \mathrm{n}=2 ; \mathrm{e}=$ exponent to alphabet " m "; an = number of atoms). If $\mathrm{e}=1$, then we have four singlets, the four bases - two pyrimidines (uracil, U; cytosine, C), with one ring in the molecule (chemically simpler), and two purine bases (adenine, A; glutamine, G), with two rings in the molecule (chemically more complex). If $\mathrm{e}=2$, then we have 16 nucleotide doublets. If these doublets are arranged in a chemical hierarchy (first simpler with two hydrogen bonds: UU, AA; then more complex, with three hydrogen bonds: CC, GG; in further steps come their variations, and first row (upper row) is made. These doublets are the same as in upper area of Rumer's Table (Table A.1). Then follows the generation of the lower row of nucleotide doublets, with the idea to present possible mirror symmetry. The result is the discovery of a "hidden" link between two sides of Rumer's Table (Table A.1): of the left side with fourcodon AAs and of the right side with non-four-codon AAs. As it is obvious, the "mirror picture" is expressed through specific "quanta" of the number of atoms in the side chains of AAs as well as through "quanta" of the sets of amino acid molecules (cf. Survey A. $1 \&$ A.2).

Survey 2. Distribution of isotopes within the PSE

## (1) Group I:

$\left\{\left[{ }_{3} \mathrm{Li}\left({ }_{(2+0)}\right)\right],\left[{ }_{11} \mathrm{Na}(\underline{\mathbf{1})}) \boldsymbol{\&}\left[{ }_{19} \mathrm{~K}(2+1)\right],{ }_{37} \mathrm{Rb}(1+1)\right],\left[{ }_{55} \mathrm{Cs}(\underline{\mathbf{1}})\right]\right\}$
$\left\{\left[{ }_{29} \mathrm{Cu}(2+0)\right],\left[{ }_{47} \mathrm{Ag}(2+0)\right],\left[{ }_{79} \mathrm{Au}(\mathbf{1})\right]\right\}$
\{[69 $\mathrm{Tm}(\mathbf{1})]\}$

## (2) Group II:

$\left\{\left[{ }_{4} \mathrm{Be}(\underline{\mathbf{1}})\right],\left[{ }_{12} \mathrm{Mg}(3+0)\right] \boldsymbol{\&}\left[{ }_{20} \mathrm{Ca}(5+1)\right],\left[{ }_{38} \mathrm{Sr}(4+0)\right],\left[{ }_{56} \mathrm{Ba}(6+1)\right]\right\}$
$\left\{\left[{ }_{30} \mathrm{Zn}(5+0)\right],\left[{ }_{48} \mathrm{Cd}(6+2)\right],\left[{ }_{80} \mathrm{Hg}(7+0)\right]\right\}$
$\{[70 \mathrm{Yb}(7+0)]\}$

## (3) Group III:

$\left\{\left[{ }_{5} \mathrm{~B}(2+0)\right],\left[{ }_{13} \mathrm{Al}(\mathbf{1})\right] \boldsymbol{\&}\left[{ }_{31} \mathrm{Ga}(2+0)\right],\left[{ }_{49} \mathrm{In}(1+1)\right],\left[{ }_{81} \mathrm{Tl}(2+0)\right]\right\}$
$\left.\left.\left\{\left[{ }_{21} \mathrm{Sc}(\mathbf{1})\right],{ }_{39} \mathrm{Y}(\mathbf{1})\right],{ }_{57} \mathrm{La}(1+1)\right]\right\}$
$\left\{\left[7{ }_{1} \mathrm{Lu}(1+1)\right]\right\}$

## (4) Group IV:

$\left\{\left[{ }_{6} \mathrm{C}(2+0)\right],\left[{ }_{14} \mathrm{Si}(3+0)\right] \&\left[{ }_{32} \mathrm{Ge}(4+1)\right],\left[{ }_{50} \mathrm{Sn}(9+1)\right],\left[{ }_{[2} \mathrm{Pb}(4+0)\right]\right\}$
$\left\{\left[{ }_{22} \mathrm{Ti}(5+0)\right],[40 \mathrm{Zr}(4+1)],\left[{ }_{72} \mathrm{Hf}(5+1)\right]\right\}$
$\{[58 \mathrm{Ce}(4+0)]\}$
(5) Group V:
$\left\{\left[{ }_{7} \mathrm{~N}(2+0)\right],\left[{ }_{15} \mathrm{P}(\mathbf{1})\right] \&\left[{ }_{33} \mathrm{As}(\mathbf{1})\right],\left[{ }_{51} \mathrm{Sb}(2+0)\right],\left[{ }_{83} \mathrm{Bi}(\underline{\mathbf{1}} \mathbf{?})\right]\right\}$
$\left\{\left[{ }_{23} \mathrm{Va}(1+1)\right],\left[{ }_{41} \mathrm{Nb}(\mathbf{1})\right],\left[{ }_{73} \mathrm{Ta}(2+0)\right]\right\}$
$\left\{\left[{ }_{59} \operatorname{Pr}(\mathbf{1})\right]\right\}$
(6) Group VI:
$\left\{\left[{ }_{8} \mathrm{O}(3+0)\right],\left[{ }_{16} \mathrm{~S}(4+0)\right] \boldsymbol{\&}\left[{ }_{34} \mathrm{Se}(5+1)\right],\left[{ }_{[2} \mathrm{Te}(6+2)\right]\right.$, $\left.\left.{ }_{84} \underline{\mathbf{P o}}(5+0)\right]\right\}$
$\left\{\left[{ }_{24} \mathrm{Cr}(4+0)\right],\left[{ }_{42} \mathrm{Mo}(6+1)\right],\left[7{ }_{74} \mathrm{~W}(4+1)\right]\right\}$
$\left\{\left[{ }_{60} \mathrm{Nd}(5+2)\right]\right\}$
（7）Group VII：
$\left\{\left[{ }_{1} \mathrm{H}(2+0)\right],\left[{ }_{9} \mathrm{~F}(\mathbf{1})\right],\left[{ }_{17} \mathrm{Cl}(2+0)\right] \boldsymbol{\&}\left[{ }_{35} \mathrm{Br}(2+0)\right],\left[{ }_{53} \mathrm{I}(\mathbf{1})\right]\right\}$
$\left\{\left[{ }_{2} \mathrm{Mn}(\mathbf{1})\right],\left[{ }_{43} \mathbf{T c}(0+0)\right],\left[{ }_{75} \operatorname{Re}(1+1)\right]\right\}$
$\{[61 \mathbf{P m}(0+0)]\}$
（8）Groups 0＋VIII：
$\left\{\left[{ }_{2} \mathrm{He}(2+0)\right],\left[{ }_{10} \mathrm{Ne}(3+0)\right],\left[{ }_{18} \mathrm{Ar}(3+0)\right] \boldsymbol{\&}\left[{ }_{36} \mathrm{Kr}(6+0)\right],\left[{ }_{54} \mathrm{Xe}(8+1)\right]\right\}$
$\left\{\left[{ }_{26} \mathrm{Fe}(4+0)\right],[44 \mathrm{Ru}(7+0)],\left[{ }_{76} \mathrm{Os}(6+1)\right]\right\}$
$\left\{\left[{ }_{62} \mathrm{Sm}(5+2)\right]\right\}$
（9）Group IX：
$\{-,-,-,-,-\}$
$\left\{\left[{ }_{27} \operatorname{Co}(\mathbf{1})\right],\left[{ }_{45} \operatorname{Rh}(\mathbf{1}],\left[{ }_{[77} \operatorname{Ir}(2+0)\right]\right\}\right.$
$\left\{\left[{ }_{63} \mathrm{Eu}(1+1)\right]\right\}$
（10）Group X：
$\{-,-,-,-,-\}$
$\left\{\left[{ }_{28} \mathrm{Ni}(5+0)\right],\left[{ }_{46} \mathrm{Pd}(6+0)\right],\left[{ }_{78} \mathrm{Pt}(5+1)\right]\right\}$
$\{[64 \mathrm{Gd}(6+1)]\}$
（11）Group XI：
$\{-,-,-,-$,
$\{-,-,-\}$
［65Tb（1］）
（12）Group XII：
$\{一,-,-,-,-\}$
$\{-,-,-\}$
$\left\{\left[{ }_{6} \mathrm{Dy}(7+0)\right]\right\}$
（13）Group XIII：
$\{一,-,-,-,-\}$
$\{一, ~-,-\}$
$\{[67 \mathrm{Ho}(\mathbf{1})]\}$
（14）Group XIV：

```
\(\{-,-,-,-,-\}\)
\(\{-,-,-\}\)
\(\left\{\left[{ }_{68} \operatorname{Er}(6+0)\right]\right\}\)
```

To proceed with new insights and analysis some explanations of Survey 2 are necessary as it follows.
I. In front of the sign " + " is the number of stable, while behind the " + " is the number of unstable primordial isotopes.
II. The order within the groups: first come intransitive elements ( $s$ or $p$ ), ${ }^{17}$ then the first transitive (d), and finally the second transitive element (f). With dark shadow tones are designated the stable elements; a total of 36: 13 odd in the odd groups and 23 even in the even groups (Survey $3 \mathrm{~b} \& 3 \mathrm{c}$ ); with light tones are unstable elements ${ }^{18}$, a total of 25 : the 8 odd in odd groups and the 17 even in even groups (Survey 3b on the left). Unshaded are the 20 stable "monoisotopic" elements ( 19 odd in odd groups, and 1 even in the even group, Be , in the second one); also unshaded are 3 radioactive elements ( $\mathrm{Tc}, \mathrm{Pm}, \mathrm{Po}$ ).
III. The presented structure of PSE is characterized by the following regularities:

1. Odd groups contain odd, and even groups contain even elements;
2. Elements of odd groups have 2 or less stable isotopes;
3. Elements of even groups, in short periods have 4 or less, while in long periods have 4 or more stable isotopes;
4. Elements of short periods have only stable isotopes (maximum of $\underline{\mathbf{0}}$ unstable primordial isotopes);
5. Elements of the odd groups of long periods have maximal $\underline{\mathbf{1}}$ unstable primordial isotope;

6 . Elements of even groups of long periods have maximal $\underline{\mathbf{2}}$ unstable primordial isotopes.

### 2.4. Specific algebraic patterns

Surveys $3 \mathrm{a}, 3 \mathrm{~b}$ and 3 c contain two key results of this research, first on the genetic code, and second one on the chemical code. Survey 3a contains the solutions of the system of two linear algebraic equations (shaded part of Survey), which appear to be in a full accordance with the distribution of codons in the genetic code through coding for $2,4,6$ and 8 amino acids (Table 5): the 25 codons encode the amino acids of the less complexity (2AAs+4AAs) [(GP)+(ALVI)] which have only carbon and hydrogen (glycine - only hydrogen!) in the side chain; and 36 codons encode the AAs of greater complexity which have, except C and H , some other elements ( $\mathrm{N}, \mathrm{O}$ or S ). The number of codons for encoding less complex AAs corresponds to the solutions of the first linear equation ( $\mathrm{x}_{1}=8$ and $\mathrm{y}_{1}=17$ ): two nonstandard hydrocarbon AAs (GP) are encoded with 8, and four standard hydrocarbon AAs (ALVI) with 17 codons. On the other hand, the number of codons for encoding more complex AAs corresponds to the solutions of the second linear equation ( $\mathrm{x}_{2}=10$ and $\mathrm{y}_{2}=26$ ): six AAs (CMFYWH) which do not have a mapping of functional groups from the "head" to the "body" (side chain), are encoded with 10, and the eight AAs (STDENQKR), which have a mapping of functional groups from the "head" to the "body" are encoded with 26 codons (Survey 3a).

[^37]
### 2.5. Key relationhips between GC and PSE

Now we go to the PSE. The solutions of the system of two linear equations (in the shaded part of Survey 3b) are in an almost wholly accordance with the distribution of chemical elements (in terms of stability/instability and odd/even parity) into periods and groups. From a total of 61 multi-isotope elements, the 25 , except stable, possess unstable primordial isotopes (light shaded tones in Survey 2); and 36 multi-isotope elements possess only stable elements (they do not have unstable primordial isotopes) (dark shaded tones in Survey 2).

| Survey 3a |  | Survey 4 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| $\begin{aligned} & y_{1}-x_{1}=3^{2} \\ & y_{1}+x_{1}=5^{2} \end{aligned}$ | $\begin{aligned} & y_{2}-x_{2}=4^{2} \\ & y_{2}+x_{2}=6^{2} \end{aligned}$ | $\begin{array}{ll} 26=\mathrm{X}=\mathbf{2 6} & 16+17+18=\mathrm{Z} \\ 26+16=\mathbf{4 2} & \mathrm{Z}=51 \\ 42+17=\mathbf{5 9} & \mathrm{Z}=\mathrm{Y} / 4 \\ 59+18=77 & \end{array}$ |  |  |  |
| $\begin{gathered} x_{1}=8 \\ y_{1}=17 \end{gathered}$ | $\begin{aligned} & x_{2}=\underline{10} \\ & y_{2}=26 \end{aligned}$ | $\begin{aligned} & 26+42+59+77=\mathrm{Y} \\ & \mathrm{Y}=204 ; \mathrm{Y} / 4=51 \end{aligned}$ |  |  |  |
| Survey 3b |  | Survey 3c |  |  |  |
| $\begin{gathered} y_{1}-x_{1}=9^{1} \\ y_{1}+x_{1}=25^{1} \end{gathered}$ | $\begin{aligned} & y_{2}-x_{2}=\frac{\mathbf{1 0}^{1}}{3} \\ & y_{2}+x_{2}=36^{1} \end{aligned}$ | a | b | c | d |
|  |  | 00 | 10 | 26 | (16) |
|  |  | 01 | 11 | 25 | (14) |
|  |  | 02 | 12 | 24 | (12) |
|  |  | 03 | 13 | 23 | (10) |
| $\begin{gathered} x_{1}=8 \\ y_{1}=17 \end{gathered}$ | $\mathrm{x}_{2}=13$ | 04 | 14 | 22 | (08) |
|  | $y_{2}=23$ | 05 | 15 | 21 | (06) |
|  |  | 06 | 16 | 20 | (04) |

The systems of linear equations as the scenarios for generating GC and PSE are given in Survey 3a and 3b, respectively; in Survey 3c there is an additional scenario for PSE with the showing why $\mathrm{x}_{2}=13$ and $\mathrm{y}_{2}$ $=23$; that comes from the fact that only in the fourth row of Surveys 3 c we have ( $03,13,23$ ), a determination with the principles of similarity and self-similarity; columns: $\mathrm{a}=\mathrm{b}-10$ and $\mathrm{d}=\mathrm{c}-\mathrm{b}$; columns "b" and "c" correspond to $\mathrm{x}_{2}$ and $\mathrm{y}_{2}$, respectively. [Survey 4 comes from Fig. 3 and Table 4 in Rakočević, 2011b. (Other details in the text).]

Further distributions are carried out through distinctions into odd and even elements - the odd elements within the odd groups and the even elements within the even groups, in both cases are in accordance with the model (the shaded part in Survey 3b). In accordance with the solutions of the first linear equations of ( $\mathrm{x}_{1}=8$ and $\mathrm{y}_{1}=17$ ), the 8 unstable and odd elements are within the odd, and 17 unstable and even elements within the even groups. On the other hand,
according to the solutions of the second linear equation ( $\mathrm{x}_{2}=13$ and $\mathrm{y}_{2}=23$ ), the 13 stable and odd elements are in odd and 23 stable and even elements in even groups. [Under the notion "unstable" we mean the chemical element, which in addition to stable isotopes, have at least one unstable primordial isotope.]

### 2.6. Some additional observations on Genetic code

At the end of the presentation of these research-insights-results, we once again return to the genetic code. Let us look at Table 3 and Table 4, in relation to Eq. (4). In Table 3 we have: monads - the numbers that appear at once; diads - twice, and triads - three times. At dark tones are the amino acids handled by enzymes of class I aminoacyl-tRNA synthetases and at light tones the amino acids handled by enzymes of class II aminoacyl-tRNA synthetases. [One can notice here a correspondence with PSE in Table 2 and with the mathematical expression in Eq. (2).]

The algorithm for "selection" of numbers in Tab. 4, going from bottom is as follows: in the first step were selected 2 numbers going up, and $\underline{\mathbf{0}}$ numbers going sideways, that is 2 vs $\underline{\mathbf{0}}$ ( $17 \&$ 18 versus nothing \& nothing); in the second step: 2 vs $\underline{\mathbf{2}}$ ( $7 \& 14$ versus $13 \& 15$ ); third step: 2 vs $\underline{4}(1 \& 4$ versus $5 \& 10$ and $8 \& 11)$; in the fourth step would be 2 vs $\underline{6}$, etc. (Eq.4).

In Table 4 we actually have the relationships within the atom number arrangement in Table 3, which arrangement corresponds with the mathematical expression in Eq. (2) in the next sense: 1 set of monads, 1 set of diads, 1 set of triads; at the same time: within the set of monads each number appears just once, within the set of diads - twice, and within the set of triads - three times. On the other hand, the "choices" presented in Eq. (4) are agreed with a specific algorithm which corresponds with Generalized Golden Mean (GGM), through "metallic means family", for $\mathrm{q}=2,6,12,20, \ldots$ (Rakočević, 2004b, p. 97).

With first choice there are $\underline{\mathbf{2}}$ number-patterns: $18 \& 17$; with the second one there are $\underline{\mathbf{6}}$ number-patterns: $(18 \& 17)+[(14 \& 07)+(13 \& 15)]$; with the third choice there are $\underline{\mathbf{1 2}}$ number-patterns: $(18 \& 17)+[(14 \& 07)+(13 \& 15)]+[(04 \& 01)+(05 \& 10)+(08 \& 11)]$. With this third choice there are all number-patterns for the number of atoms in amino acid molecules, within their side chains ( 12 patterns in Table 4 follow from 20 numbers, presented in Table 3). By all this, we can notice a regularity, valid for the GGM series, expressed in Eq. (4) and related to Eq. (5).


Remark 7. Within four diversity types of 2-4-6-8 AAs there is the number of atoms as follows. Within the "heads" 180 atoms: I.GP 18; II.ALVI 36; III.CMFYWH 54; IV.STDENQKR 72); within the
side chains 204 atoms: I.GP 9; II.ALVI 40; III.CMFYWH 74; IV.STDENQKR 81; in total, as in Eq. (5) where we have an example of self-similarity: in two inner groups, with 10 AAs, there are 204 atoms as in 20 side chains. On the other hand, in two outer groups, also with 10 amino acids, there are 180 atoms as in 20 amino acid heads. There is also a significant relation to the system, presented in Survey 4: [I.GACNP (26); II.SDTQH (42); III.YMEVL (59); IV.WRFIK (77)], which system follows from a unique arithmetical arrangement of natural numbers from 01 to 99 (Table 4 in relation to Figure 3 in Rakočević, 2011b).

Remark 8. If the Multiplication table in the decimal numbering system is written in an adequate way (Table 1.1 in: Rakočević, 2011b, p. 822) then the numbers per diagonal: $0,2,6,12,20,30, \ldots$, are also recognized as values for $q$ in the equation of the Generalized golden mean $\mathrm{x}^{2}+p \mathrm{x}=q(q=0,2,6,12,20$, $30, \ldots$ ) in the set of the family of "metallic means" (Spinadel, 1998, 1999; Rakočević, 2004b). The solutions of equations in such cases are generated from a set of natural numbers: $(0,1),(1,2),(2,3),(3$, 4), (4, 5), ...; [First family of "metallic means": "golden mean" $(\mathrm{p}=1 ; \mathrm{q}=1)$; "silver mean" $(\mathrm{p}=2 ; \mathrm{q}=1)$; "bronze mean" $(\mathrm{p}=3 ; \mathrm{q}=1), \ldots$; the second family of "metallic means": "golden mean" $(\mathrm{p}=1 ; \mathrm{q}=1)$; "copper mean" ( $\mathrm{p}=1 ; \mathrm{q}=2$ ), "nickel mean" $(\mathrm{p}=1 ; \mathrm{q}=3, \ldots)$.]

Remark 9. Double values of the numbers found on the diagonal of Multiplication table: 0, 4, 12, 24, 40, $60, \ldots$, are also recognized as values of one of the cathetus of Diophantus' triangles: $0 .(1, \underline{0}, 1), 1 .(5,4,3), 2$. $(13, \underline{12}, 5), 3 .(25, \underline{24}, 7), 4 .(41, \underline{40}, 9), 5 .(61, \underline{60}, 11), \ldots$, etc. Knowing above presented connections with the generalized golden mean, and that the genetic code is also determined by the golden mean (Rakočević, 1998b), we understand the finding of V. Shcherbak, according to which the coding of four-codon amino acids "goes" over the Pythagorian triplet $(5,4,3)$ (Shcherbak, 1994).

Remark 10. From the fact that the logic of the choices of the quantities of the number of atoms corresponds with the number sequence in Eq. (4), and this sequence ( $0,2,6,12,20 \ldots$ ) corresponds to the generalized golden mean and Diophantus' triangles at the same time, it follows that the choice of the quantitees of the number of atoms is also determined by both - by the generalized golden mean and by the set of Diophantus' triangles. [Quantities of the number of atoms: all different in monads; more quantities are the same in diads, as well as in triads, in Table 3.]

Remark 11. From the fact that Eq. (4) corresponds with Eq. (5) through the sequence of the first even numbers ( $2,4,6,8$ ), from the series of natural numbers, it follows that classification of amino acids into presented four classes is also determined by both - by the generalized golden mean and by the set of Diophantus' triangles.

Table 3. The number of atoms in the protein AAs (in their side chains)

| Monads | Diads |  | Triads |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| G 01 | C 05 | S 05 | T 08 | P 08 | N 08 |
| A 04 | V 10 | E 10 | Q 11 | M 11 | H 11 |
| D 07 | L 13 | 113 |  |  |  |
| F 14 | Y 15 | K 15 |  |  |  |
| R 17 |  |  |  |  |  |
| W 18 |  |  |  |  |  |

(Explanation in the text)

Table 4. The relationships to the atom number arrangement in Table 3

| $\mathbf{1}$ | $\mathbf{2}$ | $\mathbf{3}$ |  |  |
| :---: | :---: | :---: | :---: | :---: |
| 01 | 05 | 08 | $\boldsymbol{7}$ | $\mathbf{3}$ |
| 04 | 10 | 11 | $\rightarrow$ | $\mathbf{3}$ |
| 07 | 13 | - | $\rightarrow$ | $\mathbf{2}$ |
| 14 | 15 | - | $\rightarrow$ | $\mathbf{2}$ |
| 17 | - | - | $\rightarrow$ | $\mathbf{1}$ |
| 18 | - | - | $\rightarrow$ | $\mathbf{1}$ |
| $\mathbf{6}$ | $\mathbf{4}$ | $\mathbf{2}$ | $(12)$ |  |
| $\mathbf{6}$ | $\mathbf{8}$ | $\mathbf{6}$ | $(20)$ |  |

Table 5. The standard genetic code with new design

| 1st | 2nd letter |  |  |  | 3rd |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  | U | C | A | G |  |
| U | UUU  <br> UUC F <br> uua L <br> uug  | UCU <br> UCC <br> UCA <br> S <br> UCG |   <br> UAU  <br> UAC $\mathbf{Y}$ <br> UAA  <br> UAG CT | UGU C <br> UGC  <br> UGA CT <br> UGG $\mathbf{W}$ | $\begin{aligned} & \hline U \\ & C \\ & A \\ & G \end{aligned}$ |
| C | cuu  <br> cuc  <br> cua  <br> cug  | ccu  <br> ccc  <br> cca $\mathbf{P}$ <br> ccg  | CAU  <br> CAC $\mathbf{H}$ <br> CAA $\mathbf{Q}$ <br> CAG $\mathbf{Q}$ | CGU  <br> CGC  <br> CGA $\mathbf{R}$ <br> CGG  | $\begin{aligned} & \hline U \\ & C \\ & A \\ & G \end{aligned}$ |
| A | $\begin{array}{\|cc} \text { auu } & \\ \text { auc } & \mathbf{I} \\ \text { aua } & \\ \text { AUG } & \mathbf{M} \\ \hline \end{array}$ | $\begin{array}{\|ll\|} \hline \text { ACU } & \\ \text { ACC } & \\ \text { ACA } & \mathbf{T} \\ \text { ACG } & \\ \hline \end{array}$ | $\begin{array}{ll} \hline \text { AAU } & \mathbf{N} \\ \text { AAC } & \mathbf{N} \\ \text { AAA } & \mathbf{K} \\ \text { AAG } & \end{array}$ | AGU  <br> AGC $\mathbf{S}$ <br> AGA  <br> AGG $\mathbf{R}$ | $\begin{aligned} & \hline U \\ & C \\ & A \\ & G \end{aligned}$ |
| G | $\begin{aligned} & \text { guu } \\ & \text { guc } \\ & \text { gua } \\ & \text { gug } \end{aligned}$ | $\begin{aligned} & \text { gcu } \\ & \text { gcc } \\ & \text { gca } \\ & \text { gcg } \end{aligned}$ | GAU <br> GAC <br> D <br> GAA <br> GAG <br> E | $\begin{array}{ll} \operatorname{ggu} & \\ \text { ggc } & \mathbf{G} \\ \text { gga } & \\ \text { ggg } & \end{array}$ | $U$ $C$ $A$ $G$ |

The design responds to the classification of protein AAs into four classes, correspondently with four diversity types. The first diversity type (GP): the 8 codons in small non-bolding letters; second type (ALVI), the 17 codons in small bolding letters; third type (CMFYWH), the 10 codons in large letters and light shadow tones; fourth type (STDENQKR): the 26 codons in large letters and dark shadow tones. The three codons which are cross out, are the "stop" codons (cf. Survey 3a and Survey 4 in this paper with illustrations in Rakočević, 2011b: Tab. 4, Eq. 3 and Eq. 4 on pp. 826-827; Table. 6 on p. 829).

## 3. Discussion

For discussion of the obtained results, it is worth mentioning the current understanding of isotopy science, and hence we quote the comment of IUPAC, supplied with the official "Periodic Table of Isotopes":
> "Standard atomic weights are the best estimates by IUPAC of atomic weights that are found in normal materials, which are terrestrial materials that are reasonably possible sources for elements and their compounds in commerce, industry, or science. They are determined using all stable isotopes and selected radioactive isotopes (having relatively long half-lives and characteristic terrestrial isotopic compositions). Isotopes are considered stable (non-radioactive) if evidence for radioactive decay has not been detected experimentally" (IUPAC Project 2007-038-3-200, "Development of an isotopic periodic table for the educational community", October 1, 2013, www.ciaaw.org). ${ }^{19}$

It is understood that the discussion of isotopes of chemical elements within the scientific community is strictly limited to planet Earth, because that is what we do know from the experiments. However, if it is possible to find a theoretical model, an arithmetic-algebraic scenario, that is, at a given moment of evolution of scientific knowledge, agreed with the distribution of chemical elements in the PSE, in terms odd-even parity of elements and their isotopes stability (moreover, agreed with corresponding distributions in the GC), then it should be that this model is valid for the whole universe, due to the fact that the content of the universe consists of one and the same type of chemical elements and their isotopes.

However, having in mind the fact that the stability/instability of isotopes is experimentally determined (certainly by the best and most reliable laboratories, in terrestrial conditions), it must be said that the presented accordance with the models in Surveys 3a, 3b and 3c, although one hundred percent, or near to be one hundred percent, it is only one very distinctive trend, which should serve for further researches in both directions: for checking experimental results, and parallel with this, for checking the accordance with the models presented in Surveys 3a, 3b and 3c.

In the current state of affairs, what may possibly spoil a 100-percent accordance, it might be in the next. In relevant literature one can see that potentially three of ten isotopes of tin are radioactive, but have not been observed to decay. One of these three actually has been identified as $\mathrm{Sn}-124$, and in IUPAC sources is indicated its half-life decay larger than $1 \times 10^{17}$ years. In addition, one of the seven (stable) isotopes of Gadolinium (Gd-152) we take to be unstable with a half-life decay of $1.08 \times 10^{14}$ years, while the isotope (Gd-160) with a half-life decay larger than $1.3 \times 10^{21}$ remained in a stable status. Overall, we marked the isotopic state of Gadolinium

[^38]$(6+1)$. These are only two our interventions in relation to the IUPAC document which are, as follows from the above, also consistent with the understanding of isotopy in current science. ${ }^{20}$

### 3.1. Another understanding of the periodic system

For an additional understanding of the PSE shown in Table 1 in the form of 6 periods and 14 groups, it is necessary to include a specific variant of the PSE which is inversely related in the sense that it consists of 14 periods and the 6 groups (Table 2).

The arrangement of elements in the PSE in Table 2 is such that the odd elements are in odd and even elements in even groups, in the same way as in the PSE presented in Table 1. From this it follows that the same regularities, indicated in the explanations in Survey 2 (Section III), are valid for both, PSE in Table 1 as well as in Table 2. In addition, here we also find additional regularities. For them it is necessary to note that the arrangement of the PSE in Table 2 can be read in two ways: first, as indicated monads, diads and triads of columns, i.e. groups; and second, as odd and even groups (I, II, III, IV, V, VI). Correspondent comparisons (the left column of diads vs right column; left column of triads vs right; then, the first column vs third, the second vs fourth, etc.) show that the trend in differences, in the number of naturaly occurring isotopes, is such, that these differences, in 10 or more cases (from total 14), is less than 2 . A maximum of two times, there are differences of 2 or 3 isotopes; altogether, all differences are within the frame of the set $\{0,1,2,3\}$, that is of a "logical square".

### 3.2. Another similarities

From Table 4 it is self-evident that here we have two solutions: the number of moleculespatterns in 20 canonical AAs is 6-4-2 as the sum of number-patterns in monads-diads-triads; on the other hand real sum of amino acid molecules is $6+8+6=20$. The pattern „ $686^{\prime \prime}$ corresponds to the number 686 in decimal numbering system, which is the number of protons in 20 amino acids (within their side chains), what means a similarity and self-similarity. If we exclude the number of hydrogen atoms, that is hydrogen protons $(58+59=117)$ of all 20 side chains, then remain 569 protons +569 neutrons. At the same time, from Sukhodolets' system (Table C. 2 in this paper in relation to Table 7, p. 830 in Rakočević, 2011b) follows a symmetrical division of AAs into two sub-classes with 58 and 59 hydrogen atoms, respectively.

### 3.3. Some additional observations

The simplest chemical elements as nonmetal atoms, in the PSE, are:

$$
\begin{equation*}
\mathrm{H}+\mathrm{C}+\mathrm{N}+\mathrm{O} \Rightarrow 4 \text { simplest nonmetal atoms } \tag{6}
\end{equation*}
$$

Their simplest compounds are methane, ammonia, water and carbon monoxide:

[^39]\[

$$
\begin{equation*}
\mathrm{CH}_{4}+\mathrm{NH}_{3},+\mathrm{H}_{2} \mathrm{O}+\mathrm{CO} \Rightarrow 4 \text { related simplest molecules } . \tag{7}
\end{equation*}
$$

\]

Their functional groups are:

$$
\begin{equation*}
\mathrm{CH}+\mathrm{NH}_{2},+\mathrm{OH}+\mathrm{CO} \Rightarrow 9 \text { atoms } \tag{8}
\end{equation*}
$$

The first possible organic molecule which takes into account all these groups is the simplest possible amino acid - glycine.

Then, we ask the Shcherbak's "mathematical trace" for nucleon number in 9 atoms:

$$
\begin{equation*}
\mathrm{CH} 13+\mathrm{NH}_{2} \mathbf{1 6}+\mathrm{OH} 17+\mathrm{CO} 28=74(2 \times 37) \tag{9}
\end{equation*}
$$

So much, in fact, there are nucleons in the "head" of amino acid ( 35 protons and 39 neutrons).
To better understand the above presented facts and analogies, in a future research it would be also the worth to take into account that both, the PSE and the GC, satisfy the golden mean property. ${ }^{21}$ [The GC satisfies the golden mean, over the set of all atoms (Rakočević, 1998b, 2011b) as well as through the number of carbon atoms in 20 amino acids (Yang, 2000).] This should in particular be kept in mind for further testing "a new standpoint for addressing questions of selection vs random drift in the evolution of the code" (Swanson, 1984).

## 4. Conclusion

Considering the periodic system of chemical elements as a chemical code, then one can observe certain analogies between this code and the genetic code. This paper is just devoted to analogies between these two codes. The presented research-insights-results show that the key to these analogies are specific relationships. Namely, within the genetic code there are exactly 61 codons wich encoding amino acids, plus 3 stop codons, plus 20 protein amino acids. On the other hand, within the chemical code there are exactly 61 entities in the form of stable isotopes, plus 3 unstable isotopes (Technetium, Promethium and Polonium), plus 20 „non-isotope" entities ( 20 "monoisotope" elements). Thus, altogether there are 84 entities within the genetic as well as 84 entities within the chemical code.

Moreover, the obtained analogies contain also a deeper connection between the genetic code and the periodic system of chemical elements. For example, inside 61 codons 25 of them encode the amino acids of less complexity (GP+ALVI), and 36 codons encode the AAs of greater complexity (CMFYWH+STDENQKR). Analogies can be further expanded by splitting less complex and more complex sets of AAs into subsets (indicated in parentheses). The distribution of codons is related to solutions of the system of two linear equations presented in the upper part of Survey 3a ( 8 codons for GP and 17 codons for ALVI equals 25 codons; 10 codons for CMFYWH and 26 codons for STDENQKR equals 36 codons) (Table 5).

Analogies with chemical code are as follows. From total 61 multi-isotope elements, 25 of them, except stable, possess unstable primordial isotopes; in accordance with the solutions of the first linear equation ( $x_{1}=8$ and $y_{1}=17$ ), in Survey 3a, where the 8 unstable and odd elements are within the odd, and 17 unstable and even elements within the even groups. On the other hand,

[^40]according to the solutions of the second linear equation ( $\mathrm{x}_{2}=13$ and $\mathrm{y}_{2}=23$ ), in Survey 3b, where the 13 stable and odd elements are in odd and 23 stable and even elements in even groups.

In addition to the analogies of the number of isotopes, and the number of codons, there is an analogy more through the number of the chemical elements (in the arrangement of PSE with 6 groups - Table 2) and the number of atoms in the 20 protein AAs (Table 4): in both cases the order is made through the monads, diads and triads - with the singlets, doublets and triplets, respectively.

At the end, there is a sense to assume that regularities in the genetic code are caused, at least partially, by regularities in the periodic system of chemical elements.

## Acknowledgement

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## Appendix A. Two amino acid classes: four-codon and non-four-codon AAs

Table A.1. The Rumer's classification of amino acids into two classes

| 114 | $\begin{gathered} \hline 30 \\ 116 \end{gathered}$ | (119) | $\begin{gathered} \hline 89 \\ 108 \end{gathered}$ | 125 |
| :---: | :---: | :---: | :---: | :---: |
| Gly | GG (6) | Phe | UU (4) | Leu |
| Pro | CC (6) | Asn | AA (4) | Lys |
| Arg | CG (6) | lle | AU (4) | Met |
| Ala | GC (6) | Tyr | UA (4) | ct |
| Thr | AC (5) | His | CA (5) | Gln |
| Val | GU (5) | Cys | UG (5) | Trp |
| Ser | UC (5) | Asp | GA (5) | Glu |
| Leu | CU (5) | Ser | AG (5) | Arg |
| 125 | $\begin{gathered} 36 \\ 106 \\ \hline \end{gathered}$ | (120) | $\begin{gathered} 84 \\ 118 \end{gathered}$ | 114 |
|  | 0-66 |  | $330 \pm 00$ |  |
| $\begin{aligned} 125+114 & =239 \\ 125-114 & =11 \end{aligned}$ |  |  |  |  |

The four-codon amino acids are on the left and the non-four-codon amino acids on the right. Each of two classes is classified into two subclasses, corresponding to the number of hydrogen bonds in the nucleotide doublets. At the bottom (shaded) - the number of atoms in the amino acid molecules (side chains): within 32 amino acid molecules on the left and 29 on the right, within the set of " 61 " amino acid molecules, each molecule encoded by one codon. [There are the same results, 330-66 (as $8 \times 33$ ) and 330 (as $10 \times 33$ ) in standard GCT, both in relation with the result ( $9 \times 33$ ) $\pm 1$ as we have shown in a previous work (Rakočević, 2004a, Table 3a on p. 224).] Up/down: 119/120 atoms in 11/12 amino acids (side chains), respectively, within the set of " 23 " amino acids. [Calculations: $(30+89=119)$; $(36+84=120)$; $(30+84=$ $114) ;(36+89=125)$.] Up/down: $(116 / 1 \underline{0} 8 / / 106 / 1 \underline{8})$ as the number of atoms within nucleotide doublets. (Note: In originsl Rumer's Table only the number of hidrogen bonds is calculated; all other calculations are ours.)

Table A.2. The Shcherbak's Table of multiples of "Prime quantum 037" (Table 1 in: Shcherbak, 1994).

| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 037 | 074 | 111 | 148 | 185 | 222 | 259 | 296 | 333 |
| 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
| 370 | 407 | 444 | 481 | 518 | 555 | 592 | 629 | 666 |
| 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 |
| 703 | 740 | 777 | 814 | 851 | 888 | 925 | 962 | 999 |

The Shcherbak's basic Table indicates that the determination of the number of nucleons within amino acid molecules occurs by the multiples of number 037 (as a "Prime Quantum"), by the numbers with the same digits ( $111,222,333$ etc.) or by the permutations of the obtain different cipher multiples.

Survey A.1. Relationships between AAs in Rumer's Table in accordance with the quantumblock "Aufbau" principle


In the first four rows there are four-codon AAs (from the left side in Table A.1) and in the second four rows non-four-codon AAs (from the right side in Table A.1). In the first case, the "blocks" of AAs differ by 01 atom, and in the second case by 11 . The designations: mn - number of molecules; an - number of atoms; at the bottom: "aln" for AAs of alanine stereochemical type; "n-aln" for

AAs of non-alanine stereochemical types (Rakočević \& Jokić, 1996); "Total atom number" - the number of atoms within 23 AAs (side chains) in standard GCT.

Survey A.2. Relationships between Rumer's Table in Table A-1 and our Table in Survey 1

| 1 | Quantum "30-01" <br> (ac) T (dn, right) <br> (gc, cg) A, R (up, right) | 6 | $\begin{aligned} & \text { Quantum "89+11" } \\ & (\text { (ca, ga, ag) HQ, DE, SR (dn, right) } \\ & (\text { au, ua) IM, Y (up, right) } \end{aligned}$ | 129 |
| :---: | :---: | :---: | :---: | :---: |
| 2 | $\begin{aligned} & \text { Quantum "30" } \\ & (\mathrm{gg}, \mathrm{cc}) \text { G, P (up, left) } \\ & (\mathbf{g c}, \mathbf{c g}) \mathbf{A}, \mathbf{R} \text { (up, right) } \end{aligned}$ | 5 | $\begin{aligned} & \text { Quantum "89" } \\ & \text { (uu, aa) FL, NK (up, left) } \\ & (\text { au, ua) IM, Y (up, right) } \end{aligned}$ | 119 |
| 3 | Quantum "36" <br> (ac) T (dn, right) $(g u, c u, u c) V, L, S(d n, l e f t)$ | 8 | $\begin{aligned} & \text { Quantum "84" } \\ & \left(\begin{array}{l} \text { (ca, ga, ag) HQ, DE, SR (dn, right) } \end{array}\right. \\ & (u g) C W(d n, \text { left }) \end{aligned}$ | 120 |
| 4 | $\begin{aligned} & \text { Quantum "36+01" } \\ & (\mathrm{gg}, \mathrm{cc}) \mathrm{G}, \mathrm{P}(\mathrm{up}, \text { left }) \\ & (\mathrm{gu}, \mathrm{cu}, u c) V, L, S(d n, l e f t) \end{aligned}$ | 7 | $\begin{aligned} & \text { Quantum "84-11" } \\ & \text { (uu, aa) FL, NK (up, left) } \\ & \text { (ug) } C W \text { (dn, left) } \end{aligned}$ | 110 |

The whole arrangement is in relation to the arrangement of AAs in Survey A.1. On the left are four-codon AAs and on the right non-four-codon AAs (as in Table A.1). The designations "up", "dn" (down), "left" and "right" refer to the positions in Survey 1. Amino acids at the positions indicated by the numbers 1-8 correspond to the amino acids at the same positions in Survey A-1.

Survey A.3. Relationships between the rows in Survey A. 1

| (1-6) | $(30-1)+(89+11)$ | $=$ |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| (1-5) | $(30-1)+(89+00)$ | $=$ | 118 |  |  |
| (2-6) | $(30-0)+(89+11)$ | $=$ | 130 |  |  |
| (2-5) | $(30-0)+(89+00)$ | $=$ | 119 | 119 |  |
|  |  |  |  | 109 | 130 |
| (3-8) | $(36+0)+(84+00)$ | $=$ | 120 |  | 120 |
|  |  |  |  |  | 110 |
| (3-7) | $(36+0)+(84-11)$ | $=$ | 109 |  |  |
| (4-8) | $(36+1)+(84+00)$ | $=$ | 121 |  |  |
| (4-7) | $(36+1)+(84-11)$ | $=$ | 110 |  |  |

The relationships are such that they show changes for the unit in the first, second and / or third position in the record of the number of atoms in the amino acids (in their side chains). At the same time, it is obvious that some sequences are generated from the series of natural numbers (two last columns).

Appendix B. Two amino acid classes: AAs handled by class I and AAs handled by class II of enzymes aminoacyl-tRNA synthetases, respectively

Table B.1. The Combined Genetic Code Table (Rakočević, 2007a)


This new Table of the genetic code is realized in a specific combination of standard GCT and Swanson's Codon Path Cube (Swanson, 1984). In the combination are three different permutations from the total of 24. Bold positions (and dark tones): codons coding for AAs handled by class II of enzymes aminoacyltRNA synthetases (aaRS); non-bold positions: codons coding for AAs handled by class I of aaRS plus three "stop" codons, denoted with asterisk. As it is obvious, two groups of AAs are completely separated [Class I: (LVIM)+(YQERWC); Class II: (FSPTA)+(HDNKG)]. For the process of combining, the agreement-disagreement principle (Section 1.2) is valid as follows. In the standard GCT for all three positions in the codon (first, second and third letter), we have the maximal agreement - the same permutation (UCAG) all three times, but there is no agreement in the distinction into two classes in two separated areas (Wetzel, 1995). In the Codon Path cube the agreement in permutations is lower: for the first and second positions the UCGA and for the third position CUAG permutation; lower agreement in
permutations, but greater in terms of separation into two classes of AAs, almost complete separation with one exception (Rakočević, 1997a). Finally, if we combine the GCT and Codon Path Cube, in the way shown here, we have a more lower agreement on permutations, but the greater agreement regarding the separation into two classes, they are completely separated. Apparently, this is also an analogy with the Heisenberg principle of uncertainty. [UCAG is used in the inner part of the Table for the first letter, and in the external part is UCGA permutation; for the third letter: in the inner part of the Table is UCGA, and in the external part CUAG permutation; UCGA permutation for both parts of the Table is valid for the second letter.]

Appendix C. Two amino acid classes: AAs with odd and AAs with even number of hydrogen atoms

Table C.1. The Sukhodolets' Table of the number of hydrogen atoms

| n | Amino acids | Codon root |  |  |
| :---: | :---: | :---: | :---: | :---: |
|  |  | First letter | Secon | letter |
| 5 | Gly | G | G |  |
| 7 | Ala Ser Asp cys | $G U \quad G U$ | C C | A G |
| 8 | Asn | A | A |  |
| 9 | Pro Thr Glu His | CA G C | C C | A A |
| 10 | Gln | C | A |  |
| 11 | Val Phe Met Tyr | $G U \quad A \cup$ | U U | U A |
| 12 | Trp | U | G |  |
| 13-14 | Leu lle Arg Lys | $C \mathrm{~A}$ C A | U U | G A |

The number of hydrogen atoms ( n ) within amino acid molecules, in relation to natural numbers series: 5 , (6), 7, 8, 9, 10, 11, 12, 13, 14 (Sukhodolets, 1985). First letter plus second letter equals a codon root (nucleotide doublet). The codon root plus third letter equals a complet codon. [Cf. this regularity of the hydrogen atoms within amino acids (in relation to natural number sequence) with the regularity of total number of atoms within nucleotides in standard GCT: within 64 codons ( 192 nucleotides) there are 2 x 3456 atoms; 3456 in two inner as well as in two outer columns.]

Table C.2. The Sukhodolets' Table of the number of hydrogen atoms (Rakočević, 2011b)

| The number of H atoms (in brackets) and nucleons |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| G (01) 01 | A (03) 15 | S (03) 31 | D (03) 59 | C (03) 47 |  | 153 |  |
| $\mathrm{N}(04) 58$ | P (05) 41 | T (05) 45 | E (05) 73 | H (05) 81 | (24) | 298 | (59/58) |
| Q (06) 72 | $\mathrm{V}(07) 43$ | F (07) 91 | M (07) 75 | Y (07)107 | (34) | 388 | 569/686 |
| W (08) 130 R | $R(10) 100$ | K (10) 72 | I (09) 57 | L (09) 57 |  | 416 |  |
|  | $\begin{aligned} & 9 \text { as neutron } \\ & 9-59=627 \\ & 6-58=628 \end{aligned}$ | number and $-117$ | $686 \text { as pr }$ | oton numbe |  |  |  |

Table C.2. The Sukhodolets' system of amino acids in a $4 \times 5$ arrangement. The Sukhodolets' Table, with a minimal modification (Sukhodolets, 1985): the system of $4 \times 5$ AAs. The shadow space: AAs with even number of hydrogen atoms ( $4,6,8,10$ ); the non-shadow space: AAs with odd number of hydrogen atoms ( $1,3,7,9,11$ ). In brackets: number of hydrogen atoms (within amino acid side chain) and out of brackets the number of nucleons. Nucleon number through a specific "simulation": 569 nucleons within two outer rows, as the number of neutrons,

569 , in all 20 AAs - within their side chains; and 686 nucleons within two inner rows, as the number of protons, 686, in all 20 AAs - within their side chains. Within 20 side chains of amino acid molecules there are 569 neutrons as well as 569 non-hydrogen protons. Within 20 side chains of amino acid molecules there are 117 hydrogen protons, what means 117 hydrogen atoms at the same time $(117=59+58)$.

Appendix D. "Project Details The constitution of group 3 of the periodic table" (IUPAC document)
"Project No.: 2015-039-2-200; Start Date: 18 December 2015; Division Name: Inorganic Chemistry Division; Division No.: 200

## Objective

This project will deliver a recommendation in favor of the composition of group 3 of the periodic table as consisting either of

1. the elements $\mathrm{Sc}, \mathrm{Y}, \mathrm{Lu}$ and Lr , or
2. the elements Sc, Y, La and Ac.

The task group does not intend to recommend the use of a 32 -column periodic table or an 18 -column. This choice which is a matter of convention, rather than a scientific one, should be left to individual authors and educators. The task group will only concern itselve with the constitution of group 3. Once this is established, one is free to represent the periodic table in an 18 or 32 column format.

## Description

The question of precisely which elements should be placed in group 3 of the periodic table has been debated from time to time with apparently no resolution up to this point. This question has also received a recent impetus from several science news articles following an article in Naturê̂ magazine in which the measurement of the ionization energy of the element lawrencium was reported for the first time.

We believe that this question is of considerable importance for chemists, physicists as well as students of the subject. Students and instructors are typically puzzled by the fact that published periodic tables show variation in the way that group 3 of the periodic table is displayed. The aim of the project is to assemble a task group to make a recommendation to IUPAC regarding the membership of group 3 of the periodic table.

Various forms of evidence have been put forward in support of each version of group 3. In the basis of this evidence arguments have been proposed while appealing to chemical as well as physical properties, spectral characteristics of the elements and criteria concerning the electronic configurations of their atoms. The task force will aim to evaluate all this evidence in order to reach a conclusion that encompasses these different approaches.

## Progress

March 2016 - Project announcement published in Chem. Int. March 2016, p. 22;
http://dx.doi.org/10.1515/ci-2016-0213
Page last updated 19 March 2016" (Original text from IUPAC document)

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## 16.

# Genetic code: Chemical Distinctions of Protein Amino Acids 

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In the work it is shown that 20 protein amino acids ("the canonical amino acids" within the genetic code) appear to be a whole and very symmetrical system, in many ways, all based on strict chemical distinctions from the aspect of their similarity, complexity, stereochemical and diversity types. By this, all distinctions are accompanied by specific arithmetical and algebraic regularities, including the existence of amino acid ordinal numbers from 1 to 20. The classification of amino acids into two decades (1-10 and 11-20) appears to be in a strict correspondence with the atom number balances. From the presented "ideal" and "intelligent" structures and arrangements follow the conclusions that the genetic code was complete even in prebiotic conditions (as a set of 20 canonical amino acids and the set of $2+2$ pyrimidine / purine canonical bases, respectively); and the notion "evolution" of the genetic code can only mean the degree of freedom of standard genetic code, i.e. the possible exceptions and deviations from the standard genetic code. [This is the second version with minimal interventions in the text. In addition, one passage was added in front of the second star, with quoting of T. Jukes. Added is Remark 4 and a more adequate shading in the Table inside Box 2.]

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Atom number balance, ordinal amino acid number, genetic code, canonical amino acids, protein amino acids.

# Genetic code: Chemical Distinctions of Protein Amino Acids 

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#### Abstract

In the work it is shown that 20 protein amino acids ("the canonical amino acids" within the genetic code) appear to be a whole and very symmetrical system, in many ways, all based on strict chemical distinctions from the aspect of their similarity, complexity, stereochemical and diversity types. By this, all distinctions are accompanied by specific arithmetical and algebraic regularities, including the existence of amino acid ordinal numbers from 1 to 20. The classification of amino acids into two decades (1-10 and 11-20) appears to be in a strict correspondence with the atom number balances. From the presented "ideal" and "intelligent" structures and arrangements follow the conclusions that the genetic code was complete even in prebiotic conditions (as a set of 20 canonical amino acids and the set of $2+2$ pyrimidine / purine canonical bases, respectively); and the notion "evolution" of the genetic code can only mean the degree of freedom of standard genetic code, i.e. the possible exceptions and deviations from the standard genetic code. [This is the second version with minimal interventions in the text. In addition, one passage was added in front of the second star, with quoting of T. Jukes. Added is Remark 4 and a more adequate shading in the Table inside Box 2.]


Keywords. Genetic code; Protein amino acids; Canonical amino acids; Atom number balance; Ordinal amino acid number.

From a chemical point of view the first step of classification of protein amino acids (AAs), "the canonical amino acids" within genetic code, must be the classification into aliphatic and aromatic AAs, where on a hierarchical scale of changes by similarity and complexity, aliphatic AAs must precede the aromatic. For the same reason of the chemical hierarchy, within the class of aliphatic AAs at the beginning must be the hydrocarbon AAs (possesing in the side chain carbon and hydrogen, or hydrogen only, in the case of glycine), and at the end two sulfur AAs, quite different from preceded non-sulphuric AAs. This means that two sulfur AAs [as last in class of aliphatic AAs] must be found in a direct contact to the aromatic ones.

In further course of sequencing of AAs, in terms of changes by similarity, from the aspect of the AAs singlets and/or doublets, i.e. pairs, it should be considered appropriate distinctions in three areas: in the hydrocarbon, aromatic, and that between them. In the set of aromatic AAs, Phe came first, as the simplest, followed by Tyr, and Trp, all three with possession of a benzene ring. At the very end ultimately must be His, the only one who does not possess the aromatic benzene ring. In the set of hydrocarbon AAs, at the very beginning must be Gly as the simplest one. Follows Ala as the first possible case of hydrocarbon series with an open carbon chain. Then come Val and Pro, both with three carbon atoms in the side chain, rather than Leu and Ile with four carbon atoms. By this, Val with half-cyclic chain precedes Pro with cyclic one; also Ile precedes Leu, as more similar with Pro. [The details of the relationship between Val and Pro, see in: Rakočević \& Jokić, 1996; on the relationship between Pro and Ile, in: Rakočević 1998, Survey 4, p. 290, where the pair Pro-Ile is one of ten pairs of amino acids classified into two
classes: class I (with Ile), handled by class I of enzymes aminoacyl-tRNA synthetases, and class II (with Pro), handled by class II of enzymes aminoacyl-tRNA synthetases.]

Finally, it remains to determine the chemical distinctions of AAs in "between" area. We have already said that sulfur amino acid pair, Cys-Met, precedes aromatic amino acids. As chalcogene AAs, they must be in contact with other two chalcogene amino acids, Ser-Thr. By this, the contact have to be made via Cys because it possesses SH group, correspondent to OH group in Ser as well as in Thr.

It is to be understood that a pair of oxygen AAs with the hydroxyl $(\mathrm{OH})$ functional group in side chain must be in contact with a pair of two also oxygen AAs, but which possess the carboxyl ( COOH ) functional group: Asp-Glu. But the problem is that both of these AAs have their amide derivatives (Asn-Gln) and it is not easy, when determining the distinctions, determine which here precede and which ones follow.

It turns out, however, that the problem easier to solve when returning to the beginning, in the area of hydrocarbon AAs, to the "point" of the pair Ile-Leu. Further must follow the pair of nitrogen derivatives, Lys-Arg, and Lysine must come first with four carbon atoms in the side chain, which number is also valid for Leucine; and then, with the validity of both principles - the continuity and minimum of change - comes Arginine with three atoms (not counting carbon atom in the guanidino group). Then, chemically speaking, it is very natural that after Arginine comes Gln with its precursor, the glutamic amino acid, both (Gln-Glu) with two carbon atoms in the side chain; it is naturaly indeed that, in terms of chemical similarity, after 3C atoms occurs changes into 2 C atoms, better than into 1 C atom, as the case we have in the pair Asn-Asp. [As in the case of the guanidino functional group in arginine, no carbon atom is counting in the carboxylic or amide functional group.] With this, chemical sequencing of series of 20 AAs closes, starting from the first, glycine, and ending with very different histidine.

The main result of this pure chemical sequencing of AAs, presented in Table 1, shows that these chemical distinctions are accompanied by specific arithmetical regularities, including the existence of amino acid ordinal numbers from 1 to 20, with two decades (1-10 and 11-20) ; and also shows the full balance of the number of atoms in the 20 amino acid molecules: $102 \pm 0$ atoms in two decades, as well as on two zig-zag lines, where such a system with two zig-zag lines represents the first possible periodic system with two periods.

However, the result of the most surprising, is the result shown in Table 2. If we take the four by four AAs from Table 1 and line up they in five rows, we obtain an arrangement of AAs, as it is shown in Table 2 where the difference ratio in the number of atoms, per rows equals 11:11:11 $[(61-50=11) ;(42-31=11),(31-20=11)]$. But the surprise comes only with an insight into Table 3 in which, exactly in the 11th step of a specific number arrangement where we find the same arithmetical result (20-31-42-61-50) valid for the number of atoms in the arrangement of AAs in Table 2. [Notice that this sequence is in contact with two sequences which contain the
first pair of friendly numbers, 220-284, what is a coincidence only, or what more? ${ }^{1}$ However, knowing a previous result (Rakočević, 2011a,b) where the number of atoms in four diversity types of the protein AAs is identical to the unique arithmetical result in a unique arithmetical arrangement (Remark 1), surprises for the presented atom number sequence no longer; simply, everything is brought into a conection with the three endpoints of this arrangement: 00-11-22, in the form of a mirror mapping (00-11-22 / 22-11-00) with compression in the mirror plane (00-11-22-11-00).

Remark 1. There is a unique arrangement of the natural numbers series, such as in the "Table of minimal adding" (TMA), with changes in the values for 01 horizontally and just for 11 vertically [01, 02 , $\ldots, 09,10,11 / 12,13, \ldots, 20,21,22 / 23, \ldots, 99]$ (Rakočević, 2011b, Table 4, p. 826). Moreover, in addition to horizontal and vertical arrangement, there is also a diagonal arrangement, which we point out here in particular (Box 1 in relation to Box 2). By this one can notice that the TMA correspons with the Periodic table of chemical elements (PT), through the validity of both Mendeleev principles: the principle of continuity and the principle of minimum change. Since both these principles are also apply to the amino acid code (Swanson, 1984), all together support the hypothesis of a prebiotic complete amino acid code, i.e. genetic code (Rakočević, 2004).

The presented sequence also points to the logic of choice the uniqueness in the case of the selection of protein amino acids within the standard genetic code, minimal in two manner. So, in this paper, from the sequence ( $00-11-22-11-00$ ), located in the starting column of Table 3, generated from the initial triplet of the last column (00-11-22) in the "Table of minimal adding" (TMA), explained in Remark 1, follows: $[00+(2 \times 10)=\mathbf{2 0}],[11+(2 \times 10)=\mathbf{3 1}],[22+(2 \times$ $10)=42],[11+(5 \times 10)=61],[00+(5 \times 10)=\mathbf{5 0}]$. So, we get the sequence $(\mathbf{2 0 - 3 1 - 4 2 - 6 1 - 5 0})$, analogical to the the number of atoms in five rows of 20 AAs (within their side chains) as in Table 2;

There is also an other logic of choice the uniqueness, presented in a previous paper (Rakočević, 2011b) as follows: $[(25-36-26-16)(16-17-18)] \rightarrow[(6-5=01)(36-25=11)][(26)$, $(26+16=\mathbf{4 2}),(42+17=\mathbf{5 9}),(59+18=77)]$, we get the sequence $(26-42-59-77)$, analogical to the number of atoms in four diversity types of 20 AAs (within their side chains), dispersed in four columns of a specific arrangement (Figure 3 in Rakočević, 2011b).

In addition to the above, there are other relationships with the amino acid (genetic) code. Within TMA there are two horizontally adjacent numbers, 5 and $6(6-5=01)$ whose squares ( 25 and 36 , respectively) are vertical neighbors $(36-25=11)$; and this is a unique case, the only one in the whole TMA. Analogy (and correspondance) with the amino acid (genetic) code is in the sense that within the Table of genetic code (TGC) 25 codons are coded for ( $2+4$ ) amino acids of lower complexity (possess $\mathrm{C} \& \mathrm{H}$, or only H , in side chain), while 36 codons are coded for (6+8) amino acids of more complexity, which besides $\mathrm{C} \& \mathrm{H}$, possess even more the atoms of other elements: N, O or S (cf. Table 6 in Rakočević, 2011b, p. 829). On the other hand, in the sequence

[^41][(25-36-26-16) (16-17-18)] the sum of the three numbers with the status "to be added" is $16+17$ $+18=51$, which is a fourth of the sum of the four numbers in the given sequence: $26+42+59$ $+77=204=4 \times 51$. And this is the only such case in the TMA. For example, such a regularity does not apply to the TMA analogue sequence [(36-47-37-27) (27-28-29)], because $27+28+29=$ 84 is not a fourth of the sum of the four numbers in an analogously obtained sequence: $37+64+$ $92+121=314 \neq 4 \times 84$.

The "enigmatic" question why, in the arrangement of Table 3 (in stating column), the first three rows increase per 2 units, and the other two rows per 5 units, it stops to be mysterious when we know that the ratio of numbers 2 and 5, in binary form ( $010 / 101$ ), represents the first possible connection between the "golden route" on Farey tree and the path of the permanent change (0101010101 ...) on the binary tree of the genetic code (Rakočević, 1998). [The answer to the question why 3 rows ("per 2 units") versus 2 rows ("per 5 units") is currently not known. However, it is possible suppose that this could be due to the fact that "the limit of the golden numbers is $3 / 2^{\prime \prime}$ (Moore, 1994).]

> | Box 1. The logic of a parallel choice |
| :--- |
| The important feature of the "Table of Minimal Adding" (TMA), within the limits of the |
| two-digit arrangement of decimal number system, is a specific diagonal structure, with 10 |
| odd and 9 even of diagonals. Here, in Box 2, only odd diagonals are presented, because |
| among them there is a diagonal (the last row in the second quadrant of Box 2), which |
| analogically corresponds with a specific chemical distinct arrangement of protein amino |
| acids (Fig. 9 in Rakočević, 2011b, p. 834; here: fourth quadrant in Box 2): in $8+8$ AAs of |
| alanine stereochemical type (within their side chains) there are 91 and 81 atoms, |
| respectively; in 4+4 AAs of alanine stereochemical type plus 1+1 AAs of valine |
| stereochemical type there are 71 and 61 atoms, respectively; in 4+4 AAs of alanine |
| stereochemical type plus 1AA of glycine stereochemical type, plus 1 AA of proline |
| stereochemical type there are 41 and 31 atoms, respectively. Finally, within the set of four |
| AAs of non-alanine type, $2+2$ AAs possess 21 and 11 atoms, respectively. [About four |
| amino acid stereochemical types see in (Popov, 1989) and in (Rakočević \& Jokić, 1996.) |

Remark 2. The determination of the amino acid (genetic) code with the golden mean leads to the CIPS (Cyclic Invariant Periodic System), in which the positions of five classes of AAs are strictly determined, two in the less complex and three in the more complex superclass: 1. (SC-TM), 2. (GV-PI), 3. (DE-NQ), 4. (AL-KR), 5. (FY-HW). Less complex aliphatic AAs in the side chains, besides C \& H (Gly only H ), contain the less polar nitrogen atom ( N ), and no longer contain the polar atom of oxygen (O), while more complex AAs contain it. Aromatic AAs also fall into the superclass of more complex AAs. In addition, we recall that in all the presented AAs pairs, the first member, as a smaller molecule, belongs to class II of AAs, handled by class II of enzymes aminoacyl-tRNA synthetases, and the second one to class I. [Cf. Figs $6 \& 7$ in (Rakočević, 2011b, pp. 832-833) and 4th quadrant within Box 2 in this paper.]

| Box 2. The arrangement followed from did | structure of TMA |
| :---: | :---: |
| $(01)[1]$ $(03,13,23)[3]$ $(05,15,25,35,45)[5]$ $(07,17,27,37,47,57,67)[7]$ $(09,19,29,39,49,59,69,79,89)[9]$ | $[1](99)$ $[3](77,87,97)$ $[5](55,65,75,85,95)$ $[7](33,43,53,63,73,83,93)$ $[9](11,21,31,41,51,61,71,81,91)$ |
| $\begin{array}{ll} 11+91=102 & (91-11=\mathbf{8} \times 10) \\ 21+81=102 & (81-21=\mathbf{6} \times 10) \\ 31+71=102 & (71-31=\mathbf{4} \times 10) \\ 41+61=102 & (61-41=\mathbf{2} \times 10) \end{array}$ <br> $51 / 51$ <br> (The top two quadrants possess five diagonals each in the first and second part of the TMA, respectively. All other explanations in Box 1) |  |

At the end of this analysis of the relationship between the three arrangements, presented in the three tables (Tables 1-3), we present another more, perhaps slightly hidden, relationship. Namely, from the relationship between the first two and the last two rows of numbers in the two upper structures within Box 2, it follows that there is a correspondence between the Table of Minimal Adding (TMA) and the Multiplication Table (TM), as well as between their diagonal structures in the decimal number system. On the other hand, if TM is written adequately, systemic and systematically, ${ }^{2}$ as TMA, then, on both sides of the main diagonal, there are the numbers: $0,2,6,12,20, \ldots$ (Table 1.1 in Rakočević, 2011b), which represent the values for " q " in the equation of the generalized golden mean (Spinadel, 1998, 1999; Rakočević, 2004b, 2011b). It follows from this that it can be understood why the amino acid (genetic) code is determined by the golden mean (Rakočević, 1998, 2011b) (Remark 2).

However, if we note that the said numbers on the main diagonal of TM, taken in a double amount $(0,4,12,24,40, \ldots)$, represent the first cathete in the Pythagorean-Diophantine triangle set, and increased by one - the hypotenuse of the same triangles: $1,5,13,25,41, \ldots$ [The second cathete is "taken" from the set of odd natural numbers, respectively.] Thus, it is possible to understand why the amino acid (genetic) code was determined by the first (3-4-5) PythagoreanDiophantine triangle (Shcherbak, 1994). In addition, considering the fact that there is a

[^42]"coherence of the chemical and genetic code" (Rakočević, 1991) ${ }^{3}$, more precisely, there is an analogous unity of the chemical and genetic code (Rakočević, 2017), that is, if everything here presented, taken together, then there can be enough understanding for the standpoint that "the genetic code is an intelligent design ..." (Castro-Chavez, 2010, p. 718). ${ }^{4}$

We again look at Box 2 (quadrant fourth), from the aspect of the viewing of possible distinct chemical pairs of AAs. We see that the pairs strictly correspond to the pairs found in two classes of AAs handled by two classes of enzymes aminoacyl-tRNA synthetases (Wetzel, 1995; Rakočević, 1997a). We first consider the AAs in the non-alanine type set, and in addition, in the quantum "11" and the quantum " 21 "; the result of matching is obvious: a larger molecule in class I, while lower in class II, GV and PI, respectively. Then we look at the pairs in quantums "81" and " 91 ". In all cases, except in one, in one column there are larger molecules (class I), and in the second one smaller molecule (class II). [The exception is a par CM in quantum "81" where both AAs belong to class I, and a pair of ST in quantum "91" where both AAs belong to that class II (cf. Survey 4 in Rakočević, 1998.)] ${ }^{5}$

In reactions catalysed by the class I aminoacyl-tRNA synthetases, the aminoacyl group is coupled to the 2 '-hydroxyl of the tRNA, while, in class II reactions, the 3 '-hydroxyl site is preferred, and these two positions differ in their polarity. ${ }^{6}$ This means that the ordered arithmetical quantities, described above, correspond to the arrangement of AAs from the aspect of fine nuances in the chemical polarity of molecular classes. However, in the case that the reader doubts that this is a matter of correspondance of the arithmetical and chemical-biological entities, we also note the fact that, in the natural selection of amino acid molecules, it was necessary to "skip" the quantity 51 , and after the quantity 41 choose a quantity of 61 ; it further means that it was not possible to choose a lower quantity of a set of molecules, for example a small molecule of ornithine precedes a large molecule of arginine (in the genetic code) as Tomas

[^43]H. Jukes assumed. (Jukes, 1973, p. 24: „I have suggested that arginine displaced ornithine during the evolution of protein synthesis".) [Amicus Plato, sed magis amica veritas.]

## *

Not only in two decades (as in Table 1), the balance of the number of atoms is contained also within the halves of both decades, in four quintets: 1. GAVPI, 2. LKRQE, 3. NDSTC, 4. MFYWH. However, the said regularities are expressed (become visible) only when the four quintets develop into a system of five quartets; the five upper and five lower pairs are arranged according to the next logic: the first pair of the upper quintet with the first pair of the lower one, the second with the second, etc. (Table 4). If in fact the resulting system (with five quartets) perceived as a cyclic system (the first row in a cyclization occurs also as the last), then the balances (and symmetry) exhibit a specific self-similar arrangement more: two times appear the same quantities of the number of atoms, although with the different qualities (with different AAs) in four cases $(117,117)(118,118),(119,119),(120,120)$. Such a repetition means per se a correspondence with the principle of self-similarity (Remark 3).

Remark 3. So far, the chemical meaning for the duplicates of AAs in Table of Genetic Code (TGC) has been shown as following: SLR (Crick, 1968); SLIR (Rakočević, 2007, Table 7; Wohlin, 2015, Table 2); GP-VI (Rakočević and Jokić, 1996, Survey 1); and here in this paper: GNLM in Table 4. All these duplications, ipso facto, support the hypothesis of a prebiotic complete genetic code (Rakočević, 2004), which is now known as the standard genetic code ("Canonical genetic code"), and all other genetic codes are "deviant codes" (Weaver, 2012, pp. 568-569), or exceptions from the standard genetic code. These codes, per se, do not change nothing on the fact, when it comes to the genetic code as "amino acid code" (Swanson, 1984), because they are represented in all variants with the same 20 protein amino acids. (The only exceptions are Pyrrolyisine and Selenocysteine, presented at some very few organisms.) [Knight at al., 2001, p. 49: "The genetic code evolved in two distinct phases. First, the 'canonical' code emerged before the last universal ancestor; subsequently, this code diverged in numerous nuclear and organelle lineages".]

But, not only that, the pair 119-120 stand in relation to the same pair in the Rumer's Table of AAs and their corresponding nucleotide doublets (Table 5); The number of 118 atoms is also found as a half number of atoms within a "specific amino acid arrangement" (Rakočević \& Jokić, 1996, Survey 1$) ;^{7}$ and 117 atoms as the number of hydrogen atoms in all 20 protein AAs, within their side chains. [Also, number of hydrogen atoms within amino acid molecules appears to be in relation to natural numbers sequence; so, in side chains there are: $1,(2), 3,4,5,6,7,8,9,10$ of hydrogen atoms, and in whole molecules: $5,(6), 7,8,9,10,11,12,13,14$ (Sukhodolets, 1985) (Cf. last sentence in legend of Table 7 on page 830, in: Rakočević, 2011b).]

[^44]The principle of self-similarity extends, however, substantially broader within the amino acid (genetic) code. Moreover, this extension is present parallel with Shcherbak's principle of "analogies [of the genetic code] with quantum physics" (Shcherbak, 1994). [Details of this analogy can be seen in our previous work (Rakočević, 2017).] Thus, in the set of protein AAs, in their side chains, there is a pattern (117/87), the 117 hydrogen atoms and 87 non- hydrogen atoms. This pattern corresponds to the pattern (107/́7) where 107 is the number of all atoms in 10 polar AAs [(KR-ST-DE-NQ) + (YH)], and number 97 represents the number of atoms in 10 AAs that are not polar [(GP-AL-VI) + (CM-FW)] [The grouping of AAs follows from the distinction of AAs in four types of diversity (Rakočević, 2011a, 2011b).] In this classification calculated purely polar AAs only, and not those that are semi-polar (GP and W). Classification by the polarity criterion, however, follows from the polarity of the functional groups, that is, from the electronegativity of the atoms that make them. In view of the "chemical eyes", this polarity/nonpolarity is directly visible, and it agrees with the strict parameters for which this polarity is measured [polar requirement (Woese et al., 1966), hydropathy index (Kyte \& Doolittle, 1982) and cloister energy (Swanson, 1984)], as we have shown in previous works (Rakočević \& Jokić, 1996; Rakočević, 2004a, Section 3.3).

A direct self-evident of polarity/nonpolarity follows from the facts as stated herein: aliphatic amino acids that in the side chains possess only electropositive atoms, $\mathrm{C} \& \mathrm{H}$, or with them also possess an electropositive sulfur atom more, are nonpolar (AL-VI-CM) . [Under electropositive we consider those atoms whose electronegativity (according to Pauling) is 2.5 or less, while with values more than 2.5 , the atoms are electronegative (polar).] Aromatic amino acid phenylalanine (F), which in the side chain only has a nonpolar benzene ring, is also nonpolar amino acid. On the other hand, aliphatic amino acids that in the side chains, except carbon and hydrogen ( C \& H ), also have electronegative nitrogen atoms ( N ) and/or oxygen ( O ), are polar amino acids (KR-NQ-ST-DE); aromatic amino acid tyrosine (Y) which in the side chain has a phenol group is also a polar amino acid; Finally, the aromatic amino acid histidine $(\mathrm{H})$, which in the side chain has a polar imidazole ring, is also a polar amino acid.

On the third side, there are three more amino acids, that are not polar but semi-polar. First of them is glycine (G). Its molecule has two equivalent hydrogen atoms, which at the same time exist in both the "head" and the side chain of the glycine amino acid. Although the hydrogen atom itself is electropositive (nonpolar), the influence of the polar "head", i.e. the influence of the polar amino acid functional group is inevitable, and hence the semi-polarity of this amino acid is followed. Similarly, the proline has three nonpolar CH2 groups in the side chain, but one of the two ending allyl groups is attached to the polar nitrogen atom in the "head" of the amino acid; hence its semi-polarity follows. Aromatic tryptophan (W), which in the side chain contains an indole ring, composed of one nonpolar benzene and one polar pyrrole ring, must also be a semipolar amino acid (Remark 4).

It is understood that it makes sense to ask a question about the classification of protein amino acids into the class of strictly nonpolar amino acids (7 AAs) and the class of polar amino acids where semi-polar AAs also come (total 13 AAs). Such a classification shows a strict separation
of the TGC into polar/nonpolar as well as inner/outer space with the differences for 1 molecule and 1 atom, respectively (Rakočević, 2000, Section 3, Eq. 1-4, pp. 279-280; 2011b, Eq. 11-14 on p. 838 and Tab. A. 3 on p. 840).

Remark 4. Today, there are many different classifications of protein AAs by the criterion of their polarity. Hence, this has become a major problem not only in the analysis of protein polarities, but also in the analysis of their evolution, and it has also become a problem for understanding evolution in general. This upper representation of the polarities of AAs follows from their structure, which should become a main criterion for analyzing the structure and evolution of proteins, and also for re-examining the validity of existing parameters. In this sense, we have also demonstrated the high reliability of polar requirement (Woese et al, 1966), hydropathy index (Kyte \& Doolittle, 1982) and cloister energy (Swanson, 1984). Thus, in the case of structurally semi-polar amino acids, the state of polarity/non-polarity is as follows: Pro is polar in both parameters - hydropathy index and cloister energy, but according to the polar requirement it is not polarized, as Rumer and Konopeljchenko showed (1975, pp. 473-474); Gly and Trp are nonpolar after the cloister energy, but after polar requirement and hydropathy index are polar. On the other hand, in all other cases of strictly indicated polarity and non-polarity, there is the full agreement with hydropathy index and cloister energy (as well as with each other), while for polar requirement there are minimal deviations.

All together in the question are systemic and systematic natural arrangements, whose organization and determination correspond with the principle of self-similarity. ${ }^{8}$ The already well-known facts that genetic code represents an analogy with natural (verbal) language (First Paradigm!) are joined now to the facts about analogies between genetic code arrangements and specific arrangements within the set of natural numbers (Second Paradigm?). ${ }^{9}$ Such an agreement (through "ideal" and "intelligent" structures and arrangements) leads us to the conclusion that the genetic code was indeed complete even in prebiotic conditions (as a set of 20 canonical amino acids and the set of $2+2$ pyrimidine/purine canonical bases, respectively); and the "evolution" of the genetic code can only mean a degree of freedom of standard genetic code, i.e. the possible exceptions and deviations from the standard genetic code, as we have presented here and in previous works, and, as also other authors have pointed out (Sukhodoletc, 1981, 1985; Swanson, 1984; Rakočević, 1988a, 1988b, 2004a; Popov, 1989; Shcherbak, 2008; CastroChavez, 2010). And, secondly, there is no point in talking about the evolution of genetic code in terms of the evolution of organisms, but only about the degree of freedom of a unique coherent and harmonious system, which degree of freedom is expressed in the form of exceptions and/or deviations (Remark 3).

[^45]All the present arrangements and regularities are an addition to the previously revealed systems and arrangements of protein amino acids (as constituents of GC) in which chemical distinctions and classifications are accompanied by arithmetical and algebraic regularities, both in our previous works and in the works of other authors (Rumer, 1966; Kyte \& Doolittle, 1982; Doolittle,1985; Sukhodolets,1985; Leunissen and De Jong,1986; Taylor \& Coates, 1989; Koruga, 1992; Shcherbak, 1994; Damjanovic, 1998; Dragovich and Dragovich, 2006; Négadi, 2009; Castro-Chavez, 2010; Mišic, 2011; Petoukhov, 2016; Dragovich et al, 2017).

On the other hand, all results, presented in this paper - all together - show that the genetic code is a deeper essence than would follow only from the chemical properties of the amino acid molecules. And it also means that biological, as such, is a deeper essence than it follows only from physics and chemistry. It also proves to be a justified conclusion, at least as a hypothesis for further researches, it would make no sense to speak about the biological evolution of GC, and about its degeneration, but only about the pre-biological generation of GC, the completion of its basic ( $2 \mathrm{Py}+2 \mathrm{Pu}$ bases) and acidic ( 20 AAs ) constituents, such that their arrangements, from the aspect of physical and chemical properties, are in a correspondence with the arithmetic-algebraic arrangements of the number of molecules-atoms-nucleons in them. Existing, now known, exemptions from this generic standard GC are only necessary deviations as a result of the degree of freedom that is inevitably valid for all natural systems.

## Acknowledgement

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## TABLES

Table 1. The chemically determined order of protein amino acids


The 20 protein AAs, arranged into two decades in accordance to ordinal amino acid number, 1-10 and 11-20; the numbers presented outer: the ordinal numbers 1-20; the numbers presented inner: the number of atoms within side chain of the responding amino acid. The designations "o/e" as "odd / even". For details see the text.

Table 2. The order of five quartets of protein amino acids

|  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| $\mathrm{G}(01)$ | $\mathrm{A}(04)$ | $\mathrm{N}(08)$ | $\mathrm{D}(07)$ | $\rightarrow$ | 20 |
| $\mathrm{~V}(10)$ | $\mathrm{P}(08)$ | $\mathrm{S}(05)$ | $\mathrm{T}(08)$ | $\rightarrow$ | 31 |
| $\mathrm{I}(13)$ | $\mathrm{L}(13)$ | $\mathrm{C}(05)$ | $\mathrm{M}(11)$ | $\rightarrow$ | 42 |
| $\mathrm{~K}(15)$ | $\mathrm{R}(17)$ | $\mathrm{F}(14)$ | $\mathrm{Y}(15)$ | $\rightarrow$ | 61 |
| $\mathrm{Q}(11)$ | $\mathrm{E}(10)$ | $\mathrm{W}(18)$ | $\mathrm{H}(11)$ | $\rightarrow$ | 50 |
| $51-1$ | $51+1$ | $51-1$ | $51+1$ |  |  |

The explanation in the text.

Table 3. A specific natural numbers arrangement

| 00 | 02 | 04 | 06 | 08 | 10 | 12 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 11 | 13 | 15 | 17 | 19 | 21 | 23 |
| 22 | 24 | 26 | 28 | 30 | 32 | 34 |
| 11 | 16 | 21 | 26 | 31 | 36 | 41 |
| 00 | 05 | 10 | 15 | 20 | 25 | 30 |
| 44 | 60 | 76 | 92 | 108 | 124 | 140 |
|  | 12 | 14 | 16 | 18 | 20 | 22 |
|  | 23 | 25 | 27 | 29 | 31 | 33 |
|  | 34 | 36 | 38 | 40 | 42 | 44 |
|  | 41 | 46 | 51 | 56 | 61 | 66 |
|  | 30 | 35 | 40 | 45 | 50 | 55 |
|  | 140 | 156 | 172 | 188 | $\underline{204}$ | 220 |
|  | 22 | 24 | 26 | 28 | 30 | 32 |
|  | 33 | 35 | 37 | 39 | 41 | 43 |
|  | 44 | 46 | 48 | 50 | 52 | 54 |
|  | 66 | 71 | 76 | 81 | 86 | 91 |
|  | 55 | 60 | 65 | 70 | 75 | 80 |
|  | 220 | 236 | 252 | 268 | 284 | $\underline{300}$ |
|  | 32 | 34 | 36 | 38 | 40 | 42 |
|  | 43 | 45 | 47 | 49 | 51 | 53 |
|  | 54 | 56 | 58 | 60 | 62 | 64 |
|  | 91 | 96 | 101 | 106 | 111 | 116 |
|  | 80 | 85 | 90 | 95 | 100 | 105 |
|  | 300 | 316 | 332 | 348 | 364 | 380 |
|  | ... |  |  |  |  |  |

The arrangement represents the Table of distinct 2-5 adding (TDA) with starting column which follows from TMA, explaned in Remark 1. All other explanations in the text.

Table 4. A specific protein amino acids arrangement

| 119 |  |  |  | $\begin{aligned} & \mathbf{( 3 3 )} \\ & (40) \end{aligned}$ |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| G 01 | N 08 | L 13 | M 11 |  | 120 |
| A $04 \times$ D 07 |  | K 15 | F 14 |  |  |
| V 10 | S 05 | R17 | Y 15 | (47) |  |
| P 08 | T 08 | Q 11 | W 18 | (45) |  |
| I 13 | C 05 | E 10 | H 11 | (39) | 117 |
| G 01 | N 08 | L 13 | M 11 | (33) |  |
| 24/13 (37) | 18/23 <br> (41) | $\begin{gathered} 40 / 39 \\ (79) \end{gathered}$ | $\begin{gathered} 37 / 43 \\ (80) \end{gathered}$ | $\begin{aligned} & 118 / \mathbf{1 1 9} \\ & 117 / \mathbf{1 2 0} \end{aligned}$ |  |
|  |  | 118 |  |  |  |

The first row is repeated at the bottom, and thus one cyclic system is obtained. There are 117 atoms in two outer columns; at even positions 118, at odd 119; in two inner columns 120 atoms. On the other hand, in the lower half of the Table there are 117 atoms ones more; in the lower diagonally "wrapped" area 118, and in the upper 119; in the upper half of Table 120 atoms. The repeated four AAs at the bottom of the Table make to achieve a diagonal balance with a difference of only one atom; moreover, to establish a sequence from the series of natural numbers: 117, 118, 119, 120. (About generating the Table see in the text.)

Table 5. The Rumer's classification of amino acids into two classes (Rumer, 1966)

| 114 | $\begin{gathered} \hline 30 \\ 116 \end{gathered}$ | (119) | $\begin{gathered} \hline 89 \\ 108 \end{gathered}$ | 125 |
| :---: | :---: | :---: | :---: | :---: |
| Gly | GG (6) | Phe | UU (4) | Leu |
| Pro | CC (6) | Asn | AA (4) | Lys |
| Arg | CG (6) | lle | AU (4) | Met |
| Ala | GC (6) | Tyr | UA (4) | ct |
| Thr | AC (5) | His | CA (5) | Gln |
| Val | GU (5) | Cys | UG (5) | Trp |
| Ser | UC (5) | Asp | GA (5) | Glu |
| Leu | CU (5) | Ser | AG (5) | Arg |
| 125 | $\begin{gathered} 36 \\ 106 \\ \hline \end{gathered}$ | (120) | $\begin{gathered} 84 \\ 118 \end{gathered}$ | 114 |
|  | 0-66 |  | $330 \pm 00$ |  |
| $\begin{aligned} 125+114 & =239 \\ 125-114 & =11 \end{aligned}$ |  |  |  |  |

The four-codon amino acids are on the left and the non-four-codon amino acids on the right. Each of two classes is classified into two subclasses, corresponding to the number of hydrogen bonds in the nucleotide doublets. On the other hand, nucleon number within amino acid molecules in these two classes is determined by Pythagorian triangle (Figure 1 in Shcherbak, 1994). At the bottom (shaded) - the number of atoms in the amino acid molecules (side chains): within 32 amino acid molecules on the left and 29 on the right, within the set of "61" amino acid molecules, each molecule encoded by one codon. [There are the same results, $330-66$ (as $8 \times 33$ ) and 330 (as $10 \times 33$ ) in standard GCT, both in relation with the result $(9 \times 33) \pm 1$ as we have shown in a previous work (Rakočević, 2004a, Table 3a on p. 224).] Up/down: 119/120 atoms in 11/12 amino acids (side chains), respectively, within the set of "23" amino acids. [Calculations: $(30+89=119) ;(36+84=120) ;(30+84=114) ;(36+89=125) ;(125-114=11)$ ]; [ $(05 \times 6$ $=30 \pm 0) ;(\underline{15} \times 6=89+1) ;(\underline{06} \times 6=36 \pm 0)$; $(\underline{14} \times 6=84 \pm 0)]$; Up/down: $(116 / 1 \underline{0} / / 106 / 1 \underline{1} 8)$ as the number of atoms within nucleotide doublets. (Note: In originsl Rumer's Table only the number of hydrogen bonds is calculated; all other calculations are ours.)

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## 17.

## The Enigma of Darwin Diagram

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## Life Sciences Biochemistry, Biophysics, and Structural Biology

According to my best knowledge, for the first time here is presented a hypothesis, that the one and only "accompanying diagram" in Darwin's famous book On the Origin of Species contains, may be, a hidden code. Direct inspection reveals that the Diagram, viewed as built of four parts [(two upper and two lower / two left and two right); (two with more and two with less branches / two with multiple and two with single branches)], corresponds to the logical square of the genetic code. When, however, viewed as built of two parts (upper and lower), then it corresponds with Shcherbak's diagram (Shcherbak, 1993, 1994) of four-codon and non-fourcodon amino acids (AAs); not only by the form but also by the number of elementary quantities. [This version was storing 2015.01.06. on my website; the first one, under the title "The Darwin (hidden) code" at 2014.10.12.]

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Biochemistry, biophysics and structural biology, atom number, Darwin diagram, genetic code, nucleon number, Origin of species, Shcherbak diagram.

# THE ENIGMA OF DARWIN DIAGRAM 

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> What can be said at all can be said clearly, and what we cannot talk about we must pass over in silence. Ludwig Wittgenstein ("Tractatus")


#### Abstract

According to my best knowledge, for the first time here is presented a hypothesis, that the one and only "accompanying diagram" in Darwin's famous book On the Origin of Species contains, may be, a hidden code. Direct inspection reveals that the Diagram, viewed as built of four parts [(two upper and two lower / two left and two right); (two with more and two with less branches / two with multiple and two with single branches)], corresponds to the logical square of the genetic code. When, however, viewed as built of two parts (upper and lower), then it corresponds with Shcherbak's diagram (Shcherbak, 1993, 1994) of four-codon and non-four-codon amino acids (AAs); not only by the form but also by the number of elementary quantities. The number of nucleons in the upper part of Shcherbak's diagram (four-codon amino acids) is determined by the Pythagorean law ( $3^{\wedge} 2+4^{\wedge} 2=5^{\wedge} 2=25$ ), meaning that the total number of nucleons makes the product of the number 25 and "Prime quantum 037" (925); and the number of branches in the lower part of Darwin's diagram is determined by the law of Plato ( $3^{\wedge} 3+4^{\wedge} 3+5^{\wedge} 3=6^{\wedge} 3$ $=216)$, meaning that the total number of branches makes the product of the number 216 and "First quantum 01" (216). On the other hand, in the lower part of the Shcherbak's diagram there are 60 of "Prime quantum 037" (2220), while in the upper part of the Darwin's diagram there are 60 of "First quantum 01" (60). There are $216+60=276$ branches (in total), and this number is also the number taken from a specific and unique arithmetical system. Furthermore, it is shown that Darwin, starting from the basic structure of the Diagram, formed a sophisticated structure which strictly corresponds to the arithmetical and /or algebraic structures that also appear to be the key determinants of the genetic code (GC). Among other correspondences, there is also one in the number of entities/quantities, as follows. According to Shcherbak's account the nucleon number within the amino acid constituents of GC (in their side chains) is as follows: $[1 \times(\mathrm{G} 1+\mathrm{A} 15+\mathrm{P} 41+\mathrm{V} 43+\mathrm{T} 45+\mathrm{C} 47+\mathrm{I} 7+\mathrm{N} 58+\mathrm{D} 59+\mathrm{K} 72+\mathrm{Q} 72+\mathrm{E} 73$ + M75 + H81 + F91 + Y107 + W130) $]+[2 \times(\mathrm{S} 31+\mathrm{L} 57+\mathrm{R} 100)]=1443$. If Shcherbak's account is done, with an iteration more, for the number of atoms, the result is as follows: [2 x (G1 + A4 + C5 + D7 + $\mathrm{N} 8+\mathrm{T} 8+\mathrm{P} 8+\mathrm{E} 10+\mathrm{V} 10+\mathrm{Q} 11+\mathrm{M} 11+\mathrm{H} 11+\mathrm{I} 13+\mathrm{F} 14+\mathrm{Y} 15+\mathrm{K} 15+\mathrm{W} 18)]+[3 \mathrm{x}(\mathrm{S} 5+\mathrm{L} 13+$ R17)] $=0443$. On the other hand, within Darwin's diagram there are the next "branch" entities/quantities: 276 branches, plus 46 nodes, plus 10 branchings, in total 332 . The significant differences are as follows: 1443-332 $=1111$ and 443-332 $=111$, both determined by the unity change law. From these results it follows that Darwin with his Diagram anticipated the relationships not only in terrestrial code but in the genetic code as well, anywhere in the universe, under conditions of the presence of water, ammonia and methane, phosphine and hydrogen sulfide. If so, then Darwinian selection moves one step backwards in prebiotic conditions, where it refers to the choice of the life itself.


## 1. Introduction

As it is generally known, Darwin's book On the Origin of Species contains only a single illustration, an evolutionary tree in the form of a diagram (Figure 1.1). During the 155 years since the appearance of the first edition in 1859, this Diagram has been analyzed only qualitatively (Figure 1.2), but not quantitatively, and we shall, in this paper, do that for the first time. ${ }^{1}$ In doing so, we begin with the working hypothesis (for this and all other researches of the Diagram in future) that the diagram contains a hidden code, with strictly determined quantities, expressed in the number of branches - primary (principal, main) and secondary (minor, small) ${ }^{2}$, and also in the number of nodes and branchings; such a code, which would per se have to be biological, otherwise it would not make sense in this book, and the Diagram would not be styled as "accompanying diagram" but as an "attached diagram", or an ordinary illustration. Hence, the deeper implication of the hypothesis is that, despite the variations (and modifications) of organisms are spontaneous and random, they do not have complete freedom, but are limited by the regularity and validity of strict arithmetical and/or algebraic systems. (Cf. Box 1.)

Box 1. Citation from 1994 (I)
Rakočević, 1994, p. 14: "Darwin's diagram-binary tree, represents the first systematic informational approach to the analysis of the relations between organisms. This is the only diagram in his book Origin of Species (Darwin, 1859) and it represents a model for interpretations of origin of varieties, species, genera and higher systematic categories. By its essence, this diagram represents a code-model and code-system and by its completness and complexity it is the first example of the code model and the code system in science. Relations of the elements within this code system correspond to the relations of the elements (organisms) in natural systems. Intention (and a message) of the author of this diagram is absolutely clear: if the natural systems are at the same time the coding systems, the only adequate and complete way of description and interpretation of such systems would be the creation of adequate code models with adequately corresponding relations between the elements of one and the other model, i.e. natural system."

The analysis that we conducted showed that the relationships between these quantities are such that they are brought into mutual relationships by specific proportionalities and balances through the minimal differences in number, usually expressed in decimal units $( \pm 00, \pm 01, \pm 10$,

[^46]$\pm 11, \pm 100, \pm 111$ and so on $)^{3}$, with the validity of the principle of minimal change, and the principle of continuity. ${ }^{4}$ Moreover, all of these quantities were related and corresponding to the quantities (and their relationships) in the genetic code; with the number of codons, molecules, atoms, nucleons etc.

The obvious reason why this is so, is (according to our working hypothesis) the fact that Darwin in his Diagram built relationships taken from the specific and unique arithmetical and/or algebraic systems, based on which, as we now know, the genetic code was also built.

## 2. Methodology

Bearing in mind that the genetic code is the basic biological code, and that it has already been proven that its distinctions and classifications (within itself), are derived on the basis of physicochemical properties of the molecule, followed by (accompanied by) strict arithmetical and/or algebraic regularities and balances (Shcherbak, 1993, 1994, 2008; Damjanović, 1998, 2005, 2006; Verkhovod, 1994; Dragovich, 2009, 2011; Mišić, 2011; Négadi, 2009, 2014; CastroChavez, 2010, 2011; Dlyasin, 2011; Jokić, 1996; Rakočević, 1997, 1998, 2004, 2011, 2013), it makes sense, in analysis of the distinction and classification in Darwin's diagram, to apply the same methodology (or almost the same) by which the said regularities in the genetic code were discovered. This means that the number of branches, nodes and branchings must be determined in even and odd positions; along cross diagonals, and zigzag lines; for different parts of the Diagram, which basically boils down to the application of Mendeleevian methodology, that can be found in his original manuscript works (Kedrov, 1977).
B.M. Kedrov, who most carefully studied the archives of Mendeleev, said that he was unable to find that Mendeleev wrote about which methodology he had used in his researches. In contrast to this, handwritten sketches, drawings and diagrams show that Mendeleev clearly revealed his methodology. In the above mentioned book, Kedrov enclosed 16 photocopies (between 128 and 129 pages) ${ }^{5}$, showing the Mendeleevian methodology; which is the same methodology as we applied in the analysis of the genetic code structure as well as in the analysis of Darwin's diagram.

[^47]
## 3. Preliminaries

Already at first glance, it becomes immediately obvious that Darwin's diagram (Figure 1.1), composed of four parts (two upper and two lower / two left and two right); (two with more and two with less branches / two with multiple and two with single branches), corresponds to the logical square of the genetic code, in a reverse reading ${ }^{6}$ (Figure 2), as well as with Shcherbak's diagram at the same time (Figure 3), also in the reverse reading. ${ }^{7}$ Two lower trees are branched, multiple, and two on the top are linear, non-branched, with linear segments. In the lower left part of the Diagram, the tree consists of two large branches, and the tree on the right consists of only one. In the upper, left part of the Diagram, there are more singlet branches (eight), and on the right there are less branches (six). ${ }^{8}$

The correspondence with Shcherbak's diagram is as follows: the "heads" of amino acid molecules have the same number of nucleons each, and their bodies are completely different. It is (by analogy) similar to the Darwin's diagram: the singlet branches are implemented in the same number at every level, and the multiple branches in different number, changing from level to level.

But it is so at first glance. However, the second (deeper) look reveals a surprising fact: the total number of nucleons in the amino acid molecules in the upper part of Shcherbak's diagram is determined by the Pythagorean law $\left(3^{\wedge} 2+4^{\wedge} 2=5^{\wedge} 2=25\right)$, meaning that it is 25 of "Prime quantum 037" (925), and the number of branches in the lower part of Darwin's diagram is determined by the law of Plato ( $3^{\wedge} 3+4^{\wedge} 3+5^{\wedge} 3=6^{\wedge} 3=216$ ), meaning that the amount is 216 of the "First quantum 01" (216). On the other hand, in the lower part of the Shcherbak's diagram there are 60 of "Prime quantum 037" (2220), while in the upper part of the Darwin's diagram there are 60 of "First quantum 01 " $(60) .{ }^{9}$ [A total of nucleons is $925+2220=3145$, and a total of branches is $216+60=276$, which is again a number taken from a specific and unique arithmetical system, as the first case (Figure 4).]
[Remark 3.1. If we look at the first column in Shcherbak's original Table (Table 1 in Shcherbak, 1994): 037, 370, 703, it is clear that the first two steps can be realized by all two-digit numbers, while the third step (through module 9) is possible only for number 037 ; for example ( $037,370,703$ ) versus $(038,380,722)$.]

[^48]Darwin's diagram contains a zeroth level (undesignated) and 14 levels more, designated by Roman numerals. At the bottom of the Diagram, there are 11 English alphabet letters, A-L, ${ }^{10}$ ommiting the 10 th letter (the letter "J"). ${ }^{11}$ Because of this exclusion, the original input order: J10, K-11, L-12, (M-13) becomes the output of order K-10, L-11, (M-12). ${ }^{12}$ In support to the assumption that here the term of coding is already present, there is the fact that the branches are omitted only at the 10th level. ${ }^{13}$ On the other hand, it is also a fact that the omission of capital letters begins with "M" (the 13th, central letter in the English alphabet), and alignment of small letters on the second branch of the left tree begins (and continues) exactly with "m". In addition, only the levels 11,12 and 13 are not marked with small letters, while all the others are.

The omitting of the 10th letter makes another distinction: only the letters after the 10th letter are put into a new sequence, they are "variable". However, the letters from the $1^{\text {st }}$ to the $9^{\text {th }}$ remain unchanged, they are "stable". From that fact it follows that the main part of the Diagram is bounded by the first and by the last stable letter, "A" and "I". The species of organisms that are designated with these letters differ in other formal characteristics. Hence, we can speak about two sets of species: the first set of two, and the second set of "other nine species". In the first set of species, the branches (below the 10th level) are oblique (oblique angle), while in the second set the branches are orthogonal; within the first set there are nodes and branchings whereas within the other set there are not. By this, both types of branches (oblique and orthogonal) exist in both parts of the Diagram, in the left part, A-F, and in the right part, G-L.

The above reconciliation: 10th letter vs 10th level; "M" vs "m"; significant omission of capital letters at the start level versus reordering of the $11^{\text {th }}, 12^{\text {th }}$ and $13^{\text {th }}$ letters $(\mathrm{K}, \mathrm{L}, \mathrm{M})$, as opposed to the exclusion of small letters at the top of the Diagram at the positions $11^{\text {th }}, 12^{\text {th }}$ and $13^{\text {th }}$; all these relationships represent a kind of the specific realization of similarity principle and the principle of self-symilarity. ${ }^{14}$

[^49]
## 4. Results and discussion

### 4.1. Primary and secondary branches of species " A " and " I "

In our working hypothesis, there is a presumption that the symmetry relationships make the basis for coding, and for that reason we have analyzed the number and arrangement of branches, nodes and branchings on the 15 levels of the Diagram, at first, in symmetrical systems " $2 \times 5$ " and " $3 \times 5$ ", and then in systems derived from them. Such symmetrical systems are presented first in Table 1.1, Table 1.2 and Table 2.1.

The number of primary (main) branches on the left tree (starting with letter "a") and the right tree (starting with the ending letter "z"), for the species "A" and "I" is given in Table 1.1.. The branches are counted starting from the zeroth level onwards, until the ninth, by counting the number of branches between every two levels. The same result is, however, obtained when we follow the finalization (realization) of taxonomic entities at every next level (Table 1.2). In the latter case, we start counting with the first instead of the zeroth level and we end counting with the tenth instead of the ninth level (by this counting we realize that the number of branches is equal to the number of letters per level).

From the aspect of this vision, all primary branches are "finalized" (and marked with the corresponding small letters at the lower part of the Diagram and the unmarked ones are in the upper part of the Diagram); they are further classified into two classes: 1. Finalized, fixed (Table 1.3), and 2. Finalized, not-fixed (Tables 1.4 and 1.5). These first branches reach a certain level and do not develop further; as examples, we show the first such branch on the left tree ( $s 2$ ), and the first such branch on the right ( $t 3$ ).

If we take any of the two tables (Table 1.1 and Table 1.2) and look at the upper half of the large (left) and lower half of the small (right) tree (and vice versa), then, in this cross-connection, the number of branches is equal (28 and 28). ${ }^{15}$ But apart from these symmetrical proportionalities to the total number of primary branches $(28: 28=1: 1)$, there is one more such proportionality valid for the parts of the system ( $20: 20=1: 1$ ) (the total number of primary branches on the small tree equals the number of branches on the upper half of the large tree); ${ }^{16}$ and there are also the following proportionalities: $(36: 24=3: 2),(32: 24=4: 3),(8: 16: 24: 32=$ 1:2:3:4) etc.

In Table 2.1 we look at all primary branches, up to the $14^{\text {th }}$ level. However, prior to the analysis, an important issue should be considered. In fact, according to the said first counting procedure, on the tenth level there are no branches; according to the other procedure, however,

[^50]we say that on the tenth level, three branches on the left, and two branches on the right tree (which arrived from the previous ninth level) are finalized. Then, the question is whether, in this second sense, there are also branches (descendants) at the eleventh level? The answer was given by Darwin himself, ${ }^{17}$ from which it follows that all four levels of the upper part of the Diagram contain finalized branches, which arrived from the previous 10th level: 8 on the left and 6 on the right. ${ }^{18}$

The first thing we see in Table 2.1 is that the number of branches in the upper part of the Diagram is equal to the number of branches in the lower part of the Diagram ( $56+56=4 \times 28=$ 112); then, that the result of cross-linking system components (along the two zig-zag lines), the pattern 52/60, as well as the total number of branches (112), was taken from a specific and unique arithmetical system (Fig. 5). In addition, this number of branches (112) is just a permutation of the number $121\left(11^{\wedge} 2\right),{ }^{19}$ which is actually the number of secondary branches on both trees, for the two species, "A" and "I" (Table 2.2) ${ }^{20}$; and this number is also taken from a specific and unique arithmetical system, which we have already presented in the Preliminaries (Figure 4).

Figure 4 shows several things at the same time. First, it presents a clear and unequivocal arithmetical system which from, as we have seen, Darwin took (reconciled) the results for the total number of branches in the Diagram (276) as well as for the number of secondary branches from zero up to the 9th level of the Diagram, the number 121, for the species "A" and "I" (Table 2.2). But at the same time we see that these results follow from the determination by the first perfect number, the number 6, which also appears to be the determinant of the genetic code (Figure B.2). ${ }^{21}$
[Remark 4.1. Secondary branches do not have branchings, while the primary branches have. As examples, the two positions at the first level on the left tree: from al there is not, while from $m 1$ there is a branching; details about speaking in Section 4.4, in tables 3.1-3.3 (the nodes and branchings), in relation to tables $4-1-4-5$, where there are the sums of the primary and secondary branches.]

[^51]
### 4.2. The riddle of the genetic code

Table 2.2 is very significant. It is amazing that the sequence of quantities: $11,22,33,44,55$, 66,77 is realized. ${ }^{22}$ It is hard to believe that it could be a coincidence, especially if we know that just by these numbers a specific and unique arithmetical system, which is one of the most important determinants of the genetic code, is bounded (Table C. 1 in Appendix C) (Rakočević, 2011a, Table 4; 2011b, Table 4). The understanding of that determination is easier by illustrations given in Appendix C, where it is shown that the said arithmetical system contains the specific algebraic system, which also appears to be a significant determinant of the genetic code: it determines codon/amino acids assignment in relation to a classification into four diversity types of amino acids (AAs).

In Figure C. 1 the classification into four diversity types is shown, in linear and circular form; and Figure C. 2 shows the manner in which the circular arrangement becomes a Table of Mendeleevian type, where the molecules are arranged, mutatis mutandis, in accordance with the principles of minimum change and continuity. But what is surprising is the fact that the quantities (26, 42, 57, 77), representing the number of atoms in this Table (Figure C.2) are "taken" from the arithmetical system, given in Table C. 1 (in relation to Table C. 2 and C.3), in a manner as shown in Survey C.1. According to the algebraic equations given in Survey C.2, the 25 codons encode for less complex, and 36 for more complex AAs (Table C.4).

### 4.3. Darwin's solution to the riddle of the genetic code

The missing link in the strict determination of the genetic code by an arithmetical (Table C.1) and an algebraic system (Survey C. 2 in relation to Survey C.1) is actually in the Survey C.2. In fact, we do not know which quadruplet sequence is preceded by or which one follows a sequence of squares $\left(6^{\wedge} 2,5^{\wedge} 2,4^{\wedge} 2,3^{\wedge} 2\right)$; moreover, we do not know which sequence is initial, and if there is a more general law that all the sequences are connected with? Fortunately, there is an answer, and it is contained in Darwin's diagram (Figure $6 \& 7$ in relation to Tables 5, 6.1 and 7.1). ${ }^{23}$

The general law is actually a rule, analogue to Hückel's rule $\mathrm{N}=(4 \mathrm{n}+2)(\mathrm{n}=0,1,2,3 \ldots)$, according to which, one can calculate the number N as the number of $\pi$ electrons in the most

[^52]stable aromatic molecules; and by analogy, the number of chemical elements in the periods of the periodic system of Mendeleyev (2s, 6p, 10d, 14f ...). ${ }^{24}$ (Cf. Box 2.)

## Box 2. Citation from 1994 (II)

Rakočević, 1994, p. 14: "The main idea, which is in the basis of the diagram-binary tree, is the realization of the logic of the systematization and classification, separation of the parts within the whole, as well as the regularity of the hierarchy of the levels. The accordance of this logic with the model of classification of the number systems with the number basis $\mathrm{N}=2(2 \mathrm{n}+1)(\mathrm{n}=0,1,2,3)$ is directly obvious. ... So, we have for $\mathrm{n}=0, \mathrm{~N}=2$, what corresponds to the division of binary tree to the left tree and the right tree. It corresponds also to the Darwin's discussion of the relations during the evolution only along two lines at the beginning of which 'species (A)' and 'species (I)' occures $\ldots$ In the case when $n=1, \mathrm{~N}=6$, and this again corresponds to the division of the tree, to the left and right tree, but in this case this division is strictly indicated by only one line, the line of the letter (species) F which has a positional value of exactly 6 (this is the sixth letter in alphabet) ... The next possible relation in the system of classification and in the logic of the level hierarchy is the case when $\mathrm{n}=2$ and $\mathrm{N}=10$. This situation corresponds to a reduction of all branch outputs to three and two outputs [on the 10th level] on the left and right tree ... In the latter case, $n=3$ and $\mathrm{N}=14$, what corresponds to the end-outputs of the branches (on the 14th level) when 'we get eight species ..., all descended from (A)'...; 'and (I) will have been replaced by six ... new species'. ${ }^{25}$

By this rule, as we now see, the connection between the quadruplets of squares is determined, in a series of natural numbers, through a system of two and two linear equations, ${ }^{26}$ which are connected by an "inserted" intermedial equation. In the case of the genetic code these three equations are found in the third "quadrant" of the system in Figure 7 (correspondingly with Survey C. 1 and C.2, as well as Table C.4), with the intermedial equation as Darwin's equation $(27+09=36)$, which is found in Table 5 and Table 6.1 ; it determines the number of primary branches in the " 9 other species" (out of species "A" and "I").

[^53]Hückel's rule (more precisely, an analogue of the rule) is a generalization concerning the "travel" of quadruplet squares generated from a series of natural numbers, starting with quadruplet $1-2-3-4$, that is with $1^{\wedge} 2-2^{\wedge} 2-3^{\wedge} 2-4^{\wedge} 2$. But knowing now for this Darwin's generalization that contains Hückel's rule, (and is related to the squares), as well as for Darwin's Platonian solution, given in the Preliminaries, and it concerns cubes, a new question is: Is a generalization over the n -th degree possible ( $\mathrm{n}=1,2,3,4,5 \ldots$...) ? In our opinion, the answer to this question should include the Mendel's quadruplet, valid for „Die entwicklung der Hybriden in ihren Nachkommen". ["Bezeichnet n die Anzahl der charackteristischen Unterschiede an den beiden Stammflanzen, so gibt $3^{\mathrm{n}}\left(3^{\wedge} \mathrm{n}\right)$ die Gliederzahl der Kombinationsreihe, $4^{\mathrm{n}}\left(4^{\wedge} \mathrm{n}\right)$ die Anzahl der Individuen, welche in die reihe gehören, und $2^{n}\left(2^{\wedge} n\right)$ die Zahl der Verbindungen, welche konstant bleiben.".] ${ }^{27}$

### 4.4. Nodes and branchings

Now we observe the Diagram (Figure 1.1) compared to Table 3.1. At the zeroth level we find a node on the left tree as well as on the right tree. At the first level, there are two nodes on the left and one node on the right etc., until the ninth level, after which there is no node involvement. Some nodes branch and some do not. By this, one must notice that there is a branching only when one of the nodes is followed by at least two branches, which are finalized at the next level (and they are marked by letters). Thus, the node at the zeroth level on the left tree is at the same time a branching, while on the right it is not (Tables 3.2 and 3.3). It is easily seen that after the sixth level there is no more branching. [On the sixth level there are the following branchings: $m 6$ branches into $m 7$ and $l 7$ on the left; $z 6$ branches into $z 7$ and $w 7$ on the right.] This fact requires that, in the analysis of the number of all branches, except the splitting into the $5+5$ levels as in Table 4.1 we must analyze the splitting into $7+3$ levels ${ }^{28}$ as in Table 4.2 , and then into the $3+4$ +3 levels as in Table 4.3; and into $3+2+2+3$ levels as in Table 4.4.

The analysis shows that the number of nodes, as well as the number of branchings, along the two diagonal lines, is balanced through changes by $\pm 0$ or $\pm 1$. Thus, the number of nodes is $23 \pm 1$ (Table 3.1), and the number of branchings is $5 \pm 1$ in Table 3.2 and $5 \pm 0$ in Table 3.3. The same balances were carried out in the odd/even positions.

The essential connection of nodes and branchings allows the possibility of their addition: 46 nodes +10 branchings equals 56 group tree-entities (Tables 3.1 and 3.2) in correspondence with 56 primary branches as individual tree-entities, both in the lower and in the upper part of the Diagram (Table 1.1 and 1.2 in relation to Table 1.5).] That essential connection is related to the fact that both primary and secondary branches spring from the same nodes (Table 3.1). But what

[^54]is "unacceptable" concerning the addition is that some nodes (the ones in which there is a branching) are included in the sum twice. However, the same kind of "the unacceptable" we find in the sums of the nucleon number in the two classes of amino acids within Shcherbak's diagram (cf. legend to Figure 3).

### 4.5. Binary-code-tree in Darwin's Diagram

If we exclude (in the part of Darwin's diagram which is generated from the root "A") the nodes without branching, then we, mutatis mutandis, obtain the source Darwin's diagram (Figure 1.3). And if all secondary branches are excluded from this source Diagram, and only two primary branches are left at each node we get a "clean" binary tree, which one hundred percent corresponds to the binary tree of the genetic code (Figure 1 in Rakočević, 1998, p. 284).
[Remark 4.2. Darwin diagrams in Figures 1.3, 1.4 and 1.5 preceded to the book The Origin of Species; first two (Figures $1.3 \& 1.4$ ) as singlet ilustrations, while the third (Figure 1.5) as a set of illustrations - a unifying set of four diagrams. (For details see: Fleming, 2013.) But, what is important for us here is the fact that the Diagram in Figure 1.5 Darwin made by hand, and in it there is a small letter " j ", but as a large letter does not appear; also, there is a large letter " M " too, which does not exist in Figure 1.1. Altogether is in favor of our hypothesis that Darwin on his diagrams dealing with three sets of letters: 1. A \& I; 2. B, C, D, E, F; G, H, K, L and 3. M, N, O, P, ..., Z.]

And, as on the binary tree of the genetic code where there is only one possible alternative in each step, in Darwin's evolutionary binary tree there is only one possible alternative, as well. One by one, along a binary tree, in a very long evolutionary path, from generation to generation, the totality of alternatives (changes and modifications implemented through the process of selection) dismisses the great antinomy of the diversity of organisms (Box 3), the basis of which is the antinomy of the genetic code (Box 4). In other words, variations and modifications, which Darwin's text presents, cannot be arbitrary, but are determined and bounded by a specific and unique arithmetical and/or algebraic structures /systems, the basis of which are the following principles: the principle of symmetry, the principle of the minimal change and the continuity principle.

### 4.6. The balances of the number of branches for two species ("A" and "I")

The number of primary branches for two species, "A" and "I", at all levels (I-XIV) is given by the pattern $52+60=112$ (Table 2.1) ${ }^{29}$, which appears to be the middle case in a specific arithmetical system (Figure 5). On the other hand, the total number of secondary branches (from the zeroth to the ninth level) is such that it represents the change in $10 / 01$ in relation to the number of primary branches, respectively: 52/60 in Table 2.1 is changed to $62 / 59$ in Table 2.2 $(52+10=62$ and $60-01=59)$. But what is rather surprising is that the unit balances continue further, going from one subsystem to the other within the system of the whole of Darwin's diagram.

[^55]
## Box 3. "Irreconcilable" antinomy of organism equality and diversity

.A. Timiryazev, Istoricheskij metod v biologii, Akademiya nauk USSR, 1942, Moscow, p. 187-188: "If all organisms are related by the unity of origin (as it is proven by general observation derived from a comparison of fact classification, metamorphosis, comparative anatomy, embryology, paleontology), then the organic world [as opposed to the vast diversity] must be a merged, inseparable whole. That sharp contrast, that irreconcilable antinomy nobody managed to resolve neither before nor after Darwin. And he himself used to stop at it, until he found a solution that, logically, followed from the same principle - the principle of selection ... Natural selection provides a better chance of survival to those beings who possess some characteristics which ensure their survival under given conditions. Among such characteristics, there is some degree of difference in relation to the other closest beings and it saves them from the competition and provides, so to speak, some space for the newcomer. Thus, a differentiation, a certain degree of difference will be useful, it will mean the success of those forms which are the most different from their parents and from each other. Darwin called this the principle of characteristic divergence (divergence of characters) and he explained it by the following scheme (Figure 15 on p. 188)" (here: Figure 1.3).

## Box 4. "Irreconcilable" antinomy of the genetic code constituents equality and diversity

The genetic code antinomy can be expressed in several ways, out of which we here present only two. The first way is Shcherbak's diagram itself (Figure 3): Within 15 identical "heads" of 15 non-four-codon AAs there is the same number of nucleons, as in their 15 completely different bodies (1110). On the other hand, the number of nucleons within eight four-codon AAs - in different bodies, identical heads and whole molecules - is such as to comply with the law of Pythagoras (squares of numbers 3, 4 and 5, multiplied by the "Prime Quantum 037", respectively). Despite the fact that 19 out of 20 canonical AAs are derivatives of the same AA (glycine), they build a huge number of different proteins; and the four nucleotide bases, which are derivatives of the same molecule (pyrimidine), build a number of different and various DNA/RNA macromolecules, genes and genomes.

Thus, the total number of branches (primary + secondary branches, in the classification into $5+5$ levels), shown in Table 4.1, along the two diagonal lines is such that it constitutes a change of $\pm 01$ compared to the arithmetic mean, i.e. compared to the value of the central pair of numbers: the result $90 / 87$ in relation to $89 / 88$. In the next step (primary + secondary, in the classification into $7+3$ levels) as shown in Table 4.2, a change by $\pm 10$ in the result $90 / 87 \rightarrow$ $80 / 97^{30}$ is realized. In the next step (primary + secondary branches, in the classification into $3+$ $4+3$ ) as shown in Table 4.3, the arithmetic mean, i.e. the central pair of numbers (88/89) is realized.

Classifications and distinctions in Tables 4.1-4.4 do not affect the number of branches at even and odd positions, respectively, which is $82 / 95 ;{ }^{31}$ but in the fourth step (Table 4.4), in the result of the two zigzag lines, there is a change in $\pm 01$ exactly related to the result $(82 / 95 \rightarrow$

[^56]83/94). The fifth step is associated with a number of branches, from the upper part of the Diagram as well (arrangement $5+5+5$ ) (Table 4.5), and the result of the two zigzag lines represents a change of $\pm 02$ related to the arithmetic mean $(116 / 117 \rightarrow 114 / 119)$.

### 4.7. The 'Prime Quantum 037"

It is clear, from the results presented so far, that the key principle of classification is actually a (symmetric) distinction of the system, a splitting into two parts, in proportion $1: 1$ (5:5). Concerning the distinction 7:3, however, there must be some additional (hidden?) ${ }^{32}$ reason; maybe the appearance of the "Prime quantum 037" or a connection to Lucas's sequence (Figure D.1), or something else? But whatever it may be, the analysis of quantitative relations in the Diagram shows that precisely this distinction (Table 4.2), with the sub-distinction 3:4:3 (Table 4.3) is the most significant. Taken together, in unity, they show that the quantities are chosen in such a way that in the final result (along the diagonal lines) they represent the realization of $3^{\text {rd }}, 2^{\text {nd }}$ and $1^{\text {st }}$ of multiples of "Prime quantum 037". Moreover, they show (the sub-distinction in Table 4.3) that the "Prime Quantum 037" is a part of a broader arithmetical system (Table B. 1 and Survey B.1) ${ }^{33}$ what we have also presented in several previous works, which from here we present just one (Rakočević, 2008, Tab. 3).

Interestingly, in an also hidden way, the "Prime Quantum 037" is also found in Mendeleev's calculations. ${ }^{34}$ At this point Mendeleev calculates the differences of atomic masses of elements, and in three cases makes two "mistakes". Instead of writing 30/27/67, what is actually the result, he writes 30/37/77 (Appendix B, Survey B.4).

### 4.8. Primary and secondary branches for "other nine species"

Table 5 provides an overview of the number of branches for the remaining nine species, B-F on the left part and G-H \& K-L on the right part. First, we see the number of primary branches at all levels (I-XIV): $27+09=36$ (Table 6.1), ${ }^{35}$ as a result through which Darwin solves "the riddle of the genetic code" (Section 4.3). [Review of counting through levels for primary branches is given in Tables 6.1 and 6.2.] On the right of the result, in Table 5, the result of the total number

[^57]of secondary branches is given $(3+4=7),{ }^{36}$ from the zeroth to the sixth level, because there are none of them on other levels, as shown by the specific counting in the Diagram (Table 6.3). ${ }^{37}$ Therefore, the total number of branches (primary + secondary) for "other nine species," from the zeroth to the 14 th level is $36+07=43$ (Table 6.4), and from the zeroth to the 9 th level is $32+07=39$ (Table 6.5). ${ }^{38}$

In Table 6.1 we see that the number of primary branches for "other nine species", at 0-14 levels, is balanced in the odd/even positions, as well as along the two zigzag lines $(18+18)$. It is clear that there is balance at levels $0-9$ in odd/even positions $(16+16)$, and that there is no balance for four units of the two diagonal lines (Table 6.2). For secondary branches the balance in the same spatial situations is realized with $\pm 1$ difference (3/4) (Table 6.3); for the sum of primary and secondary branches (at levels $0-14$ ) the balance is also realized with $\pm 1$ difference (21/22) (Table 6.4), and this balance is disrupted for three units at 0-9 level (Table 6.5).

### 4.9. Primary and secondary branches for all 11 species

Table 7.1 shows that in Darwin's diagram, we find a total of 276 branches; a number that, in union with the number 121 (which represents the total number of secondary branches of "first two species", "A" and "I"), represents the first case of a specific and unique arithmetical system (as we have shown in the Preliminaries and in Figure 4). The total number of branches splits into two sets, 60 branches in the upper part of the Diagram (with singlet branches) and 216 branches (Plato's number!) in the lower part of the Diagram, with multiple branches (Table 7.2). ${ }^{39}$ Table 7-2 also shows that the number of branches of the first and of the second five levels, represents a change of $\pm 10$ in relation to the arithmetic mean of the total number of branches in the lower part of the Diagram $[(216: 2=108) ;(108+10=118) ;(108-10=98)]$. The same model is valid for the whole Diagram, for the total number of primary (Tables 7.3) and secondary branches (Table 7.4), but in relation to the total number of branches, number $276[(276: 2=138) ;(138+10=$ 148); $(138-10=128)]$.

[^58]Table 7.5 presents the results of the total number of branches from the zeroth to the ninth level, as in Table 7.4, of the total number of secondary branches. (A Table in analogy with Table 7.3 for the secondary branches is not possible, because there are no secondary branches in the upper part of the Diagram.) In addition to the other balances, Table 7.5 shows an obvious determination through the sequence of a series of natural numbers: 42, 43, 44, 45, 46.

### 4.10. Improbable and unexpected result

In Section 4.3 we have shown that Darwin's equation naturally "fits" the two linear equations which determine the connection between codons and amino acids. And there is nothing surprising in that. Darwin understood (and there is no doubt about that) the existence of a specific and unique system, and with that system he adjusted his (hidden) code stored in the Diagram. However, there is another, perhaps more direct link with the genetic code, for which there is almost no explanation. This connection is revealed by comparing Darwin's result, presented in Table 4.3 to the result which represents the number of atoms in the amino acid molecules, as it is shown in the standard GC Table, if Shcherbak's calculation method is applied.

Shcherbak's calculation procedure is as follows: the number of nucleons in one-meaning AAs is taken into account once, and in two-meaning AAs (L, S, R) twice. ${ }^{40}$ Thus, for example, for the number of nucleons in side chains of AAs he got the following result: [1 x (G1+A15+ $\mathrm{P} 41+\mathrm{V} 43+\mathrm{T} 45+\mathrm{C} 47+\mathrm{I} 57+\mathrm{N} 58+\mathrm{D} 59+\mathrm{K} 72+\mathrm{Q} 72+\mathrm{E} 73+\mathrm{M} 75+\mathrm{H} 81+\mathrm{F} 91+\mathrm{Y} 107+$ W130) $]+[\mathbf{2} \times(\mathrm{L} 57+\mathrm{S} 31+\mathrm{R} 100)]=\underline{1} 443$. If, however, Shcherbak's calculation procedure, is performed with an iteration more, for the number of atoms, the result is as follows: [2 x (G1+ $\mathrm{A} 4+\mathrm{C} 5+\mathrm{D} 7+\mathrm{N} 8+\mathrm{T} 8+\mathrm{P} 8+\mathrm{E} 10+\mathrm{V} 10+\mathrm{Q} 11+\mathrm{M} 11+\mathrm{H} 11+\mathrm{I} 13+\mathrm{F} 14+\mathrm{Y} 15+\mathrm{K} 15+$ $\mathrm{W} 18)]+[3 \mathrm{x}(\mathrm{S} 5+\mathrm{L} 13+\mathrm{R} 17)]=\underline{\mathbf{0}} 443$. On the other hand, the number of all "branch" entities/quantities in Darwin's diagram is: 276 branches (Table 4.5 in relation to Table 5) plus 46 nodes (Table 3.1) +10 branchings (Table 3.2) equals 332 . From this result, the significant differences in relation to GC are: 1443-332 = 1111 and 443-332 $=111$, in both cases determined by a strict balance, expressed through the law of unity change (four and three unit positions, respectively). But that is not all. If the above iteration is derived in a Mendelevian system of AAs (Table E.1) we get the result of two parts which are related to each other also through the unit change law: $277-166=111$. What is, however, surprising is the fact that this result written in the form 166-111-2 77 , strictly corresponds with Darwin's result $\mathbf{0} 66-111-\underline{1} 77$, also through the unit change law (cf. Table 4.2 with Table E.1). From all these results it follows that Darwin's diagram contains a prediction of relationships not only in terrestrial but the genetic code anywhere in the universe, under conditions of the presence of water, ammonia and methane, phosphine and hydrogen sulfide. If so, then Darwinian selection moves one step backwards in prebiotic conditions, where it refers to the choice of the life itself.

[^59]
### 4.11. More than improbable result

This raises the question: whether, perhaps, it is possible to find an arithmetical system that will show all Darwin's quantities, which he used to determine the relations in the Diagram, gathered in one place? Yes, this is the system shown in the Survey B.4. Even more than that, it is a system that demonstrates that Darwin's hidden code is in the unity with the Mendeleev's hidden code (Section 4.7), as well as with the genetic code (Survey B. 5 in relation to Survey B. 6 and B.7), and without that unity none of these three codes [one natural (genetic code) and two created (Mendeleev code and Darwin code)] can be understood.

## 5. Concluding remarks

1. Presenting in this paper a possible Darwin's hidden code, and the arguments in favor of the working hypothesis, given in the Introduction (for this and all other researches of the Diagram in future) of the actual existence of such a code, we hope that we are now also closer to the answer to Shcherbak's crucial question about the nature of arithmetical regularities in the genetic code. ${ }^{41}$ The essence of Darwin's coding is that the principle of selection must also refer to the pre-biological conditions, when it comes to selection of life itself. In some way, unknown to us, Darwin grasped and understood that biological organization must be in correspondence with the organization of unique arithmetical and/or algebraic systems; precisely as we now know that it is so in the genetic code, as presented in this, and in the previous works of several authors. Hence, the whole Darwin's book On the Origin of species is actually a qualitatively expressed biological code and the diagram represents a quantitative evidence of the same code.
2. The working hypothesis, however, can only be considered as proven, provided that one should first understand (and that is our intention, so throughout the paper, we have provided arguments to support it) that Darwin consciously and deliberately encoded everything; in other words, it is proven that the relations presented in Darwin's diagram were not randomly presented. In addition to the aforesaid, it is enough to look at Figures 4 and 5 where two special arithmetical systems are presented, both in relation to the "arithmetical-logical square 11-12-13-14", presented in Table A.1. From the aspect of the probability theory the question is not the probability with which we can accidentally "extract" the numbers one by one, but three numbers at once [in Figure 4, the numbers are: 12-23-276, 23-34-782, etc., where the first case is Darwin's case (Table 7.1$)^{42}$; in Figure 5 there are: $26-36-62,52-60-112$, etc., where the second case is
[^60]Darwin's case ${ }^{43}$ (Table 2.1) $]^{44}$. This, then, means that there is the question of the selection probability of not only these two arithmetical systems, but of all other arithmetical / algebraic systems presented here, correspondent with Darwin's quantities that appear as important determinants in the Diagram.
3. However, independently of the future, we present the probabilities for the two systems in Figures 4 and 5. The probability of a "favorable" event being realized, within the system in Figure 4 (for example, to "derive" the triple 12-23-276) ${ }^{45}$, the probability is $1: 6 \times 10^{\wedge} 12$; and to derive all triples listed in Figure 4 (seven triples), the probability is $1: 10^{\wedge} 79$. As for the system in Figure 5, regarding the fact that the system reaches the end of the three-digit and not four-digit numbers, and that only four cases are presented, the probability is slightly higher $1: 10^{\wedge} 33$. But since these two systems are independent, with the independent events, the probability to draw both systems (in the given lengths) is $1: 10^{\wedge} 112$. It is clear that both systems in their totality, tend to reach the infinity, whereas the probability tends to reach zero, that is to say, to the impossible event.

Everything would be the same if we would like to determine the appereance probability for the elements of the system, presented in the Survey B. 7 (which is in a conection with the system in Survey B.6). However, in favor of the intention and the disqualification of randomness, there is a fact of conditional probability occurrence: with the appearance of the triple 177-277-377, its analogue triple 066-166-266 automatically appears; then, with the triple $288-388-488$ there is its analogue 177-277-377 etc. In addition to this, there is one fact more: the first case is additionally significant, because it contains the Darwin's solution (177-066) in the first position, and the genetic code solution (277-166) in the second position (Table E.1).
4. Based on the findings, presented in this paper, it makes sense to set up a hypothesis (prediction!) according to which a future research will show that life, in all its levels (presented here in the unity and coherence of physical-chemical laws and arithmetical-algebraic regularities) is manifested in proportionalities and harmonious balance. ${ }^{46}$ In addition to that, we

[^61]expect that the results presented here will help in resolving some dilemmas - Darwinism or Intelligent design, ${ }^{47}$ as well as the dilemma: if cultural evolution is subject to Darwinian selectionism or is it a "communal exchange" (Gabora, 2013; Kaufman, 2014). ${ }^{48}$
5. It is so with hypothesis for the future, but if I am to express my opinion, here and now, just based on these results, then, here it is: Concerning the intelligent design, I have nothing to add to what I said in the previous work (here: footnote 47). As for culture, I believe that professors L. Gabora and S. Kaufman (footnote 48) are wrong. As a Darwinian selection has to move one step backwards in prebiotic conditions, it has to move one step forward, as well, where it refers to human consciousness and its "products," such as human society.

All kinds of "communal exchanges" are primarily found in the input, and when it comes to the final output (which language and which culture survive and which languages and cultures disappear), they must necessarily be the result of Darwinian selection, as the most general law valid for all manifestations of life, starting with the problem of its origin in the immaterial, through all the manifestations of actual life, until the problem of appearance and manifestation of consciousness and meaningfulness, including the evolution of human society itself.

## Acknowledgement

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[^62]
## FIGURES



Figure 1.1. The "accompanying diagram" in Darwin's book "On the Origin of Species" (London, 1859)


Figure 1.2. The qualitative analysis of Darwin's diagram (www.biologydirect/darwin)


Figure 1.3. The Darwin's binary tree in his initial, preliminary draft „The foundations of origin of species", 1842 (after: Kliment A. Timiryazev, Istoricheskij metod v biologii, Akademiya nauk SSSR, 1942, Moskva, Figure 15 on p. 188).


Figure 1.4. In mid-July 1837 Darwin started his "B" notebook on Transmutation of Species, and on page 36 he wrote "I think" above his first evolutionary tree.


Figure 1.5. In mid-July 1837 Darwin started his "B" notebook on Transmutation of Species, and on page 36 he wrote "I think" above his first evolutionary tree.


Figure 2. The logic square of the Genetic code: two single versus two double molecules; two with two and two with three hydrogen bonds (after: Rakočević, 1994, p. 8).


Figure 3. The Shcherbak's diagram of classification into four-codon and non-four-codon amino acids. The one-meaning AAs are included in the sum once while two-meaning AAs (L, S, R) are included twice (Shcherbak, 1994, Fig. 1 ).

| $\left(0^{\text {th }}\right.$ ) | 01 | X | 12 | $=$ | 012 |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| (1) |  |  |  |  |  | 264 |  |  |
| $\left({ }^{\text {st }}\right.$ ) | 12 | X | 23 | $=$ | 276 |  | 242 |  |
| (2) |  |  |  |  |  | 506 |  |  |
| ( $2^{\text {nd }}$ ) | 23 | X | 34 | $=$ | 782 |  | 242 | 121 |
| (3) |  |  |  |  |  | 748 |  |  |
| $\left(3^{\text {rd }}\right)$ | 34 | X | 45 | $=$ | 1530 |  | 242 |  |
| (4) |  |  |  |  |  | 990 |  |  |
| $\left(4^{\text {th }}\right.$ ) | 45 | X | 56 | = | 2520 |  | 242 |  |
| (5) |  |  |  |  |  | 1232 |  |  |
| $\left(5^{\text {th }}\right)$ | 56 | x | 67 | = | 3752 |  | 242 | 121 |
| (6) |  |  |  |  |  | 1474 |  |  |
| (6 ${ }^{\text {th }}$ ) | 67 | X | 78 | = | 5226 |  | 242 |  |
| (7) |  |  |  |  |  | 1716 |  |  |
| $\left(7^{\text {th }}\right)$ | 78 | X |  | $=$ | 6942 |  | 242 |  |
| $(50=49+01)$ |  | $(49+121=170)$ |  |  | $(170+07=177)(121=121 \pm 00)$ |  |  |  |

Figure 4. The multiples of $[(1+11 n)(12+11 n)](n=0,1,2, \ldots)$. The pattern „276" appers to be Darwin's determinant as the total number of branches in the Diagram (Table 7.1); as well as the pattern „121" which also appears to be Darwin's determinant as the total number of secondary branches for two species (A and I) in the Diagram (Table 2.2).

| 0 | x | 13 | $=$ | 00 | 12 | $\underline{0} 12$ |  |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| 1 | x | 12 | $=$ | 12 |  |  | 50 |
| 2 | x | 13 | $=$ | 26 |  |  | 50 |
| 3 | x | 12 | $=$ | 36 | 10 | 062 |  |
| 4 | x | 13 | $=$ | 52 |  |  | 50 |
| 5 | x | 12 | $=$ | 60 |  | 112 |  |
|  |  |  |  |  |  |  | 50 |
| 6 | x | 13 | $=$ | 78 | 06 | 162 |  |
| 7 | x | 12 | $=$ | 84 |  |  | 50 |
| 8 | x | 13 | $=$ | 104 |  |  |  |
| 9 | x | 12 | $=$ | 108 | $\underline{212}$ |  |  |
| $(50=49+01)$ | $(49+121=170)$ | $(170+07=177)$ |  |  |  |  |  |

Figure 5. The multiples of numbers 13 and $12 ; 13$ by even, and 12 by odd numbers from natural numbers sequence. The Darwin's pattern $(52+60=112)$ is presented in the dark tones area in Table 2.1.


Figure 6. The generation of the squares of natural numbers through two linear equations. Darwin's equation is in the third quadrant, in the area of dark tones (Tables 5 and 6.1) surrounded by two linear equations valid in the genetic code (Table C.2), presented in Survey C.2.


Figure 7. This Figure follows from the previous one, Figure 6. Three linear equations within each of the four quadrants in relation to the quadruplets of natural numbers' squares. In the third quadrant: two equations are valid in the genetic code (Table C.2) and one (in the middle position, dark tone) is given as Darwin's equation (Tables 5 and 6.1). [Notice a paradox (Darwin's paradox), valid for number 1 in the first quadrant: the negative value of number 1 cannot be - negative?!]

| $1^{\wedge} 2$ | + | $2^{\wedge} 2$ | + | $3^{\wedge} 2$ | $=$ | 14 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $1^{\wedge} 1$ | + | $2^{\wedge} 1$ | + | $3^{\wedge} 1$ | = | 06 |
| $1^{\wedge} 3$ | + | 2^3 | + | 3^3 | = | $6^{\wedge} 2$ |
| 1 |  | 8 |  | 27 |  |  |
|  | 9 |  | + | 27 | = | 36 |
| G | H | K | L |  |  |  |
| 6:1 | 2:1 | 0:1 | 1:1 | $3 \wedge 2+$ | $3 \wedge 3$ | $=6^{\wedge} 2$ |
| 8 |  | 1 |  |  |  |  |
|  |  | 9 |  | $9+$ | 27 |  |
| $\mathrm{x}^{\wedge} \mathrm{n}$ | + | $\mathrm{y}^{\wedge} \mathrm{n}$ | = | $\mathrm{z}^{\wedge} \mathrm{n}-1$ | Valid only for $\mathrm{n}=3$ |  |
| $\mathrm{x}^{\wedge} 3$ |  | $y^{\wedge} 3$ | = | $\mathrm{z}^{\wedge} 2$ |  |  |
| 1^3 | + | 2^3 | $=$ | 3^2 |  |  |
| 1 |  | 8 | $=$ | 9 |  |  |

Figure 8. The relationships between the first three natural numbers. On the top area: the first row shows that the sum of the the first three numbers' squares equals 14 - a half of the second perfect number; the second row shows the sum of the first three numbers as the first perfect number, the number 6 ; the third row shows that the sum of the cubes of the first three numbers equals the square of the first perfect number; in the fourth row we see the values which follow from the third row; the fifth row shows the Darwin's equation (Tables 5 and 6.1). In the central area, on the left there is the number of primary (bold) and secondary branches, valid for the species G, H, K, L and on the right there is a part of Darwin's diagram. [Notice that there are two manners to understand Darwin's approach for a splitting into $8+1=9$ branches: in relation to „species-I" position (left G \& H and right K \& L); and in relation to the zeroth position (there is no primary branches in K position).] In the middle area, on the right: the second variant of the generation of Darwin's equation; the second, in relation to the 5th row in the top area. Down: the intermedial step in generation of Darwin's equation is shown $(1+8=9)$.

| 3^2 | + | $2^{\wedge}$ | + | $1^{\wedge} 2$ | $=$ | 14 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 9 |  | 4 |  | 1 |  |  |
| 5 |  |  |  |  |  |  |
| 3 |  | 3 |  |  |  |  |
| 1 |  | 1 |  | 1 |  |  |
|  |  |  |  |  |  |  |
| $2^{\wedge} 3$ | + | 2^2/ | + | $2^{\wedge} 1$ | $=$ | 14 |
| 8 |  | 4 |  | 2 |  |  |

Figure 9. The relationships within the periodic system of chemical elements (PSE) in correpondence with the equation which we have taken from the first row in Figure 8; also in correpondence with the reverse form of this equation. The arrangement is as follows: 5 elements of $s$-type or $p$-type, 3 elements of $d$-type and 1 element of $f$-type. This pattern is realized (in Periodic Table) 8 times; The following pattern has 3 elements of $d$-type and 1 element of $f$-type, and it is realized 2 times; Finally, we have the form of 1 element of $f$-type, which is repeated four times. [Cf. Table 18, p. 180 in Rakočević, 1997b; by this one must notice that in PSE, in Table 18, there are $1+14$ groups (" 1 " as zeroth group), analogously to $1+14$ elements in Mendeleev's Table: 1 is the lanthanum and 14 are the lanthanides (the last, lutetium, was not known for the life of Mendeleyev, but he is still indicated it, as it is presented in Table 16, in Kedrov, 1977, p. 188); also, analogously to $1+14$ levels in Darwin's diagram.]

## T A B L E S

| $\underline{\mathbf{a}}_{9} \quad 03$ $\mathrm{a}_{8} \quad 03$ $\begin{array}{ll}\mathbf{a}_{7} & 05\end{array}$ $\mathrm{a}_{6} \quad 05$ $\mathbf{a}_{5} \quad 04$ | $\begin{array}{ll} 02 & \mathbf{Z}_{9} \\ 02 & \mathbf{Z}_{8} \\ 03 & \underline{Z}_{7} \\ 03 & \mathbf{Z}_{6} \\ 02 & \mathbf{Z}_{5} \end{array}$ | $\begin{aligned} & \underline{a}_{9} 03 \\ & a_{8} \\ & \hline \end{aligned}$ | 20 (32) 12 | $\begin{aligned} & 02 \underline{Z}_{9} \\ & 02 \mathbf{Z}_{8} \\ & 03 \underline{Z}_{7} \\ & 03 \\ & \mathbf{Z}_{6} \\ & 02 \underline{Z}_{5} \end{aligned}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\begin{array}{ll} \mathrm{a}_{4} & 04 \\ \underline{\mathrm{a}}_{3} & 04 \\ \mathrm{a}_{2} & 03 \\ \mathbf{a}_{1} & 03 \\ \mathrm{a}_{0} & 02 \\ \hline \end{array}$ | $\begin{array}{ll} 02 & Z_{4} \\ 01 & \underline{Z}_{3} \\ 02 & \mathbf{Z}_{2} \\ 02 & \underline{Z}_{1} \\ 01 & Z_{0} \end{array}$ | $\left\|\begin{array}{ll} \mathrm{a}_{4} & 04 \\ \mathbf{a}_{3} & 04 \\ \mathrm{a}_{2} & 03 \\ \mathbf{a}_{1} & 03 \\ \mathrm{a}_{0} & 02 \end{array}\right\|$ | $16 \text { (24) } 08$ | $\begin{array}{ll} 02 & Z_{4} \\ 01 & \mathbf{Z}_{3} \\ 02 & \mathbf{Z}_{2} \\ 02 & \underline{Z}_{1} \\ 01 & Z_{0} \end{array}$ |
| Odd 19 Even 17 | $\begin{aligned} & (29) 10 \\ & (27) \\ & \hline \end{aligned}$ | $\begin{array}{\|l} 27 \\ 29 \end{array}$ | $28 / 28$ <br> (00) |  |
| 36 | 20 | 56 | 56 |  |

Table 1.1. All primary branches at $0-9$ levels (for two species: A and I) in the splitting $(5+5)$. The counting starts from every initial level at which the branching occurs $(\underline{\mathbf{0}}-1, \underline{\mathbf{1}}-2, \underline{\mathbf{2}}-3, \ldots, \underline{\mathbf{9}}-10)$, and the $9^{\text {th }}$ level is the last.

| $\mathrm{a}_{10} 03$ | $02 Z_{10}$ | $a_{10} 03$ |  | $02 Z_{10}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\underline{\underline{a}}_{9} 03$ | $02 \underline{Z}_{9}$ | $\underline{\mathbf{a}}_{9} 03$ |  | $02 \underline{Z}_{9}$ |
| $\mathrm{a}_{8} 05$ | $03 \mathrm{Z}_{8}$ | $\mathrm{a}_{8} 05$ |  | $03 \mathrm{Z}_{8}$ |
| $\underline{a}_{7} 05$ | $03 \underline{Z}_{7}$ | $\underline{a}_{7} \quad 05$ | 20 (32) 12 | $03 \underline{Z}_{7}$ |
| $\mathrm{a}_{6} 04$ | $02 \mathrm{Z}_{6}$ | $\mathrm{a}_{6} 04$ |  | $02 \mathrm{Z}_{6}$ |
| $\underline{a}_{5} 04$ | $02 \underline{Z}_{5}$ | $\mathrm{a}_{5} \quad 04$ |  | $02 \underline{Z}_{5}$ |
| $\mathrm{a}_{4} 04$ | $01 \mathrm{Z}_{4}$ | $\mathrm{a}_{4} 04$ |  | $01 \mathbf{Z}_{4}$ |
| $\underline{\mathbf{a}}_{3} 03$ | $02 \underline{Z}_{3}$ | $\underline{\mathbf{a}}_{3} \quad 03$ |  | $02 \underline{Z}_{3}$ |
| $\mathrm{a}_{2} 03$ | $02 Z_{2}$ | $\mathrm{a}_{2} 03$ | 16 (24) 08 | $02 Z_{2}$ |
| $\underline{\underline{a}}_{1} 02$ | $01 \underline{Z}_{1}$ | $\underline{\mathbf{a}}_{1} 02$ |  | $01 \underline{Z}_{1}$ |
| Even 19 | (29) 10 | (27) | $28 \text { / } 28$ |  |
| Odd 17 | (27) 10 | (29) |  |  |
| 36 | 20 | 56 | 56 |  |

Table. 1.2. All primary branches at $1-10$ levels (for two species: A and I) in the splitting ( $5+5$ ). The counting starts from each subsequent level at which the branch is finalized $(1,2,3, \ldots, 10)$, and the $10^{\text {th }}$ level is the last.

| $a_{10} 00$ <br> $\underline{a}_{9} \quad 00$ <br> $\mathrm{a}_{8} \quad 02$ <br> $\underline{a}_{7} \quad 00$ <br> $a_{6} \quad 00$ | $\begin{array}{lll} 00 & \mathrm{Z}_{6} \\ 00 & \mathbf{Z}_{9} \\ 01 & \mathrm{Z}_{8} \\ 00 & \underline{Z}_{7} \\ 00 & \mathrm{Z}_{6} \end{array}$ | $\left\lvert\, \begin{array}{ll} a_{10} & 00 \\ \underline{a}_{9} & 00 \\ a_{8} & 02 \\ a_{7} & 00 \\ a_{6} & 00 \end{array}\right.$ | $02(03)$ | $\begin{array}{ll} 00 & Z_{10} \\ 00 & \underline{Z}_{9} \\ 01 & Z_{8} \\ 00 & \underline{Z}_{7} \\ 00 & Z_{6} \end{array}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\underline{a}_{5} \quad 01$ <br> $a_{4} \quad 01$ <br> $\underline{\mathbf{a}}_{3} \quad 00$ <br> $\mathrm{a}_{2} 01$ <br> $\underline{\mathbf{a}}_{1} \quad 00$ | $\begin{array}{lll} 00 & \underline{Z}_{5} \\ 00 & \mathbf{Z}_{4} \\ 01 & \mathbf{Z}_{3} \\ 00 & \mathrm{Z}_{2} \\ 00 & \mathbf{Z}_{1} \end{array}$ | $\left.\begin{array}{ll} \underline{\mathbf{a}}_{5} & 01 \\ \mathbf{a}_{2} & 01 \\ \mathbf{a}_{3} & 00 \\ \mathbf{a}_{2} & 01 \\ \underline{\mathbf{a}}_{1} & 00 \end{array} \right\rvert\,$ | $03 \text { (04) } 01$ | $\left\lvert\, \begin{array}{ll} 00 & \mathbf{Z}_{5} \\ 00 & \mathbf{Z}_{4} \\ 01 & \underline{Z}_{3} \\ 00 & \mathbf{Z}_{2} \\ 00 & \underline{Z}_{1} \end{array}\right.$ |
| Even 04 Odd 01 | $\left\|\begin{array}{l} (05) \\ (02) \\ 01 \end{array}\right\|$ | $\begin{aligned} & (02) \\ & (05) \end{aligned}$ | $03 \text { / } 04$ |  |
| 05 | 02 | 07 | 07 |  |

Tab. 1.3. All primary, finalized, fixed branches at 1-10 levels (for two species: A and I) in the splitting $(5+5)$. The counting is as in Table 1.2. (Notice the results in the form of the sequence: 1, 2, 3, 4, 5.)

| $\mathrm{a}_{10} \quad 03$ | $02 \mathrm{Z}_{10}$ | $a_{10} 03$ |  | $02 \mathrm{Z}_{10}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\underline{\underline{a}}_{9} \quad 03$ | $02 \underline{Z}_{9}$ | $\underline{\mathbf{a}}_{9} \quad 03$ |  | $02 \underline{Z}_{9}$ |
| $\mathrm{a}_{8} \quad 03$ | $02 \mathrm{Z}_{8}$ | $\mathrm{a}_{8} \quad 03$ |  | $02 \mathrm{Z}_{8}$ |
| $\underline{\underline{a}}_{7} \quad 05$ | $03 \quad \underline{Z}_{7}$ | $\begin{array}{ll}\mathbf{a}_{7} & 05\end{array}$ | 18 (29) 11 | $03 \underline{Z}_{7}$ |
| $a_{6} \quad 04$ | $02 \mathrm{Z}_{6}$ | $a_{6} 04$ |  | $02 \mathrm{Z}_{6}$ |
|  | $02 \quad \mathbf{Z}_{5}$ | $\mathrm{a}_{5} 03$ |  |  |
| $\mathrm{a}_{4} 03$ | 01 | 03 |  |  |
| $\underline{\mathbf{a}}_{3} \quad 03$ | $01 \underline{Z}_{3}$ | $\underline{\mathbf{a}}_{3} \quad 03$ |  | $01 \underline{Z}_{3}$ |
| $\mathrm{a}_{2} 02$ | $02 \mathrm{Z}_{2}$ | $\mathrm{a}_{2} 02$ | 13 (20) 07 | $02 \mathrm{Z}_{2}$ |
| $\underline{\underline{a}}_{1} \quad 02$ | $01 \quad \underline{Z}_{1}$ | $\underline{\underline{a}}_{1} \quad 02$ |  | $01 \underline{Z}_{1}$ |
| Even 15 | (24) 09 | 25 | $25 \text { / } 24$ |  |
| Odd 16 | (25) 09 | 24 |  |  |
| 31 | 18 | 49 | 49 |  |
| $(31-20=11)(29-18=11)$ |  |  |  |  |
| Fixed $7\left(7^{1}\right)+49\left(7^{2}\right)$ non-fixed $=56$ primary |  |  |  |  |

Tab. 1.4. All primary, finalized, non-fixed branches at 1-10 levels (for two species: A and I) in the splitting (5+5). The counting is as in Table 1.2.

| $\mathrm{a}_{14} 08$ | $06 Z_{14}$ | $a_{14} 08$ |  | $06 \mathbf{Z}_{14}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\underline{\mathbf{a}}_{13} 08$ | $06 \underline{Z}_{13}$ | $\underline{\mathbf{a}}_{13} 08$ |  | $06 \underline{Z}_{13}$ |
| $\mathrm{a}_{12} 08$ | $06 \mathbf{Z}_{12}$ | $\mathrm{a}_{12} 08$ | 32 (56) 24 | $06 \mathbf{Z}_{12}$ |
| $\underline{\mathbf{a}}_{11} 08$ | $06 \underline{Z}_{11}$ | $\underline{a}_{11} 08$ |  | $06 \underline{\underline{Z}} 11$ |
| $\mathrm{a}_{10} 00$ | $00 \mathrm{Z}_{10}$ | $\mathrm{a}_{10} 00$ |  | $00 Z_{10}$ |
|  |  |  |  |  |
| $\mathrm{a}_{10} 03$ | $02 Z_{10}$ | $\mathrm{a}_{10} 03$ |  | $02 Z_{10}$ |
| $\underline{\mathbf{a}}_{9} \quad 03$ | $02 \underline{Z}_{9}$ | $\underline{a}_{9} 03$ |  | $02 \underline{Z}_{9}$ |
| $\mathrm{a}_{8} \quad 03$ | $02 \mathrm{Z}_{8}$ | $\mathrm{a}_{8} 03$ | 18 (29) 11 | $02 \mathrm{Z}_{8}$ |
| $\underline{\mathbf{a}}_{7} \quad 05$ | $03 \underline{Z}_{7}$ | $\underline{a}_{7} 05$ |  | $03 \underline{\underline{Z}}_{7}$ |
| $\mathrm{a}_{6} \quad 04$ | $02 \mathrm{Z}_{6}$ | $a_{6} 04$ |  | $02 \mathbf{Z}_{6}$ |
| $\begin{array}{ll}\mathbf{a}_{5} & 03\end{array}$ | $02 \underline{Z}_{5}$ | $\underline{\mathbf{a}}_{5} 03$ |  | $02 \underline{Z}_{5}$ |
|  |  | $\begin{array}{ll}a_{4} & 03 \\ \mathbf{a}_{3} & 03\end{array}$ | 13 (20) 07 |  |
| $\begin{array}{ll}\underline{a}_{3} & \\ \mathrm{a}_{2} & 02\end{array}$ | $\begin{aligned} 01 & \leq 3 \\ 02 & \mathrm{Z}_{2} \end{aligned}$ | $\begin{array}{ll} \mathbf{a}_{3} & 03 \\ \mathbf{a}_{2} & 02 \end{array}$ |  | $\left\|\begin{array}{ll} 01 & \mathbf{Z}_{3} \\ 02 & \mathrm{Z}_{2} \end{array}\right\|$ |
| $\underline{\underline{\mathbf{a}}}_{1} 02$ |  | $\underline{a}_{1} 02$ |  |  |
| Even 31 | (52) 21 | 53 | $49 / 56$ |  |
| Odd 32 | (53) 21 | 52 |  |  |
| 63 | 42 |  | 5 (216-11 |  |
| $(105=56+49)[233-105=128(121+7)]$ |  |  |  |  |

Tab. 1.5. All primary, finalized, non-fixed branches on 1-14 levels (for two species: A and I) in the splitting (3x5). The counting is as in Table 1.2. Notice the self-similarity expressed through quantities on two zigzag lines: 49 as non-fixed branches (Table 1.4), 56 as total number of primary branches in the lower as well as in the upper part of the Diagram (Table 2.1). The result 105 follows from this distinction: all 112 primary branches (Table 2.1) minus 7 fixed branches (Table 1.3). The balance and self-similarity: 105 as all primary, finalized, non-fixed branches $=216$ as all the branches in the lower part of the Diagram ( $0-9$ levels, for all 11 species) minus 111 "undefined" units. [Self-similarity is present here because 111-105 = $\mathbf{6}$ and 177 (in Table 4.1) minus 111 equals $\mathbf{6 6}$ as in Table 4.2 (Notice the determinants 6 and 66 in Table B.1).]

| $\begin{array}{ll} \mathrm{a}_{14} & 08 \\ \mathbf{a}_{13} & 08 \\ \mathrm{a}_{12} & 08 \\ \mathbf{a}_{11} & 08 \\ \mathbf{a}_{10} & 00 \end{array}$ | $\left\|\begin{array}{ll} 06 & \mathbf{Z}_{14} \\ 06 & \mathbf{z}_{13} \\ 06 & \mathbf{Z}_{12} \\ 06 & \mathbf{z}_{11} \\ 00 & \mathbf{Z}_{10} \end{array}\right\|$ | $a_{14} 08$ <br> $\underline{a}_{13} 08$ <br> $\mathrm{a}_{12} 08$ <br> $\underline{a}_{11} 08$ <br> $a_{10} 00$ | $32(56) 24$ | $\begin{aligned} & 06 \mathbf{Z}_{14} \\ & 06 \\ & \mathbf{Z}_{13} \\ & 06 \\ & \mathbf{Z}_{12} \\ & 06 \\ & \mathbf{Z}_{11} \\ & 00 \end{aligned}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\underline{a}_{9} \quad 03$ <br> $\mathrm{a}_{8} \quad 03$ <br> $\underline{a}_{7} 05$ <br> $a_{6} \quad 05$ <br> $\underline{a}_{5} \quad 04$ | $\left\|\begin{array}{ll} 02 & \mathbf{Z}_{9} \\ 02 & \mathbf{Z}_{8} \\ 03 & \mathbf{Z}_{7} \\ 03 & \mathbf{Z}_{6} \\ 02 & \mathbf{Z}_{5} \end{array}\right\|$ | $\underline{a}_{9} 03$ <br> $\mathrm{a}_{8} 03$ <br> $\underline{a}_{7} 05$ <br> $a_{6} 05$ <br> $\underline{a}_{5} 04$ | $20(\mathbf{3 2}) 12$ | $\begin{array}{ll} 02 & \underline{Z}_{9} \\ 02 & \mathbf{Z}_{8} \\ 03 & \underline{Z}_{7} \\ 03 & \mathbf{Z}_{6} \\ 02 & \underline{Z}_{5} \end{array}$ |
| $\begin{array}{ll} \mathbf{a}_{4} & 04 \\ \mathbf{a}_{3} & 04 \\ \underline{a}_{2} & 03 \\ \mathbf{a}_{1} & 03 \\ \mathbf{a}_{0} & 02 \\ \hline \end{array}$ | $\left\|\begin{array}{ll} 02 & Z_{4} \\ 01 & \underline{Z}_{3} \\ 02 & Z_{2} \\ 02 & \underline{Z}_{1} \\ 01 & Z_{0} \end{array}\right\|$ | $a_{4} 04$ <br> $\underline{a}_{3} \quad 04$ <br> $\mathrm{a}_{2} 03$ <br> $\underline{\mathbf{a}}_{1} 03$ <br> $a_{0} 02$ | $16 \text { (24) } 08$ | $8\left(\left.\begin{array}{ll} 02 & Z_{4} \\ 01 & \underline{Z}_{3} \\ 02 & \mathbf{Z}_{2} \\ 02 & \underline{Z}_{1} \\ 01 & \mathbf{Z}_{0} \end{array} \right\rvert\,\right.$ |
| $\begin{gathered} \text { Even } 33 \\ \text { Odd } 35 \end{gathered}$ | $\left\|\begin{array}{l} \text { (55) } 22 \\ (57) \\ 22 \end{array}\right\|$ | $\begin{aligned} & 57 \\ & 55 \end{aligned}$ | $52 \text { / } 60$ |  |
| $\begin{aligned} & 08 \\ & 24 \\ & 32 \end{aligned}$ | $\begin{aligned} & 06 \\ & 18 \\ & 24 \end{aligned}$ | $\begin{aligned} & 14 \text { (wel } \\ & 42 \text { (non } \\ & 56 \\ & \hline \end{aligned}$ | rked on 11-13 | vel) levels) |
| 36 | 20 | 56 (well- | marked on 00-09 | -94 ${ }^{\text {th }}$ levels) |
| 68 | 44 | 112 (4 | x 28) total |  |
| 44 | 26 | 70 well-m | marked (with lett | ters) |

Tab. 2.1. All primary branches for two species, "A" and "I", with the splitting into (3x5) levels. The pattern $52+62=112$ appears to be the middle case in a specific arithmetical system (Figure 5). Notice that 56 branches are in the upper as well as in the lower part of the Diagram. (Notice the differences between pattern 52 / 60 / 112, valid for all primary branches (in this Table) and the pattern 62 / 59 / 121 (in Table 2.2 ), valid for secondary branches, where the changes are $\pm 10$ and $\pm 01$. Notice also that the first pattern $52 / 60 / 112$ is the middle case within a specific arithmetical system, presented in Figure 5.)


Table 2.2. All secondary branches for two species, "A" and "I", with the splitting into $(5+5)$ levels. There are none of them after the 9th level. [Cf. pattern 74/77 with the pattern 64/66 in Table 4.1; then $44 / 46$ with the pattern $64 / 66$ also in Table 4.1.]

| $\underline{\mathbf{a}}_{9} \quad 03$ <br> $\mathrm{a}_{8} \quad 03$ <br> $\underline{a}_{7} 05$ <br> $a_{6} 04$ <br> $\underline{a}_{5} 03$ | $\begin{array}{ll} 02 & \underline{Z}_{9} \\ 02 & \mathbf{Z}_{8} \\ 03 & \underline{Z}_{7} \\ 02 & \mathbf{Z}_{6} \\ 02 & \underline{Z}_{5} \\ \hline \end{array}$ | $\underline{a}_{9} 03$ <br> $\mathrm{a}_{8} 03$ <br> $\underline{a}_{7} 05$ <br> $\mathrm{a}_{6} 04$ <br> $\underline{a}_{5} 03$ | 18 (29) 11 | $\begin{array}{ll} 02 & Z_{9} \\ 02 & Z_{8} \\ 03 & \underline{Z}_{7} \\ 02 & \mathbf{Z}_{6} \\ 02 & \underline{Z}_{5} \end{array}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\begin{array}{ll} \mathrm{a}_{4} & 03 \\ \mathbf{a}_{3} & 03 \\ \mathbf{a}_{2} & 02 \\ \mathbf{a}_{1} & 02 \\ \mathrm{a}_{0} & 01 \end{array}$ | $\begin{array}{ll} 01 & Z_{4} \\ 01 & \underline{Z}_{3} \\ 02 & \mathrm{Z}_{2} \\ 01 & \underline{Z}_{1} \\ 01 & \mathrm{Z}_{0} \end{array}$ | $\begin{array}{ll} \mathrm{a}_{4} & 03 \\ \mathbf{a}_{3} & 03 \\ \mathbf{a}_{2} & 02 \\ \mathrm{a}_{2} & \\ \mathbf{a}_{1} & 02 \\ \mathrm{a}_{0} & 01 \end{array}$ | $11(17) 06$ | $\begin{array}{ll} 01 & Z_{4} \\ 01 & \underline{Z}_{3} \\ 02 & Z_{2} \\ 01 & \underline{Z}_{1} \\ 01 & Z_{0} \end{array}$ |
| $\begin{array}{\|ll} \text { Odd } 16 \\ \text { Even } & 13 \end{array}$ | $\begin{array}{\|l} (25) \\ (21) \\ \hline \end{array} 09$ | $\left(\begin{array}{l} (22) \\ (24) \end{array}\right.$ | $24 \text { / } 22$ |  |
| 29 | 17 | 46 | 46 |  |
| $46+10=56$ |  |  |  |  |

Tab. 3.1. All nodes for two species, "A" and "I", with the splitting into ( $5+5$ ) levels. The balances are self-evident. [Notice a special balance: 46 nodes +10 branchings (Tables 3.1 and 3.2) equals 56 group tree-entities in correspondence with 56 primary branches (Table 1.1) as individual tree-entities.]


Tab. 3.2. All branchings for two species, "A" and "I", with the splitting into (4+3) levels. This is due to the fact that there are branchings in the Diagram just from the zeroth to the 6th level. This finding requires that in the analysis of the number of all branches, except for splitting into the (5+5) levels as in Table 4.1, we must as well analyze the splitting into $(7+3)$ levels as in Table 4.2 , and then into $(3+4+3)$ as in Table 4.3 and $(3+2+2+3)$ as in Table 4.4. The balances are self-evident. [Notice that the left tree of the Diagram (Figure 1.1) contains two large branches; and on the left branch there are only two branchings (bold, underlined units in the second column).]

| $\begin{array}{ll}a_{6} & 1\end{array}$ | $1 \mathrm{Z}_{6}$ | $a_{6} 1$ |  | $1 \mathrm{Z}_{6}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\underline{a}_{5} 1$ | $0 \underline{Z}_{5}$ | $\underline{a}_{5} 1$ |  | $0 \underline{Z}_{5}$ |
| $\mathrm{a}_{4} \quad 1$ | $1 Z_{4}$ | $\mathrm{a}_{4} 1$ | 04 (06) | $2{ }_{1} Z_{4}$ |
| $\underline{a}_{3} \quad 1$ | $0 \underline{Z}_{3}$ | $\underline{\mathrm{a}}_{3} 1$ |  | $0 \underline{Z}_{3}$ |
| $\mathrm{a}_{2} \quad 1$ | $0 \mathrm{Z}_{2}$ | $\mathrm{a}_{2} 1$ |  | $0 \mathrm{Z}_{2}$ |
| $\underline{\mathbf{a}}_{1} \quad 1$ | $1 \underline{Z}_{1}$ | $\underline{a}_{1} 1$ | 03 (04) | $11 \underline{Z}_{1}$ |
| $\mathrm{a}_{0} \quad 1$ | $0 \mathrm{Z}_{0}$ | $\mathrm{a}_{0}$ |  | $0 \mathrm{Z}_{0}$ |
| Even 04 | (06) 02 | (05) | $05 / 05$ |  |
| Odd 03 | (04) 01 | (05) |  |  |
| 07 | 03 | 10 | 10 |  |
| $10+40=56$ (cf. legend in Tab. 3.1) |  |  |  |  |

Tab. 3.3. All branchings for two species, "A" and "I", with the splitting into (3+4) levels as a reverse way in relation to Table 3.2. Notice that the splitting of 7 levels into 3 and 4 ( $3+4=7$ ) represent a correspondence with the Lucas numbers series at the same time (Figure D.1).

| $\underline{a}_{9} \quad 11$ <br> $\mathrm{a}_{8} \quad 12$ <br> $\begin{array}{ll}\underline{a}_{7} & 18\end{array}$ <br> $a_{6} \quad 11$ <br> $\underline{a}_{5} \quad 14$ | $\begin{array}{ll} 07 & \mathbf{Z}_{9} \\ 08 & \mathbf{Z}_{8} \\ 10 & \mathbf{Z}_{7} \\ 07 & \mathbf{Z}_{6} \\ 08 & \mathbf{Z}_{5} \end{array}$ | $\underline{a}_{9} 11$ <br> $\mathrm{a}_{8} 12$ <br> $\underline{a}_{7} 18$ <br> $a_{6} 11$ <br> $\underline{a}_{5} 14$ | 66 (106) 40 | $\begin{cases}07 & \mathbf{Z}_{9} \\ 08 & \mathbf{Z}_{8} \\ 10 & \mathbf{Z}_{7} \\ 07 & \mathbf{Z}_{6} \\ 08 & \underline{Z}_{5}\end{cases}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\left\|\begin{array}{ll} \mathbf{a}_{4} & 13 \\ \mathbf{a}_{3} & 11 \\ \mathbf{a}_{2} & 08 \\ \mathbf{a}_{1} & 09 \\ \mathbf{a}_{0} & 06 \end{array}\right\|$ | $\begin{array}{ll} 06 & \mathbf{Z}_{4} \\ 04 & \underline{Z}_{3} \\ 06 & \mathbf{Z}_{2} \\ 03 & \underline{\mathbf{Z}}_{1} \\ 05 & \mathbf{Z}_{0} \end{array}$ | $\begin{array}{ll} \mathrm{a}_{4} & 13 \\ \mathbf{a}_{3} & 11 \\ \mathbf{a}_{2} & 08 \\ \mathrm{a}_{1} & 09 \\ \mathbf{a}_{0} & 06 \end{array}$ | 47 (71) 24 | $\left\|\begin{array}{ll} 06 & Z_{4} \\ 04 & \underline{Z}_{3} \\ 06 & Z_{2} \\ 03 & \underline{Z}_{1} \\ 05 & Z_{0} \end{array}\right\|$ |
| Odd 63 <br> Even 50 | $\left\|\begin{array}{l} \text { (95) } \\ 32 \\ (82) \\ 32 \end{array}\right\|$ | $\begin{array}{\|l} (82) \\ (95) \end{array}$ | $90 / 87$ |  |
| 113 | 64 | 177 | 177 |  |
| $(177=88+89)(90-89=01)(88-87=01)$ |  |  |  |  |

Tab. 4.1. All branches (primary + secondary) for two species, "A" and "I", with the splitting into (5+5) levels. The pattern $90 / 87$ appears to be an inverse result $80 / 97$ which appears by the splitting into ( $7+3$ ) levels (Table 4.2) and a strict balance in relation to $89 / 88$ (the balance in frame of $\pm 1$ ) by the splitting into ( $3+4+3$ ) levels (Table 4.3). [Cf. pattern 64/66 with pattern $74 / 77$ and pattern $44 / 46$ in Table 2.2.]

| $\begin{array}{ll}\underline{\mathbf{a}}_{9} & 11 \\ \mathrm{a}_{8} & 12 \\ \underline{\mathbf{a}}_{7} & 18\end{array}$ | $\begin{array}{ll} 07 & \mathbf{Z}_{9} \\ 08 & \mathrm{Z}_{8} \\ 10 & \underline{Z}_{7} \end{array}$ | $\begin{array}{ll} \begin{array}{ll} \mathbf{a}_{9} & 11 \\ \mathrm{a}_{8} & 12 \\ \boldsymbol{a}_{7} & 18 \end{array} \\ \hline \end{array}$ | $41(66) 25$ | $\begin{array}{ll} 07 & Z_{9} \\ 08 & Z_{8} \\ 10 & \underline{Z}_{7} \end{array}$ |
| :---: | :---: | :---: | :---: | :---: |
| $a_{6} \quad 11$ | $07 \mathrm{Z}_{6}$ | $a_{6} 11$ |  |  |
| $\underline{a}_{5} \quad 14$ | $08 \underline{Z}_{5}$ | $\mathrm{a}_{5} 14$ |  | $08 \underline{Z}_{5}$ |
| $\mathrm{a}_{4} \quad 13$ | $06 \mathrm{Z}_{4}$ | $a_{4} 13$ |  | $06 \mathbf{Z}_{4}$ |
| $\underline{\underline{a}}_{3} \quad 11$ | $04 \underline{Z}_{3}$ | $\underline{a}_{3} 11$ | 72 (111) 39 | $04 \underline{Z}_{3}$ |
| $\mathrm{a}_{2} 08$ | $06 \mathrm{Z}_{2}$ | $\mathrm{a}_{2} 08$ |  | $06 \mathbf{Z}_{2}$ |
| $\underline{\mathbf{a}}_{1} 09$ | $03 \underline{Z}_{1}$ | $\underline{\mathbf{a}}_{1} 09$ |  | $\mathbf{Z}_{1}$ |
| $\mathrm{a}_{0} 06$ | $05 \mathrm{Z}_{0}$ | $a_{0} 06$ |  | $05 \mathrm{Z}_{0}$ |
| Odd 63 | 95) 32 | 82 | $80 / 97$ |  |
| Even 50 | (82) 32 | 95 |  |  |
| 113 | 64 | 177 | 177 |  |
| (066-111-177) vs (166-111-2 $\mathbf{2 0}^{\text {7 }}$ ) in Tab. E. 1 |  |  |  |  |

Tab. 4.2. All branches (primary + secondary) for two species, "A" and "I", with the splitting into (7+3) levels with pattern 80/97 corresponding to the pattern $90 / 87$ which appears by the splitting into ( $5+5$ ) levels in Table 4.1. On the other hand pattern $\underline{\mathbf{0} 66-111-\underline{1} 77}$ corresponds to pattern $\underline{\mathbf{1} 66-111-\underline{\mathbf{2}} 77 \text { in genetic }}$ code (Appendix E). All other balances are self-evident.

| $\underline{\underline{a}}_{9} \quad 11$ | $07 \underline{Z}_{9}$ | $\underline{a}_{9} 11$ |  | $07 \underline{Z}_{9}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\mathrm{a}_{8} 12$ | $08 \mathrm{Z}_{8}$ | $\mathrm{a}_{812}$ | 41 (66) 25 | $08 \mathrm{Z}_{8}$ |
| $\underline{\underline{a}} 77^{18}$ | $10 \underline{Z}_{7}$ | $\mathbf{a}_{7} 18$ |  | $10 \underline{Z}_{7}$ |
| $a_{6} \quad 11$ | $07 \mathrm{Z}_{6}$ | $a_{6} 11$ |  | $07 Z_{6}$ |
| $\begin{array}{ll}\mathbf{a}_{5} & 14\end{array}$ | $08 \underline{Z}_{5}$ | $\underline{a}_{5} 14$ | 49 (74) 25 | $08 \underline{Z}_{5}$ |
| $\begin{array}{ll}\mathrm{a}_{4} & \\ & \\ \end{array}$ | ${ }_{06} \mathrm{Z}_{4}$ | $\mathrm{a}_{4}{ }_{13}$ |  | $\mathrm{Z}_{4}$ |
| $\underline{\mathbf{a}}_{3} \quad 11$ | $04 \underline{Z}_{3}$ | $\underline{\mathbf{a}}_{3} 11$ |  | $04 \underline{Z}_{3}$ |
| $\mathrm{a}_{2} \quad 08$ | $06 \mathrm{Z}_{2}$ | $\mathrm{a}_{2} 08$ |  | $06 Z_{2}$ |
| $\begin{array}{ll}\mathbf{a}_{1} & 09\end{array}$ | $03 \underline{Z}_{1}$ | $\underline{a}_{1} 09$ | 23 (37) 14 | $03 \underline{Z}_{\mathbf{1}}$ |
| $\mathrm{a}_{0} \quad 06$ | $05 \mathrm{Z}_{0}$ | $a_{0} 06$ |  | $05 Z_{0}$ |
| Odd 63 | ( 95) 32 | 82 | $89 / 88$ |  |
| Even 50 | (82) 32 | 95 |  |  |
| 113 | 64 | 177 | 177 |  |
| $37+74=111$ |  |  |  |  |

Tab. 4.3. This Table follows from Table 4.2. The formal splitting into $(3+4+3)$ levels corresponds to an extended Cantor triadic set (Figure D.2). On the other hand, the number of the branches follows from the splitting of the first Shcherbak's quantum of "the same symbols" (111 in previous Table) into two quantums "arranged by the cyclic permutation" $(037+074)$ where the quantum 037 is the "Prime quantum 037"; all these quantums in relation to number 66, and altogether in connection with a specific and unique arithmetical system (Table B. 1 and Survey B. 1 in Appendix B).

| $\underline{\mathbf{a}}_{9} \quad 11$ | $07 \underline{Z}_{9}$ | $\underline{a}_{9} 11$ |  | $07 \underline{Z}_{9}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\mathrm{a}_{8} \quad 12$ | $08 \mathrm{Z}_{8}$ | $\mathrm{a}_{812}$ | 41 (66) 25 | $08 \mathrm{Z}_{8}$ |
| $\underline{\mathbf{a}}_{7} 18$ | $10 \underline{Z}_{7}$ | $\underline{a}_{7} 18$ |  | $10 \underline{Z}_{7}$ |
| $\mathrm{a}_{6} \quad 11$ | $07 \mathrm{Z}_{6}$ | $\mathrm{a}_{6} 11$ | 25 (40) 15 | $07 \mathrm{Z}_{6}$ |
| $\underline{\mathbf{a}}_{5} 14$ | $08 \underline{Z}_{5}$ | $\underline{a}_{5} 14$ |  | $08 \underline{Z}_{5}$ |
| $\begin{array}{ll} \mathbf{a}_{4} & 13 \\ \mathbf{a}_{3} & 11 \end{array}$ | $\begin{aligned} & 06 \mathrm{Z}_{4} \\ & 04 \underline{Z}_{3} \end{aligned}$ | $\begin{array}{ll}a_{4} & 13 \\ \underline{a}_{3} & 11\end{array}$ | 24 (34) 10 | $06 \mathbf{Z}_{4}$ |
| $\mathrm{a}_{2} \quad 08$ | $06 \mathrm{Z}_{2}$ | $\mathrm{a}_{2} 08$ |  | $06 \mathrm{Z}_{2}$ |
| $\underline{\mathbf{a}}_{1} 09$ | $03 \underline{Z}_{1}$ | $\underline{a}_{1} 09$ | 23 (37) 14 | $03 \underline{Z}_{1}$ |
| $\mathrm{a}_{0} 06$ | $05 \mathrm{Z}_{0}$ | $a_{0} 06$ |  | $05 \mathrm{Z}_{0}$ |
| 63 | ( 95) 32 | 82 | 94/83 |  |
| 50 | (82) 32 | 95 |  |  |
| 113 | (13) 64 | 177 | 177 |  |
| $(94 / 83$ vs $82 / 95)(94-83=11)$ |  |  |  |  |

Tab. 4.4. All branches (primary + secondary) for two species, "A" and "I", with the splitting into $(3+2+2+3)$ levels. The balances are self-evident.

| $\begin{aligned} & \mathbf{a}_{14} \\ & \mathbf{a}_{13} \\ & \mathrm{a}_{12} \\ & \mathbf{a}_{11} \\ & \mathrm{a}_{10} \end{aligned}$ | $06 Z_{14}$ <br> $06 \underline{Z}_{13}$ <br> $06 Z_{12}$ <br> $06 \underline{Z}_{11}$ <br> $00 Z_{10}$ | $\left\lvert\, \begin{array}{ll} a_{14} & 08 \\ \mathbf{a}_{13} & 08 \\ a_{12} & 08 \\ \mathbf{a}_{11} & 08 \\ a_{10} & 00 \end{array}\right.$ | $32(56) 24$ |  |
| :---: | :---: | :---: | :---: | :---: |
| $\begin{array}{ll}\underline{\mathbf{a}}_{9} & 1 \\ \mathrm{a}_{8} & 12 \\ \mathbf{a}_{7} & 18 \\ \mathrm{a}_{6} & 1 \\ \underline{a}_{5} & 1\end{array}$ | $\begin{array}{ll} 07 & \underline{Z}_{9} \\ 08 & \mathbf{Z}_{8} \\ 10 & \underline{\mathbf{Z}}_{7} \\ 07 & \mathbf{Z}_{6} \\ 08 & \underline{Z}_{5} \end{array}$ | $\mathbf{a}_{9} 11$ <br> $a_{8} \quad 12$ <br> $\underline{a}_{7} 18$ <br> $a_{6} 11$ <br> $\underline{a}_{5} \quad 14$ | 66 (106) 40 | $\begin{array}{ll} 07 & \underline{Z}_{9} \\ 08 & \mathbf{Z}_{8} \\ 10 & \underline{Z}_{7} \\ 07 & \mathbf{Z}_{6} \\ 08 & \underline{Z}_{5} \end{array}$ |
| $\begin{array}{ll}\mathrm{a}_{4} & 13 \\ \underline{\mathbf{a}}_{3} & 1 \\ \mathrm{a}_{2} & 08 \\ \underline{\mathbf{a}}_{1} & 09 \\ \mathrm{a}_{0} & 0\end{array}$ | $\begin{array}{ll} 06 & Z_{4} \\ 04 & \underline{Z}_{3} \\ 06 & Z_{2} \\ 03 & \underline{Z}_{1} \\ 05 & Z_{0} \end{array}$ | $a_{4} \quad 13$ <br> $\underline{a}_{3} \quad 11$ <br> $a_{2} \quad 08$ <br> $\underline{\mathbf{a}}_{1} 09$ <br> $a_{0} 06$ | 47 (71) 24 | $+\begin{array}{ll} 06 & Z_{4} \\ 04 & \underline{Z}_{3} \\ 06 & Z_{2} \\ 03 & \underline{Z}_{1} \\ 05 & Z_{0} \end{array}$ |
| Even 6 Odd 7 | $\left\|\begin{array}{ll} (110) & 44 \\ (123) & 44 \end{array}\right\|$ | $\begin{array}{\|l\|} \hline 123 \\ 110 \\ \hline \end{array}$ | $114 \text { / } 119$ |  |
| 145 | 88 | 233 | 233 |  |
| $(233=116+117)$ |  |  |  |  |

Tab. 4.5. All branches (primary + secondary) for two species, "A" and "I", with the splitting into ( $3 \times 5$ ) levels, $0-14$. The balances are self-evident.

| Primary |  | Secondary |  |
| :---: | :---: | :---: | :---: |
| B 00 | 06 G | B 01 | 01 G |
| C 01 | 02 H | C 01 | 01 H |
| D 02 | 00 K | D 01 | 01 K |
| E 10 | 01 L | E 00 | 01 L |
| F 14 |  | F 00 |  |
| 2709 |  | 0304 |  |
| 36 (43) 07 |  |  |  |
| $\begin{aligned} & (233+43=276) \\ & (276+56=332) \end{aligned}$ |  |  |  |
| 99 |  |  |  |
| $276=216_{\text {down }}+60^{\text {up }}$ |  |  |  |

Table 5. All branches (primary + secondary) for "other nine species" for the left and the right part of the Diagram, at all 15 levels. The equation $27+09=36$ appears to be a special Darwin's equation, valid to determination of the genetic code (Figure 6, $7 \& 8$ and Table 6.1); and the equation $03+04=07$ corresponds to the first three members of Lucas number series (Figure D.1).The number 233 comes from Table 4.5 and together with this result (43) makes 276 which is the total number of branches within the Diagram. In addition: $56=46$ nodes plus 10 branchings, and from that all "branch" entities/quantities equal 332 as a mirror pattern of the 233 .


Table 6.1. All primary branches for 9 species (B, C, D, E, F on the left and G, H, K, L on the right) at 0 14 levels. The final result is the Darwin's equation $(27+09=36)$ (cf. Figures $6 \& 7)$.

| $\begin{array}{ll} \begin{array}{ll} \hat{\mathbf{a}}_{9} & 02 \\ \hat{\mathbf{a}}_{8} & 02 \\ \hat{\mathbf{a}}_{7} & 02 \\ \hat{\mathrm{a}}_{6} & 02 \\ \hat{\mathbf{a}}_{5} & 02 \\ \hline \end{array} \end{array}$ | $\begin{array}{ll} 00 & \hat{\mathbf{Z}}_{9} \\ 00 & \hat{\mathbf{Z}}_{8} \\ 00 & \hat{\mathbf{z}}_{7} \\ 00 & \hat{\mathbf{Z}}_{6} \\ 01 & \hat{\mathbf{Z}}_{5} \end{array}$ |  | 10 (11) 01 | $\begin{aligned} & 00 \\ & 00 \\ & 00 \\ & \hat{Z}_{8} \\ & 00 \\ & 00 \\ & 00 \\ & \hat{Z}_{7} \\ & 01 \\ & 01 \end{aligned} \underline{\underline{Z}}_{5}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\hat{a}_{4} \quad 02$ <br> $\underline{a}_{3} \quad 02$ <br> $\hat{a}_{2} \quad 02$ <br> $\underline{\underline{a}}_{1} \quad 03$ <br> â 04 | $01 \hat{Z}_{4}$ <br> $01 \underline{\underline{Z}}_{3}$ <br> $01 \hat{Z}_{2}$ <br> $02 \underline{\underline{Z}}_{1}$ <br> $03 \hat{Z}_{0}$ | $\begin{aligned} & \hat{a}_{4} 02 \\ & \hat{a}_{3} \\ & \underline{a}_{3} \\ & \hline \hat{a}_{2} \\ & \hat{a}_{2} \\ & \hat{\mathbf{a}}_{1} \\ & \hat{a}_{03} \\ & \mathbf{a}_{0} \end{aligned}$ | \% 13 (21) 08 | $\begin{array}{ll} 01 & \hat{Z}_{4} \\ 01 & \hat{\mathbf{Z}}_{3} \\ 01 & \hat{\mathbf{Z}}_{2} \\ 02 & \hat{\mathbf{Z}}_{1} \\ 03 & \hat{\mathbf{Z}}_{0} \end{array}$ |
| Odd 11 <br> Even 12 | $\left\lvert\, \begin{aligned} & (15) \\ & (17) \\ & (17) \\ & \hline \end{aligned}\right.$ | $\begin{aligned} & (16) \\ & (16) \end{aligned}$ | $18 / 14$ |  |
| 23 | 09 | 32 | 32 |  |
| $56+32=88$ |  |  |  |  |

Table 6.2. Primary branches for 9 species (B, C, D, E, F on the left and G, H, K, L on the right) at 0-9 levels.

| $\hat{\mathbf{a}}_{9} \quad 00$ $\hat{a}_{8} \quad 00$ $\hat{\mathbf{a}}_{7} \quad 00$ $\hat{a}_{6} \quad 00$ $\underline{\underline{a}}_{5} \quad 00$ | $\begin{array}{lll} 00 & \hat{\mathbf{Z}}_{9} \\ 00 & \hat{\mathbf{Z}}_{8} \\ 00 & \hat{\mathbf{Z}}_{7} \\ 01 & \hat{\mathbf{Z}}_{6} \\ 00 & \hat{\mathbf{Z}}_{5} \\ \hline \end{array}$ | $\begin{aligned} & \begin{array}{l} \hat{\mathbf{a}}_{9} \\ \hat{a}_{8} \\ \hat{a}_{8} \end{array} 00 \\ & \hat{\mathbf{a}}_{7} \\ & \hat{\mathrm{a}}_{6} \\ & \mathrm{a}_{6} \\ & \hat{\mathbf{a}}_{5} \end{aligned}$ | 00 (01) 01 |  |
| :---: | :---: | :---: | :---: | :---: |
| $\begin{array}{ll} \hat{\mathbf{a}}_{4} & 00 \\ \hat{\mathbf{a}}_{3} & 00 \\ \hat{\mathrm{a}}_{2} & 01 \\ \hat{\mathbf{a}}_{1} & 01 \\ \hat{\mathrm{a}}_{0} & 01 \\ \hline \end{array}$ | $00 \hat{\mathbf{Z}}_{4}$ <br> $00 \underline{\underline{Z}}_{3}$ <br> $01 \hat{\mathbf{Z}}_{2}$ <br> $01 \underline{\underline{Z}}_{1}$ <br> $01 \hat{Z}_{0}$ | $\begin{aligned} & \hat{a}_{4} 00 \\ & \hat{a}_{3} \\ & \hat{a}_{3} 00 \\ & \hat{a}_{2} \\ & \hat{a}_{01} \\ & \mathbf{a}_{1} 01 \\ & \hat{\mathbf{a}}_{0} \end{aligned}$ | $03 \text { (06) } 03$ | $\begin{array}{ll} 00 & \hat{Z}_{4} \\ 00 & \hat{Z}_{3} \\ 01 & \hat{Z}_{2} \\ 01 & \hat{\mathbf{Z}}_{1} \\ 01 & \hat{\mathbf{Z}}_{0} \end{array}$ |
| Odd 01 <br> Even 02 | $\left\lvert\, \begin{aligned} & (02) \\ & (05) \\ & (03) \end{aligned}\right.$ | $\begin{array}{\|l\|} \hline 03 \\ 04 \\ \hline \end{array}$ | $03 \text { / } 04$ |  |
| 03 | 04 | 07 | 07 |  |
| $121+07=128$ |  |  |  |  |

Table 6.3. All secondary branches for 9 species (B, C, D, E, F on the left and G, H, K, L on the right) at $0-9$ levels.


Table 6.4. All branches (primary + secondary) for 9 species (B, C, D, E, F on the left and G, H, K, L on the right) at 0-14 levels. Notice the balances: 21/22 versus 19/24 as a change for $\pm 2$; then: 27 as $9 \times 3$ and 30 as $10 \times 3$.

| $\begin{array}{ll}\hat{\mathbf{a}}_{9} & 02 \\ \hat{a}_{8} & 02 \\ \hat{\mathbf{a}}_{7} & 02 \\ \hat{a}_{6} & 02 \\ \underline{\mathbf{a}}_{5} & 02\end{array}$ | $\begin{array}{lll} 00 & \hat{\mathbf{Z}}_{9} \\ 00 & \hat{\mathrm{Z}}_{8} \\ 00 & \hat{\mathbf{Z}}_{7} \\ 01 & \hat{\mathrm{Z}}_{6} \\ 01 & \hat{\mathbf{Z}}_{5} \end{array}$ | $\begin{array}{\|l\|l} \left\lvert\, \begin{array}{l} \hat{a}_{9} \\ \hat{a}_{8} \\ \mathbf{a}_{8} \end{array} 02\right. \\ \hat{a}_{7} & 02 \\ \hat{a}_{6} & 02 \\ \hat{a}_{6} & 02 \\ \hat{a}_{5} & 0 \end{array}$ | 10 (12) 02 | $2 \begin{array}{ll} 00 & \hat{\mathbf{Z}}_{9} \\ 00 & \hat{\mathbf{Z}}_{8} \\ 00 & \hat{\mathbf{Z}}_{7} \\ 01 & \hat{\mathbf{Z}}_{6} \\ 01 & \hat{\mathbf{Z}}_{5} \end{array}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\begin{array}{ll} \hat{\mathbf{a}}_{4} & 02 \\ \hat{\mathbf{a}}_{3} & 02 \\ \hat{\mathrm{a}}_{2} & 03 \\ \hat{\mathbf{a}}_{1} & 04 \\ \hat{\mathrm{a}}_{0} & 05 \\ \hline \end{array}$ | $\begin{array}{ll} 01 & \hat{\mathrm{Z}}_{4} \\ 01 & \hat{\mathbf{Z}}_{3} \\ 02 & \hat{\mathrm{Z}}_{2} \\ 03 & \hat{\mathbf{Z}}_{1} \\ 04 & \hat{\mathbf{Z}}_{0} \end{array}$ |  | \% 16 (27) 11 | $\left(\begin{array}{l} 01 \hat{\mathbf{Z}}_{4} \\ 01 \\ 01 \\ \hat{\mathbf{Z}}_{3} \\ 02 \hat{\mathbf{Z}}_{2} \\ 03 \\ 03 \underline{\mathbf{Z}}_{1} \\ 04 \hat{\mathbf{Z}}_{0} \end{array}\right.$ |
| Odd 12 <br> Even 14 | $\left\|\begin{array}{l} \text { (17) } 05 \\ (22) \\ \hline \end{array}\right\|$ | $\left(\begin{array}{l} (19) \\ (20) \end{array}\right.$ | $21 / 18$ |  |
| 26 | 13 | 39 | 39 |  |
| The sums: $17,18,19,20,21,22$ |  |  |  |  |

Table 6.5. All branches (primary + secondary) for 9 species (B, C, D, E, F on the left and G, H, K, L on the right) at 0-9 levels.

| $\begin{array}{ll} \begin{array}{ll} \hat{\mathbf{a}}_{14} & 09 \\ \hat{\mathbf{a}}_{13} & 09 \\ \hat{\mathbf{a}}_{12} & 09 \\ \hat{\mathbf{a}}_{11} & 09 \\ \hat{\mathbf{a}}_{10} & 00 \end{array}, \begin{array}{l} \end{array}{ }^{2} \\ \hline \end{array}$ | $\begin{array}{ll} 06 & \hat{\mathbf{Z}}_{14} \\ 06 & \hat{\mathbf{Z}}_{13} \\ 06 & \hat{\mathbf{Z}}_{12} \\ 06 & \hat{\mathbf{Z}}_{11} \\ 00 & \hat{\mathbf{Z}}_{10} \end{array}$ | $\begin{array}{ll} \left.\begin{array}{ll} \hat{\mathbf{a}}_{14} & 09 \\ \hat{\mathbf{a}}_{13} & 09 \\ \hat{\mathbf{a}}_{12} & 09 \\ \hat{\mathbf{a}}_{11} & 09 \\ \hat{\mathbf{a}}_{10} & 00 \end{array} \right\rvert\, \end{array}$ | 36 (60) 24 | $\left\lvert\, \begin{array}{ll} 06 & \hat{\mathbf{Z}}_{14} \\ 06 & \hat{\mathbf{z}}_{13} \\ 06 & \hat{\mathbf{Z}}_{12} \\ 06 & \hat{\mathbf{z}}_{11} \\ 00 & \hat{\mathbf{Z}}_{10} \end{array}\right.$ |
| :---: | :---: | :---: | :---: | :---: |
| $\underline{\underline{a}}_{9}$ 13 <br> $\hat{\mathrm{a}}_{8}$ 14 <br> $\hat{\mathrm{a}}_{7}$ 20 <br> $\hat{\mathrm{a}}_{6}$ 13 <br> $\underline{\mathrm{a}}_{5}$ 16 | $\begin{array}{ll}07 & \hat{\mathbf{Z}}_{9} \\ 08 & \hat{\mathbf{Z}}_{8} \\ 10 & \hat{\mathbf{Z}}_{7} \\ 08 & \hat{\mathbf{Z}}_{6} \\ 09 & \underline{\mathbf{Z}}_{5}\end{array}$ | $\begin{array}{ll}\hat{\mathbf{a}}_{9} & 13 \\ \hat{\mathrm{a}}_{8} & 14 \\ \hat{\mathbf{a}}_{7} & 20 \\ \hat{\mathrm{a}}_{6} & 13 \\ \underline{\hat{a}}_{5} & 16\end{array}$ | 76 (118) 42 | $\begin{array}{ll} 07 & \hat{\mathbf{Z}}_{9} \\ 08 & \hat{\mathbf{Z}}_{8} \\ 10 & \hat{\mathbf{Z}}_{7} \\ 08 & \hat{\mathbf{Z}}_{6} \\ 09 & \hat{\mathbf{Z}}_{5} \end{array}$ |
| $\begin{array}{ll}\hat{\mathbf{a}}_{4} & 15 \\ \hat{\mathbf{a}}_{3} & 13 \\ \hat{\mathbf{a}}_{2} & 11 \\ \hat{\mathbf{a}}_{1} & 13 \\ \hat{\mathbf{a}}_{0} & 11\end{array}$ | $\begin{array}{ll} 07 & \hat{\mathbf{Z}}_{4} \\ 05 & \hat{\mathbf{Z}}_{3} \\ 08 & \hat{\mathbf{Z}}_{2} \\ 06 & \hat{\mathbf{Z}}_{1} \\ 09 & \hat{\mathbf{Z}}_{0} \end{array}$ | $\begin{array}{ll}\hat{\mathbf{a}}_{4} & 15 \\ \hat{\mathbf{a}}_{3} & 13 \\ \hat{\mathbf{a}}_{2} & 11 \\ \hat{\mathbf{a}}_{1} & 13 \\ \hat{\mathrm{a}}_{0} & 11\end{array}$ | $63(98) 35$ | $\left[\begin{array}{ll} 07 & \hat{\mathbf{Z}}_{4} \\ 05 & \underline{\mathbf{Z}}_{3} \\ 08 & \hat{\mathbf{Z}}_{2} \\ 06 & \underline{\mathbf{Z}}_{1} \\ 09 & \hat{\mathbf{Z}}_{0} \end{array}\right.$ |
| $\begin{array}{\|cc} \text { Even } 82 \\ \text { Odd } 93 \end{array}$ | $\begin{array}{\|l\|} \hline(134) \\ \text { (142) } 49 \\ \hline \end{array}$ | $\begin{aligned} & 145 \\ & 131 \end{aligned}$ | $141 \text { / } 135$ |  |
| 175 | 101 | 276 | 276 |  |
| $\begin{aligned} & (1 \times 496)-220=276)(496 \\ & (2 \times 028)+220=276 \end{aligned}$ |  |  |  |  |

Table 7.1. All branches (primary + secondary) for all the 11 species at $0-14$ levels. Notice the balances: $131 / 145$ versus $141 / 135$ as a change for $\pm 10$; then $141 / 135$ versus $142 / 134$ as a change for $\pm 1$. Notice also the relations to the second (28) and the third (496) perfect number as well as the relation to the first pair of friendly numbers (220 and 284). In addition: the total number of branches (276) appears to be the first case in a specific and unique arithmetical system (Figure 4).

| $\begin{array}{ll} \hline \hat{\mathbf{a}}_{9} & 13 \\ \hat{\mathbf{a}}_{8} & 14 \\ \hat{\mathbf{a}}_{7} & 20 \\ \hat{\mathbf{a}}_{6} & 13 \\ \hat{\mathbf{a}}_{5} & 16 \\ \hline \end{array}$ | $\begin{array}{ll} 07 & \hat{\mathbf{Z}}_{9} \\ 08 & \hat{\mathbf{Z}}_{8} \\ 10 & \hat{\mathbf{Z}}_{7} \\ 08 & \hat{\mathbf{Z}}_{6} \\ 09 & \hat{\mathbf{Z}}_{5} \end{array}$ | $\underline{a}_{9} 13$ <br> $\hat{a}_{8} \quad 14$ <br> $\hat{a}_{7} 20$ <br> $\hat{a}_{6} \quad 13$ <br> $\underline{\underline{a}}_{5} \quad 16$ | $76 \text { (118) } 42$ | $\begin{array}{ll} 07 & \hat{\mathbf{Z}}_{9} \\ 08 & \hat{\mathbf{Z}}_{8} \\ 10 & \hat{\mathbf{Z}}_{7} \\ 08 & \hat{\mathbf{Z}}_{6} \\ 09 & \underline{\mathbf{Z}}_{5} \end{array}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\begin{array}{ll} \hat{\mathbf{a}}_{4} & 15 \\ \hat{\mathbf{a}}_{3} & 13 \\ \hat{\hat{\mathbf{a}}}_{2} & 11 \\ \hat{\mathbf{a}}_{1} & 13 \\ \hat{\mathrm{a}}_{0} & 11 \end{array}$ | $\begin{array}{ll} 07 & \hat{\mathbf{Z}}_{4} \\ 05 & \hat{\mathbf{Z}}_{3} \\ 08 & \hat{\mathbf{Z}}_{2} \\ 06 & \underline{\mathbf{Z}}_{1} \\ 09 & \hat{\mathbf{Z}}_{0} \end{array}$ | $\begin{array}{ll} \hat{a}_{4} & 15 \\ \hat{\mathbf{a}}_{3} & 13 \\ \hat{a}_{2} & 11 \\ \hat{\mathbf{a}}_{1} & 13 \\ \underline{a}_{1} & 1 \end{array}$ | $63(98) 35$ | $\begin{aligned} & 07 \hat{Z}_{4} \\ & 05 \\ & 08 \\ & 08 \\ & \hat{\mathbf{Z}}_{2} \\ & 06 \\ & 06 \hat{\mathbf{Z}}_{1} \\ & 09 \\ & \hat{Z}_{0} \end{aligned}$ |
| Odd 75 Even 64 | $\left\lvert\, \begin{aligned} & \text { (112) } 37 \\ & \text { (104) } 40 \end{aligned}\right.$ | $\begin{aligned} & (101) \\ & (115) \end{aligned}$ | $111 / 105$ |  |
| 139 | 77 | 216 | 216 |  |

Table 7.2. All branches (primary + secondary) for all the 11 species at $0-9$ levels. Notice the balances: $101 / 115$ versus $111 / 105$ as a change for $\pm 10$; then $111 / 105$ versus $112 / 104$ as a change for $\pm 1$. Notice that the total number 216 is Plato's number, that is to say, the cube of number $6\left(3^{\wedge} 3+4^{\wedge} 3+5^{\wedge} 3=6^{\wedge} 3=\right.$ 216). The results $98 / 108$ appear to be in relation to a half of Plato's number, as a change for $\pm 10$ (108 $\pm 10$ ).

|  | $\begin{array}{ll} 06 & \hat{\mathbf{Z}}_{14} \\ 06 & \hat{\mathbf{Z}}_{13} \\ 06 & \hat{\mathrm{Z}}_{12} \\ 06 & \hat{\mathbf{z}}_{11} \\ 00 & \hat{\mathbf{Z}}_{10} \end{array}$ | $\begin{array}{ll} \begin{array}{ll} \mathbf{a}_{14} & 09 \\ \hat{\mathbf{a}}_{13} & 09 \\ \mathbf{a}_{12} & 09 \\ \hat{\mathbf{a}}_{10} & \\ \hat{\mathbf{a}}_{11} & 09 \\ \hat{a}_{10} & \end{array}{ }^{2} \\ \hline \end{array}$ | 36 (60) 24 | $\left(\begin{array}{ll} 06 & \hat{\mathbf{Z}}_{14} \\ 06 & \hat{\mathbf{Z}}_{13} \\ 06 & \hat{\mathbf{Z}}_{12} \\ 06 & \hat{\mathbf{Z}}_{11} \\ 00 & \hat{\mathbf{Z}}_{10} \end{array}\right.$ |
| :---: | :---: | :---: | :---: | :---: |
| $\begin{array}{ll} \hat{\mathbf{a}}_{9} & 05 \\ \hat{\mathrm{a}}_{8} & 05 \\ \hat{\mathbf{a}}_{7} & 07 \\ \hat{\mathrm{a}}_{6} & 07 \\ \underline{\mathrm{a}}_{5} & 06 \end{array}$ | $\begin{array}{ll} 02 & \hat{\mathbf{Z}}_{9} \\ 02 & \hat{\mathbf{Z}}_{8} \\ 03 & \hat{\mathbf{Z}}_{7} \\ 03 & \hat{\mathbf{Z}}_{6} \\ 03 & \underline{\mathbf{Z}}_{5} \\ \hline \end{array}$ | $\begin{array}{ll}\hat{\mathbf{a}}_{9} & 05 \\ \hat{\mathrm{a}}_{8} & 05 \\ \hat{\mathrm{a}}_{7} & 07 \\ \hat{\mathrm{a}}_{6} & 07 \\ \hat{\mathrm{a}}_{5} & 06\end{array}$ | $30(43) 13$ | $\begin{array}{ll} 02 & \hat{\mathbf{Z}}_{9} \\ 02 & \hat{\mathbf{Z}}_{8} \\ 03 & \hat{\mathbf{Z}}_{7} \\ 03 & \hat{\mathbf{Z}}_{6} \\ 03 & \underline{\mathbf{Z}}_{5} \end{array}$ |
| $\begin{array}{ll}\hat{\mathrm{a}}_{4} & 06 \\ \hat{\mathbf{a}}_{3} & 06 \\ \hat{\mathrm{a}}_{2} & 05 \\ \hat{\mathbf{a}}_{1} & 06 \\ \hat{\mathrm{a}}_{0} & 06\end{array}$ | $\begin{array}{ll} 03 & \hat{\mathbf{Z}}_{4} \\ 02 & \hat{\mathbf{Z}}_{3} \\ 03 & \hat{\mathbf{Z}}_{2} \\ 04 & \hat{\mathbf{Z}}_{1} \\ 04 & \hat{\mathbf{Z}}_{0} \\ \hline \end{array}$ | $\begin{array}{ll}\hat{a}_{4} & 06 \\ \hat{\mathbf{a}}_{3} & 06 \\ \hat{\mathrm{a}}_{2} & 05 \\ \hat{\mathbf{a}}_{1} & 06 \\ \hat{\mathrm{a}}_{0} & 06\end{array}$ | $29(45) 16$ | $\left[\begin{array}{ll} 03 & \hat{Z}_{4} \\ 02 & \hat{\mathbf{Z}}_{3} \\ 03 & \hat{\mathbf{Z}}_{2} \\ 04 & \hat{\mathbf{Z}}_{1} \\ 04 & \hat{\mathbf{Z}}_{0} \\ \hline \end{array}\right.$ |
| Even 4 <br> Odd 48 | $\begin{aligned} & \text { (74) } 27 \\ & \text { (74) } 26 \end{aligned}$ | $\begin{aligned} & 75 \\ & 73 \end{aligned}$ | $78 / 70$ |  |
| 95 | 53 | 148 | 148 |  |

Table 7.3. All primary branches for all the 11 species at $0-14$ levels. The total number 148 appears to be in relation to the half of the total number of branches (of number 276 from Table 7.1) $(148=138+10)$. Notice the balances: 78/70 in this Table versus $68 / 60$ in Table 7.4 as a change for $\pm 10$; then $74 / 74$ versus $73 / 75$ as a change for $\pm 1$. The result $43 / 45$ appears to be in relation to the arithmetic mean $44 / 44$ as a change for $\pm 1$.

| $\begin{array}{ll} \underline{\hat{\mathbf{a}}}_{9} & 08 \\ \hat{\mathrm{a}}_{8} & 09 \\ \hat{\mathbf{a}}_{7} & 13 \\ \hat{\mathrm{a}}_{6} & 06 \\ \hat{\hat{a}}_{5} & 10 \\ \hline \end{array}$ | $\begin{array}{ll} 05 & \hat{\mathbf{Z}}_{9} \\ 06 & \hat{\mathbf{Z}}_{8} \\ 07 & \hat{\mathbf{Z}}_{7} \\ 05 & \hat{\mathbf{Z}}_{6} \\ 06 & \hat{\mathbf{Z}}_{5} \end{array}$ | $\underline{a ̂}_{9} 08$ <br> $\hat{a}_{8} 09$ <br> $\hat{a}_{7} 13$ <br> $\hat{a}_{6} 06$ <br> $\underline{\hat{a}}_{5} 10$ | 46 (75) 29 |  |
| :---: | :---: | :---: | :---: | :---: |
| $\begin{array}{ll} \hat{\mathrm{a}}_{4} & 09 \\ \hat{\mathbf{a}}_{3} & 07 \\ \hat{\hat{a}}_{2} & 06 \\ \hat{\mathbf{a}}_{1} & 07 \\ \underline{\hat{a}}_{0} & 05 \\ \hat{a}^{2} \end{array}$ | $\begin{array}{lll} 04 & \hat{\mathbf{Z}}_{4} \\ 03 & \hat{\mathbf{Z}}_{3} \\ 05 & \hat{\mathbf{Z}}_{2} \\ 02 & \hat{\mathbf{Z}}_{1} \\ 0 & \hat{\mathbf{Z}}_{0} \end{array}$ | $\left\lvert\, \begin{array}{ll} \hat{a}_{4} & 09 \\ \hat{a}_{3} & 07 \\ \underline{\hat{a}}_{3} & 07 \\ \hat{a}_{2} & 0 \\ \hat{a}_{1} & 07 \\ \hat{a}_{0} & 05 \end{array}\right.$ | $34 \text { (53) } 19$ | $\begin{aligned} & 04 \hat{\mathbf{Z}}_{4} \\ & 03 \hat{\mathbf{Z}}_{3} \\ & 05 \hat{\mathbf{Z}}_{2} \\ & 02 \hat{\mathbf{Z}}_{1} \\ & 05 \hat{\mathbf{Z}}_{0} \end{aligned}$ |
| Odd 45 <br> Even 35 | $\begin{aligned} & (70) 25 \\ & (58) \\ & 23 \end{aligned}$ | $\begin{array}{\|l} 60 \\ 68 \\ \hline \end{array}$ | $65 \text { / } 63$ |  |
| 80 | 48 | 128 | 128 |  |
| $121+7=128$ |  |  |  |  |

Table 7.4. All secondary branches for all the 11 species at $0-9$ levels. [The secondary branches do not exist in the upper part of the Diagram (levels 11-14)]. The total number 128 appears to be in relation to the half of the total number of branches (of number 276 from Table 7.1) $(128=138-10)$. Notice the balances: $60 / 68$ versus $70 / 58$ as a change for $\pm 10$; then $68 / 60$ in this Table versus $78 / 70$ in Table 7.3 as a change for $\pm 10$; then $74 / 74$ in Table 7.3 versus $64 \pm 1$ in this Table.

| $\begin{array}{ll}\hat{\mathbf{a}}_{9} & 05 \\ \hat{\mathbf{a}}_{8} & 05 \\ \hat{\mathbf{a}}_{7} & 07 \\ \hat{\mathbf{a}}_{6} & 07 \\ \underline{\mathbf{a}}_{5} & 06\end{array}$ | $\begin{array}{ll} 02 & \hat{\mathbf{Z}}_{9} \\ 02 & \hat{\mathbf{Z}}_{8} \\ 03 & \hat{\mathbf{Z}}_{7} \\ 03 & \hat{\mathbf{Z}}_{6} \\ 03 & \underline{\mathbf{Z}}_{5} \\ \hline \end{array}$ | $\|$$\hat{\mathbf{a}}_{9}$ 05 <br> $\hat{\mathbf{a}}_{8}$ 05 <br> $\hat{\mathbf{a}}_{7}$ 07 <br> $\hat{\mathbf{a}}_{6}$ 07 <br> $\underline{\mathbf{a}}_{5}$ 06 | 30 (43) 13 | $\begin{array}{ll} 02 & \hat{\mathbf{Z}}_{9} \\ 02 & \hat{\mathrm{Z}}_{8} \\ 03 & \hat{\mathbf{Z}}_{7} \\ 03 & \hat{\mathrm{Z}}_{6} \\ 03 & \underline{\hat{\mathbf{Z}}}_{5} \\ \hline \end{array}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\begin{array}{ll}\hat{\mathbf{a}}_{4} & 06 \\ \hat{\mathbf{a}}_{3} & 06 \\ \hat{\mathrm{a}}_{2} & 05 \\ \hat{\mathbf{a}}_{1} & 06 \\ \hat{\mathrm{a}}_{0} & 06\end{array}$ | $\begin{array}{ll} 03 & \hat{\mathbf{Z}}_{4} \\ 02 & \hat{\mathbf{Z}}_{3} \\ 03 & \hat{\mathbf{Z}}_{2} \\ 04 & \hat{\mathbf{Z}}_{1} \\ 04 & \hat{\mathbf{Z}}_{0} \\ \hline \end{array}$ | $\begin{array}{ll}\hat{\mathbf{a}}_{4} & 06 \\ \hat{\mathbf{a}}_{3} & 06 \\ \hat{\hat{a}}_{2} & 05 \\ \hat{\mathbf{a}}_{1} & 06 \\ \hat{\hat{a}}_{0} & 06\end{array}$ | $29(45) \quad 16$ | $\left[\begin{array}{ll} 03 & \hat{\mathbf{Z}}_{4} \\ 02 & \hat{\mathbf{Z}}_{3} \\ 03 & \hat{\mathbf{Z}}_{2} \\ 04 & \hat{\mathbf{Z}}_{1} \\ 04 & \hat{\mathbf{Z}}_{0} \end{array}\right.$ |
| Even 29 Odd 30 | $\begin{aligned} & \text { (44) } 15 \\ & (44) 14 \end{aligned}$ | $\begin{aligned} & (45) \\ & (43) \end{aligned}$ | $46 / 42$ |  |
| 59 | (88) 29 | 88 | 88 |  |
| $56+32=88)$ |  |  | $(59+36=95)$ |  |

Table 7.5. All primary branches for all the 11 species at $0-9$ levels. The total number 88 as a result of 148 (all primary branches in Table 7.3) minus 60 branches in the upper part of the Diagram at levels 11-14 (Table 7.3). Notice the balances: $44 / 44$ versus $43 / 45$ as a change for $\pm 1$; then $43 / 45$ versus $42 / 46$ as a change for $\pm 1$; then 29/30 in even/odd positions versus 29/30 in up/down positions; also15/14 in even/odd positions versus $16 / 13$ in up/down positions.

## Appendix A

$\left.\begin{array}{|l|l|l|l|}\hline & 11 \times 1=11 & 11 \times 1=11 & \\ 0 & 11 \times 2=22 & 11 \times 2=22 & 11^{2}=121 \\ 11 \times 3=33 & 11 \times 3=33 & \\ \hline 1 & 12 \times 1=12 & 21 \times 1=21 & \\ \hline & 12 \times 2=24 & 21 \times 2=42 & 12^{2}=144 \\ & 12 \times 3=36 & 21 \times 3=63 & 21^{2}=441 \\ \hline & 13 \times 1=13 & 31 \times 1=31 & \\ \hline 3 & 13 \times 2=26 & 31 \times 2=62 & 13^{2}=169 \\ \hline & 14 \times 1=14 & 31 \times 3=93 & 31^{2}=961 \\ & 14 \times 2=28 & 41 \times 2=82 & 14^{2}=196\end{array}\right]$.

Table A.1. The arithmetical logic square: the space of the maximum possible inversions within decimal numbering system (Rakočević, 1994, p. 235).

## Appendix B

|  |  |  |  |  |
| :--- | :--- | :--- | :--- | :--- |
| $\mathbf{5}$ | F | 14 | 15 | Y |
| 4 | L | 13 | 04 | A |
| $\mathbf{3}$ | Q | 11 | 08 | N |
| $\mathbf{2}$ | P | 08 | 13 | I |
| $\mathbf{1}$ | T | 08 | 11 | M |
| $\mathbf{1}$ | S | 05 | 05 | C |
| 2 | G | 01 | 10 | V |
| $\mathbf{3}$ | D | 07 | 10 | E |
| $\mathbf{4}$ | K | 15 | 17 | R |
| $\mathbf{5}$ | H | 11 | 18 | W |
|  |  |  |  |  |

Figure B.1. "The Cyclic Invariant Periodic System (CIPS) of canonical AAs. ... In the middle position there are chalcogene AAs (S, T \& C, M); then - in the next „cycle" - there are the AAs of non-alaninic stereochemical types ( $\mathrm{G}, \mathrm{P} \& \mathrm{~V}, \mathrm{I}$ ), then two double acidic AAs with their two amide derivatives ( $\mathrm{D}, \mathrm{E}$ \& $\mathrm{N}, \mathrm{Q}$ ), the two original aliphatic AAs with two amine derivatives ( $\mathrm{A}, \mathrm{L} \& \mathrm{~K}, \mathrm{R}$ ); and, finally, four aromatic AAs (F,Y \& H, W) - two up and two down. The said five classes belong to two super classes: primary superclass in light areas and secondary superclass in dark areas. Notice that each amino acid position in this CIPS is strictly determined and none of them can be changed" (Rakočević, 2009, Table 3; 2011, Fig. 2).


Figure B.2. This Figure follows from CIPS, presented in Figure B.1. First, there are five charged AAs. Then three other quintets follow in accordance to the three principles: principle of minimum change, principle of continuity and principle of dense packing. As it is self-evident, the system is determined by the first perfect number - the number 6. For the lower part of the Figure cf. the determination of GC by Golden mean (Rakočević, 1998a).

| Multiples of 01, 6, 66, 666, 037 |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: |
| 01 | 6 | 66 | 666 | 037 |
| $162=216-(2 \times 27)$ |  |  |  |  |
| 27 | 162 | 1782 | 162 | 999 |
| 26 | 156 | 1716 | 17316 | 962 |
| 25 | 150 | 1650 | 16650 | 925 |
| 13 | 78 | 858 | 8658 | 481 |
| 12 | 72 | 792 | 7992 | 444 |
| 11 | 66 | 726 | 7326 | 407 |
| $\ldots$ |  |  |  |  |
| 03 | 18 | 198 | 1998 | 111 |
| 02 | 12 | 132 | 1332 | 074 |
| 01 | 6 | 66 | 666 | 037 |
| The 216 as Plato's number ( $6^{\wedge} 3=216$ ) |  |  |  |  |

Table B.1. The multiples of the numbers are presented in the first row. The $13^{\text {th }}$ case is the sum of the first four perfect numbers $(6+28+496+8128=8658)$.

| $6=1 / 3=(0.333 \ldots) \times 18$ | $6 \times 11=\mathbf{6 6}(60+06)$ |
| :--- | :--- |
| $66=11 / 3=0.666 \ldots) \times 18$ | $66 \times 11=726(660+066)$ |
| $666=111 / 3=\quad \mathbf{0 3 7} \times 18$ |  |
| $(1 \times 066 \times 11=7326(6660+0666)+(2 \times 037)=111$ | $111+66=177$ |

Survey B.1. This first "mirror" corresponding case (66) and the first integer case (037) correspond to Darwin's diagram through the results in Table 4.3.

| Multiples of 01, 7, 77, 777, 037 |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| 01 | 7 | 77 | 777 | $\mathbf{0 3 7}$ |  |
| $189=216-(1 \times 27)$ |  |  |  |  |  |
| 27 | $\mathbf{1 8 9}$ | 2079 | 20979 | $\mathbf{9 9 9}$ |  |
| 26 | 182 | 2002 | 20202 | 962 |  |
| 25 | 175 | 1925 | 19425 | $\mathbf{9 2 5}$ |  |
| $\ldots$ |  |  |  |  |  |
| 13 | 91 | 1001 | 10101 | $\mathbf{4 8 1}$ |  |
| 12 | 84 | 924 | 9324 | $\mathbf{4 4 4}$ |  |
| 11 | 77 | 847 | 8547 | $\mathbf{4 0 7}$ |  |
| $\ldots$ |  |  |  |  |  |
| 03 | 21 | 231 | 2331 | $\mathbf{1 1 1}$ |  |
| 02 | 14 | 154 | 1554 | $\mathbf{0 7 4}$ |  |
| 01 | 7 | 77 | 777 | $\mathbf{0 3 7}$ |  |
| The 216 as Plato's number (6^3=216) |  |  |  |  |  |

Table B.2. The multiples of the numbers presented in the first row. The $13^{\text {th }}$ case corresponds to the line of maximal changes (the change in each following step) on the binary tree (Rakočević, 1998).

| $7=1 / 3=(0.333 \ldots) \times 21$ | $7 \times 11=77(70+07)$ |
| :--- | :--- |
| $77=11 / 3=0.666 \ldots) \times 21$ | $77 \times 11=847(770+077)$ |
| $777=111 / 3=\quad \mathbf{0 3 7} \times 21$ |  |
| $(1 \times 037)+(2 \times 037)=111$ | $111+77=188$ |

Survey B.2. This first "mirror" corresponding case (77) and the first integer case (037) correspond to Darwin's diagram through the results in Survey B. 4 (middle area with dark tones).

| Multiples of 01, 8, 88, 888, 037 |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 01 | 8 | 88 | 888 | $\mathbf{0 3 7}$ |  |
| $216=216 \pm(0 \times 27)$ |  |  |  |  |  |
| 27 | $\mathbf{2 1 6}$ | 2376 | 23976 | $\mathbf{9 9 9}$ |  |
| 26 | 208 | 2288 | 23088 | 962 |  |
| 25 | 200 | 2200 | 22200 | $\mathbf{9 2 5}$ |  |
| $\ldots$ |  |  |  |  |  |
| 13 | 104 | 1144 | $\mathbf{1 1 5 4 4}$ | $\mathbf{4 8 1}$ |  |
| 12 | 96 | 1056 | 10656 | $\mathbf{4 4 4}$ |  |
| 11 | 88 | 968 | 9768 | 407 |  |
| $\ldots$ |  |  |  |  |  |
| 03 | 24 | 264 | 2664 | $\mathbf{1 1 1}$ |  |
| 02 | 16 | 176 | 1776 | $\mathbf{0 7 4}$ |  |
| 01 | 8 |  | 88 | 888 | $\mathbf{0 3 7}$ |
| $\left(3^{\wedge} 3=27\right)\left(6^{\wedge} 3=216\right)$ |  |  |  |  |  |

Table B.3. The multiples of the numbers are presented in the first row. The Plato's number 216 (the cube of number 6) appears as the last result in column of number " 8 ".

| $8=1 / 3=(0.333 \ldots) \times 24$ | $8 \times 11=\mathbf{8 8}(80+08)$ |
| :--- | :--- |
| $88=11 / 3=0.666 \ldots) \times 24$ | $88 \times 11=968(880+088)$ |
| $888=111 / 3=\quad \mathbf{0 3 7} \times 24$ | $888 \times 11=9768(8880+0888)$ |
| $(1 \times 037)+(2 \times 037)=111$ | $111+88=199$ |

Survey B.3. This first "mirror" corresponding case (88) and the first integer case (037) correspond to Darwin's diagram through the results in Survey B. 4 (middle area in dark tones).

| $\begin{aligned} & (1 \times 037)+(2 \times 037)=111 \\ & \mathbf{2 7} \times 037=\mathbf{9 9 9} \end{aligned}$ |  | $\begin{aligned} & 111+66=177 \\ & 177-56=121 \end{aligned}$ | $\begin{aligned} & 177-65=112 \\ & 121+112=233 \end{aligned}$ |
| :---: | :---: | :---: | :---: |
| $\begin{aligned} & (30 / 37 / 77) \\ & (30 / 27 / 67) \end{aligned}$ | $\begin{aligned} & 6^{\wedge} 1=6 \\ & 5^{\wedge} 2=25(31) \\ & \hline \end{aligned}$ | $\begin{aligned} & 177+077=254 \\ & 177=50+127 \end{aligned}$ | $\begin{aligned} & 254=117+137 \\ & 254=50+204 \end{aligned}$ |
| $\begin{aligned} & (1 \times 037)+(2 \times 037)=111 \\ & \mathbf{2 7} \times 037=\mathbf{9 9 9} \end{aligned}$ |  | $\begin{aligned} & 111+77=188 \\ & 188-67=121 \end{aligned}$ | $\begin{aligned} & 188-76=112 \\ & 121+112=233 \end{aligned}$ |
| $\begin{aligned} & (30 / 37 / 77) \\ & (30 / 27 / 67) \end{aligned}$ | $\begin{aligned} & 7^{\wedge} 1=7 \\ & 6^{\wedge} 2=36(43) \end{aligned}$ | $\begin{aligned} & 188+088=276 \\ & 188=60+128 \end{aligned}$ | $\begin{aligned} & 276=128+148 \\ & \mathbf{2 7 6}=\mathbf{6 0}+\mathbf{2 1 6} \end{aligned}$ |
| $\begin{aligned} & (1 \times 037)+(2 \times 037)=111 \\ & \mathbf{2 7} \times 037=\mathbf{9 9 9} \end{aligned}$ |  | $\begin{aligned} & 111+88=199 \\ & 199-78=121 \end{aligned}$ | $\begin{aligned} & 199-87=112 \\ & 121+112=233 \\ & \hline \end{aligned}$ |
| $\begin{aligned} & \hline(30 / 37 / 77) \\ & (30 / 27 / 67) \\ & \hline \end{aligned}$ | $\begin{aligned} & 8^{\wedge} 1=8 \\ & 7^{\wedge} 2=49(57) \\ & \hline \end{aligned}$ | $\begin{aligned} & 199+099=298 \\ & 199=70+129 \end{aligned}$ | $\begin{aligned} & 298=139+159 \\ & 298=70+228 \\ & \hline \end{aligned}$ |

Survey B.4. The first area corresponds to Table B. 1 and Survey B.1; the second (in dark tones) to Table B. 2 and Survey B.2; and the third area corresponds to Table B. 3 and Survey B.3. The middle area is especially significant because it, mutatis mutandis, contains all Darwin's quantities in relation to Mendeleev's quantitatives (the same area, on the left: 30/37/77 versus 30/27/67) (cf. Section 4.7, last paragraph, and Mendeleev's manuscript photocopy - Photocopy X in Kedrov, 1977, pp. 128-129).


Survey B.5. A hypothetical model for the connection between the quantities/entities in Tables B.1, B. 2 and B. 3 and $6-7-8$ proton determined chemical elements ( $\mathrm{C}-\mathrm{N}-\mathrm{O}$ ) as constituents of life anywhere in the universe. On the left: 6, 7, 8 protons for first three elements in IV-V-VI group of Periodic system of chemical elements, respectively; then $12,14,16$ nucleons of these elements; then $12,13,15,16$ atoms in four $\mathrm{Py} / \mathrm{Pu}$ bases, with the relation to the half of second perfect number (28); in the last row, there is the number of atoms within four nucleotide molecules in relation to the cube of the first perfect number, number 6. [Notice that the number of nucleons in the second row and the number of atoms in the third row represent a unique type of self-similarity.] On the right: 3,4 and 5 chemical elements as constituents of protein amino acids - the constituents of proteins. Notice that the last case on the right represents five elements in amino acid molecules (C,N,O,S,H) and five elements in nucleotide molecules (C,N,O,P,H) at the same time. Notice also that hydrogen, as a nonmetal, exists within the seventh group of Periodic system. Altogether it is self-evident that the neighbor positions of life-elements are determined with the three principles: principle of minimum change, principle of continuity and the principle of neighborhood.

| (6) | 1332 |  |  | (6) | 832 |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | 2553 |  |  |  | 1553 |
| (5) | 1221 |  |  | (5) | 721 |  |
|  |  | 2331 |  |  |  | 1331 |
| (4) | 1110 |  |  | (4) | 610 |  |
|  |  | 2109 |  |  |  | 1109 |
| (3) | 999 |  |  | (3) | 499 |  |
|  |  | 1887 |  |  |  | 887 |
| (2) | 888 |  |  | (2) | 388 |  |
|  |  | 1665 |  |  |  | 665 |
| (1) | 777 |  | ${ }_{646}{ }_{16}$ | (1) | 277 |  |
|  | (111) | 1443 | $1 / 2[1660]_{10}$ |  | (111) | 443 |
| (1) | 666 |  |  | (1) | 166 |  |
|  |  | 1221 |  |  |  | 221 |
| (2) | 555 |  |  | (2) | 055 |  |
|  |  | 999 |  |  |  | -001 |
| (3) | 444 |  |  | (3) | -056 |  |
|  |  | 777 |  |  |  | -223 |
| (4) | 333 |  |  | (4) | -167 |  |
|  |  | 555 |  |  |  | -445 |
| (5) | 222 |  |  | (5) | -278 |  |
|  |  | 333 |  |  |  | -667 |
| (6) | 111 |  |  | (6) | -389 |  |

Survey B.6. If multiples 666 (Table B.1) and 777 (Table B.2) have a middle position within the system of presented multiples, then it becomes obvious that there are the relations to the number of nucleons as well as of atoms within amino acid molecules as constituents of the Genetic code. Number 1443 as the number of nucleons within 23 amino acid molecules, within their side chains, in Shcherbak's diagram (Figure 3). Notice that number 1443 is $1 / 6$ of the sum of the first four perfect numbers $(6+28+496+8128=8658=6 \times 1443)$ and the sum of all multiples in the second column of this Table at the same time. Within 23 amino acid "heads" (amino acid functional groups) there are 1702 nucleons written in decimal numbering system, or $6(10) 6$ (i.e. 6A6) in hexadecimal system (see the window in the middle frame area). Number 443 as the number of atoms within 43 amino acid molecules (within their side chains) after the arrangement in Table E. 1 (row "d"). Within 43 amino acid "heads" there are 387 atoms. The sum $443+387$ equals $1 / 2$ of 1660 written in decimal numbering system. [Notice the two designations: $6(10) 6$ for nucleon number and 1660 for atom number express a specific self-similarity.]

| (6) 732 | (6) 832 | (6) 932 |
| :---: | :---: | :---: |
| 1353 | 1553 | 1753 |
| (5) 621 | (5) 721 | (5) 821 |
| 1131 | 1331 | 1531 |
| (4) 510 | (4) 610 | (4) 710 |
| 909 | 1109 | 1309 |
| (3) 399 | (3) 499 | (3) 599 |
| 687 | 887 | 1087 |
| (2) 288 | (2) 388 | (2) 488 |
| 465 | 665 | 865 |
| (1) 177 | (1) 277 | (1) 377 |
| (111) 243 | (111) 443 | (111) 643 |
| (1) 066 | (1) 166 | (1) 266 |
| 021 | 221 | 421 |
| (2) -045 | (2) 055 | (2) 155 |
| -201 | -001 | 199 |
| (3) -156 | (3) -056 | (3) 044 |
| -423 | -223 | -023 |
| (4) -267 | (4) -167 | (4) -067 |
| -645 | -445 | -245 |
| (5) -378 | (5) -278 | (5) -178 |
| -867 | -667 | -467 |
| (6) -489 | (6) -389 | (6) -289 |
| -1089 | -889 | -689 |
| (7) -600 | (7) -500 | (7) -400 |

Survey B.7. The arithmetical system which is in relation with the system, presented in Survey B.6. (Notice that the last difference in "Darwin's column" is $1089=33 \wedge 2$; in "Genetic code's" column 1089-200, and in the third, the "neutral" column it is 1089 - 400.)

|  |  | N | $\mathrm{a}_{1}, \mathrm{a}_{2}$ | A | D | $\mathrm{d}_{1}$ | $\mathrm{~d}_{2}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $(4)$ | 999 | 1887 | 499 |  |  | 887 | 776 |
| $(3)$ | 888 | 1111 | 111 |  |  |  |  |
| $(2)$ | 777 | 1665 |  | 277 | 665 | 554 | 1111 |
| $(1)$ | 666 | 1443 | 166 | 443 | 332 | 1111 | 111 |
| $(0)$ | 555 | 1221 | 055 | 221 | 110 | 1111 | 111 |
| $(-1)$ | 444 | 999 |  |  |  |  |  |
| $(-2)$ | 333 | 777 |  |  |  |  |  |
| $(-3)$ | 222 | 555 |  |  |  |  |  |
| $(-4)$ | 111 | 333 |  |  |  |  |  |

Survey B.8. An insert from Survey B.6; N: the numbers in relation to nucleon number 1443; $a_{1}$, $\mathrm{a}_{2}$ : the numbers in relation to atom number 166 and 277 , respectively; A : the numbers in relation to atom number 443; D: the numbers in relation to Darwin's number 332 as the total number of "branch" quantities/entities in his Diagram (Table 5); $\mathrm{d}_{1}$ : all differences in relation to the difference $1443-332=1111 ; \mathrm{d}_{2}$ : all differences in relation to the difference $443-332=111$.

## Appendix C



Figure C.1. Four diversity types of protein amino acids: 2 AAs with non-standard and $\mathbf{4}$ AAs with standard hydrocarbon side chain; then 6 AAs with different, and $\mathbf{8}$ with the same "head" $/$ "body" functional groups: linear and circular arrangement, which from - through the principles of minimum change and continuity - follows a new arrangement, such as in Figure C. 2 (Rakočević, 2011a, Fig. 2; 2011b, Fig. 2 on p. 822).


Figure C.2. A specific AA classification and systematization which follow from four diversity types (Figure C.1) in correspondence with a unique arithmetical arrangement (Table C.2). The ordering through the validity of two Mendeleev principles: minimum change and continuity ( $1,5,15,18$ of atoms in the first row), ( $1,4,5,8$ of atoms in the first column) (Rakočević, 2011a, Fig. 1; 2011b, Fig. 3 on p. 828).

|  | $\ldots$ |  |  |  |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $(-2)$ | $\ldots$ |  |  |  |  |  |  |  |  | $\ldots$ | -22 |  |  |
| $(-1)$ | -21 | -20 | -19 | -18 | -17 | -16 | -15 | -14 | -13 | -12 | -11 |  |  |
| $(0)$ | -10 | -09 | -08 | -07 | -06 | -05 | -04 | -03 | -02 | -01 | 00 |  |  |
| $(1)$ | 01 | 02 | 03 | 04 | 05 | 06 | 07 | 08 | 09 | 10 | 11 |  |  |
| $(2)$ | 12 | 13 | 14 | 15 | $-16-$ | -17 | -18 | 19 | 20 | 21 | 22 |  |  |
| $(3)$ | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 |  |  |
| $(4)$ | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 |  |  |
| $(5)$ | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 |  |  |
| $(6)$ | 56 | 57 | 58 | 59 | 60 | $5 B$ | 62 | 63 | 64 | 65 | 66 |  |  |
| $(7)$ | 67 | 68 | 69 | 70 | 71 | 72 | $6 D$ | 74 | 75 | 76 | 77 |  |  |
| $(8)$ | 78 | 79 | 80 | 81 | 82 | 83 | 84 | $7 F$ | 86 | 87 | 88 |  |  |
| $(9)$ | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 |  |  |
| (A) | A0 | A1 | A2 | A3 | A4 | A5 | A6 | A7 | A8 | A9 | AA |  |  |
| (B) | B1 | B2 | B3 | B4 | B5 | B6 | B7 | B8 | B9 | BA | BB |  |  |

Table C.1. The Table of minimal addition in decimal numbering system. A specific arrangement of natural numbers in decimal numbering system, going from 01 to 11 and so on (Rakočević, 2011a, Tab. 4; 2011b, Tab. 4 on p. 826).

$$
\begin{array}{lll}
26 & =26 & 26+42+59+77=Y \\
26+\mathbf{1 6}=42 & Y=204 & \mathbf{1 6}+\mathbf{1 7}+\mathbf{1 8}=\mathrm{Z} \\
42+\mathbf{1 7}=59 & \mathrm{Y} / 4=51 & \mathrm{Z}=51 \\
59+\mathbf{1 8}=77 & & \mathrm{Z}=\mathrm{Y} / 4
\end{array}
$$

Survey C.1. The unique arithmetical relations which follow from the system presented in Table C. 1 (Rakočević, 2011a, Equations 4.1; 2011b, Equations 3 on p. 826).

$$
\begin{array}{|ll|}
\hline \mathrm{x}_{1}+\mathrm{y}_{1}=36=\mathbf{6}^{2} & \left(\mathrm{x}_{1}=26 ; \mathrm{y}_{1}=10\right) \\
\mathrm{x}_{2}+\mathrm{y}_{2}=25=\mathbf{5}^{2} & \left(\mathrm{x}_{2}=17 ; \mathrm{y}_{2}=08\right) \\
\mathrm{x}_{1}-\mathrm{y}_{1}=16=\mathbf{4}^{2} & \\
\mathrm{x}_{2}-\mathrm{y}_{2}=09=\mathbf{3}^{\mathbf{2}} &
\end{array}
$$

Survey C.2. The unique algebraic relations which follow from the system presented in Table C. 1 (Rakočević, 2011a, Equations 4.2; 2011b, Equations 4 on p. 827).

|  | $\ldots$ |  |  |  |  |  |  |  |  |  |  |  |  |
| ---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $(-2)$ | $\ldots$ |  |  |  |  |  |  |  |  | $\ldots$ | -22 |  |  |
| $(-1)$ | -21 | -20 | -19 | -18 | -17 | -16 | -15 | -14 | -13 | -12 | -11 |  |  |
| $(0)$ | -10 | -09 | -08 | -07 | -06 | -05 | -04 | -03 | -02 | -01 | 00 |  |  |
| $(1)$ | $\underline{0} 1$ | 02 | 03 | 04 | 05 | 06 | 07 | 08 | 09 | 10 | 11 |  |  |
| $(2)$ | $\underline{12}$ | 13 | 14 | 15 | $-16-$ | -17 | -18 | 19 | 20 | 21 | 22 |  |  |
| $(3)$ | $\underline{2} 3$ | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 |  |  |
| $(4)$ | $\underline{3} 4$ | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 |  |  |
| $(5)$ | $\underline{4} 5$ | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 |  |  |
| $(6)$ | $\underline{5} 6$ | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 |  |  |
| $(7)$ | $\underline{6} 7$ | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 |  |  |
| $(8)$ | $\underline{78}$ | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 |  |  |
| $(9)$ | $\underline{8} 9$ | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 |  |  |
| $(10)$ | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 |  |  |
| $(11)$ | 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 |  |  |

Table C.2. This Table is the same as Table C.1, except the first, highlighted column and the left diagonal, so that the following law is to be detected: the left diagonal appears as the sum of all neighboring pairs in the first column minus 10 n , where $\mathrm{n}=0,1,2, \ldots$

| $01(-10)$ | -9 | -8 | -7 | -6 | -5 | -4 | -3 | -2 | -1 | 0 |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :--- | :--- | :--- |
|  | 21 | 32 | 43 | 54 | 65 | 76 | 87 | 98 | 109 | 120 |  |
| 12 | 012 | 024 | 036 | 048 | 060 | 072 | 084 | 096 | 108 | 120 | $(220)$ |
|  | 241 | 252 | 263 | 274 | 285 | 296 | 307 | 318 | 329 | 340 |  |
| 23 | 253 | 276 | 299 | 322 | 345 | 368 | 391 | 414 | 437 | 460 | $(220)$ |
|  | 461 | 472 | 483 | 494 | 505 | 516 | 527 | 538 | 549 | 560 |  |
| 34 | 714 | 748 | 782 | 816 | 850 | 884 | 918 | 952 | 986 | 1020 | $(220)$ |
|  | 681 | 692 | 703 | 714 | 725 | 736 | 747 | 758 | 769 | 780 |  |
| 45 | 1395 | 1440 | 1485 | 1530 | 1575 | 1620 | 1665 | 1710 | 1755 | 1800 | $(220)$ |
|  | 901 | 912 | 923 | 934 | 945 | 956 | 967 | 978 | 989 | 1000 |  |
| 56 | 2296 | 2352 | 2408 | 2464 | 2520 | 2576 | 2632 | 2688 | 2744 | 2800 | $(220)$ |
|  | 1121 | 1132 | 1143 | 1154 | 1165 | 1176 | 1187 | 1198 | 1209 | 1220 |  |
| 67 | 3417 | 3484 | 3551 | 3618 | 3685 | 3752 | 3819 | 3886 | 3953 | 4020 | $(220)$ |
|  | 1341 | 1352 | 1363 | 1374 | 1385 | 1396 | 1407 | 1418 | 1429 | 1440 |  |
| 78 | 4758 | 4836 | 4914 | 4992 | 5070 | 5148 | 5226 | 5304 | 5382 | 5460 | $(220)$ |
|  | 1561 | 1572 | 1583 | 1594 | 1605 | 1616 | 1627 | 1638 | 1649 | 1660 |  |
| 89 | 6319 | 6408 | 6497 | 6586 | 6675 | 6764 | 6853 | 6942 | 7031 | 7120 |  |

Table C.3. The Table follows from Table C. 2 with the multiplication of all neighbouring pairs in first column (the numbers on the diagonal), of their predecessors (the numbers for the diagonal) and of their successors (the numbers after the diagonal). The differences increase by 11 , and the differences of differences by the twentieth multiple of 11 , the number 220, which is the first friendly number. Here one must notice that the numbers on the left diagonal are the same numbers which appear in the arithmetical system presented in Figure 4.


Table C.4. The standard Genetic Code Table. This Table represents the relations within the so cold "standard Genetic code" with designation of four diversity types of protein amino acids and corresponding codons: the first and the second type without color (in light and dark tones, respectively), but the third and the fourth in color. The codon number: for the first type 08 , the second 17 , the third 10 and the fourth 26, just as in algebraic system in Survey C. 2 (Rakočević, 2011a, Fig. 3; 2011b, Tab. 6 on p. 829).

## Appendix D

| Fibonacci | $\mathbf{0}$ | $\mathbf{1}$ | $\mathbf{1}$ | $\mathbf{2}$ | $\mathbf{3}$ | $\mathbf{5}$ | $\mathbf{8}$ | $\mathbf{1 3}$ | $\ldots$ |
| :--- | :--- | :--- | :--- | :---: | :---: | :---: | :---: | :---: | :---: |
| Fibonacci | $\mathbf{1}$ | $\mathbf{2}$ | $\mathbf{3}$ | $\mathbf{5}$ | $\mathbf{8}$ | $\mathbf{1 3}$ | $\mathbf{2 1}$ | $\mathbf{3 4}$ | $\ldots$ |
| Fibonacci | $\mathbf{2}$ | $\mathbf{3}$ | $\mathbf{5}$ | $\mathbf{8}$ | $\mathbf{1 3}$ | $\mathbf{2 1}$ | $\mathbf{3 4}$ | 55 | $\ldots$ |
| Lucas | $\mathbf{3}$ | $\mathbf{4}$ | $\mathbf{7}$ | $\mathbf{1 1}$ | 18 | 29 | $\mathbf{4 7}$ | 76 | $\ldots$ |
|  | 4 | 5 | 9 | 14 | 23 | 37 | 60 | 97 | $\ldots$ |
|  |  |  |  |  |  |  |  |  |  |
| $\mathbf{0}$ | $\mathbf{1}$ | $\mathbf{1}$ | $\mathbf{2}$ | $\mathbf{3}$ | $\mathbf{5}$ | $\mathbf{8}$ | $\mathbf{1 3}$ | $\mathbf{2 1}$ | $\mathbf{3 4}$ |
| $\mathbf{1}$ | $\mathbf{1}$ | $\mathbf{2}$ | $\mathbf{3}$ | $\mathbf{5}$ | $\mathbf{8}$ | $\mathbf{1 3}$ | $\mathbf{2 1}$ | $\mathbf{3 4}$ | 55 |
| $\mathbf{2}$ | $\mathbf{1}$ | 3 | $\mathbf{4}$ | $\mathbf{7}$ | 11 | 18 | 29 | 47 | 76 |
| 3 | 4 | 4 | 5 | 9 | 14 | 23 | 37 | 60 | 97 |
| 4 | 4 | 5 | 6 | 14 | 17 | 28 | 45 | 73 | 118 |
| $\ldots$ |  |  |  |  |  |  |  |  |  |

Figure D.1. The "golden" series: all the number series which are not crossed out correspond with the Golden Mean (Golden section).


Figure D.2. The "evolution" of a triadic Cantor set (the simplest possible fractal), placed in the zeroth position; the evolution through the divergence for one unit in all three positions. From the first position onwards there is an "Extended triadic Cantor set" through the number of quantities at levels. Here a paradoxical situation becomes obvious: the farther we move from the beginning, the closer to it we get!? The biological meaning could be this: after a million years since the origin of life on Earth there were a lot of different species of organisms, but one and the same genetic code; after a hundred million years even a greater number and a greater variety of the species existed and the code remains the same; After a billion years everything is still enormously increased, but the code remained the same. The third case (dark tones) corresponds with the splitting of levels into Darwin's diagram, presented in Table 4.3. Also, the sums designated on the right of Figure (4-7-10-13- ...) correspond with the Shcherbak's numbering systems: The analogs to "Prime quantum 037" have the numbering systems with the basis $\mathrm{q}=4$, $7,10,13, \ldots$.
II\|

Figure D.3. The visualization of the Cantor triadic set as an infinite binary tree.

## Appendix E

| (a) |  |
| :---: | :---: |
| 49 | 74 |
| $\mathrm{V}_{10} \mathrm{~L}_{13} \quad \mathrm{C}_{05}$ | $E_{10} Q_{11} \left\lvert\, \begin{array}{llllll}11 & I_{13} & R_{17} & W_{18} & Y_{15}\end{array}\right.$ |
| $\mathrm{G}_{01} \mathrm{~A}_{04}$ | $\begin{array}{c\|ccc} \mathrm{D}_{07} \mathrm{~N}_{08} \mathrm{~T}_{08} \mathrm{P}_{08} & \mathrm{~K}_{15} & \mathrm{H}_{11} & \mathrm{~F}_{14} \\ 56 \end{array}$ |
|  | (56) 130 |
| (c) | (222 / 221) |
| (b) | 9156 |
|  |  |
|  | 147 |
| (d) 166 | (111) 277 (443) |
| (e) |  |
| $\begin{array}{r} 113 \\ \text { (Tab.4.1) } 47 \end{array}$ | $066$ |
| (Tab.4.1) <br>  <br>  | 177 |
| (f) |  |
| $24$ | (32) 66 |
| (Tab.4.1) 40 | (32) \% 47 (Tab.4.1) |
| 64 | 113 |
| (g) |  |
| (Darwin code) | $\begin{aligned} & 233 / 443 \quad(\text { Gen. code }) \\ & (443-332=111) \end{aligned}$ |

Table E.1. (a) The first class of AAs is in the upper row, and in the lower row there is the second class (Rakočević, 1997a): "Two classes of amino acids handled by two classes of enzymes. (Class II with 81 and Class I with 123 atoms.) The ten amino acid pairs, natural pairs from the chemical aspect, are classified into two classes. Class I contains larger amino acids (larger within the pairs), all handled by class I of enzymes aminoacyl-tRNA synthetases. Class II contains smaller amino acids, all handled by class II of synthetases. ... The order follows the number of atoms within side chains of class II AAs (given here as index); from left to right: first there are aliphatic, and then aromatic AAs. ...[Notice that the pair $\mathrm{F}-\mathrm{Y}$ is simpler as only aromatic and $\mathrm{H}-\mathrm{W}$ is more complex as aromatic heterocyclic.]" (Rakočević, 2011, Table 2.1). Shcherbak's account of nucleon number within the amino acid constituents
of GC, in their side chains (Figure 1.1) is as follows: $[\mathbf{1} \times(\mathrm{G} 1+\mathrm{A} 15+\mathrm{P} 41+\mathrm{V} 43+\mathrm{T} 45+\mathrm{C} 47+\mathrm{I} 57+\mathrm{N} 58$ $+\mathrm{D} 59+\mathrm{K} 72+\mathrm{Q} 72+\mathrm{E} 73+\mathrm{M} 75+\mathrm{H} 81+\mathrm{F} 91+\mathrm{Y} 107+\mathrm{W} 130)]+[2 \mathrm{x}(\mathrm{S} 31+\mathrm{L} 57+\mathrm{R} 100)]=1443$. If Shcherbak's account is done, with an iteration more, for the number of atom, the result is as follows: [ 2 x $(\mathrm{G} 1+\mathrm{A} 4+\mathrm{C} 5+\mathrm{D} 7+\mathrm{N} 8+\mathrm{T} 8+\mathrm{P} 8+\mathrm{E} 10+\mathrm{V} 10+\mathrm{Q} 11+\mathrm{M} 11+\mathrm{H} 11+\mathrm{I} 13+\mathrm{F} 14+\mathrm{Y} 15+\mathrm{K} 15+$ $\mathrm{W} 18)]+[3 \mathrm{x}(\mathrm{S} 5+\mathrm{L} 13+\mathrm{R} 17)]=0443$ (here: row $d$ ). On the other hand, within Darwin's diagram there are the next "branch" entities/quantities: 276 branches plus 46 nodes +10 branchings, in total 332 . The significant differences are as follows: 1443-332 = 1111and 443-332 = 111, both determined by the unity change law (here: row g); (b) Atom number within 23 amino acid molecules as in (a), except that twomeaning AAs (L,S,R) participate twice in the account: $204+35=239=92+147$. (c) The result of the „crossing" sumation: $74+147=221$ and $130+92=222$; (d) The result of two sumation: $74+92=166$ and $130+147=277$; (d) The sumation of two sumations: $166+277=443$; (e) The results from Darwin's diagram as in Tables 4.1 and 4.2; (f) The results from Darwin's diagram ( $66-64=\underline{\mathbf{2}}$ ) as in Tables 4.1 in correspondence with two results in genetic code: $92-91=\underline{\mathbf{1}}$ and $74-74=\underline{\mathbf{0}}$; (g) Final result in GC (443) in relation to the final Darwin's result (233), taken from Tables 4.5 and 5.

## Appendix F. A simple syllogism

1. Darwin's diagram corresponds with the presented arithmetical / algebraic systems
2. Genetic code corresponds with presented arithmetical / algebraic systems
3. Therefore, Darwin's diagram corresponds with the Genetic code

| Distrib. of AAs after Cloister energy and atom number |  | Relations | Chemical pairs |
| :---: | :---: | :---: | :---: |
|  $\underline{\mathbf{H}}$ 0.00 1.46 $\underline{\mathbf{K}}$  <br> 44 A -0.09 0.91 $\underline{Q}$ 60 <br> 45 $\underline{\mathbf{G}}$ -0.16 0.87 $\underline{\mathbf{R}}$ 45 <br> $\mathbf{8 9}$ $\underline{\mathrm{~W}}$ -0.25 0.71 $\underline{\mathrm{E}}$ $\mathbf{1 0 5}$ <br>  $\underline{\mathbf{V}}-0.52$ 0.69 $\underline{\mathbf{D}}$   <br> $\mathbf{1 9 4}$      |  H 0.00 1.46 K  <br> 57 A -0.09 0.91 Q 68 <br> 54 G -0.16 0.87 R 54 <br> $\mathbf{1 1 1}$ W -0.25 0.71 E $\mathbf{1 2 2}$ <br>  V -0.52 0.69 D  <br>  L -0.54 0.52 N  | $\begin{aligned} & (44+44=88)^{49} \\ & (60+56=116)^{50} \end{aligned}$ | $\begin{gathered} (\mathrm{H}-\mathrm{W}) \\ (\mathrm{A}-\mathrm{G}) \\ \mathrm{V}-\mathrm{L} \\ (\mathrm{~K}-\mathrm{R}) \\ \mathrm{Q}-\mathrm{E} \\ \mathrm{D}-\mathrm{N} \end{gathered}$ |
|  L -0.54 0.52 N  <br> 56 $\underline{\mathbf{I}}$ -0.56 0.46 $\underline{\mathbf{P}}$ 44 <br> 45 F -0.56 0.42 Y 45 <br> $\mathbf{1 0 1}$ $\underline{\mathbf{M}}$ -0.57 0.27 $\underline{\mathbf{T}}$ $\mathbf{8 9}$ <br>  $\mathbf{C}$ -0.73 0.24 S  <br>       |  |  | $\begin{gathered} (\mathrm{I}-\mathrm{P}) \\ \mathrm{F}-\mathrm{Y} \\ (\mathrm{M}-\mathrm{T}) \\ \mathrm{C}-\mathrm{S} \end{gathered}$ |
| 190 | 151 | $\begin{array}{ll} 125 & (102+23) \\ 79 & (102-23) \end{array}$ | $\begin{aligned} & 125=57+68 \\ & 79=43+36 \end{aligned}$ |
| Odd 46 $(102-1)$ 55 <br> Even 54 $(102+1)$ 49 | $102 \pm \mathrm{x}$ (For x = 23 we have the correspondence with 276) |  |  |

Table F.1. Distribution of amino acids after Cloister energy (Swanson, 1984) and atom number
[Note F.1. The chemical pairs after (Dlyasin, 1998, 2011; Rakočević, 1998, Survey 4, p. 290; Rakočević, 2004, Figures 1 and 2, p. 222). The pairs G-A and V-L as well as S-T and C-M after Dlyasin; in a vice versa logic: G-V and A-L as well as S-C and T-M after Rakočević; all other is the same].

[^63]\[

$$
\begin{aligned}
& (111+01=\mathbf{1 1 2})^{52} ;(122-01=\mathbf{1 2 1})^{53} ;\left[89+89=178 ;(178-01=\mathbf{1 7 7})^{54}\right. \\
& \left(101+105=206(206+10=\mathbf{2 1 6})^{55} ;\right. \\
& (2 \underline{\mathbf{0}} 6+17 \underline{\mathbf{8}}=384)^{56} \\
& (2 \underline{1} 6+17 \underline{7}=393) ; \quad(384+393=777)^{57} \\
& (116+\mathbf{2 1 6}=\mathbf{3 3 2}) ;{ }^{58}(\mathbf{8 8}+\mathbf{1 8 8}=\mathbf{2 7 6})^{59} \\
& (190-151=\mathbf{3 9})^{60} \\
& (233-194=\mathbf{3 9})
\end{aligned}
$$
\]

Survey F.1. Relations between quantitatives of Genetic code and existing quantitatives within Darwin's diagram (I)

| $(194-151=43)^{61}$ | $44+44=\mathbf{8 8}$ | $\left[(233)+(43)^{62}=(\mathbf{2 7 6})\right]$ |
| :--- | :--- | :--- |
| $(233-190=\mathbf{4 3})$ | $60+56=\mathbf{1 1 6}$ |  |

Survey F.2. Relations between quantitatives of Genetic code and existing quantitatives within Darwin's diagram (I)

[^64]
## Appendix G. The number of hydrogen bonds within the set of four nucleotides

Why 2-3 and not 1-2 hydrogen bonds within the set of four nucleotides (UA connected with two and CG with three hydrogen bonds)? The answer follows from the relationships presented in Tables G. 1 and G.2. If we have the alphabet of four letter (UCAG in Table G.1), then there are six their pairs (UC, AG, UA, CG, UG, CA). Also there are two possibilities for bonding (Tables G. 1 \& G.2). Going from the arrangement in Table G. 1 to the arrangement in Table G. 2 the pairs UG, CA appear to be invariant, but other four (two and two: UC/AG and UA/CG) variant. By this, from the chemical aspect we must speak: $\underline{\mathbf{2}}$ original pairs (UC/AG or UA/CG), $\underline{\mathbf{6}}$ derived pairs (UC, AG, UA, CG, UG, CA), $\underline{\mathbf{1 0}}$ hydrogen bonds ( $5+5$ or $4+6$ ). Altogether this is the correspondence with the Hückel's formula, in form $N=2(2 n+1)(n=0,1,2,3)$ as it is presented in Section 4.3 and Box 2. In Table G. 1 we can find this arrangement only it the case with 2-3 hydrogen bonds, in wich case the principles of continuity and minimum change are also valid.

One must notice that the pattern 4-5-5-6 of hydrogen bonds corresponds with the same system existing within Rumer's Table of nucleotide doublets. (Cf. Tables $1 \& 2$ in Book of Abstracts - Theoretical Approaches to Bioinformation Systems,TABIS 2013, 17-22 September 2013, Belgrade, Serbia.) (Proceedings in press.) Notice also that this pattern corresponds with the 4-5-5-6 amino acid pairs, presented in this paper in Table F.1.


Table G.1. The number of real and hypothetical hydrogen bonds (I)


Table G.2. The number of real and hypothetical hydrogen bonds (II)

Appendix H. Some citations from Darwin's book
[Darwin, Ch. (1876) The Origin of Species, John Murray, 6th ed., with additions and corrections, London]

## Citation 1a (p. 90). The accompanying diagram ...

> The accompanying diagram will aid us in understanding this rather perplexing subject. Let A to L represent the species of a genus large in its own country; these species are supposed to resemble each other in unequal degrees, as is so generally the case in nature, and as is represented in the diagram by the letters standing at unequal distances. I have said a large genus, because
"... letters ... distances" (Explanation 1a)
Explanation 1a. It is clear that Darwin here insists on the letters as such. In this case in the question are large letters below, under the zeroth level.

## Citation 1b (p. 92). In our diagram ...

and the more their moditied progeny will increase. In our diagram the line of succession is broken at regular intervals by small numbered letters marking the successive forms which have become sufficiently distinct to be recorded as varieties. But these breaks are imaginary, and might have been inserted anywhere, after intervals long enough to allow the accumulation of a considerable amount of divergent variation.
"... by small numbered letters .... as varieties" (Explanation 1b)
Explanation 1b. At the levels 1-10 all varieties are designated "by small numbered letters". However, at the levels 11-14, only varieties at the level 14 are with letters and other ( $3 \times 14=42$ varieties) at 11-13 levels are without letters (see Citations $2 \& 3$ ).

## Citation 2 (p. 91): The intervals ...

The intervals between the horizontal lines in the diagram, may represent each a thousand or more generations. After a thousand generations, species (A) is supposed to have produced two fairly well-marked varieties, namely $a^{1}$ and $m^{1}$. These two varieties will

"After a thousand generations ...well-marked varieties" (Explanation 2)

Explanation 2. Varieties as the primary branches, and as the letters to the 10 th level, at the same time; well-marked also at the level 14. H. 1

## Citation 3 (p. 91): In the diagram ... a condensed and simplified form

> and some failing to produce any. Thus the varieties or modified descendants of the common parent (A), will generally go on increasing in number and diverging in character. In the diagram the process is represented up to the ten-thousandth generation, and under a condensed and simplified form up to the fourteen-thousandth generation.
" ... to the fourteen-thousand generation" (Explanation 3)
Explanation 3. If "to the fourteen", then that means at $11^{\text {th }}, 12^{\text {th }}$ and the $13^{\text {th }}$ at the same time.

From this small discussion it follows: from all primary branches (varieties) in two species (,,A" and „I"), them 112, organized in form of two trees, and presented in Table 2.1, the 70 ( 5 x 14) are „well-marked" by 70 letters and 42 ( $3 \times 14$ ) are not marked with the letters. (The 56 primary branches on the levels I-X, marked with the letters, plus 14 on the $14^{\text {th }}$ level, equals 70 "well-marked" primary branches; then $70+42=112$.)

On the other hand, from all primary branches (varieties) in remaining 9 species, them 36 , organized without of two trees, and presented in Table 6.1, the $3(1 \times 3)$ are well-marked by 3 letters (E \& F at the $10^{\text {th }}$ level and $F$ at $14^{\text {th }}$ level) and $33(11 \times 3)$ are not marked with the letters. Altogether, $70+3=73$ well-marked and $42+33=075$ not marked $(75+73=148$ as in Table 7.3). (Cf. first two cases in last columns of Tables H.1, H. 2 and H.3). By this one must notice that the result 075 corresponds with the middle position in Table H. 1 ( $\underline{7} 75$ vs $\underline{1} 85$ ). Also, from these relationships it follows that the number " 73 " we can read as 73 branches and as 73 letters. Analogously with Shcherbak's method (L, S, R two times in calculation) it makes sense to have the sum of all branch-letters entities, that means: $73+148=\mathbf{2 2 1}$, which result we have in the GC (Table E.1, a,b,c: $147+74=221$ and $92+130=222$ ), where Shcherbak's method (with one iteration more) also acts. On the other hand, the 73 well-marked primary branches and 75 nonmarked, appear to be in the ratio $74 \pm 1$ (Table H.3), what a balance is and where the 74 is also a Shcherbak's number as the number of nucleons within the amino acid "head".

In addition to the said: there is a whole Darwin Diagram Space, i.e. the Darwin Diagram System (DDS), consisting of "tree-space" (left tree „A" \& right tree „I") and "non-tree-space" [left part (B,C,D,E,F) \& right part (G,H,K,L)]. Within whole DDS there are 73 letters, and within "tree-space" there are 112 primary branches (Table 2.1 ). From this facts, it makes sense to calculate the sum $73+112=185$. Why? Because the 73 are branch-letters in whole DD system,
and 112 are branches in DD sub-system; the sub-system as a „half" of whole system. [„Whole" and „half" as a condition for the realization of the „symmetry in the simplest case" (Marcus, 1989, p. 103).]

And now, as we see from Table H.1, the number of 185 „branch" entities, appers to be in the middle position within a specific arithmetical system, the system of relationships between multiples of second perfect number 28 and Shcherbak's „Prime quantum 37".

Within whole DDS there are 148 primary branches (Table 7.3), and within "tree-space" (as a „half" of „whole") there are 70 letters ( 73 of total letters minus E \& F on the 10th and F on the 14th level); the sum of 148 primary branches in both spaces (tree-space and non-tree-space as a whole) plus 70 letters in tree-space (as a „half") $=218$; these 218 quantitatives (as a new whole), minus 33 primary non-marked branches (as a new „half") equals 185 once more. (Note: The 33 primary non-marked branches we have within "non-tree-space", if we subtract 3 from 36 in Table 6.1; these 3 are - the 3 well-marked primary branches, designated with E \& F at 10th and F at 14th level.)

|  | Multiples of 14 \& 37 |  |  | Sums | Double values |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1 | 14 | (23) | 37 | 51 | 28 | (46) | 74 |
| 2 | 28 | (46) | 74 | 102 | 56 | (92) | 148 |
| 3 | 42 | (69) | 111 | 153 | 84 | (138) | 222 |
| 4 | 56 | (92) | 148 | 204 | 112 | (184) | 296 |
| 5 | 70 | (115) | 185 | 255 | 140 | (230) | 370 |
| 6 | 84 | (138) | 222 | 306 | 168 | (276) | 444 |
| 7 | 98 | (161) | 259 | 357 | 196 | (322) | 518 |
| 8 | 112 | (184) | 296 | 408 | 224 | (368) | 592 |
| 9 | 126 | (207) | 333 | 459 | 252 | (414) | 666 |

Table H.1. The arithmetical relationships between second perfect number 28 and Shcherbak's "Prime quantum 37 ". There are some GC significant numbers: 204 as the number of atom within 20 amino acid side chains; the number $\underline{\mathbf{0}} 255$ corresponds with the total number ( $\mathbf{1 2 5 5}$ ) of nucleons within 20 AA side chains; the number 74 as the number of nucleon within AA "head". (Notice an analogy between this pattern $\underline{\mathbf{0}} 255$ / $\underline{\mathbf{1}} 255$ and the pattern $\underline{\mathbf{0}} 443$ / $\underline{\mathbf{1}} 443$ in Table E.1, valid for the number of atoms and nucleons, respectively.)

| Tab. H. 2 | 1 | 2 | 3 |  |  | 4 | 5 |  | 6 |  | 3+6 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| I | (24 | 18 | 42) |  |  | 240 | 09 |  | 33) |  | $75^{65}$ |
| 11 | (44 | 26 | 70) |  |  | 03 | 00 |  | 3) ${ }^{6}$ |  | $73^{68}$ |
| I+II | (68 |  | 112) |  |  | (27 0 | 09 |  | 6) |  | $148{ }^{/ 1}$ |
| III | (77 |  | 121 |  |  | 03 | 04 | 07 | 7) |  | $128^{74}$ |
| I+II+III | (145 | 88 | 233 |  |  |  |  |  | 3) |  | $276{ }^{\prime \prime}$ |

Table H.2. Distributions and Distinctions within Darwin Diagram, DDDD-1: "tree-space" $(1,2,3)$ versus "non-tree-space" $(4,5,6)$ on $0-14$ levels; I.1: The left tree-space ("A"): the 24 non-marked primary
${ }^{63}$ The results 24-18-42 (non-marked primary branches on 11-13th levels) (non-marked by the small letters) in relation to total primary branches on both trees (A \& I): 68-44-112 (Table 2.1).
${ }^{64}$ The results 24-09-33 (non-marked primary branches on 0-14th levels) (non-marked by the small letters) in relation to total primary branches at the left and right non-tree-space, respectively (left: B,C,D,E,F; right: G,H,K,L): 27-09-36 (Table 6.1).
${ }^{65}$ The total number of non-marked primary branches (varieties non-designated with small letters).
${ }^{66}$ The results 44-26-70 as well-marked primary branches within tree-space, on the trees "A" and "I" (Table 2.1 and Figure 5).
${ }^{67}$ The results 03-00-03 as well-marked primary branches within non-tree-space (only within the left space: B,C,D,E,F; that, because within the right space: G,H,K,L the well-marked primary branches do not exist (Table 6.1).
${ }^{68}$ The total number of well-marked primary branches (varieties designated with small letters).
${ }^{69}$ The total number of primary branches within tree-space, on the trees "A" and "I" (Table 2.1 and Figure 5).
${ }^{70}$ The total number of primary branches within non-tree-space (left: B,C,D,E,F; right: G,H,K,L) (Table 6.1). At the same time e: The Darwin's equation as in Table 6.1 and in Figure 6.
${ }^{71}$ The total number of primary branches within tree-space ("A" \& "I") and non-tree-space (left: B,C,D,E,F; right: $\mathrm{G}, \mathrm{H}, \mathrm{K}, \mathrm{L}$ ). The number 148 together with the subsequent number below (128) appears to be a change for $\pm 10$ in relation to the half of number 276 as total number of branches within the Diagram ( $2 \times 138=276$ ) (cf. Table 7.3 with Table 7.1).
${ }^{72}$ The total number of secondary branches (non-varieties) (Table 2.2 and Figure 4).
${ }^{73}$ All secondary branches for 9 species (B, C, D, E, F on the left and G, H, K, L on the right) at 0-9 levels (Table 6.3 ).
${ }^{74}$ The total number of secondary branches within tree-space ("A" \& "I") and non-tree-space (left: B,C,D,E,F; right: $\mathrm{G}, \mathrm{H}, \mathrm{K}, \mathrm{L}$ ) (Table 6.1). The number 128 together with the subsequent number above (148) appears to be a change for $\pm 10$ in relation to the half of number 276 as total number of branches within the Diagram ( $2 \times 138=276$ ) (cf. Table 7.4 with Table 7.1). The number 128 as the sum of $121+7$.
${ }^{75}$ The total number of branches (primary plus secondary) within tree-space ("A" \& "I") (Table $4.5 \&$ Table 5; both in relation to Table E.1, g).
${ }^{76}$ The total number of branches (primary plus secondary) within non-tree-space (left: B,C,D,E,F; right: G,H,K,L) at $0-14$ levels (Table 6.4).
${ }^{77}$ The total number of branches (primary plus secondary) within tree-space ("A" \& "I") and non-tree-space (left: B,C,D,E,F; right: G,H,K,L) (Table 7.1). The 276 as the sum of $233+43$.
branches ( $3 \times 8=24$ ) on 11-13th levels; I.2: The right tree-space ("I"): the 18 non-marked primary branches ( $3 \times 6=18$ ) on 11-13th levels; I.3: The sum of previous two (Table 2.1); I.4: The left non-treespace (B,C,D,E,F): the 24 non-marked primary branches ( 21 on the levels $0-9$ and 3 on the levels 11-13); I.5: The right non-tree-space ( $\mathrm{G}, \mathrm{H}, \mathrm{K}, \mathrm{L}$ ): the 9 non-marked primary branches (all 9 on the levels $0-5$ ); I.6: The sum of previous two (Table 6.1); II.1: The left tree-space ("A"): the 44 well-marked primary branches ( 36 on the levels $0-9$ and 8 on the level 14); II.2: The right tree-space ("I"): the 26 well-marked primary branches ( 20 on the levels $0-9$ and 6 on the level 14); II.3: The sum of previous two (Table 2.1); II.4: II.4: The left non-tree-space (B,C,D,E,F): the 3 well-marked primary branches (E \& F with the start on the level $9^{\text {th }}$ and the finalization on the level $10^{\text {th }}$; plus F with the start on the level $13^{\text {th }}$ and the finalization on the level $14^{\text {th }}$ ); II.5: The right non-tree-space ( $\mathrm{G}, \mathrm{H}, \mathrm{K}, \mathrm{L}$ ): without well-marked primary branches; II.6: II.6: The sum of previous two (Table 6.1). With all these facts it must be noted that the vertically shaded field is in connection with arithmetical systems in Figures 4 \& 5, and the horizontally shaded field with the Darwin's equation, observed in Table 6.1 and presented in Figure 6.

| Tab.H.3 | 1 | 2 | 3 |  | 4 | 5 | 6 |  | $3+6$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| I | 24 | 24 | $\mathbf{4 8}$ |  | 18 | 09 | $\mathbf{2 7}$ | 75 |  |
| II | 44 | 03 | $\mathbf{4 7}$ |  | 26 | 00 | $\mathbf{2 6}$ | 73 | $\pm 74$ |
| I+II | 68 | 27 | 95 |  | 44 | 09 | 53 | 148 |  |
| III | 77 | 03 | 80 |  | 44 | 04 | 48 | 128 |  |
| I+II+III | 145 | 30 | 175 |  | 88 | 13 | 101 | 276 |  |

Table H.3. Distributions and Distinctions within Darwin Diagram, DDDD-2: Left part of Darwin Diagram (DD) versus Right part, 1-14 levels. All data in columns 1, 2, 4, 5 are the same as in Table H.2, except the interchange of two columns: $2 \& 4$, respectively. The horizontally shaded fields correspond with the Darwin's equation as it is presented in Tables H. 4 and H.5; The vertically shaded field is in connection with a unique situation in a specific arithmetical system, presented in Table H.6.

| Table H.4 |  |  |  | -09 |  | -09 |  | -18 |  | -18 |  |
| :--- | :--- | :--- | :--- | :--- | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1 | 09 | 09 | 18 | 2 | 00 | 09 | 09 | -09 | 09 | 00 | $\cdots$ |
| 2 | 18 | 09 | 27 | 3 | 09 | 09 | 18 |  | 00 | 09 | 09 |
| 3 | 27 | 09 | 36 | 4 | 18 | 09 | 27 |  | 09 | 09 | 18 |
| 4 | 36 | 09 | 45 | 5 | 27 | 09 | 36 |  | 18 | 09 | 27 |
| 5 | 45 | 09 | 54 | 6 | 36 | 09 | 45 |  |  |  |  |
| 6 | 54 | 09 | 63 | 7 | 45 | 09 | 54 | 09 | 36 |  |  |
| 7 | 63 | 09 | 72 | 8 | 54 | 09 | 63 | 09 | 45 |  |  |
| 8 | 72 | 09 | 81 | 9 | 63 | 09 | 72 |  | 09 | 16 | $\ldots$ |
| 9 | 81 | 09 | 90 | 10 | 72 | 09 | 81 | 09 | 36 |  |  |
|  | $\ldots$ |  |  |  |  |  |  |  |  |  | 53 |

Table H.4. An arithmetical system of multiples of number 9 with an inclusion of Darwin's equation in the darker ton (Variant I).

| Table H. 5 |  |  |  |  | -1 | -1 | -2 |  | -2 |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1 | 09 | 09 | 18 | 2 | 08 | 09 | 17 | 07 | 09 | 16 | $\ldots$ |
| 3 | 27 | 09 | 36 | 4 | 26 | 09 | 35 |  | 25 | 09 | 34 |
| 5 | 45 | 09 | 54 | 6 | 44 | 09 | 53 |  | 43 | 09 | 52 |
| 7 | 63 | 09 | 72 | 8 | 62 | 09 | 71 |  | 61 | 09 | 70 |
| 9 | 81 | 09 | 90 | 10 | 80 | 09 | 89 |  | 79 | 09 | 88 |
|  | $\ldots$ |  |  |  |  |  |  |  |  |  |  |

Table H.5. An arithmetical system of multiples of number 9 with an inclusion of Darwin's equation in the darker ton (Variant II).

| $2,2,2$ | 10 | 25 | 35 | $2,2,2$ | 10 | 25 | 35 | $2,2,2$ | 10 | 25 | 35 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| ${ }_{2}, 2,2$ | 20 | 35 | 55 | $2,2,2$ | 20 | 35 | 55 | $2,2,2$ | 20 | 35 | 55 |
| $2,2,2$ | 30 | 45 | 75 | $2,2,2$ | 30 | 45 | 75 | $2,2,2$ | 30 | 45 | 75 |
| $2,2,2$ | 40 | 55 | 95 | $2,2,2$ | 40 | 55 | 95 | $2,2,2$ | 40 | 55 | 95 |
| $2,2,3$ | 50 | 65 | 115 | $2,2,3$ | 50 | 65 | 115 | $2,2,3$ | 50 | 65 | 115 |
| $2,2,3$ | 60 | 75 | 135 | $2,2,3$ | 60 | 75 | 135 | $2,2,3$ | 60 | 75 | 135 |
| $2,2,3$ | 70 | 85 | 155 | $2,2,3$ | 70 | 85 | 155 | $2,2,3$ | 70 | 85 | 155 |
| $2,2,3$ | 80 | 95 | 175 | $2,2,3$ | 80 | 95 | 175 | $2,2,3$ | 80 | 95 | 175 |
| $2, \mathbf{3}, 3$ | 90 | 105 | 195 | $2, \mathbf{3}, 3$ | $\mathbf{9 0}$ | 105 | 195 | $2, \mathbf{3}, 3$ | 90 | 105 | 195 |
| $\mathbf{3 , 3 , 3}$ | 100 | 115 | 215 | $\mathbf{3}, 3,3$ | 100 | 115 | 215 | $\mathbf{3}, 3,3$ | 100 | 115 | 215 |
| $3,3,3$ | 110 | 125 | 235 | $3,3,3$ | 110 | 125 | 235 | $3,3,3$ | 110 | 125 | 235 |
| $3,3,3$ | 120 | 135 | 255 | $3,3,3$ | 120 | 135 | 255 | $3,3,3$ | 120 | 135 | 255 |
| $3,3,3$ | 130 | 145 | 275 | $3,3,3$ | 130 | 145 | 275 | $3,3,3$ | 130 | 145 | 275 |
| $3,3,3$ | 140 | 155 | 295 | $3,3,3$ | 140 | 155 | 295 | $3,3,3$ | 140 | 155 | 295 |
|  |  |  |  | $3,3,3$ | 150 | 165 | 315 | $3,3,3$ | 150 | 165 | 315 |
|  |  |  |  |  |  |  |  | 160 | 175 | 335 | $3,3,3$ |
| $3,3,3$ | 160 | 175 | 335 |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  | 170 | 185 | 355 |  |
| $3,3,3$ | 180 | 195 | 375 |  |  |  |  |  |  |  |  |

Table H.6. A specific arithmetical system with two or three digit numbers. In relation to left and right area, the middle area appears to be unique: the central row ( $80-95-175$ ) is in a direct connection with only one situation where appears a digit-triplet with the Gray code changes (2-2-3 / 2-3-3/3-3-3). Just this case is also the Darwin's case in third column of Table H.3. (Notice the correspondence with Table H. 1 from the aspect of appearance of two-three digit numbers.)

## Appendix K. Another correspondence with the genetic code ${ }^{78}$

From Table K. 1 follow Tables K. 2 and K. 3 with first half of AAs in first column and the second one in the second column. For each AA is given atom number in whole molecule. As we can see, atom number within 12 AAs in second column is 233 ; exactly as the number of all branches (primary plus secondary) in two trees, A \& I, within Darwin's diagram (Table 4.5); and in first column 233-1=232.

| $\begin{aligned} & 1 \text { st } \\ & \text { lett. } \end{aligned}$ | 2nd letter |  |  |  |  |  |  |  | 3rd lett. |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | U |  | C |  | A |  | G |  |  |
|  | 00. UUU | F | 08. UCU |  | 32. UAU | Y | 40. UGU | C | $U$ |
|  | 01. UUC |  | 09. UCC |  | 33. UAC |  | 41. UGC |  | C |
| U | 02. UUA | L | 10. UCA | S | 34.UAA | CT | 42. UGA | CT | A |
|  | 03. UUG |  | 11. UCG |  | 35.UAG |  | 43. UGG | W | $G$ |
|  | 04. CUU |  | 12. CCU |  | 36. CAU | H | 44. CGU |  | $U$ |
|  | 05. CUC |  | 13. CCC |  | 37. CAC |  | 45. CGC |  | C |
| C | 06. CUA | L | 14. CCA | P | 38. CAA |  | 46. CGA | R | A |
|  | 07. CUG |  | 15. CCG |  | 39. CAG | Q | 47. CGG |  | $G$ |
|  | 16. AUU |  | 24. ACU |  | 48. AAU | N | 56. AGU |  | U |
|  | 17. AUC | I | 25. ACC |  | 49. AAC | N | 57. AGC | S | C |
| A | 18. AUA |  | 26. ACA | T | 50. AAA |  | 58. AGA |  | A |
|  | 19. AUG | M | 27. ACG |  | 51. AAG | K | 59. AGG | R | G |
|  | 20. GUU |  | 28. GCU |  | 52. GAU |  | 60. GGU |  | $U$ |
| G | 21. GUC | V | 29. GCC | A | 53. GAC |  | 61. GGC | G | C |
| G | 22. GUA | V | 30. GCA | A | 54. GAA | E | 62. GGA | G | A |
|  | 23. GUG | $V$ | 31. GCG |  | 55. GAG | E | 63. GGG |  | G |

Table K.1. „The Table of the standard genetic code (GCT). Total codon space is divided into three parts in correspondence with the harmonic mean $(\mathrm{H})$ of the whole codon space sequence (a) and its half (b), where $\mathrm{a}=63, \mathrm{~b}=31.5$ and $\mathrm{H}=42 \ldots$ In the central area, the three stop codons (CT, codon terminations) are crossed out" (Rakočević, 2013, Table 1). By this one must noice now the correspondence and selfsimilarity between patterns of quantitives: $\underline{\mathbf{0}} 22 / \underline{\mathbf{0}} 21$ of codons in this Table versus $\underline{\mathbf{1}} 22$ / $\underline{\mathbf{1}} 21$ of atoms in Table K.3.

[^65]

Table K.2. The Table follows from Table 1: odd /even atom number distinctions.

| F | 23 | 20 | H |  | (d)65 ... $=1.53$ (e) |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| L | 22 |  | Q |  |  |  |
| L | 22 | 17 | N |  | 63 -.- ${ }^{-1}$ |  |
| I | 22 | 24 | K |  |  |  |
| M | 20 | 16 | D |  | $244-233=0 \underline{11}$ |  |
| V | 19 | 19 | E |  |  |  |
| Crossing Horizontal Vertical |  |  |  | $\begin{aligned} & 1 \underline{2} 8+1 \underline{16}=244(2 \times 122) \\ & 1 \underline{1} 8+1 \underline{2} 6=244(2 \times 122) \\ & 1 \underline{1} 8+1 \underline{2} 6=244(2 \times 122) \end{aligned}$ |  |  |
|  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |
| V | 19 | 14 | C |  | (f) $49 \ldots$  <br> $55 \ldots$ .$-66(\mathrm{~g})$ <br> $\cdots$  |  |
| S | 14 | 27 | W |  |  |  |
| P | 17 | 26 | R |  |  |  |
| T | 17 | 14 | S |  |  |  |
| A | 13 | 26 | R |  | $\begin{aligned} & 232-121=\mathbf{1 1 1} \\ & 100+122=222 \end{aligned}$ |  |
| Y | 24 | 10 | G |  |  |  |
| 232233 |  |  |  | $\begin{aligned} & \text { C } 100+121=221(1 \times 221) \\ & \text { H } 1 \underline{1} 5+\underline{0} \underline{6}=221(1 \times 221) \\ & \text { V } \underline{\underline{0}} 4+1 \underline{1} 7=221(1 \times 221) \\ & \hline \end{aligned}$ |  |  |
| $233-232=001$ |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |
| $232-122=110$ |  |  |  | $384-100=284$ |  |  |

Table K.3. The Table follows from Table K.2. For details cf. Surveys K.1 and K.2.

| n -VPA (49) +p -WSG (51) $=100$ (The reference sequence) |  |  |  |
| :---: | :---: | :---: | :---: |
| FLM (a) HND | FLM | (d) | QKE |
| LIV ${ }^{\text {- }}$ - ${ }^{\text {- }}$ | LIV | (e) | HND |
| VPA (b) STY | V | (f) | WSG |
| CWG (c) RSR | STY | (g) | CRR |

Survey K.1. This survey is the key for the reading and understanding of amino acid arrangement in Tables K. 2 and K.3, in odd/even positions, respectively. Also, after our hypothesis (and prediction) - the key of positioning and hierarchy of AAs within proteins. By this the key of the key is the reference sequence (above) with the unity of arithmetical and physico-chemical balance: $50 \pm 1$ of atoms in nonpolar and polar sub-sequence, respectively; balance-nuancing in polarity/nonpolarity: Valine \& Alanine as nonpolar; Proline as nonpolar in polar requirement (Woese, et al., 1966; Konopel'chenko and Rumer, 1975) and polar in hydropathy index (Kyte and Doolittle, 1982) and cloister energy (Swanson, 1984); Serine as polar; Tryptophan and Glycine as polar in hydropathy index, and nonpolar in cloister energy. Except this way, the balance-nuancing is evident through realization of three logics: (a) nonpolar AAs on the left and polar on the right; (b) AAs in odd positions are nonpolar and AAs in even positions are polar; (c) outer AAs, CWG, are nonpolar (in cloister energy) and inner, RS, polar. The arrangement on the right, the sequences $\mathrm{d}-\mathrm{g}$, in correspondence with their arithmetical solutions in Table K.3, shows further nuancing and unity of arithmetical balances and polarity / nonpolarity.


Survey K.2. "The determination of the series of the numbers 0-63. When we look closely into the structure of the sequence $0-63$ of the series of the natural numbers we come to the obvious and selfevident explanation of the reason
anifestation in the form of the Gray why the genetic code must be six-bit code, no matter if it is the manifestation in the form of the Gray
Code model (Swanson, 1984, p 188), or it is in the form of the Binary tree (Rakočević, 1994, p. 38). There must be 8 codon, i.e. amino acid classes. The structure of the sequence $0-63$ is strictly determined by third perfect number (496) and the sum consisted of the first pair of the friendly numbers (220+284)" (Rakočević, 1997b, p. 60). [Cf. with the same pair of friendly numbers, in form 110-284, in Table K.3, below.]

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## ADDENDA

## A. 1

## THREE-DIMENSIONAL MODEL OF THE GENETIC CODE

## ACTA

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## REWIEV ARTICLE

# THREE-DIMENSIONAL MODEL OF THE GENETIC CODE 

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#### Abstract

The classical table of the genetic code does not reflect all the relations among the codons. This paper demonstrates that the three--dimensional topological model - cube enveloping a sphere - is the source of all the relations within the genetic code: eight cogate codons, disposed at the corners, make up the main cube; then, according to the superposition principle, these eight cubes make up a bigger (common) cube containing all the 64 codons. The topological relation between the cube and the sphere inscribed in the cube is expressed by Euler's theorem of homeomorphic translation. Using this three-dimensional model, a new table and a new matrix of the genetic code can be worked out, representing the relations among encoding words (codons), in the actual DNA and RNA molecules far more precisely than the classical ones.


## Introduction

In spite of its adequate name from the vary beginning of investigations in molecular biology, the genetic code has not been sufficiently and comprehensively explored as a code, i.e. as a mathematical essence of the relations. This task, however, has been present since 1963 , when all the 64 codons were practically known. The fact that the genetic code is in full accordance with the mathematical model for generating three-letter words out of a four-letter alphabet (third class variations with repetition, out of a four-element set $4^{3}$ ), led to further necessary and evident deductions. So, after 1966, when the genetic code table was finally established, it was necessary to search for a solution of the obvious problem of two sites in the table being ,,occupped" by serine and two by arginine. The main purpose of both the previous (Rakocevice, 1988a; 1988b) and this work was actually that necessary deduction, based on appropriate theoretical and experimental data.

The whole project has proved to make sense, since it has led to a significant result, which may be summarized as follows:

The genetic code, as a unity of a nucleotide and an amino acid component (the encoding words and encoded elements from the first and the second alphabet, respectively) is in full accordance with the three-dimensional topological model of a cube with an inscribed sphere, their mutual relation being described by Euler's theorem of homeomorphic translatron. The degree of difference between codons (which occupy the cube corners on the toplogical model) corresponds precisely to mutal distances between the corners: 1 step (or 1 bit in the binary record) if the codons are at opposite ends of the edges; 2 steps, if they are at opposite ends of face diagonals, and 3 steps if they are at opposite ends of the cube dagonals. In the matrix of distances between the codons (Table 1), which is derived directly from this three-dimensional model, zeros are consistently situated on the diagonal (one does not differ from itself), while unities follow as the next number sequence along the dagonail. They testify to the optimum quality of the genetic code revealed in the regular one-unit distance between adjacent codons, according to similarity-dissimilarity criterium.

Table 3. 64 codons for 20 amino acids and 1 ,Stop" command.

ween codon groups with $U$ and $A$ as the middle bases and codons with $G$ and $C$ as the middle bases are also in contact. The arrangement of the encoding words (codons) within the genes is in full accordance with this table, (Blalock et. al., 1986; Rakočević, 1988a). Periodicity and complementarity can be read directly from this table; in addition, the pro-


Fig. 1. The optimal amino acid ring
blem of serine and arginine ,,occupying" two places each, has been solved in this way.

On the basis of the topological genetic code model, it is possible to construct a „mutational amino acid ring" (Fig. 1), which corresponds to the interrelationships between amino acids, first of all in terms of similarity dissimilarity of their physico-chemical characteristics. In fact, all the relations exatly correspond to the relations between the elements of the cube, as described in introduc-
tion.

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## A. 2

THE UNIVERSAL CODE AS A REALITY OF HOLISM

# THE UNIVERSAL CODE AS A REALITY OF HOLISM 

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#### Abstract

From ancient times it was thought that the codes and conventions are the basis of all cultural phenomena, and they have divided the world culture from the world of nature. The nature is governed by objective immutable laws, whereas the culture is produced by mutable conventions of the human mind. However, the discovery of the genetic code in the early 1960s, like a bolt from the blue, shown that the barrier between nature and culture does not exist. It turned out that the genetic code, in its essence, is a metaphor, a secondary structure such as a computer program which allows us to represent the physical and chemical properties of molecules writing only the binary numbers. In my researches of the genetic code, from early 1980s until now, I understood coding process as a correspondence between two systems, one realistic and second symbolic. Thus, the genetic code as well as periodic system of chemical elements appears to be only the aspects of a universal code which structure and composition is determined by the best possible symmetry, harmony and proportion. Later I viewed that the possible aspects of such a universal code can be found among the creations of the human mind, as there are examples of poetic structures and compositions of classical literature (Homer, Dante, Shakespeare, Goethe, Pushkin, Njegosh, Tolstoy ...); then the structure of Bible, I Ching and so on. In recent times I see that so-and-such universal code is nothing else than the reality of a possible holism, which connection is just the subject of this communication.


Keywords: code, convention, genetic code, universal code, holism, culture, nature, metaphor, symbolic system, symmetry, harmony, proportion, poetic structures, human mind, classical literature, Bible, I Ching

## 1. Introduction

The idea of the universal code of nature I presented in several papers of which only a few mentioned here [1-4]. The very idea resulted from my researches of the genetic code that were started in the 1973rd, when the Genetic Code Table (GCT) before long time has been definitely established [5-6]. If genetic information can be written out and then be translated, that at least means an analogy with natural (speaking) language. With this reason the route toward the universal code has already been set [7]. But during the time came new questions: why just 64 coding words in the genetic code, does this have to do with 64 boxes of chess and with the 64 hexagrams presented in one of the oldest books, in the Chinese book I Ching [8]? If such a connection exists, and it turned out to be, then we are at the heart of understanding the universal code. The Pavle Bidev's book Chess, a symbol of the universe [9] has prompted a new question: is Njegoš's poem Luča mikrokozma (The Light of Microcosm) only a metaphor or this title indicates the essence, the symbol and a code?

So I found first by Njegoš, and then by other literary classics (Homer, Dante, Shakespeare, Goethe, Pushkin, Tolstoy ...) that these authors, consciously and deliberately, built the structure and composition of their poetic works in accordance with structures determined by the best possible symmetry, harmony and proportion (golden mean); such structures as, for example, the structures of the genetic code and the periodic system of chemical elements, in an analogical comparison $[10-13]^{1}$. Within this work we will present only the basic elements of such
${ }^{1}$ My friends and colleagues, Prof. Djuro Koruga and Prof. Dejan Raković, do not agree with me that these authors intentionally do this. According to the first of them this is the result of the existence of a general intelligence of the universe; according to the second one, this is, par excellence, the result of the holographic universal connectivity. We can say that these three standpoints are, mutatis mutandis, the key models of alignment when it comes to the attitudes of researchers in such
structures, relying on our already published works, but for the first time we will also present $a$ hypothesis that such a universal code represents by itself the reality of holism.

## 2. A Possible Approach to Universal Code

It was easy to see that from the aspect of optimality and validity of two principles, the principle of continuity and the principle of minimum change (change in unit), four-letter alphabet is one and only possible solution. Namely, from the four-letter alphabet it makes sense to generate three-letter words, from five-letter alphabet fourletter words and so on. ${ }^{2}$ Then, three-letter words have the root of two letters, and the root is preceded by the smallest possible unit - a single letter. Altogether, it is implemented a complete and homogeneous hierarchical system (4-3-2-1), and so it is not possible in any other case.

If the system of 64 coding words of GCT develop into a binary tree $0-63$ [10], we obtain the same binary tree that is found in the aforementioned Chinese book I Ching, for the 64 hexagrams. A full line in each hexagram corresponds to a binary zero, and each broken line corresponds to unit (binary number 1) on the six-bit binary tree. But not only this, such a binary tree (with a system of 64 words) is the only one that strictly corresponds to the first four perfect numbers. The sum of the ordinal numbers for the first four words (in the first quartet), $0-3$, makes number 6 what is the first perfect number; the sum of the first eight numbers, $0-7$, gives the 28 (the second perfect number!). Then there comes the realization of a half of the system, $0-31$, with the sum of 496 , which is the third perfect number. If, however, it is going to end, 0-63, and returned to the beginning (cycling!), we have the sum of the first 128 numbers, from 0 to 127 , which is 8128 , the fourth perfect number. In general, the determination with perfect numbers is related to the realization of 2 -bit, 3 -bit, 5 -bit and 7 -bit binary trees, where again we have a strict order ${ }^{3}$ - the order of the first four prime numbers: 2-3-5-7. "Skipped" is the determination of 4-bit and 6-bit binary tree, where we have 4 classes, each of 16 and 8 classes, each of the eight words, which logic is also the aspect of uniqueness and validity of the principle of self-similarity ${ }^{4}\left[\left(2^{4}=4^{2}\right),\left(2^{6}=8^{2}\right),\left(2^{6} \rho 6^{2}\right)\right]$. (Note: Notice that 16 stay in relation with 16 two-letter words, and 64 in relation with 64 three-letter words.)

From the aspect of determination by generalized golden mean, the four-letter alphabet, through six-bit binary tree, appears also to be the optimal and appropriate composition, i.e. the best possible solution [10-11]. This is because the exact determination is possible only within the decimal numbering system, from $\phi^{0}$ to $\phi^{9}[10, \mathrm{Tab}$. $2]^{5}$. The 22 years ago five U.S. scientists have presented still an another property of four-letter alphabet, more exactly for its 64 three-letter words: "the number of all distributions in the set of 64 codons [words] is 1741630 " [16]. After the publishing of this result, I showed that the number 1741630 also follows from the number of verses in the Iliad and the Odyssey ([3, Fig. 13], [17-18], [18, Fig. 5, p. 191]), as well as from the number of verses in the first Njegoš's triptych [18, p. 60]. ${ }^{6}$

Otherwise, the total cumulative number of verses of the Iliad and the Odyssey can be generated from the binary sequence $2^{n}(2 \exp n)(n=0,1,2,3, \ldots, 14)$. At first, the obtained 15 numbers must be grouped into three

[^66]fives and then comes the choice: from the first and third fives select two first and two last numbers, and from the second (central) five select only the number 128, a middle number ([3, Fig. 12], [18, Fig. 4, pp. 189-190]). ${ }^{7}$ However, without a genial thought of Dante Alighieri it would be hard today to understand the essence of the universal code. The selection of the number of verses in 100 songs of The Divine Comedy performed by a unique pattern, which we present through the examples of four songs from Hell (Inferno): VIII 130 (4), IX 133 (7), X 136 (10), XII 139 (13). If we take any of 100 songs, no song is out of this pattern (4-7-10-13). Just in our time the same model is found in the genetic code [19]. It was found, namely, that the number of nucleons within the amino acid constituents of the genetic code is corresponding to the multiples of 037, a unique two-digit numbers in the decimal numbering system $(\mathrm{q}=10) .{ }^{8}$ But it is also found that the same property possesses the analogues of 037 ( $13,25,37,49 \ldots$...) in the numbering systems with the $\mathrm{q}=4,7,10,13,16,19$, etc..., respectively. As we can see the first four cases, are actually the Dante's numbers. ${ }^{9}$

It should be noted that the first digit in a series of analogues comes from the series of natural numbers, and the second one from a series of odd natural numbers. But despite this simplicity, I needed a very lot of time (and work) until I realized an arrangement of natural numbers in form of a matrix, with such numbers in the first diagonal which possesses the form of Shcherbak's (and of Dante's?) numbers. In such an arrangement unique are also the neighbors of the number 37 (the numbers 26 and 48). ${ }^{10}$ (Table 1).

### 2.1 Some uniqueness in relation to the universal code

We will consider Table 1 more broadly. If the first diagonal neighbour of the number 26, the number 16 ( 26 $16=10$ ) is added to the number 26 and its two followers (17 and 18) are successively added to the obtained result, we get the results as in Solution (1):

$$
\begin{array}{lll}
26 \quad=26 & & 26+42+59+77=\mathrm{Y} \\
26+\mathbf{1 6}=42 & & \mathrm{Y}=204  \tag{1}\\
42+\mathbf{1 6}=59 & & \mathrm{Z}=51 \\
59+\mathbf{1 8}=77 & & \mathrm{Y} / 4=51
\end{array}
$$

With three addings $(16+17+18=51=\mathrm{Z})$ we obtained three new results, and with the inclusion of the initial number 26 - four results. Their sum is $204(26+42+59+77=204=Y=4 Z)$, exactly four times greater than the sum of the three addings $(16+17+18=51=\mathrm{Z})$. But this connection of two equalities is a single and unique case in the entire system of numbers within Table 1 , in other words within the set of natural numbers. ${ }^{11}$
 8192, 16384). Njegoš's choice are all numbers which are not the Homer's choice: printed version + manuscript version of The Mountain Wreath: $2819+1528=4347$ verses; plus the number of person-scenes: $318+150=468$; plus pages for printing as well as for manuscript version: $116+33=149$; altogether: $4347+468+149=4964$. Finelly, Homer's choice plus Njegoš's choice: $27803+4964=32767$, what is 77777 in octal numbering system.
${ }^{8}$ The uniqueness is because the multiplication through the modulo ( $q-1$ ) preserves all three digits: $(1 \times 037=037 ; 10 \times 037$ $=370 ; 19 \times 037=703),(2 \times 037=074 ; 11 \times 037=407 ; 20 \times 037=740)$ etc.
${ }^{9}$ To satisfied my friends, Prof. Koruga and Prof. Raković (and non-confidential readers) that Dante intentionally build his poetic structures, I will mention the Dante's verses which say that a hidden doctrine is lying under the verses, that is teaching or science: "O ye who have undistempered intellects, / Observe the doctrine that conceals itself / Beneath the veil of the mysterious verses! "(" O voi ch'avete you 'ntelletti sani, / safely without che la dottrina s'asconde / sotto' I I say de li versi side ") (Div. Comm., Inferno, IX, 61-63).
${ }^{10}$ In further text follows the explanation of the uniqueness of the number 26 , but about uniqueness of the number 48 see ref. [15].
${ }^{11}$ Moreover, it appears that this is the zeroth case in the $4^{\text {th }}$ column of Table 1 in the decimal numbering system, and also the zeroth case within all Shcherbak's numbering systems ( $\mathrm{q}=4,7, \underline{10}, 13,16, \ldots$ ); in all other cases, discrepancies arise $[15$, Tables C 1 and C 2 ].

Table 1. A specific arrangement of natural numbers in decimal numbering system

|  | $\ldots$ |  |  |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $(-2)$ | $\ldots$ |  |  |  |  |  |  |  |  | $\ldots$ | -22 |  |
| $(-1)$ | -21 | -20 | -19 | -18 | -17 | -16 | -15 | -14 | -13 | -12 | -11 |  |
| $(0)$ | -10 | -09 | -08 | -07 | -06 | -05 | -04 | -03 | -02 | -01 | 00 |  |
| $(1)$ | 01 | 02 | 03 | 04 | 05 | 06 | 07 | 08 | 09 | 10 | 11 |  |
| $(2)$ | 12 | 13 | 14 | 15 | , $\mathbf{1 6}$ | $-\mathbf{- 1 7}^{-}$ | $-\mathbf{1 8}$ | 19 | 20 | 21 | 22 |  |
| $(3)$ | 23 | 24 | 25 | $\mathbf{2 6}$ | 27 | 28 | 29 | 30 | 31 | 32 | 33 |  |
| $(4)$ | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 |  |
| $(5)$ | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 |  |
| $(6)$ | 56 | 57 | 58 | 59 | 60 | $5 B$ | 62 | 63 | 64 | 65 | 66 |  |
| $(7)$ | 67 | 68 | 69 | 70 | 71 | 72 | $6 D$ | 74 | 75 | 76 | 77 |  |
| $(8)$ | 78 | 79 | 80 | 81 | 82 | 83 | 84 | $7 F$ | 86 | 87 | 88 |  |
| $(9)$ | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 |  |
| (A) | A0 | A1 | A2 | A3 | A4 | A5 | A6 | A7 | A8 | A9 | AA |  |
| (B) | B1 | B2 | B3 | B4 | B5 | B6 | B7 | B8 | B9 | BA | BB |  |

The uniqueness of the number 26 is expressed not only through the difference 26-10=16, but also through the sum $26+10=36$, where number 36 , as the second diagonal neighbour of the number 26 , appears to be the member of a unique pair 25-36; unique case in the entire system of numbers within Table 1, and that means within the set of natural numbers. Namely, the numbers 25 and 36 are neighbours in third column of Table 1 with a difference of 11 as in all other cases, in all columns. But their square roots, as integers, appear to be also neighbours, and that is the said uniqueness [Solution (2)]:

$$
\begin{align*}
& x_{1}+y_{1}=36=\mathbf{6}^{2}\left(x_{1}=26 ; y_{1}=10\right) \\
& x_{2}+y_{2}=25=\mathbf{5}^{2}\left(x_{2}=17 ; y_{2}=08\right)  \tag{2}\\
& x_{1}-y_{1}=16=\mathbf{4}^{2} \\
& x_{2}-y_{2}=09=\mathbf{3}^{2}
\end{align*}
$$

### 2.2 The unity of two realities - mathematical and physical

Through a purely chemical analysis it is possible to find such an arrangements of protein amino acids that fully correspond to the observed arithmetical regularities, related to the uniqueness of numbers 26 ; as if we are dealing with an "intelligent" imitation, in one possible classification and systematization. Namely, Figure 1 shows an arrangement of AAs (in the $4 \times 5$ system), with the number of atoms as in Solution (1). This arrangement follows from a classification and systematization of 20 protein AAs into four diversity types ${ }^{12}$, as it is shown in Figure 2: first row from the vertical line of the circular model; fourth row from the horizontal line; second row from four middle points of circular model; third row make two left and two right AAs in relation to two middle points (M \& D); finally, fifth row make two left and two right AAs in relation to two middle points (A \& R). By this, each sequence in Figure 1 is arranged by the size of molecules, i.e. by the number of atoms in the side chains, ${ }^{13}$ going from left to right; and the order of sequences is determined by the size of the first amino acid

[^67]molecule in the sequence. ${ }^{14}$ Only with such a precise and strictly regulated system can we get the desired result, the sequence 26-42-59-77, signifying the number of atoms in the four columns of AAs (in their side chains) [cf. Table 1, Solution (1) and Figures $1 \& 2$ ].

| G 01 | S 05 | Y 15 | W 18 | 39 | 78 | 102 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| A 04 | D 07 | M 11 | R 17 | 39 |  |  |
| C 05 | T 08 | E 10 | F 14 | 37 | 24 | 102 |
|  |  |  |  |  | 13 |  |
| N 08 | Q 11 | V 10 | 113 | 42 |  |  |
| P 08 | H 11 | L 13 | K 15 | 47 |  |  |
| 26 | 42 | 59 | 77 |  |  |  |
| 16 |  | 17 | 18 |  |  |  |
| (1 x 68) |  | (2 x 68) |  |  |  |  |

Figure 1. A specific classification and systematization of amino acids, which follow from four diversity types (Figure 2). In the shadow space there are 20 AAs with atom number in molecules side chains. Within first two and last two columns: $1 \times 68$ and $2 \times 68$ atoms, respectively. Within two inner and two outer columns: $102 \pm 1$ atoms. Regarding at the rows: there are 78 atoms within first two and 78 $+11=89$ within last two rows; within first half of the middle row 13 , and within the second one $13+11$ atoms. Within two halves of shadow spaces (light and dark) there is also a specific balance: $102 \pm 00$ atoms. All amino acid sequences are of the growing series from the aspect of number of atoms; all but one, in which Q-11 precedes V-10, because different stereochemical types have been distinguished: N Q belongs to alanine but V-I to valine type.

Bearing in mind that an arithmetical law, presented in Solution (1), is fully confirmed, it makes sense to set up a working hypothesis, related to an algebraic law, presented in Solution (2): it must be that the quantities, given in Solution (2), $\mathrm{x}_{1}=26, \mathrm{y}_{1}=10$ as well as $\mathrm{x}_{2}=17, \mathrm{y}_{2}=08$ in a way also contained in the genetic code. Figure 3 is an obvious and direct evidence for this. The first diversity type of AAs ( $\mathrm{P}, \mathrm{G}$ ) and corresponding $\mathbf{0 8}$ codons appears to be diagonally on the right within Genetic Code Table (GCT), designated in Figure 3 in lightest tones; the second one ( $\mathrm{L}, \mathrm{I}, \mathrm{V}, \mathrm{A}$ ) with $\mathbf{1 7}$ codons diagonally on the left (in a little dark tones); altogether, in both diversity types of chemically low-level-functions there are 25 codons.

The third diversity type of AAs and corresponding 10 codons follows, within GCT, in the next order (more dark tones): in column " U " up and down, and in columns " A " and " G " only up. The fourth type, with $\mathbf{2 6}$ codons (the most dark tones), in column " C " up and down, and in columns " A " and " G " only down; altogether, in two diversity types of chemically high-level-functions there are 36 codons.

[^68]

Figure 2. Four diversity types of protein amino acids in a linear arrangement in form of the sequence 2-$4-6-8$; then in a circular arrangement, in form of the sequence $5-5-5-5$. From this last sequence it is possible a new arrangement in form of the sequence $4-4-4-4-4$ as in system, presented in Figure 1.

| 1st letter | 2nd letter |  |  |  |  |  |  |  | 3rd letter |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | $U$ |  | C |  | A |  | G |  |  |
|  | UUU |  | UCU |  | UAU |  | UGU |  | U |
|  | UUC | F II | UCC |  | UAC | Y I | UGC | C I | C |
| $u$ | UUA |  | UCA | S II | UAA |  | UGA |  | A |
|  | UUG | L I | UCG |  | UAG | CT | UGG | $\begin{gathered} \text { CT } \\ \text { W } \end{gathered}$ | G |
|  |  |  |  |  |  |  |  |  |  |
|  | CUC |  | CCC |  | CAC | H II | CGC |  | C |
| c | CUA | L I | CCA | P II | CAA |  | CGA | R I | A |
|  | CUG |  | CCG |  | CAG | Q I | CGG |  | G |
|  | AUU |  | ACU |  | AAU |  | AGU |  | U |
|  | AUC |  | ACC |  | AAC | N II | AGC | S II | C |
| A | AUA |  | ACA | T II | AAA |  | AGA |  | A |
|  | AUG |  | ACG |  | AAG | K II | AGG | R I | $G$ |
|  |  | M I |  |  |  |  |  |  |  |
|  | GUU |  | GCU |  | GAU |  | GGU |  | $U$ |
|  | GUC |  | GCC |  | GAC | D II | GGC |  | C |
| $G$ | GUA | V I | GCA | A II | GAA |  | GGA | G II | A |
|  | GUG |  | GCG |  | GAG | E I | GGG |  | G |

Figure 3. The standard Genetic Code Table with designation of four diversity types of protein amino acids and corresponding codons (lightest, light, more dark and most dark tones): 08, 17,10 and 26, respectively ( $8+$ $17=25=5 \times 5$ and $10+26=36=6 \times 6$ ). The roman numbers designate class I and class II of aminoacyltRNA synthetases. For details see the text.


Figure 4. This Figure follows from Figure 3. The designations I-IV: Four diversity types of amino acids. In first quadrant there is the number of three-letter words, i.e. codons within GCT (in total 61), while in other three quadrants - the number of letters. The rule valid for zigzag line is given in two last paragraphs of Section 2.2. (a) The first half of Table in Figure 3. (b) The second half of Table in Figure 3. In column $a$ there are codons of pyrimidine kind, regarding at the middle position in codon, whereas in column $b$ of purine. The validity of two principle (continuity and minimum change) is self-evident; also the changes for 01,10 and 11.
The positioning of codons within the system of GCT in the terms "up" and "down" at first glance seem to be arbitrary and optional. However, if such a classification is viewed from the aspect of key qualificatives - the first half of the GCT (of pyrimidine kind) is of lower rank, and the second half of a higher rank (of purine kind) - then we get here also to the very strict quantitative relations (Figure 4). The Figure 4, in fact, shows that the principle of self-similarity (through the alignment into $25 / 36$ codons) achieved in another way. First, if a series of I-II-IIIIV types is taken as splitting into two classes, then in the first class belong two types from odd positions, and in the second one two types from even positions. Then (in a holistic way?) there "enters" at the scene the validity of the following regularity: the number of low-ranking codons in two types at the odd positions, plus the number of higher-ranking codons in the two types at the even positions is the same as the number of all codons in the first two diversity types (25). The reverse is true for the reverse situation: the number of low-ranking codons in the two types placed at the even positions, plus the number of higher-ranking codons in two types placed at the odd positions is the same as the number of all codons in the second two diversity types, the third and fourth, just 36.

As we see, here we are in a situation that is both very simple and very complicated. Simple, because here all comes to be a balance, expressed through two zigzag lines (Figure 4), which balance we have so often found in the classifications of the genetic code constituents ( $[10,21]$ ). Complicated, because this balance is mediated by
more wholeness, each of more parts. On the one hand we have the wholeness of low-ranking codons in all four diversity types, then the wholeness of higher-ranking codons; finally, the wholeness of all codons. And the results are such that as the parts of all of these wholeness also provide information on the number of codons in all individual wholeness, and all individual parts, as well as to have their own internal "awareness" about all this. This and such situation leads us (inevitably) to the conclusion that for the solution of the problem we need to seek help from the possible holistic approach.

## 3. A Hypothesis About Possible Relation Between Universal Code and Holism

With this inter-title I deliberately insist on the relation to holism, and not the connection or identity and so on. This is because the holism is itself still hypothetical idea, and my hypothesis requires a proper interpretation of the interdependence of the two realities presented above. The first reality makes the system of natural numbers in the arrangement given in Table 1, the arithmetic system introduced in Solution 1 and the algebraic system presented in the second Solution. Within the second reality there are the constituents of the genetic code represented in Figures 1, 2, $3 \& 4$, while both realties contained in Tables $2,3 \& 4$ (see in further text). The question is, whether here is a classic Bohmian dilemma, a relationship between the original (material) and holographic reality? In other words, the question is what the reality is here and what the "illusion"? But, in the comparison of these two realities, it is not difficult to see that first we have to deal with the problem of coding, and just in terms of holism, not only in terms of coding what is seen in the information theory, though that coding, per se, is also present (the connection between the two alphabets: 4 Py-Pu bases vs 20 AAs ). As we understand the formation of holograms that holographic film contains an encoded image, is here the same, in Bohmian or a different holism? The answer to this question should give future researches.

Table 2. Four types of diversity of protein amino acids

| G P | A L V I | C M F Y W H | R K Q N E D T S |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| 01 | 08 | 04131013 | 051114151811 | 1715110810070805 |  |
| $9+18=27$ | $40+36=76$ | $74+54=128$ | $81+72=153$ |  |  |
| $(27+153=\mathbf{1 8 0})(76+128=\mathbf{2 0 4})$ |  |  |  |  |  |
|  |  |  |  |  |  |

The relationships between four diversity types of protein amino acids $(2+4+6+8)$. In second row there is the number of atoms within side chains of amino acids. The calculations: within 10 AAs of two inner types there are 180 atoms, just as within 20 amino acid "heads", i.e. 20 amino acid functional groups ( 20 x $9=180$ ). On the other hand, within 10 AAs of two outer types there are 204 atoms, just as within 20 amino acid side chains. This specific "simulation" is analogue to the "simulation", valid for the number of protons and neutrons in Table 3.

Another thing that reminds us of the Bohmian reality access is the issue of order. The Bohm's idea of different hierarchy and levels in the order, here, in these two realities also maximal comes into play; as under the reality of molecules, exists a deeper order of existence, embodied in a specific mathematical reality. However, what we can be very sure (or, perhaps, we cannot?) is that the primary (mathematical) level of reality does not rise buildings, not bearing molecules and their particles ${ }^{15}$, but only the birth of the interdependence of these

[^69]molecules, when, and if they do, find in an active system; ${ }^{16}$ such interdependence, which is the "image", "hologram" - the mathematical reality is mirrored in the physical? ${ }^{17}$

Table 3. The Sukhodolets' system of amino acids in a $4 \times 5$ arrangement

| The number of H atoms (in brackets) and nucleons |  |  |  |  |  |
| :--- | :--- | :--- | :--- | :--- | :--- |
| $G(01) 01$ | $A(03) 15$ | $\mathrm{~S}(03) 31$ | $\mathrm{D}(03) 59$ | $\mathrm{C}(03) 47$ | $(\mathbf{1 3})$ |

The Sukhodolets' Table, with a minimal modification [25]: the system of $4 \times 5$ AAs. The shadow space: AAs with even number of hydrogen atoms ( $4,6,8,10$ ); the non-shadow space: AAs with odd number of hydrogen atoms ( $1,3,7,9,11$ ). In brackets: number of hydrogen atoms [25] and out of brackets the number of nucleons. Nucleon number through a specific "simulation": 569 within two outer rows, as the number of neutrons, 569 , in all 20 AAs: within their side chains; and 686 nucleons within two inner rows, as the number of protons, 686, in all 20 AAs: within their side chains. [Note: Within 20 side chains of amino acid molecules there are 569 neutrons as well as 569 non-hydrogen protons. Within 20 side chains of amino acid molecules there are 117 hydrogen protons, what means 117 hydrogen atoms at the same time ( $117=59+58$ ).]

Table 4. The harmonic structure with two "acidic" and three "basic" amino acid quartets

|  |  |  |  |  | a | b | c | d | M |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| D | N | A | L | $\rightarrow$ | $\mathbf{1 8 9}$ | $\mathbf{1 8 9}$ | $\mathbf{2 2 1}$ | $\mathbf{2 2 1 + 3}$ | $485.49 \approx 485$ |
| R | F | P | I | $\rightarrow$ | 289 | 289 | 341 | $341+\mathrm{O}$ | $585.70 \approx 586$ |
| K | Y | T | M | $\rightarrow$ | 299 | 299 | 351 | $351+2$ | $595.71 \approx 596$ |
| H | W | S | C | $\rightarrow$ | 289 | 289 | 331 | $331+1$ | $585.64 \approx 586$ |
| E | Q | G | $\mathrm{V} \rightarrow \mathbf{1 8 9}$ | $\mathbf{1 8 9}$ | $\mathbf{1 8 2 1}$ | $\mathbf{2 2 1 + 3}$ | $485.50 \approx \mathbf{4 8 5}$ |  |  |
|  |  |  |  |  | 1255 | 1255 | 1465 | $1465+9$ | 2738.04 |
|  |  |  |  |  |  |  |  | $2(37 \times 37)$ |  |

The two "acidic" AAs because D \& E are acidic and the three "basic" AAs because R, K \& H are basic. Four choices after four types of isotopes: (a) Number of nucleons within 20 AAs side chains, calculated from the first, the lightest nuclide ( $\mathrm{H}-1, \mathrm{C}-12, \mathrm{~N}-14, \mathrm{O}-16, \mathrm{~S}-32$ ). (b) The number of nucleons within 20 AAs side chains, calculated from the nuclide with the most abundance in the nature [the same patterns as in (a): $\mathrm{H}-1, \mathrm{C}-12, \mathrm{~N}-14, \mathrm{O}-16, \mathrm{~S}-32$; at heavier nuclides of other bioelements the data by (a) and (b) are not the same]. (c) The number of nucleons within 20 AAs side chains, calculated from the nuclide with the less abundance in the nature ( $\mathrm{H}-2, \mathrm{C}-13, \mathrm{~N}-15, \mathrm{O}-17, \mathrm{~S}-36$ ); (d) The number of nucleons within 20 AAs side chains, calculated from the last, the heaviest nuclide (H-2, C-13, N-15, O-18, S-36). (M) The AAs molecule mass. Notice that (d) is greater from (c) for exactly one modular cycle (in module 9) and that total molecules mass is equal to $2(37 \times 37)$. Notice also that molecule mass within five rows is realized through the same logic-patterns of notations as the first nuclide, i.e. isotope [21].

[^70]Just as every part of a hologram contains the whole picture, so in every part of the universe, says Bohm, is contained implicate ("enfolded") order, which is in relation to explicate ("unfolded") order of our level of existence [22-23]. ${ }^{18}$ If not entirely, some of these ideas about the relationship between the whole and part can also be found in the genetic code system. Table 2 contains, namely, a system that suits Bohmian holism. The parts contain information about the whole system: within 10 molecules of two external diversity types there are, in total, 180 atoms; so exactly as how many is in all 20 molecular "heads" of all four types. On the other hand, within 10 molecules of two internal diversity types there are, in total, 204 atoms, so exactly as how many is in all 20 molecular "body" of all four types.

A similar logic we have also in Table 3, except that here the word is on the number of nucleons. In 20 amino acid molecules there are 569 neutrons and 686 protons. In doing so, the number of protons contains 569 nonhydrogen and 117 hydrogen protons $(569+117=686)$. As we see within external part (the first and fourth row) there are, in total, 569 nucleons (protons and neutrons together), exactly as the amount of neutrons in the whole system. The reverse is true for the inner part of the system (the inner two rows: the second and third); here there are 686 of nucleons, as there are protons in the whole system. But not only that, in the last row of Table 3 is presented that the quantities of " 569 " and " 686 " contain the information on the total number of hydrogen protons (117), as well as the medians as well as arithmetic mean of total number of nucleons within 20 side chains ( 1255 $=627+628 ; 1255: 2=627.5$ ). Without reference to holism, Bohm's or another, these results would be difficult to explain.

### 3.1 A "phantom" molecular mass

To understand and explain the relationships within the system presented in Table 4, even more we need Bohmian "dualism", but also Pribram's understanding of the holographic nature of the brain. ${ }^{19}$ We can, in fact, understand the symmetry of the molecular mass distribution as well as of the nucleon number within first nuclides which possesses the most abundance in nature ( $\mathbf{a}, \mathrm{b}$ and M ). But how to understand the symmetry in the distribution of nucleon number within nuclides (columns $\mathbf{c}$ and $\mathbf{d}$ ) which possesses a minimal abundance? Despite this fact, the balance can be obtained only when all the nucleons are included in the account, in one hundred percent!? As it appears the information ("consciousness") of the presence of a huge mass, which is a pure illusion, because most of these masses in fact do not exist in reality; information, analogous to sensations in the brain, in the case of the so-called phantom parts of body. ${ }^{20}$

## 4. Conclusion

In this paper, through a short scientific discussion, we tested a hypothesis of a possible relation between the universal code of nature and holistic approach to understanding natural structures and phenomena. By this, the access to the universal code has been made through the understanding that the genetic code as well as periodic system of chemical elements must be the aspects of such a universal code, whose structures and compositions are

18 "One of Bohm's most starting assertions is that the tangible reality of our everyday lives is really a kind of illusion, like a holographic image. Underlying it is a deeper order of existence, a vast and more primary level of reality that gives birth to all the objects and appearances of our physical world in much the same way that a piece of holographic film gives birth to a hologram. Bohm calls this deeper level of reality the implicate (which means 'enfolded') order, and he refers to our one level of existence as the explicate, or unfolded, order. He uses these terms because he sees the manifestation of all forms in the universe as the result of countless enfolding and unfolding between these two orders" [23, p. 47].
19 "This was precisely the feature that got Pribram so excited, for it offered at last a way of understanding how memories could be distributed rather than localized in the brain. If it was possible for every portion of a piece of holographic film to contain all the information necessary to create a whole image, then it seemed equally possible for every part of the brain to contain all of the information necessary to recall a whole memory" [23, p. 17].
${ }^{20}$ The phantom limb is the sensation that an amputated or missing limb (even an organ) is still attached to the body and is moving appropriately with other body parts. Phantom sensations may also occur after the removal of body parts other than the limbs.
determined by the best possible symmetry, harmony and proportion (golden mean). The same - to be an aspect of universal code - is valid for all other natural, as well as possible artificial harmonic structures; especially the structures found among the creations of the human mind. Among other possible connections between these and such structures in this paper we were interested mainly for the bond that is established through a coding process, understood as a correspondence between two systems, one realistic and second symbolic.

Our discussion, with a high degree of reliability, shown that there are grounds for the placed hypothesis. What is more, and it turned out, that some recent results of my own researches of the genetic code are far easier to explain with the help of a holistic approach.

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## Appendix 1. The Completeness of the legend to Figure 4

|  | a | b |  | U,C | A,G | U,G C,A |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| I | 04 | 04 | 25 | 12 | 12 | 12 | 12 |
| II | 17 | 00 |  | 31 | 20 | 31 | 20 |
| III | 03 | 07 | 36 | 20 | 10 | 19 | 11 |
| IV | 08 | 18 |  | 30 | 48 | 29 | 49 |
|  | 25 |  |  | 100 | 83 | 100 | 83 |
|  | 36 |  |  |  |  | (91) (92) |  |
|  |  |  |  | (93) | (90) |  |  |
|  | U C | A G |  | U,A | C,G | 75 |  |
| 1 | 0210 | 0210 | 75 | 04 | 20 |  | 11 |
| II | 1912 | 0812 |  | 27 | 24 | 86 |  |
| III | 1406 | 0505 | 108 | 19 | 11 | $97^{11}$ |  |
| IV | 1020 | 2919 |  | 39 | 39 |  |  |
|  | 96 | 87 |  | 86 | 97 |  |  |
|  |  |  |  | (89) | (94) |  |  |

Figure 4. This Figure follows from Figure 3. The designations I-IV: Four diversity types of amino acids. In first quadrant there is the number of three-letter words, i.e. codons within GCT (in total 61), while in other three quadrants - the number of letters. The rule valid for zigzag line is given in two last paragraphs of Section 2.2. (a) The first half of Table in Figure 3. (b) The second half of Table in Figure 3. In column $a$ there are codons of pyrimidine kind, regarding at the middle position in codon, whereas in column $b$ of purine. The validity of two principle (continuity and minimum change) is self-evident; also the changes for 01,10 and 11 . Besides the obvious, there are some "hidden" regularities as, for example, the redistribution of 75/108 letters through the doublets. Thus, in the first two types (I, II), which possess chemical features of lower rank, we have: UC43 - AG32 = 11 and CA43 - CA32 $=11$. On the other hand, the doublets AG32 and CA32 appear to be in a unit change relation with UA31; then, the doublets UC43 and UG43 with CG44. Similarly, is in doublets of two other types (III, IV), which possess chemical features of higher rank: CA60 - UC50 $=10$ and AG58 - UG $48=10$. On the other hand, the doublets AG58 and UC50 appear to be in a zeroth change relation with the doublets UA58 and CG50.

## A. 3

DOES UNIVERSAL CONSCIOUSNESS EXIST?
Emerging Logic of the Periodic System of Elements, Genetic Code and Human Consciousness


# Toward A Scientific Basis for Consciousness An Interdisciplinary Conference 

## ACKNOWLEDGMENTS

In the planning stages, this meeting benefited from the ideas, inspirations and work of many.<br>We offer our deepest thanks to these people.<br>In addition, we offer our gratitude to those who have made a financial contribution.<br>They include:<br>The University of Arizona Department of Anesthesiology The University of Arizona Cognitive Neuroscience Center and<br>Gordon E. Olson, M.D., Sierra Vista, Arizona

## Toward A Scientific Basis for Consciousness

## Consciousness

What is consciousness? Ignored, denied, and mystified in the past, consciousness is now recognized as one of the greatest scientific frontiers facing humanity. It is being approached across a spectrum ranging from reductionism (the mind is the brain) to dualism (the mind is distinct and merely interacts with the brain). Between these extremes lie ample evidence, theory, and tools to begin to unravel the mind/brain "problem." Representatives from psychology, neuroscience, computer science, physics, mathematics, medicine, philosophy, and other fields will gather to discuss these issues at an international, interdisciplinary scientific conference on consciousness.

Communication across disciplinary lines isn't always easy; each field has jargon and biases that get in the way. We hope to promote understanding through an atmosphere of open discussion and festive challenge. While focusing on objective scientific approaches to consciousness, we also recognize the importance of subjective experiences and hope to provide avenues for discussing them. Join us in finding a common synergy among different fields, and help us move toward a new understanding of what "consciousness" really means.

# Toward a Scientific Basis for Consciousness An Interdisciplinary Conference APRIL 12-17, 1994 

## TUESDAY, APRIL 12

6:30-8:30 PM Welcoming Reception, Arizona Inn

## WEDNESDAY, APRIL 13

DuVal Auditorium, The University of Arizona Health Sciences Center
8:00-8:30 AM Continental Breakfast

Philosophy of Mind

| 8:30-9:15 AM | Owen Flanagan, PhD, Department of Philosophy, Duke University <br> "Constructive naturalism and consciousness: philosophic perspectives" |
| :--- | :--- |
| 9:15-9:45 AM | Alvin Goldman, PhD, Department of Philosophy, University of <br> Arizona <br> "Philosophy of mind: defining consciousness" |
| 9:45-10:15 AM | David Chalmers, PhD, Department of Philosophy, Washington <br> University, St, Louis, Missouri <br> "On explaining consciousness scientifically: choices and challenges" |
| 10:15-10:45 AM | Break |

COGNITIVE APPROACHES
10:45-11:30 AM Bernard Baars, PhD, Wright Institute, Berkeley, California "Cognitive theory of consciousness"

# Toward a Scientific Basis for Consciousness An Interdisciplinary Confarence April 12-17, 1994 

## Poster Presentations

1. Richard Amoroso, Director of the Noetic Institute, Orinda, California "Consciousness: A radical definition"
2. Britt Anderson, MD, Thomas Head, MD, Department of Neurology and the Alzheimer's Disease Center, University of Alabama at Birmingham, Birmingham, Alabama
"Evidence for covert language comprehension in a severe ‘sensory' aphasic"
3. Adam Atkin, PhD, Briarcliff Manor, New York
"Mind is more than mechanism: A new-old consciousness paradigm"
4. Richard P. Atkinson, PhD, Heath Earl, Weber State University
"Enhanced vigilance in guided meditation: Perceptual implications of altered consciousness"
5. Parthasarathi Banerjee, PhD, National Institute of Science, Technology and Development Studies, New Delhi, India
"The four spaces of consciousness"
6. J. Baribeau, PhD, Director of Neurophysiology and Neuropsychology Laboratory, Department of Psychology, Concordia University, Montreal, Canada
"Neurophysiological correlates of levels of consciousness and anesthesia"
7. Miloje M. Rakocevic, Department of Chemistry, University of Nis, Nis, Serbia, Yugoslavia
"Does universal consciousness exist?"
8. Dejan Rakovic, Faculty of Electrical Engineering, University of Belgrade, Belgrade, Serbia, Yugoslavia
"Neural networks, brainwaves and ionic structures; biophysical model for states of consciousness?"
9. Peter A. Raynolds, PhD, Gennie H. Raynolds, Management and Organizational Behavior, Northern Arizona Univeristy, Flagstaff, Arizona "The projective differential (PD) response phenomenon: New tool for consciousness research?"
10. Antti Revonsuo, Department of Philosophy and Center for Cognitive Neuroscience, University of Turku, Finland "Semantic processing without conscious understanding in global aphasia"

DOES UNIVERSAL CONSCIOUSNESS EXIST?<br>Emerging Logic of the Periodic System of Elements, Genetic Code and Human Consciousness<br>Miloje M.Rakocevic<br>Department of Chemistry, Faculty of Science<br>University of Nis, 2 Cirila i Metodija, 18000 Nis Serbia, Yugoslavia

There are many approaches to investigate consciousness. We propose one which use logic ( from ancient Greece logos, something what was at the beginning).

In the scientific work of D.I. Mendeleev, espeialy his original works, three important aspects of periodic law were examined, which in 20th century science have never been adequately understood. These are: (1) the system relations among elements, (2) spaciousness (three-dimensionality, and (3) cyclicity. In fact these aspects are of the great importance today when it is being demonstrated system entity, spatiality, periodicity and cyclicity are the most important characteristic of the genetic code.

This paper, in fact deals with very topic: the chemical code, built on the very principles mentioned and in complete accordance with the genetic code. Such a surprisingly simple model at the same time represents the Logical-Informational and Geometrical-HomeomorhicTopological (LIGHT) system of the cube-hypercube with an inscribed sphere-hyperspere.

This paper also shows that all the relations in the chemical code and the genetic code are in accordance with periodicity and cyclicity of the natural number system with the base $N_{1}=2^{\prime \prime} \quad(n=1, .6)$ and $\mathrm{N}_{2}=2(2 \mathrm{n}+1)$, where $\mathrm{n}=0,1 \ldots 5$. These mathematical number systems lead to Golden Mean, as one of the most important law in the Nature.
Human consciousness in some specific way express itself through the masterpieces like Goethe, Shakespeare, Tolstoy, Njegos have written. We fined that their masterpieces have been written ity same law as the chemical and the genetic codes possess, Golden Mean.

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## A. 4

# THE UNIVERSAL CONSCIOUSNESS ON THE UNIVERSAL CODE 

- An integrated approach 1996


# CONSCIOUSNESS 

Scientific Challenge of the 21st Century

# THE UNIVERSAL CONSCIOUSNESS ON THE UNIVERSAL CODE - An integrated approach - 

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#### Abstract

There are many approaches to investigate the consciousness. In this paper we will show that it makes sense to speak about the consciousness as about the comprehension of something. Furthermore, to speak about the universal consciousness as about the universal comprehension of the universal code; the comprehension from different investigators, in different creativeness, through different epochs. We propose one approach which utilizes the logic in the sense of logos (from the ancient Greek logos meaning coding, as a something that was at the beginning). For living beings their matter logos point of departure is the periodic system of elements because genetic code is its second hand side. In the scientific work of D. I. Mendeleev the important aspects of periodic law were examined, which the 20th century scientists have never adequately understood. Also, Darwin's diagram, in his book Origin of Species, represents a specific code, which is the first example of the code model and the code system in biological science. What is the point of departure of mind logos it is difficult to say, but on the consciousness level, after five thousand years in the development of the binary numbering system, the time has become ripe for a unification of the two different approaches in studying the universe and human beings: the global-integral method of the Ancient East, based primarily on speculation (logic of speculative mind), and the single-partial method of the Modern West, based primarily on experimentation (the logic of natural mind). Even more, today it is becoming evident that a scientific basis of human consciousness cannot be understood without such unification. Before such a unification can be done, one possible general hypothesis about the existence of a universal Mind/ Matter code should be tested and proven. This paper is subject of that kind of consideration.


Key words: logic, periodic system of elements, genetic code, microtubules, water, Yin-Yang code, consciousness

## 1. INTRODUCTION

There are many approaches to investigate the consciousness. First of all, the physiological and psychological approaches. But, more in accordance with Russell's [1], and Vygotsky's [2] and less with Ashby's [3] and Arbib's [4] views, our hypothesis (in establishing our approach) is that the investigation of the consciousness must always consider the consciousness as a whole system, as a unity of physiological (including biochemical and biophysical) and psychological-logical characteristics. If so, if physiological characteristics must be in relation with physiological, and these in relation with logical characteristics, then the consciousness itself must also be $a$ relation (Russell, p. 168: "... we are said to be 'conscious of' something; in this sense, 'consciousness' is a relation"; p. 170: "The ... relation to an 'object', it could be said, is characteristic of every kind of consciousness", p. 173: "Nevertheless we can distinguish 'mental' events from others ..."; Vygotsky, first chapter: "... consciousness is a unity of all functions"; Arbib, p. 1: "... all the functioning of the nervous system relevant to our study is mediated solely by passage of electrical impulses by cells we call neurons"; Ashby, p. 11: "... the book deals with only one of the properties of the brain, and with property - learning - that has long been recognized to have no necessary dependence on consciousness"; p. 12: " And until such a method ... the facts of consciousness cannot be used in scientific method").
Considering this concept, together with Russell's idea about consciousness as a relation to objects in sense to be 'consciousness of' something, with Sartre's idea [5] that any consciousness is the consciousness about something, with Petronijevic's idea [6] that the contents of the consciousness are the notions, and finally, with Einstein's idea [7] that all notions within 'natural laws' are from the space-time nature, we will show that it makes sense to speak about the consciousness as about the comprehension of something (to comprehend - to be in relation to something within the consciousness of someone!). By this if we can speak about a universal
concept of the organization of a whole from the parts, then it makes sense to speak about a universal consciousness of such an organization. On the other hand, if within such an organization must exist a universal code, then it makes sense to speak about the universal comprehension of the universal code.

Further, based on the said, it makes sense to investigation how human consciousness, in form of a comprehension, has been expressed itself through different epochs: in some specific ways, or in one and the same universal way? In this paper we will show that that was the case: in the various works, by different creative investigators, within very different epochs, an exactly universal code has been expressed. On the other words, we will show that human consciousness was always in relation with a universal code through a specific manner.

## 2. PRELIMINARIES

More than any other scientists, Crick and Einstein are responsible for our link between the molecular basis of life and consciousness. Crick made first and important step, with arguments that consciousness is a property of molecular activities in neurons and networks of neurons in our brain [8], while a serious analysis of complete works of Einstein lead to the conclusion that when he speaks about the four-dimensional continuum of space-time, he means in fact three-four-dimensionality. This opens a possibility to speak about coding coordinates and coding spaces; by doing this, each Boole's space characterized by three-quaternity must be taken as Boole-Einstein's space. In fact Coding Space (CS) unavoidably should to be Coding SpaceTime (CST), what is subject of the information physics as a new scientific discipline of space-time structures $[9,10]$.

Remark 2.1. All the three elementary types of symmetries (1. in relation to the point, i.e. center, 2. in relation to the line or axis and 3. in relation to the plane) can be represented by the binary symmetry of the segment line, i.e. by the symmetry of the entities $A \leftrightarrow A^{\prime}$ (or $A \leftrightarrow B$ ) in relation to the central entity $C$ - the center of symmetry (whether or not it exists, represented only by
a point), where $A C=C A^{\prime}=n$ and $A A^{\prime}=2 n$. If so, then: the entity $C$ contains (in itself) the quantity $c(c=n)$, which represents the arithmetical mean for $A C$ and $C A$ '. This is the essence of binary symmetry as the "symmetry in the simplest case" (Marcus, 1989, p 103: "In its simplest form, in a onedimensional Euclidean space, symmetry is defined with respect to one point. Given two points $A$ and $B$ in this space, the symmetric point $C$ of $A$ with respect to $B$ is one such that the distance from $C$ to $B$ is equal to the distance from $A$ to $B$, whereas the distance from $C$ to $A$ is the sum of these two distances"; Notice that our $B$ or $A^{\prime}$ 'is Marcus' $C$ and vice versa). This simplicity is the reason why we can consider the binary symmetry as the best possible symmetry. There is also the entity $M$ which contains (in itself) the quantity m , where $m=4 / 3 n$, which represents the harmonic mean for $A C$ and $A A^{\prime}$ (the essence of binary harmony!); $A A^{\prime}$ can be, in infinitely numerous ways, divided into two unequal parts; $A A^{\prime}$ can, in a finite number of ways, be divided into two parts which are proportional to each other (the essence of binary proportionality!) ...There is exactly one of pair of parts $(a, b)$ which represent the golden section along the segment line $A A^{\prime}$ ' (the essence of infinite division and the best possible proportion!).

Remark 2.2. The binary symmetry $A \leftrightarrow A^{\prime}$ (or $A \leftrightarrow B$ ) in this paper is still understood, except by S. Marcus, in the sense used by P. Hilton and J. Pederson (1989, pp 73-74) so that the given entity from the pair $A, A^{\prime}($ or $A, B)$ "may admit several different combinatorial structures and each structure will be regarded as combinatorial distinct. You should thus be warned that [entities] which we regard as the same (i.e. combinatorial equivalent), you may hitherto have regarded as different; and [entities] which we regard as different (i.e. combinatorial distinct), you may hitherto have regarded as the same." For a better understanding of this we present a possible correspondence between their visual representations and our Figure 3 in this paper. The entity of their "cube" corresponds to the pyrimidine entity (in 32 combinations, or to be more correct, variations) on the left branch of the binary tree in our Fig. 3. On the other hand, their "prism" corresponds to our purine entity on the right side (also in 32 variations) in Figure 3. The entity on the left side of any one of the $4+4$ classes of codons on the binary tree, in our Figure 3, corresponds to their left entity in their visual representation; a simpler cube model corresponds to our simpler pyrimidine ( U ) and/or simpler purine (A) entity; their right entity - a more complex cube model - corresponds to our more complex pyrimidine (C) and/or more complex purine (G) entity on the right side in Figure 3 (cf. analogous "cubes" and "prisms" in Fig. 3.5 in Dubinin, 1985, p 81).

Remark 2.3. Since the genetic code can be reduced to the Gray code model (Fig. 1 in Swanson, 1984,p 188) and to a binary tree (Fig. 1 in [14b] and Fig. 3 in this paper), with a starting codon UUU 000000 and a final codon GGG 111111, it follows that as to questions of symmetry in relation to the genetic code the mathematical group theory holds only partially (our hypothesis and a prediction of this remains for future researches). This results from the fact that the set Q of rational numbers, including zero, does not form a group with respect to a multiplication operation. The above mentioned is the reason why we won't use the mathematical group theory to research the symmetries of the genetic code in this paper.

The basic parameters which determine physico-chemical characteristics of $a$ system of stable chemical elements are: atomic number, number of period, number of the group and number of isotopes. Mendeleev never used word Table, what we usually do, to present his work, but System. His original System of elements is different from our today's Table of elements. Science of 20th century escapes Mendeleev "mysterious" form of his system of elements, saying that Mendeleev made some arithmetical errors (ref. [11], p. 185). Mendeleev's "errors", or our inadequate understanding of his work, is the information (coding system $3^{4}=81$ and $4^{3}=64$ ) approach to elements. Information approach as coding approach. The coding system $3^{4}=81-$ because within first 84 chemical elements (from $\mathrm{H}=1$ to the $\mathrm{Po}=84$ ) there are exactly 81 stable elements. The coding system $4^{3}=64$ - because 84 minus 20 "mono-isotope" elements equals 64 (cf. ref. [12], ch. 27, sect. "Relations odd-even", where Gould says that all even elements to the polonium, $\mathrm{Po}=84$, have minimally two stable isotopes, except beryllium (cf. ref. [13], where it has been said that within chemical code there are exactly 84 elements; cf. also 64 hexagrams in Fig. 5 and 81 tetragrams in Fig. 6). Mendeleev clearly and precisely gave the system of chemical elements as a four-dimensional Boolean hypercube [14a]. The same approach, based on Boolean hypercube, has been used recently by Kauffman to explain the origins of order as point of departure of self-organization and selection in evolution [15].


Figure 1. The universal consciousness on the universal code of the nature: the Mendeleev's system of chemical elements oddityevenness principle; the valence trinity-quaternity system; the atomic mass distances integer system.

In the scientific work of D.I. Mendeleev, especially his original manuscript works (see ref. [11], pp. 128-129), three important aspects of periodic law were examined, which have never been adequately understood by $20^{\text {th }}$ century science. These are: (1) the system relations among elements including odd-even principle, (2) spaciousness ie. three-dimensionality (Figs. 1-2), and (3) cyclicity (photocopy XII in Kedrov: $\mathrm{Cu}, \mathrm{Ag}, \mathrm{Au}$ within first and after that within eighth group at the end, parenthetically). From these facts it follows that the third dimension of the periodic system as a "New dimension for Mendeleev" [16] is not necessary because Mendeleev was conscious of dimension 100 years ago. Also, Mendeleev was conscious of the problem of "rare earth", although there are different opinions (ref. [16], p. 13: "The two versions differ simply in their arrangements to accommodate elements such as the rare earths, but the result must be to
leave many with the impression that Mendeleev had not made up his mind about something of importance"). In his long periods Table (ref. [11], p. 188) Mendeleev gave a specific position to the first element of "rare earth", i.e. lantanides (Ce) - not in the third but in fourth group; then still 13 groups for 13 lantanides. If so, Mendeleev must have been seen conscious that the short periods Table with 8 groups of elements corresponds with cube, and long periods Table with a hypercube ( 8 group of non-rare earth elements plus 14 group of yes-rare earth elements with a superposition equal 14 groups; then: 14 groups plus the first group at the end, and plus the zeroth group equal 16 groups). On the other hand, Mendeleev was conscious of the fact that there must be 4 types of elements with correspondence to the square (for details see ref. [14a], pp. 197-200). Bearing in mind all these Mendeleev's insights, it was possible to determine the definitive real positions of elements within 3-4 dimensional periodic system (ref. [13], pp. 19-22). Other creative investigators, primarily Darwin and Mendel [14a] were conscious of square-cube-hypercube relations within natural systems.

Darwin's diagram, binary tree, represents the first systematic information approach to the analysis of the relations between organisms [17]. This is the only diagram in his book Origin of Species and it represents a model of interpretations of the origin of varieties, species, genera and higher systematic categories. By its essence, his diagram represents a specific codemodel and code-system as the first example in biological science. Relations of the noted elements within this code system correspond to the relations of the organisms in the natural systems. Hidden message of this diagram now is clear: if the natural systems are at the same time the coding systems, the only adequate and complete way of description and interpretation of such systems would be the creation of adequate code models with adequately corresponding relations between the elements of the one and the other model.


Figure 2. The universal consciousness on the universal code of the nature: the Mendeleev's three-dimensional periodic system as unity of cube-sphere; cube: through the three coordinates; sphere: the noble elements are at all three coordinates.

The main idea which is in the basis of the diagram - binary tree, is the realization of the logic of systematization and classification, separation of the parts within the whole, as well as the regularity of the hierarchy of the levels. The accordance of this logic with the model of classification of the number systems with the number basis $N_{2}=2(2 n+1)$, where $n=0,1,2,3$, is directly obvious. So, we have for $n=0, N=2$, which corresponds to the division of the binary tree to the left tree and the right tree. This is exactly what Darwin discussed on the relations during the evolution only along two lines at the beginning of which "species (A)" and "species (I)" occur: " These two species (A) and (I), were also supposed to be very common and
widely diffused species, so that they must originally have had some advantages over most of the other species of the genus". The obvious characteristic of the Darwin's diagram of the binary tree is that each transition to the next level completely follows the logic of the Gray code, since only a unit change is allowed [14a].

## 3. LOGIC OF THE EXISTENCE OF LIFE MOLECULES

The problem of accordance-discordance of the genetic code $\left(4^{3}=64\right)$ and its physico-chemical basis was firstly stated by Crick who demonstrated that this problem is impossible to separate from the questions related to the ratio of probabilistic and deterministic in the coding process: the fact that codons $X_{1}, X_{2}, X_{3} \ldots$ are coding for amino acid $Y$ results from numerous accidental processes during the evolution, or here strict (deterministic) reasons could be also included $[18,19]$.

The very approach to the three-four-dimensional system of both the chemical code (Mendeleev) and the genetic code should be integral one: it has to be emerging logic approach. We have shown [14a] that atomic mass and number of isotopes represent the principal determinants of the chemical code $\left(3^{4}=81\right)$, while binary values of codons and amino acids represent the principal determinants of the genetic code $\left(2^{6}=64\right)$. (Figs. 3-4).

### 3.1.The Number of Trinity-Quaternity

The basic concept from which we start is the Boolean logical square. This hidden square exists within the Gray code model of genetic code [20,21]. The Gray code model of the genetic code can be per se developed in two types of the binary tree: (1) the binary tree which keeps the logic of the Gray code having characteristic that "two adjacent symbols differ at only one bit" [20], and (2) the binary tree with the logic of natural numbers series "for the numbers 0-63" [21]. With the first type of binary tree, the distances between codons are the unit Hamming distances if "measured" by weight,
i.e. by norm of Boolean vector, while with the second type of binary tree the distances are also the unit ones if "measured" via the vector number.


Figure 3. The universal consciousness on the universal code of the nature: the genetic code binary tree is in full accordance with the yin-yang binary tree in the oldest book - I Ching. The relations between 64 codons and 64 hexagrams: to each zero corresponds a broken line; to each one corresponds an unbroken line (see ref. [14a], p. 274). This binary tree of the genetic code with the order of the eight families of codons (rosettes), which corresponds to the series of natural numbers ( $0-7$ ). The four 16 -codon families begin with broken lines for + Yin and/or +Yang states; full lines for -Yin and/or -Yang states, reflecting the greater or lesser influence of bases of the Py and/or Pu type.

According to the logic of the Boole's square, longitudinal diagonal of the Boole's cube has to be labeled by the following sequence of corners: 1076. The end-corner, 1776, in the diagonal is optimal only in the system of trinity-quaternity $(T Q): 1076+700=1776$ (trinity because it is cube; quaternity because there are four positions; optimal because the corner 7 of the three-digit-record does not change position during "transition" to four-
digit-record). $T Q$ system should be understood as the unity of BooleEinstein's cube-hypercube: there are two sevens at the longitudinal diagonal as a result of permanent coping 0-7 and 7-0 (within the frame of the cube) and/or as a result of permanent motion from starting to middle point and backwards, i.e. from end-point to middle point and backwards (within the frame of the hypercube). Sevens from longitudinal diagonal are intercrossed by two sevens of the middle diagonal (within the frame of hypercube) which appear as a result of permanent coping 7-8 and 8-7. Therefore, at each moment of time, there is a system 0777-7777 in Boole-Einstein's coding space, and/or 1776-17776, if we take into account cyclicity of the system.


Figure 4. The universal consciousness on the universal code of nature: The Logical-Informational and Geometrical-HomeomorphTopological (LIGHT) system of the Boolean cube-hypercube with an inscribed sphere-hypersphere, as the model of the genetic code, in full accordance with Mendeleev's cube-sphere model (Fig. 2) of the chemical code (for details see ref. [14a], p. 54).

### 3.2. The Genetic Code as TQ System

Analysis of the Crick's papers published immediately after 1966, upon definitive establishment of the Table of codons, demonstrates his sagacious observation of the problems imposed by Table itself, in spite of its beauty and symmetry. Determination of the number of problems and their denomination are ours, while the original statements are those of Crick.
(1) Problem of the alphabets (problem of coding): Four-letter language of the nucleic acids has been studied in the meantime and we know how it controls 20-letter language (amino acids) of the proteins. However, in spite of the fact that numerous problems remained unsolved, this knowledge is certain;
(2) Problem of the neighborhood (both codons and amino acids): Neighbor amino acids are coded for by neighbor codons;
(3) Problem of similarity of codons: It is sure that triplets coding for the same amino acid are most often very similar;
(4) Problem of the position of base I, II, III in triplet: In any case triplets with U and C at the end of the codon are coding for the same amino acid, and this is also very often the case with the triplets containing A and G as the end base;
(5) Problem of selectivity of base I, II, III within a codon: Amino acid is chosen mainly by the first two bases in a triplet;
(6) Problem of a sign: Is the allotment of a triplet to amino acids at random, or there are structural reason for this?
(7) Problem of the meaning: What is the sense of the synonymy through the third base, and what is the sense of the exceptions?
(8) Problem of the form: Form of the genetic code is established with a considerable certainty;
(9) Problem of the essence (what is the "corner stone"): Genetic code is an important corner stone at the long path of molecular biology and biological life;
(10) Problem of the origin and evolution of the genetic code: When we answer all these questions, the question of the origin of the genetic code will
remain as the major problem. Is the genetic code the result of a series of evolutional coincidences? The origin of the genetic code will remain as the major problem.

Two amino acids; serine and arginine have been the main problem not only for Crick, but also for all other researchers undertaking serious studies on the essence of the genetic code. The codons coding for these two amino acids for each of them are very different and even separated in the table. This is then the reason Crick could not claim with certainty that similar codons code for similar amino acids (this should be expected on the basis of chemistry) or that neighbor codons code for the same amino acid. So, Crick could only say that they are "the most often very similar". Position of the third base within a triplet makes new problems. Coding process is not affected when pyrimidine bases ( U and C ) appear in the third position, i.e. the same amino acid is coded (synonymy). If we use information-topological model of the genetic code it is practically possible to solve all ten Crick's problems of genetic code: four-letter language is at the same time the language and the chemical essence; similar codons indeed code for similar amino acid and again without an exception; neighbor codons code for the same amino acid and again without an exception. In our information geometry approach [14a] genetic code is completely characterized by entity of $T Q$ system. Two pyrimidine ( $P y$ ) and two purine ( $P u$ ) bases are inevitably expressed in the coding space as the system $3+1$ (three with oxo-group and one without it, or three with amino group and one without it$)$. Therefore the number of codons in the table of the genetic code by positions in four groups should read from an aspect of the main coding position. In spite of this distinction $3+1$ only on the basis of numbers presented in this manner it is impossible to understand possible physico-chemical meaning of $T Q$ system in the genetic code without an analysis of the internal structure. Each position consisting of 16 units can be taken as position with the structure $8: 8$ what makes sense from a physico-chemical aspect, since 16 families of codons $(1 \cdot 16) \cdot 4=64$ could be understood also as a system of $(2 \cdot 8) \cdot 4=64$ codons. In one family of higher order (eight-membered one) there can be 8 codons with Py base in the first position, and/or 8 codons with $P u$ base in
the first position. However, there is a question whether classifications such as $(8-1):(8+1),(8-2):(8+2)$, or some others make sense? We will put forward the hypothesis that the classification (8-1): $(8+1)$, so $7: 9$ makes sense also from an aspect of strictly determined physico-chemical parameters such as hydropathy $(\mathrm{H})$ or polarity ( P ), as well as from an aspect of the principal parameter of the binary value. (For details see ref. [14a], pp. 253 and 255260). It was proposed the existence of binary values for the entities of two pyrimidine and two purine bases: $U(00), C(01), G(10), A(11)$ [22]. Swanson made the same assumption, but with a significant difference: $U(00), C(01)$, $A(10), G(11)[20]$. She showed that the binary record of a codon must begin with the second (middle) and not the first base, as was proposed by Schonberger. When we used our $T Q$ coding system we satisfied all Crick's genetic code problems and find similarity with quantization the magnetic quantum number ( $-3,-2,-1,0,+1,+2,+3$ ). This indicate the basic biomolecular information processing associate with quantum field trough coding. Our results of genetic code are summarized in ref. [14a]. We can say that genetic code is preamble of biological consciousness which arise in proteins-water interaction and through activities of cell (molecular networks), body network, neural networks and brain, that lead human beings to be conscious ([8], 10]).

### 3.3. The Microtubules Coding System

Microtubules coding system was identified by Koruga [23]. There is microtubule coding system of two codes; $K_{1}\left[13,2^{6}, 5\right]$ and $K_{2}\left[24,3^{4}, 13\right]$. First code, $K_{1}$, is result of tubulin subunits, packing in proto-filaments by screw symmetry. This code has 64 codewords, length 13 and distance 5 (the best known binary error-correcting code).


Figure 5. A speculative system of ancient China, based on hexagonal arrangement: It consists of 64 hexagrams $\left(2^{6}=64\right)$, which display every possible combination of archetypal human situations - along with thousands of variations caused by changing lines. Notice that an inverse countdown is possible. In such a case the 63 rd number is zeroth.

The second code, K2, is result of interaction of 24 tubulin subunits and high molecular weight MAP (microtubule-associated proteins). This code has 81 code-words, length 24 and distance 13 (the best efficient code for information transmission) (cf. these 64 and 81 code-words with analogous "code-words" within chemical code, mentioned in Preliminaries).

### 3.4. The Biological Water "Mystery"

The essential role of water has been recognized in all studies of biological processes, but it is a paradox that we know very little about order and properties of "biological water". Water seems to be the fastest solvent, because simulations predict and experiments verified femtosecond dynamics of water [24a]. It is well known that water molecules may be organized in different ways but one of the most promising is the clusters organization.

Water clusters may exist with 10 to 1000 water molecules. An approach of water cluster cellular automata (WCCA) may be the right way to solve the problem of its "mysterious" role in biological information processes.


Figure 6. A speculative system of ancient China, based on tetragrams arrangement: A tetragram is constructed from four stacked lines of three types (solid, broken, and twice-broken). There are 81 possible combinations of these three types of lines ( $3^{4}=81$ ). It is no accident that ancient Chinese book Tao Te Ching has eighty-one chapters, what is also a significant number to those Chinese philosophers who treasured the symmetry of numbers. Notice that an inverse countdown is possible. In such a case the 81 st number is zeroth. If so, then $3 \cdot 4$ and $3^{4}$ are the numbers of lines and tetragrams, respectively.

However, how much "Water mystery" is only an extraordinary otherness and specificity of the water, it has been shown in Ref. [24b]. Among other things, it is quoted the work of Russian biologist Afanasii Semenovich Troshin, from 1957, in which he set forth the hypothesis that the plain water and the water of cytoplasm within the cells differ. This corresponds with our hypothesis that the chemistry of life is more than the chemistry in the laboratory. ${ }^{1}$

## 4. LOGIC OF SPECULATIVE MIND

The logic of natural mind is primary result of human brain adaptation through its interaction with environment (Nature), while the logic of human speculative mind is primary result of human field based mind interaction with Mind Itself. The best example of speculative mind related to natural mind is Chinese concept of Yin-Yang, while Chinese concept of Dao may be related to Mind Itself. Schonberger was the first to point the possibility of making the I Ching and the genetic code conform to the same model by using binary records [22].

[^71]






$A C I D{ }_{0}^{x} \times B A S E / A C I O$



Pu

Figure 7. The universal consciousness on the universal code of Nature: the Boolean logical square of the genetic code is in full accordance with the Aristotelian (Boolean) logical square of four entities (cf. Fig. 8) (For details see ref. [14a], p. 8).

### 4.1. The Dao and Mind Itself

From a scientific point of view we do not know yet what Mind Itself is, but if we identified Mind Itself with Dao we can learn that

The Dao that can be expressed
Is not the Dao of Absolute.
The name that can be named Is not the name of the Absolute.

The Dao is empty and yet useful;
Somehow it never fills up.
So profound!
It resembles the source of All Things.

### 4.2. Yin-Yang and Natural Mind

We shall demonstrate the underlying meaning of the link, coherence and interdependence of the natural code (natural mind) and the I Ching code (speculative mind). We shall show that there is a complete and perfect correspondence between the Yin-Yang entities in the I Ching code $\left(2^{6}=64\right)$ and the pyrimidine-purine entities in the genetic code. Our starting point has been Stent's discovering that Yang (the male or light principle) is identified with the purine bases and Yin (the female or dark principle) with pyrimidine bases [25]. It was known in the ancient China that the Yin-Yang entities may be extended, so there can be +Yin (Great Yin) and -Yin (Lesser Yin) or +Yang (Great Yang) and -Yang (Lesser Yang), what lead us to new conclusions, which can be summed up in Figs. 3-8 and the following points:
(1) Boole's logical square lies at the heart of the I Ching as well as of all natural codes. The logical square of the four entities of the I Ching should be turned $180^{\circ}$ to make it correspond to the logic square of the four elements known to Aristotle: Air and Fire associated with Yang, and Earth and Water with Yin (Fig. 8).
(2) There is complete congruence and correspondence between the sixbit binary records for the 64 codons and the binary records for the 64 hexagrams in the I Ching (Fig. 5).


Figure 8. The universal consciousness on the universal code of Nature: the Alchemists' (Boolean) logical square follows from Aristotelian square; both are in accordance with the yin-yang system and with the genetic code logical square (cf. Fig. 7); further, they are in accordance with the fundamental particles square: neutrino ( 00 ), electron ( 01 ), quark down (10), quark up (11). For the (Boolean) logical square regarding the fundamental particles see ref. [14a], p. 283.
(3) The binary tree of the I Ching should be turned $180^{\circ}$ for it to fit exactly over the binary tree of the genetic code; then both binary trees correspond to Farey's binary tree, which determines the quasiperiodical transition to deterministic chaos (cf. ref. [14a], p. 280).
(4) The eight trigrams in the I Ching are analogous to the eight rosettes, i.e. eight families of codons on the binary tree of the genetic code (Fig. 3). However, the system: +Yang, -Yang, +Yin, -Yin may be presented as $3^{4}=81$ (Fig. 6). This indicates that Yin-Yang coding system is the same as microtubules coding system.

## 5. FINAL COMMENTS

In fact the three quoted aspects of periodic law are of great importance today, when it has been demonstrated that the system entity, spatiality, periodicity and cyclicity are the most important characteristics of the genetic code (Figs. 3-4). From these figures it is clear why it is sensible to speak about the chemical code in connection with the genetic code. There are certain aspects of correspondence and coherence of the two codes: (1) within the genetic code there are exactly 61 amino acid (stable aggregation) meaning codon situations, plus 3 breaks in amino acid meaning ( 3 "stop" codons), plus 20 non-codon situations ( 20 protein amino acids); (2) within the chemical code there are exactly 61 situations (in the form of stable aggregations) which have multiisotope meaning, plus 3 breaks in stable isotope ( 3 "stop" situations: Tc, Pm, Po), plus 20 non-(stable) isotope situations ( 20 "mono isotope" elements). Thus altogether there are 84 entities within both the genetic, and chemical codes. This, is the very topic: the chemical code, built on the very principles mentioned and in complete accordance with the genetic code. Such a surprisingly simple model at the same time represents the Logical-Informational and Geometrical-Homeomorphous-Topological (LIGHT) system of the Boolean cubehypercube with an inscribed sphere-hypersphere (Fig. 4). The 8 vertices of the cube in Fig. 4 correspond with the 8 rosettes on the binary tree in Fig. 3 ( 8 families of codons); the 16 vertices of imagined hypercube correspond with 16 families of codons on the binary tree.

| d | c | b | a | e | f |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  | - | 1 |
| 1 | 0 | 1 | 00001 |  |  |
| 1 | 0 | 1 | 00002 | 2 | 9 |
| 1 | 1 | 0 | 00004 | 1 | 1 |
| 1 | 0 | 1 | 00008 |  |  |
| 1 | 0 |  | 00016 | 2 | 12 |
| 1 | 1 | 0 | 00032 |  |  |
| 1 | 1 | 0 | 00064 |  |  |
| 1 | 0 | 1 | 00128 | 1 | M |
| 1 | 1 | 0 | 00256 |  |  |
| 0 | 1 | 0 | 00512 |  |  |
| 1 | 0 | 1 | 01024 |  |  |
| 1 | 0 | 1 | 02048 | 2 | 12 |
| 0 | 1 | 0 | 04096 | 1 | 1 |
| 0 | 0 | 1 | 08192 |  |  |
|  |  | 1 | 16384 | 2 | 9 |
|  |  |  |  | - | 1 |

Figure 9. The universal consciousness on the universal code of Nature: the Homer's and Njegoš's (Boolean) space sequence, $\mathrm{N}=2^{\mathrm{n}}$. (a) The binary sequence whose sum is $2^{15}-1=32767$; (b) Homer's choice: $27803_{10}=66233_{8}=$ $110110010011011_{2}$ (the number of verses for Iliad plus Odyssey); (c) Njegoš's choice: $4964_{10}=11544_{8}=001001101100100_{2}$ (The Mountain Wreath: printed version 2819 verses plus 318 person-scenes, plus 116 pages for printing $=$ 3253; manuscript version 1528 verses plus 150 person-scenes plus 033 pages $=$ 1711; all together - the total spaces of The Wreath: $3253+1711=4964$ ); Homer's plus Njegoš's system: $66233_{8}+11544_{8}=77777_{8}$; (d) Homer's choice: $3583_{10}=6777_{8}=000110111111111_{2}$. The number 3583 represents the
difference of Iliad and Odyssey: 15693-12110 = 3583. The relation between two numbers $77777_{8}$ and $6777_{8}$ was given through a logic program: to exclude first position, and then - to write the result $\left(7777_{8}\right)$; after that: to exclude first unit in the first position, and, then to write the result $\left(6777_{8}\right)$. The choice logic for the number $3583_{10}=6777_{8}$ is as follows. From the total sequence $\left(2^{15}-1\right)$ to exclude all the situations that contain the whole third perfect number 496; (e) The number of Homer's yes-choice and non-choice situations; (f) The (in literary science) known composition sequence of Iliad: from the middle point Mission to Achilles) 1 day full, 9 empty of events etc.

The basic (main) relations, determinants and invariants within the binary tree, i.e. within the system of cube-hypercube are the relations of a Boolean logical square. There are 4 types of molecules within the genetic code: Uracil $(\mathrm{U}=00)$ with number 0 of Boolean vector, Cytosine $(\mathrm{C}=01)$ with number 1 , Adenine $(A=10)$ with number 2 and guanine $(G=11)$ with number 3 of Boolean vector (Fig. 7). Also, there are 4 types of chemical elements: $s(00), p(01), d(10)$ and $f(11)$ in relations of the Boolean logical square; plus 4 types of fundamental particles: neutrino (00), electron (01), quark down (10) and quark up (11). Fig. 8 illustrates the consciousness about logical square relations within the Universe of Aristotle and Alchemists. The periodicity and cyclicity within the genetic, as well as within the chemical code, are in accordance with periodicity and cyclicity of the natural number systems with the base $N_{1}=2^{n}(n=1, \ldots, 6)$ and $N_{2}=2(2 n+1)=4 n+2(n$ $=0, \ldots, 5)$. The relations within these mathematical number systems lead to the Golden Mean, as one of the most important Laws in Nature (for details, see ref. [14a]). It could be said that these number systems are the natural number systems. And then a new surprise: human consciousness in some specific way expresses itself through masterpieces such as those written by Goethe, Shakespeare, Tolstoy, Njegoš. We find their compositions were written according to the same Law as possessed by the chemical and genetic codes - the Golden Mean. Fig. 9 shows how Homer and Njegoš generated their works from the binary sequence $N_{1}=2^{n}$.

From this discussion it follows: it makes sense to give some separate hypotheses for further investigation. For example: (1) Human consciousness as a specific brain-computer code must be determined by Boolean spaces; (2) Human consciousness in the form of human language must be determined by Boolean logical square (Fig. 10); (3) Human consciousness as logical reason (syllogism etc.) must also be determined by Boolean logical square (Fig. 11).

FRINCIPES DE FIHONOLOGIE
On obtient ainsi le schéma des variations possibles :

|  | 1 | 11 | III | IV |
| :---: | :---: | :---: | :---: | :---: |
| $a$ $b$ $c$ $d$ | Expiration Art. bucc. | Expiration Art. bucc. | Explation Art. bucc. I] | Explration Art. bucc. |

La colonne I désigne les sons sourds. Il les sons sonores, III les sons sourds nasalisés, IV les sons sonores nasalisés.
Mais une inconnue subsiste : la nature de l'articulation buccale ; il importe donc d'en déterminer les variétés possibles.

Figure 10. The universal consciousness on the universal code of Nature: De Saussure's sound system of natural language can be seen as a specific Boolean logical square: $\mathrm{I}(00), \mathrm{III}(01), \mathrm{II}(10)$, IV (11) ... (cf. De Saussure's natural language designation system ref. [26], p. 70 and R. Swanson's genetic code designation system ref. [14a], p. 10).

## 6. CONCLUSIONS

The periodicity and cyclicity within the periodic system of elements, genetic code, microtubule code and Yin-Yang system, are in accordance with periodicity and cyclicity of the natural number systems with the base $N_{1}=2^{n}$ $(n=1, \ldots, 6)$ and $N_{2}=2(2 n+1)(n=0, \ldots, 5)$. The relation within these mathematical number systems is the Golden Mean.

To understand the biophysical mechanism of information processes the main investigation should be done in both fields water coding system(s) and water-biomolecules interaction. There is a strong indication that water code(s) should be given by natural systems, $N_{1}$ and/or $N_{2}$.

Our main hypothesis in establishing our approach is that investigation of consciousness must always consider the whole system as a unity of mind/matter. We have shown that speculative mind (Yin-Yang) and matter (periodic system of elements and genetic code) have the same coding system. The link between Mind (as quantum field entity of empty space pure vacuum) and Matter (as mass organized entities) are microtubules and their interaction with water.


Figure 11.The universal consciousness on the universal code of Nature: Aristotle's syllogism "square of opposition" can be seen as specific Boolean logical square: No S is $\mathrm{P}(00)$, Some S is not P (01), Some S is $\mathrm{P}(10)$, All S is $\mathrm{P}(11) \ldots$ (cf. ref. [27], p. 341).

We believe, based on our knowledge, that human consciousness as mind/matter unity arises from this interaction. Considering this concept,
together with Russel's idea about consciousness as a relation to an object in the sense of being conscious of something, we believe that human consciousness in some specific ways has expressed human being itself in the various works by different creative investigators through different epochs.This universal code as the basis of separate natural codes (chemical, genetic codes etc.) must be determined by Boolean spaces. Thus follows the hypothesis that human consciousness must also be determined by Boolean logical spaces.

This Boolean logical spaces concept of the universal consciousness must be provided by further investigation from different aspects. For example, from the aspect of an existing or not existing accordance with the quantum physics concept [28] and information physics [9].

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## A. 5

THE UNIVERSAL CONSCIOUSNESS AS A UNIVERSAL COMPREHENSION OF THE UNIVERSAL CODE

# THE UNIVERSAL CONSCIOUSNESS AS A UNIVERSAL COMPREHENSION OF THE UNIVERSAL CODE 

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#### Abstract

There are many approaches to investigate the consciousness. In this paper we will show that it makes sense to speak about the consciousness as about the comprehension of something. Furthermore, to speak about the universal consciousness as about the universal comprehension of the universal code; the comprehension from different investigators, in different creativeness, through different epochs.


Key words: universal consciousness, universal comprehension, universal code, logic, periodic system of chemical elements, genetic code, microtubules code, yin-yang code.

## 1 Introduction

There are many approaches to investigate the consciousness. First of all, there are the physiological and psychological approaches. But, other approaches are also possible ... More in accordance with Russell's [1], and Vygotskii's [2] and less with Ashby's [3] and Arbib's [4] views, our hypothesis (in establishing our approach) is that the investigation of the consciousness must always consider the consciousness as a whole system, as a unity of physiological (including biochemical and biophysical) and psychological-logical characteristics. If so, if physiological characteristics must be in a relation to psychological, and these in a relation to logical characteristics, then the consciousness itself must also be a relation to objects (Russell, p. 168: "... we are said to be 'conscious of something'; in this sense, 'consciousness' is a relation"; p. 170: "The ... relation to an 'object', it could be said, is characteristic of every kind of consciousness"; p. 173: "Nevertheless we can distinguish 'mental' events from others..."; Vygotskii, first chapter: "... consciousness is a unity of all functions"; Arbib, p. 1: "... all the functioning of the nervous system relevant to our study is mediated solely by passage of electrical impulses by cells we call neurons"; Ashby, p. 11: "... the book deals with only one of the properties of the brain, and with property - learning - that has long been recognized to have no necessary dependence on consciousness"; p. 12: " And until such a method [exists] ... the facts of consciousness cannot be used in scientific method").

Considering our concept, together with Russell's idea about consciousness as a relation to objects in sense to be 'consciousness of' something', with Sartre's
idea [5] that any consciousness is the consciousness about something, with Petronijević's idea [6] that the contents of the consciousness are the notions, and finally, with Einstein's idea [7] that all notions within 'natural laws' are from the space-time nature, we will show that it makes sense to speak about the consciousness as about the comprehension of something (to comprehend - to be in relation to something within the consciousness of someone!). By this, if we can speak about a universal concept of the organization of a whole from the parts, then it makes sense to speak about a universal comprehension of such an organization. On the other hand, if within such an organization a universal code must exist, then it makes sense to speak about the universal comprehension of the universal code.

In the light of the said, it makes sense to investigat how human consciousness, in form of a comprehension, has been expressed itself through different epochs: in some specific ways, or in one and the same - universal way? In this paper we will show that that was the case: in various works, by different creative investigators, within very different epochs, an exactly universal code has been expressed, in one and the same - universal way. In other words, we will show that human consciousness was always in relation to a universal code through a specific manner.

## 2 Universal Comprehension of the Universal Code

What is the universal code? That is any system organized as a whole, consisting of parts; the system organized through the unity of the best possible symmetry, best possible harmony and best possible proportion; the unity based on the Logos (Logos itself is more than law, principle and scenario, altogether). Because the objects within the reality are organized through three dimensions (coordinates), and because orthogonality principle is valid for reality, the universal model of the universal code must be that, which is presented in Fig. 1, and which must be based on the model (logical square) presented in Fig. 2. On the other hand, it must be so that there exist the best examples of the realization of the universal code, as we will show in further text.

First of all, the best possible example is the genetic code, represented by the model, presented in Fig. 3, in correspondence with the models, presented in Figs. 46 , the best possible (best plus best!) is also the chemical code, represented by models, presented in Figs. 7-10; then can follow: the human masterpiecescode, represented by models, presented in Figs. 12, 13; the human language-code, represented by models, presented in Figs. 14, 15; and the human logic-syllogism-code, represented by model, presented in Fig. 16, etc.


Figure 1 The LIGHT (Logical-Information-Geometric-Homeomorphic-Topological) model of the genetic code. It is in full accordance with Mendeleev's cube-sphere model (Fig. 7) of the chemical code (for details see ref. [10], p.54).


Figure 2 The Alchemists' (as a Boolean) logical square. It follows from the Aristotleian square; both are in accordance with the yin-yang system and with the genetic code logical square (cf. Fig. 4). Further, they are in accordance with the fundamental particles square: neutrino (00), electron (01), quark down (10), quark up (11). For the (Boolean) logical square regarding the fundamental particles see ref. [10], p. 283 .

Remark 1. All the three elementary types of symmetries can be represented by the binary symmetry of the segment line
(n) (or $\mathrm{A} \leftrightarrow \mathrm{B}$ ) with the middle point $M$, where $\mathrm{AM}=\mathrm{MB}$. The point $M$ contains (in itself) the quantity $m=1 / 2 n$ which represents the arithmetic mean of $A M$ and $M B$. This is the essence of binary symmetry as the "symmetry in the simplest case" $[8,9]$. Its simplicity is the reason why we can consider binary symmetry as the best possible symmetry. On the segment line $n$ or $\mathrm{A} \leftrightarrow \mathrm{B}$ there is also the point $H$ which contains (in itself) the quantity $h=2 / 3 n$, representing the harmonic mean, where lies the key for the triadic Cantor set, valid for the genetic code, not only in form of a binary tree, but in form of a fractal structure, as it is shown in [10,11]. The link of the harmonic mean and triadic Cantor set is the essence of the binary harmony, also valid for the genetic code, more exactly, for the classification of the genetic code constituents as it is shown in [12], p 137. The segment line $n$ can be, in infinitely numerous ways, divided into two unequal parts; one of these is the golden mean as the best possible proportion. (About the validity of the golden mean for the genetic code, see in [11], p 68).
Remark 2. Since the genetic code can be reduced to the Gray code model (Fig. 1 in [13], p 188) and to a binary tree (Fig. 2 in this paper), with a starting codon UUU 000000 and a final codon GGG 111111, it follows that as to question of symmetry in relation to the genetic code the mathematical group theory does not hold. This follows from the fact that set Q of rational numbers, including zero, does not form $a$ group with respect to a multiplication operation.


Figure 3 The genetic code binary tree. It is in full accordance with the yin-yang binary tree in the oldest book I Ching. The relations between 64 codons and 64 hexagrams: to each zero corresponds a dotted line; to each one corresponds a full line (see ref. [10], p. 274).


Figure 4 The Boolean logical (LIGHT) square of the genetic code. It is in full accordance with the Aristotleian (Boolean) logical square of four entities (cf. Fig. 2) (For details see ref. [10], p. 8).

### 2.1 The Important Examples

1. A serious analysis could show that Crick and Einstein, more than any other scientists, are responsible for our understanding of the link between the molecular basis of life and consciousness, and between both these and the universal code of the Nature. Crick made first and important step, not only in the research of the genetic code (see References in [10,11]), but also first and important step in argumentation that consciousness is a property of molecular activities in neurons and networks of neurons in our brain [14]. On the other hand, Einstein was the first led to arrive at the conclusion of the continuum of the space-time of the Universe. But here we must understand that when he speaks about the four-dimensional continuum of space-time, he means in fact on the three-four-dimensionality; and when he speaks about the space he speaks also about a space, which is "the space of counting". This opens a possibility to speak about coding coordinates and coding spaces accordingly to universal code model as a union of cube-sphere (presented here in Fig. 1) and hypercube-hypersphere (not presented in this figure); the model, valid at the same time for Crick's macromolecular structures as well as for Einstein's three-four-dimensional space-time. By this, the word is not only about the real space, and not only about the Boolean Logical space, but about a Logical-Information-Geometric-Homeomorphic-Topological space, altogether and at the same time (about LIGHT model and system see in [10], pp 61-63). From the said it follows that any LIGHT space, characterized by three-four-dimensionality, must be taken as BooleEinstein's LIGHT space.
2. The second example can be the chemical code, represented here by some Mendeleev's original works (Figs. 7-10). The Mendeleev's System of elements is different from our today's Table of elements. The 20th century science escapes Mendeleev "mysterious" form of his system of elements, saying that Mendeleev made some "arithmetical errors" (Fig. 10; cf. [15], p. 185). However, Mendeleev's "errors", or our inadequate understanding of his work, is the LIGHT approach to the system of chemical elements. That is a coding system of $3^{4}=81$ and $4^{3}=64$ entities and a LIGHT approach as a coding approach. The coding system of $3^{4}=81$ entities, because within the set of first 84 chemical elements (from $\mathrm{H}=1$ to the $\mathrm{Po}=84$ ) there are exactly 81 stable elements. The coding system $4^{3}=64$, because 84 minus 20 "monoisotope" elements equals 64 (cf. [16], chapt. 27, sect. "Relations odd-even", where Gould says that all even elements to the polonium, $\mathrm{Po}=84$, have minimally two stable isotopes, except beryllium; cf. [17], where it is said that within chemical code there are exactly 84 elements; cf. 64 hexagrams in Fig. 5 and 81 tetragrams in Fig. 6). Thus, the conclusion that Mendeleev clearly and precisely gave the system of chemical elements as a three-dimensional Boolean LIGHT cube, as we can read from the Figs. 7, 8.


Figure 5 The Yin-Yang system of ancient China based on hexagram arrangement: it consists of 64 hexagrams $\left(2^{6}=\right.$ 64 ), which display every possible combination of archetypal human situations - along with thousands of variations caused by changing lines. Notice that an inverse countdown is possible. In such a case the 63 rd number is zeroth. If so, then $2 \times 6$ and $2^{6}$ are the numbers of lines and hexagrams respectively.


Figure 6 The Yin-Yang system of ancient China based on tetragram arrangement: a tetragram is constructed from four stacked lines of three types (full, broken, and twicebroken). There are 81 possible combinations of these three types of lines $\left(3^{4}=81\right)$. It is no accident that ancient Chinese book Tao Te Ching has eighty-one chapters. Notice that an inverse countdown is possible. In such a case the 81 st number is zeroth. If so, then $3 \times 4$ and $3^{4}$ are the numbers of lines and tetragrams, respectively.

The periodic system of the chemical elements is really three-dimensional, but not in the sense expressed through the Leland C. Allen's model [18,19], as here it is presented in Fig. 11, but in the sense expressed through the original Mendeleev's model as it is presented in Figs. 7,8, which model is in accordance to the model of universal code, presented in Fig. 1 (Cf. [18], p 9003: "It is argued that electronegativity is the third dimension of the Periodic Table"; and [19], p 1510: " It is clear that something is missing ... Configuration energy (CE), the average one-electron valence shell energy of a ground-state free atom, is the missing third dimension".) Accordingly to Mendeleev, the same groups of the elements are at all three coordinates (i.e. dimensions) at the same time, as it follows from the model presented in Fig. 7. Notice that within Fig. 7, in relation to Fig. 8, the noble gases are at the end in all three cases. That comes from the fact that the groups of elements must be at the vertices of the LIGHT cube, i.e. at the vertices of the model of the universal code, presented here in form as in Fig. 1.


Figure 7 The Mendeleev's three-dimensional periodic system as unity of cube-sphere; cube: through the three coordinates; sphere: through the noble elements, which are at the end of all three coordinates.

From these facts it follows that the third dimension of the periodic system as a "New dimension for Mendeleev" [20] is not necessary, because Mendeleev was conscious of this dimension 100 years ago. Also, Mendeleev was conscious of the problem of "rare earth", although there are different opinions ([20], p. 13: "The two versions differ simply in their arrangements to accommodate elements such as the rare earths, but the result must be to leave many with the impression that Mendeleev had not made up his mind about something of importance").
Remark 3. In his long periods Table ([15], p. 188), Mendeleev gave a specific position to the first element of "rare earth", i.e. lantanides, Ce , not in the third but in fourth group; then still 13 groups for 13 lantanides. If so, Mendeleev must have conscious by seen that the short periods Table with 8 groups of elements (Fig. 10) corresponds with cube, and long periods Table with a hypercube (for details see [10], pp. 197-200). ... Bearing in mind all the said Mendeleev's insights, it was possible to
determine the definitive real positions of elements within 34 dimensional periodic system ([10], pp 61-63 and [11], pp 180-182).


Figure 8 The Mendeleev's project for the three-dimensional periodic system, presented in Fig. 7. A half volume of the cube is realized with the realizations of the line 2-3-4-5, and the whole volume with the line 2-3-4-6-7 (half : whole $=1$ : 2). Notice that from the point 4 there are two possibilities. First: the realization of one step, 4-5, i.e. a half of the volume; second: the realization of two steps, 4-6 and 6-7, i.e. $a$ whole of the volume ( $1: 2$ still once; cf. Remark 1 ).


Figure 9 The Mendeleev's system of chemical elements oddity-evenness principle; the valence trinity-quaternity system; the atomic mass distances integer system.

Remark 4. From figures presented it is clear why it is sensible to speak about the chemical code in connection with
the genetic code. There are certain aspects of correspondence and coherence of the two codes: (I) within the genetic code there are exactly 61 codon situations (stable aggregations) with amino acid corresponding meaning, plus 3 breaks in that meaning ( 3 "stop" codons), plus 20 noncodon situations ( 20 protein amino acids); (II) within the chemical code there are exactly 61 situations (in the form of stable aggregations) which have multi-isotope meaning, plus 3 breaks in stable isotopy ( 3 "stop" situations: Tc, Pm, Po), plus 20 non-stable isotope situations ( 20 "mono isotope" elements). Thus, altogether there are 84 entities within each: within the genetic, and within the chemical code too. This is the very topic: the chemical code, built on the very principles mentioned and in complete accordance with the genetic code.


Figure 10 Two Mendeleev's arithmetical "errors" (?!) ([15], pp 128-129, photocopy X ). For details see [10], pp 197-200.


Figure 11 Electronegativity as a "third dimension" of the periodic system [18].
3. The grandiose creative investigators as Charles Darwin and Gregor Mendel were also conscious that a universal harmonious whole-parts system-model (the universal code) must exist in the nature. So, the one and only Darwin's diagram (binary-code tree with 16 levels, exactly as Mendeleev's Periodic system, with 16 groups) in Origin of Species represents the first systematic information approach (LIGHT approach) to the analysis of the evolution relations between organisms [21]. (For details see in [10,11]; for Mendel's universal code in [10], pp. 14-19 and 21-25.)

### 2.2 The Significant Characteristics

The genetic code is an example of the Boolean logical (LIGHT) square-cube-hypercube realized through four nucleotide molecules: $\mathrm{U}(00), \mathrm{C}(01)$, $\mathrm{A}(10), \mathrm{G}(11)$ [10,11,13,22-26]; or, realized through the four rosettes (classes of the codons) on the binarycode tree, presented in Fig. 3, in a full accordance with the Yin-Yang code of the I Ching ([27], p 223). The microtubules system was identified also as a code [28]; more exactly as two codes: $K_{1}\left[13, \mathbf{2}^{6}, 5\right]$ and $K_{2}\left[24,3^{4}, 13\right]$ (cf. these 64 and 81 codewords with analogous "codewords" within chemical code, mentioned above; also cf. $\mathbf{2}^{6}$ with 64 hexagrams in Fig. 5 and $3^{4}$ tetragrams in Fig. 6).

| d | c | b | a | e | f |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  | - | 1 |
| 1 | 0 | 1 | 00001 |  |  |
| 1 | 0 | 1 | 00002 | 2 | 9 |
| 1 | 1 | 0 | 00004 | 1 | 1 |
| 1 | 0 | 1 | 00008 |  |  |
| 1 | 0 | 1 | 00016 | 2 | 12 |
| 1 | 1 | 0 | 00032 |  |  |
| 1 | 1 | 0 | 00064 | 2 | 3 |
| 1 | 0 | 1 | 00128 | 1 | M |
| 1 | 1 | 0 | 00256 |  |  |
| 0 | 1 | 0 | 00512 | 2 | 3 |
| 1 | 0 | 1 | 01024 | 2 | 12 |
| 1 | 0 | 1 | 02048 |  |  |
| 0 | 1 | 0 | 04096 | 1 | 1 |
| 0 | 0 | 1 | 08192 |  |  |
| 0 | 0 | $\underline{1}$ | 16384 | 2 | 9 |
|  |  |  |  | - | 1 |

Figure 12 The Homer's and Njegoš's (Boolean) space sequence, $\mathrm{N}=2^{\mathrm{n}}$. (a) The binary sequence whose sum is $2^{15}$ $1=32767$; (b) Homer's choice: $27803_{10}=66233_{8}=$ $110110010011011_{2}$ (the number of verses for Iliad plus Odyssey); (c) Njegoš's choice: $4964_{10}=11544_{8}=$ $001001101100100_{2}$ (The Mountain Wreath: printed version 2819 verses plus 318 person-scenes, plus 116 pages for printing $=3253$; manuscript version 1528 verses plus 150 person-scenes plus 033 pages $=1711$; all together - the total spaces of The Wreath: $3253+1711=4964$ ); Homer's plus Njegoš's system: $66233_{8}+11544_{8}=77777_{8}$; (d) Homer's choice: $3583_{10}=6777_{8}=000110111111111_{2}$. The number 3583 represents the difference of Iliad and Odyssey: 15693$12110=3583$. The relation between two numbers $77777_{8}$ and $6777_{8}$ was given through a logic program: to exclude first position, and then - to write the result (77778); after that: to exclude first unit in the first position, and, then to write the result $\left(6777_{8}\right)$. The choice of logic for the number $3583_{10}=6777_{8}$ is as follows. From the total sequence ( $2^{15}-$ 1) to exclude all the situations that contain the whole third perfect number 496; (e) The number of Homer's yes-choice and non-choice situations; (f) The (in literary science) known composition sequence of Iliad: from the middle point (Mission to Achilles) 1 day full, 9 empty of events etc.

On the other hand, the comparison of the Boolean logical squares (more exactly: LIGHT squares), presented in Figs. 2,4 shows that both codes, genetic code and Yin-Yang code, correspond to the logical square of the four "elements" of the Universe, known to Aristotle and to Alchemists: Fire as +Yang (11), Air as -Yang (01), Earth as +Yin (00) and Water as Yin (10).

As the third, the binary tree of the I Ching and the binary tree of the genetic code, both correspond to Farey's binary tree, which determines the quasiperiodical transition to deterministic chaos (cf. ref. [10], pp 182 and 280).
Remark 5. The binary-code tree presented in Fig. 3 corresponds ipso facto with the Farey tree ([11], pp 182 and 280), which represents the rational numbers relationships within the interval $(0 / 1,1 / 1)$, what means the relations of parts within $a$ whole; all positions within the binary-code tree correspond to all fraction locations within the Farey tree - each to each [29]. In fact both trees are the binary trees because each generation within both is simply a power of 2 . The essential characteristic of the Farey tree is the Golden mean route realized through the binary digit notation 101010 within the first full zigzag line on the right at the model, presented in Fig. 3 (the best possible symmetry - the binary symmetry).


Figure 13. The two Homer's epics. The both have 24 cantos each: 12 the first, 12 the second; 12 even and 12 odd. The final result 1741630 is the same as within the genetic code: "The number of all distributions in the set of 64 codons is 1741630 " [22, p 191]; cf. Fig. 12. Notice that $1751589=63$ x 27803 (Iliad plus Odyssey); the 63 is the last point on the binary tree of the genetic code in Fig. 3; the 21 is the last point on the Floor-table of genetic code (Table 4.1 in [10], p.56).

## 3 Final Comments

Finally, a surprise: human consciousness, in the form of a comprehension, expresses itself, in some specific way, through the human masterpieces-code, the human language-code, and the human logic-syllogism-code. Masterpieces such as those written by Homer, Dante, Shakespeare, Goethe, Pushkin, Njegoš, Tolstoy. We find their compositions were written according to the same Law as possessed by the chemical and genetic codes - the Golden Mean. Figure 4.1 shows how Homer and Njegoš generated the verse number for their works from the binary sequence $2^{n}$. On the other hand, Fig. 14 shows De Saussure's sound
system within the human natural language-code [30]. But that what is very interesting is the fact that the model in Fig. 14 (logical square) can be also valid for the language-accent. For example, in Serbian (for the words) there are two and two and still once two and two (first law of the logical square) types of the accent: two long and two short; then two falling and two rising. At the same time there are one and three (the second law of the logical square) types of the accent: one fast (short-falling) and other three (shortrising, long-rising and long-falling) are slow. In French (for sounds) there is one $e$ without accent (to relation $e$ mute) and three $e$ with the accents: $e ́, \hat{e}$ and $\grave{e}$. In English (for sentences) the intonation (cf.[31], pp 8-24) realizes itself through a logical square as it is shown in Fig. 15 (start 00, end 11 and two intermediate situations: rising 01 and falling 10). At the end we show that human consciousness in the form of a logical reason (syllogism etc.) must also be determined by Boolean logical square, more exactly by LIGHT square as it is presented in Fig. 16 [32].
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On obtient ainsi le schéma des variations possibles :

|  | 1 | 11 | III | IV |
| :---: | :---: | :---: | :---: | :---: |
| $\square$ | Expiration | Explration | Explation | Explration |
| $b$ | Art, bucc. | Art. bucc. | Art. buce. | Art. buce. |
| c | [] | $\sim$ | I] | $\sim$ |
| d | I | [] |  | $\cdots \cdot \cdots$ |

La colonne I designe les sons sourds. II les sons sonores,
III les sons sourds nasalists, IV les sons sonores nasalisés. Mais une inconnue subsiste : la nature de l'articulation buccale; il importe done d'en déterminer les variétés possibles.

Figure 14 De Saussure's sound system of natural language. It can be seen as a specific Boolean logical square: $I(00)$, $\mathrm{III}(01), \mathrm{II}(10), \mathrm{IV}(11) \ldots$ (cf. two very similar designation systems: De Saussure's natural language designation system, ref. [30], p.70, and R. Swanson's genetic code designation system, ref. [13], p. 188).


Figure 15 The sentence intonation within English language. A "hidden" logical square seems to be self-evident: (00) starting, (01) rising, (10) falling, (11) ending.

In conclusion we can say that our concept of the universal consciousness as a universal comprehension must be tested by further investigations from different aspects and in relations to the other different approaches. For example in relation to the quantum physics concept [33] and information physics concept [ 34,35$]$. By this, our two previous papers related to consciousness $[36,37]$ also must be included in the testing.


Figure 16 The Aristotle's syllogism "square of opposition" can be seen as specific Boolean logical square: No S is P (00), Some S is not $\mathrm{P}(01)$, Some S is $\mathrm{P}(10)$, All S is P (11) ... (cf. ref. [32], p. 341).

Acknowledgments: This research is dedicated to the soul of Petar Petrović Njegoš (1813-1851), who wrote the poem "Mountain Wreath" in accordance with the Harmonic mean and Golden mean laws, 150 years ago.

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## A. 6

## MENDELEYEV'S ARCHIVE

# MENDELEYEV'S ARCHIVE 

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Mendeleev's archive of St. Petersburg State University, founded in 1911 upon the initiative of D. I. Mendeleev's students and colleagues. The memorial study, which became the centre of studying and promoting his legacy, was enlarged and in 1953 reorganised into a science archive and museum (the formation of the science exposition was completed by 1956). The exposition shows Mendeleev's main scientific activities, presents a collection of unique equipment with many pieces constructed by Mendeleev himself; the library contains about 20,000 books. The scholar's personal archive with manuscripts, letters, and diaries counts over 16,000 items. The archive annually serves as a research venue for some 500 researchers from different countries.

Mendeleyev's manuscript works most completely studied B.M. Kedrov; the 16 of them are presented, firstly in his famous monography [„Прогнозы Д. И. Менделеева в атомистике - неизвестные елементы" (Атомиздат, Москва, 1977)] and, secondly, here for further study. ${ }^{1}$

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Фотокопия I. Черновой набросок, составленный Д. И. Менделеевым в ходе открытия периодического закона (в ходе раскладывания «хпмнческого пасьянса»). 17 февраля/ 1 марта 1869 г.


Фотожопия II. Отдельный листок «Опыт системы элементов, основанной на пх атомном весе и химическом сходетвея, разосланный иностранным химикам. $1 / 13$ марта 1869 г.


Фотокопия III. «Грушшы по величине атома». Элементы, стоящие в середине и в конце больших периодов (с их атомными объемами), Июнь/июль? 1869 г.



Фотокопия IV. Легкие элементы, разделенные на нечетно- и четноатомные. Феврать/март 1869 г.


Фотокопия $V$. Первый варнант короткой таблицы элементов с подразделешем рядов на чет-


Фотокопия VI. Набросок короткой таблицы элементов с выявленным диагональным направлением. Лето или осень 1870 г.


Фотокопия VII. «Объемы металлов». Короткая таблица элементов с уточненными аломнымми объемами. Јето илй осень 1870 г.


Фотокопия VIII. Черновнк короткой «Спстемы әлемептов» с детально разработанными днагональными направлениями. 17/29 ноября 1870 г.


Фотокопия $I X$. Таблица с центральной частью больших периодов и выделенным из нее полем-блоком. Конец 1870 г. первая половина 1871 г.



Фотокопия XI. Автограф периодической системы әлементов с включениом 0 группы, $12 / 25$ марта 1902 г.


Фотокопия XII. Правка в таблице әлементов из седьмого издания «Основ химии» при подготовке восьмого издания. 1904 г.


Фотокопии XIII и XIV. Рамка с фотографиями химиков Л. Нильсона, J. де Буабодрана, Б. Браунера и К. Винклера и надписи, сделанные на ее обороте (см. оборот этой страницы)


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Фотокопия $X V$. Автограф первой страннцы рукописи заметки об открытии галлия. Ноябрь 1875 г.


Фотокопия XVI. Автограф сопроводительного письма, адресованного Дюма в Париж. $5 / 17$ ноября 1875 г.

## Изображение периодической таблщцы элементов в системе коордннат

 (по Д. И. Менделееву) с нулевой грушшой в качестве осп абсцисе



## A. 7

## Universal Poetic Structures

The work shows that the structure of the Homer Iliad and Odyssey, and Dante Divine Comedy, as well as Njegosh Mountain Wreath are built on the same principles, on which is built the structure of the universal code, which aspects are genetic code and chemical code.

# UNIVERSAL POETIC STRUCTURES 

## (Homer Dante and Njegosh)

Ejolim Civecokar, individual researcher

## 1. INTRODUCTION

When the greatest poet of South Slavic region, Petar II Petrovic sent the first of his three works (the famous triptych: The Ray of Microcosm, The Mountain Wreath, The False Tsar Steven the Small) to Belgrade to his former teacher Simo Milutinovic Sarajlija, to have it printed, he also attached a letter containing the program statement: "And I, as the intellectual substance of the Creator, must needs follow the general accord. " Njegosh therefore attempted, through a hidden code, to create poetic structures built on the same principles on which the entire Universe was built. Hence there comes the title of this article, in which we will show that Njegosh, in his attempt, only joined the poets of classic literature - Homer, Dante, Shakespeare and Goethe, who had incorporated the same idea into their works.

Njegosh's creation plan was not an ordinary plan, in terms of affiliation to this or that aesthetic category, this or different structures and compositions, which had been more or less already known, but it was also, at the same time, a plan of the Universe, the general accord, the implementation plan, a plan of harmonious relation between the whole and its parts; such relation which implies that those parts of the whole must be in the best possible - symmetry, proportion and harmony, the basis of which is the golden mean. And the unity of harmony, symmetry and proportion is also the basic plan, which must inevitably be the plan of creating any natural system, and accordingly the whole World, that is to say the Universe.

In my previous works I presented that Njegosh was not only aware of the plan, but following it through his own work, in form of two triptychs, ${ }^{2}$ he built a Poetic Universe, strictly correspondent to and in accordance with the Universe - World, where all living and nonliving things exist, and where we all exist. The manner in which Njegosh, through his two triptychs, together with several separate works, made the general accord I have presented in a two volume book $^{3}$ and here I will show the relations of Njegosh's accordance with, almost exactly the same accordance, inherently and consistently implemented in Homer's and Dante's works.

[^73]
## 2. THE CONCEPT OF THE CODE AND THE UNIVERSAL CODE

In contemporary information science, cybernetics and system theory, under the term of coding we understand the process of linking the alphabet 1 - with the alphabet 2 , where the rule to move from one alphabet -1 character to the corresponding alphabet -2 character - is given as a list of connections, that is to say, a code. On the other hand, in semiotics (semiology) the very characters are the code, the characters which always represent a certain relation between the signifier and the signified, or language itself is the code meaning that every natural language is a kind of a special code.

Starting from the above presented definitions, it is not difficult to go a step further in generalizing and to define the code as correspondence, according to a certain rule and / or law, of any of the two subsystems (parts) within one natural system (the whole). If, thus, we take into account the systems whose organization of parts within the whole is such that they are in the best possible harmony, ${ }^{4}$ and, that at the same time there is a correspondence of the system structure with the sequence of natural numbers structure, then it makes sense to say that it is a universal code.

However, one has to bear in mind that under the term of "natural" system one must understand not only any real (by definition given) natural system, as the system of chemical elements, Bioelements system, the system of constituents of the genetic code, etc., but also the man-made "experiential" systems, as in the examples of the classic literary masterpieces (Homer, Dante, Shakespeare, Goethe, Pushkin, Njegosh, Tolstoy), of Athens' palaces and Egyptian pyramids built in the relation to the golden mean, and the like.

If, considering everything mentioned above, one also understands that in the definition of the universal code, the term 'numbers' must also mean 'numbers-relations', relations which are spatially logical, ${ }^{5}$ i.e. Boolean, generated from a universal cube, [Boolean space $B{ }^{n}(n=0,1$, $2,3 \ldots)]$, it becomes clear that the universal code must manifest itself in the form of spatially logical 'characters ': logical segment line, logical square, cube, hypercube, etc..
Ideal examples (aspects, that is, forms) of the universal code, according to the given definition, are the genetic code and Mendeleev's System of chemical elements (the chemical code). Here we deliberately refer to the System as "Mendeleev's" and not as any other (modern) system, because of the fact that only in the original Mendeleev's manuscript we can find confirmation of the above said. No one, neither before nor after Mendeleev, realized that this was the best possible harmony. No one, if not aware of the relation, between the system of chemical elements and the system of constituents of the genetic code. When, however, we are aware of this relation, then it is evident that even the ancient Chinese were aware of it five thousand years ago. Their

[^74]system of 64 hexagrams, presented in the "Book of Changes - I Ching" is a hundred percent accurate 6 -bit record of 64 codons within the genetic code. ${ }^{6}$ If, on the other hand, one analyzes the binary-code tree of the genetic code, ${ }^{7}$ also present in I Ching, and reads it as a trinityquaternity system or as the union of the cube and the hypercube, then it is evident that this is the same hypercube found in a three-dimensional system of chemical elements, drawn by Mendeleev himself. ${ }^{8}$ And that is practically, the same hypercube found in Darwin's diagram, the only illustration given in his famous book The Origin of Species, and also the same hypercube that was so ingeniously grasped by the Moldavian monk, one of the greatest devotees - devotees of science - Gregor Johann Mendel by the formula $1{ }^{n} 2{ }^{n} 3{ }^{n} 4{ }^{n}$ (numbers 1, 2, 3 and 4 with an exponent $n$, (where $n$ is the number of characteristics at the intersection, with the values $n=1$, $2.3, \ldots$ ) which reveals an unbreakable bond and unity: one refers to the parenting pair, and two, three and four refer to a phenotype, genotype and type of an individual, respectively.

## 3. HOMER'S AND NJEGOSH'S CHOICE

Without the binary sequence $2^{\mathrm{n}}(2 \exp \mathrm{n}),(\mathrm{n}=0,12,3 \ldots)$ the ancient Egyptians did not use the multiplication table either (according to the evidence found in Rhind papyrus and in Moscow mathematical papyrus); but they, in fact, reduced all the multiplication to repeated addition. Thus, whenever they multiplied two numbers, they asked which number, from the sequence of numbers $1,2,4,8$, and so on, should be added in order to obtain the required result. To understand the meaning of this kind of arithmetic it is important to find the key determinant of the multiplication table in terms of logic of the best possible harmony. If we know the fact that in the decimal numeral system, numerical basis is $q=10$, then it is easy to realize that the key determinant has to appear in the process of multiplication by a half, i.e. by number 5 , in the octal numeral system, where $q=8$, it is multiplication by number 4 , in the hexadecimal system where $\mathrm{q}=16$, it is the multiplication by number 8 , etc.; in all cases, that key determinant is found in multiplication by number 3 .

Let us reveal why this is so, in the example of the decimal numeral system. If we multiply number 5 by 1 and 2 , the border of the numeral system basis where $\mathrm{q}=10$ is still not crossed. Only when multiplied by 3 , the first case of "crossing the border" appears. Therefore, the key determinant of the multiplication table in the decimal numeral system is "Three times five equals fifteen"; in octal numeral system it is "three times four equals twelve," and in the hexadecimal numeral system it is "three times eight equals twenty-four" etc.

Bearing in mind the above mentioned facts, we could make an interesting task involving both the Egyptian sequence of numbers 1-2-4-8-16 - etc. and the key determinant of the multiplication table, for example, in the decimal numeral system, if it is reasonable to isolate the decimal numeral system as specific and (possibly) more powerful than any other system of numbers in "matters" of the Nature. Here is the task. We need to take 3 groups of 5 numbers from the Egyptian sequence 1-2-4-8-16-32-... etc.., but in such a way that these numbers are in the best possible symmetric-proportional-harmonious relation.

[^75]Here is the key to a solution to this problem: [11011] - [00100] - [11011]. The key is given as a palindrome, which means that it reads the same from both left and right. The solution is the following: $[1-\underline{2}-(4)-\underline{8}-\underline{16]}-[(32-64)-\underline{128}-(256-512)]-[1024-2048-(4096)-\underline{8192-}$ 16384]. If we add up all the underlined numbers (out of round brackets), we get the number 27803, which is exactly the sum of the number of verses in Homer's Iliad and Odyssey. [If this number (27803) is translated into the binary numeral system ( $\mathrm{q}=2$ ) from the decimal numeral system ( $\mathrm{q}=10$ ), the result is exactly the number we have already observed in the form of the code key: $11,011,001,001,1011$. In the octal numeral system ( $q=8$ ) number symmetry is obvious: 66,233] However, if we add up all other numbers (within round brackets), we get a total "space" of Njegosh's Mountain Wreath (total space: the number of verses, the number of persons, the number of pages, etc., as we have shown in our previous works) (cf. Box 1). ${ }^{9}$ Njegosh chose exactly what Homer did not choose. If you add Homer's (27803) to Njegosh's number (4964), the number 32767 appears as the result, and in the octal numeral system ( $\mathrm{q}=8$ ) that number is 77777 .

## Box 1. The Homer's and Njegosh's (Boolean) space sequence, $\mathrm{N}=2^{\mathrm{n}}$

(a) The binary sequence whose sum is $2^{15}-1=32767$ (2 exp 15); (b) Homer's choice: $27803_{10}=66233_{8}=$ $110110010011011_{2}$ (the number of verses for the Iliad plus the Odyssey); (c) Njegosh's choice: $4964_{10}=$ $11544_{8}=001001101100100_{2}$ (The Mountain Wreath: printed version 2819 verses plus 318 person-scenes, plus 116 pages for printing $=3253$; manuscript version 1528 verses plus 150 person-scenes plus 033 pages $=1711$; all together - the total space of The Wreath: $3253+1711=4964$ ); Homer's plus Njegosh's system: $66233_{8}+11544_{8}=77777_{8}$; (d) Homer's choice: $3583_{10}=6777_{8}=000110111111111_{2}$. The number 3583 represents the difference between the Iliad and the Odyssey: 15693-12110 = 3583; (e) The number of Homer's choices (1) and non-choices (0); (f) The (in literary science) known composition sequence of the Iliad: from the middle point (Mission to Achilles): 1 day full, 9 empty of events etc., all adequate with choice and non-choice patterns, respectively.

## 4. RELATIONS WITH THE GENETIC CODE AND I CHING

In previous papers (listed in footnote 9, and elsewhere), we have shown that the logic of the arrangement of 64 hexagrams on the binary tree, in Chinese book "I Ching", also corresponds to the arrangement of 64 codons on the binary tree of the genetic code (as we presented in the book: Logic of The Genetic Code, Scientific Book, Belgrade, 1994). Since

[^76]exactly 50 years ago ${ }^{10}$ we have known that the Genetic Code language is a four-letter "alphabet" (uracil, cytosine, adenine, guanine) ( $\mathrm{U}, \mathrm{C}, \mathrm{A}, \mathrm{G}$ ), and three-letter words generated from this alphabet. Logic (of Nature?) is this: if the alphabet is a quartet, the principle of minimal change requires the realization of triplets, doublets and singlets. Thus, in case of this (the only optimal?) alphabet, 64 triplets, 16 doublets and 4 singlets are possible to be derived. And that is exactly the same as found in the Chinese Book of Changes "I Ching", written at least five thousand years ago; and exactly the same on the binary tree, as well, identical in both cases, with 6-bit binary records: in the genetic code there are records of zeros and units (six digits per each codon), and in I Ching records are made using full and broken lines (six lines in each hexagram). The question is whether both cases are connected with the fact that number six is the first perfect number.

At the time when I realized the facts about these 6-bit and 6-hexagram records, I had already found that the genetic code was determined by perfect and friendly numbers. ${ }^{11}$ The possiblity that Njegosh was influenced by the Biblical "Hexaemeron" (fully discussed in the book "Njegosh's Primordial Logos") ${ }^{12}$ does not, however, contradict the possibility of having been influenced by the number six perfection ${ }^{13}$, since, according to St. Augustine, God actually created the world in six days because of the fact that number six is the first perfect number. In his famous work Civitas Dei, St. Augustine, alias Aurelius Augustine, in the thirtieth chapter of the eleventh book, discussing perfect numbers, also presents the reason "why the Bible says that creation was completed in six days," and says that "God ... did not need any period of time, "but he chose the perfect number six" to symbolize the perfection of his work $" .{ }^{14}$ As we can see, according to St. Augustine, even God acts by "general laws", exactly as Njegosh says: "The laws of universal order are/ My behest and the life of nature" (The Ray of Microcosm III, 261-262).

To emphasize it again: in the genetic code, the basic four-letter alphabet is represented by four nucleotide molecules, two simple pyrimidine molecules (cytosine and uracil) and two complex purine ones (adenine and guanine); in the "I Ching" system it is represented by two simple characters (a small Yin and a small Yang), and two complex ones (a big Yin and a big Yang). But in the genetic code, there is also a 20-letter "alphabet", made of 20 amino acid molecules. The link between 64 codons and 20 amino acids is actually given in the genetic code. However, the number of theoretical possibilities of joining (of these codons to these amino acids) has also been calculated - exactly 1741630 (one million seven hundred forty-one thousand six hundred and thirty). ${ }^{15}$

[^77]This number refers to all the possibilities (through every possible variation) of joining 64 codons, to every single amino acid (out of the 20 amino acids) as mediated by the genetic code. If we pay attention to the Chinese 4-letter alphabet (small and big YIN, and small and big YANG), which generates 64 6-bit "words", it cannot be directly seen that there was the awareness of the inevitability of the other, 20-letter alphabet (indirectly, however, it can be seen, but it is a matter of a separate research). Njegosh's result, which is identical to Homer's (Figure 5, p. 191, second volume of our book "Njegosh's Primordial Logos") (Njegošev iskonski logos), gives evidence of the presence of such an awareness of both the authors.

However, there is a surprising fact - the fact that everything is arranged in such a manner that it is reduced to the balance level ( 202020 ), corresponding with and analogous to the binary sequence of the biggest change in the binary tree (101010). Having put the sequence 202020 in the operating association with the digit record (11111), Njegosh also implemented the number 1,741,630, which is, as we have seen, an important determinant of the genetic code (p. 60 in Volume II of the above mentioned book). What, however, is particularly important from the aspect of this analysis is the fact that the same number follows from the distribution of the verse number in the 24 poems in The Iliad and in the 24 poems in The Odyssey (if they are related in the following way: the first 12 and the second 12, 12 in even and 12 in odd positions) (Ibid, p. 191).

## 5. PYTHAGORAS, DANTE AND NJEGOSH

If we know that in the sequence of natural numbers there is only one triplet (3-4-5) for which the Pythagoras' law is valid, it is inevitable to conceive the sequence of natural numbers as a sequence of triangles: $0-1-2,3-4-5,6-7-8,9-10-11$, etc. In addition, all the triangles geometrically read in the Boolean space are actually Pythagoras', whereas in the arithmetic reading, only one is Pythagoras' (3-4-5). However, if we consider only the central "vertices" of the triangles, then we get the following sequence of numbers: $1,4,7,10,13,16$, etc... Numeral systems which take numbers from this sequence (except number 1) as the q basis, have specific characteristics. Thus, in the decimal numeral system $(\mathrm{q}=10)$ number 037 is the only two-digit number (read from three positions) which is able to generate full cycles according to module 9 . Thus $1 \times 037=037,10 \times 037=370$ and $19 \times 037=703,2 \times 037=074,11 \times 037=407$ and $20 \times$ $037=740$ and so on. ${ }^{16}$ Everything that is possible for number 037 in the numeral system where q $=10$, can also be adequate for corresponding numbers in numeral systems with the following bases 4, 7, (10), 13, 16, etc.. This was first presented by Vladimir Shcherbak in 1993-1994. ${ }^{17}$ when he, at the same time, showed that number 013 in the quaternary numeral system ( $\mathrm{q}=4$ ) determines the cyclicity of 64 codons in the genetic code, and number 037 in the decimal numeral system $(\mathrm{q}=10)$ determines the corresponding cyclicity which is valid for the system of 20 protein amino acids that have the status of "canonical" amino acids in the genetic code.

Thus, it was Shcherbak who first realized that this is the ability of number 037 in the decimal numeral system, and also the ability of its analogues, generated in numeral systems through moving in three steps. It is our insight, however, that these numeral systems are

[^78]generated from the system of triangles in a sequence of natural numbers. However, our observations are also illustrating that all of this, before all of us was understood by Dante Alighieri, who, with an ultimate precision, expressed it in his Divine Comedy (La Divina Commedia). How did he do that? He took care that the number of verses in any of his 100 songs could only be a number whose sum of digits had to be $4,7,0$ or 13 and in the second cycle of addition $1,4,7$, and that is actually the realization of the central figures of the first three triangles in the sequence mentioned above. The answer to the question why Dante stopped at number 13, today remains unknown, but we can present the principle which extends right up to that number. The sequence of analogues of number 037 (10) for the above given numerical bases is the following: 013 (4), 025 (7), 037 (10) 049 (13), 05B (16) 06D (19) ... We perceive that the figures, only up to number 13, are given in the decimal numeral system, and if we proceed, we must borrow the figures from hexadecimal numeral system and from other higher systems of numbers.

Portuguese mathematician L. de Freitas revealed (1989.) that the last verse of Dante's Divine Comedy is a palindrome. In the old-Italian original it reads: "En giro torte sol ciclos et rotor igne," and in contemporary Italian: "L'amor che move il sole e l'altre stele", in Serbian: "Ljubav pokretac sunca i svih zvezda. " (Near the last verse there is another palindrome: "In girum imus nocte et consumimur igni.") ${ }^{18}$. Stijepo Kastrapeli, a renowned researcher of Njegosh's works of the late nineteenth and early twentieth century, states that Njegosh read and studied the Divine Comedy together with his teacher Simo Milutinovic Sarajlija. If so, then could it be possible that, just under the influence of these Dante's twists (palindromes), Njegosh did what he did: He wrote the names of all those wrong-doers of the past (or perhaps of the present as well) in the wrong way. Thus, there are all of them, (in The Ray of Microcosm): Napoleon, Caesar, Alex, Prince of the Evil, Evil Spirit, The Head of the Evil and so on. ("Satan’s sinners head to him after mutual agreement... Live eht fo Daeh, Tirisp Live, Live eht fo Ecnipr ... Noelopan, Raseac and Xela") [ In Serbian: Napoleon, Cezar, Aleksa, Knez zla, Duh zli, Glava zla etc. ("Satanini zloumišljenici idu k njemu s opšteg dogovora ... Alzzenk, Ilzhud i Alzavalg Gordi ... Noelopan, Razec i Askela") ]. Our answer to the question is affirmative.

[^79]
## Box 2 Numbers on bones

In Natural History Museum in Brussels there is a small, 10 centimetres long animal bone, which was found in Central Africa near the Lake Isango, in Congo, on the border with Uganda, about 1960. The bone was found in a village near the lake covered with ash after the eruption of a volcano (some kind of prehistoric Pompeii). On the basis of the modern radiocarbon dating, the bone is estimated to be over twenty thousand years old. On this bone, there are notches in small groups, arranged in three rows. In one of the rows there are groups of 9,11, 19 and 21 notches (making a total of 60 ), in the second row there are groups of $11,13,17$ and 19 notches - these are the prime numbers between 10 and 20 - again, making a total of 60 ... Apparently, in the times of illiteracy, somebody "played" with numbers and presented prime numbers, ("atoms" of arithmetic) to future generations. This is, actually, the oldest known testimony of mathematical culture (Gunter Ziegler, Can I count - math stories, Mathematical Institute SANU, Belgrade, 2012).

The fact that prime numbers were presented (as well as the exact number of prime numbers between 10 and 20) is what we know about this oldest testimony of mathematical culture. However, more than that can be concluded. Having presented the fact, that between 10 and 20 there are four prime numbers whose sum is 60 , and that we get the same sum by adding up their neighbouring numbers (one prime number together with one composite number: [ $(9+11)+(19$ $+21)=60]$ ), the oldest known "mathematician" was actually studying the decimal numeral system. If one would search the Lake better, I presume that at least one bone with similar records would be found, and not in the decimal but in the octal numeral system, because of the complementary situation: $[(7+9)+(15+17)=48] .{ }^{19}$

If one wanted to know how come that Homer, Dante and Njegosh dealt with mathematics, before answering this question, one should keep in mind this old mathematical record.

## 6. CONCLUSION

Everything presented above leads to the conclusion that Njegosh's intention to make "the general accord" really refers to the correspondence of poetic structures with the structures of natural systems, in the same manner in which that correspondence was achieved in the works of Njegosh's precursors (forerunners), Homer and Dante.

[^80]
## ABOUT AUTHOR

Prof. Dr. Miloje M. Rakočević was born in the village of Sponce, Medvedja near Leskovac. Studied in high school in Leskovac and Priština, studies of biology and chemistry at the College of Education in Pristina, followed by chemistry studies, master's degree and doctorate at the Faculty of Sciences in Belgrade. He is full professor at the Chemistry Department of the Faculty of Natural Sciences and Mathematics in Niš (since october 2003, the pension). He also teaches in postgraduate studies at the Centre for Molecular Machines of the Faculty of Mechanical Engineering in Belgrade (the theory of the genetic code and information biology). He is primarily dealing with investigations of the possible existence of a universal code of nature on examples of the genetic code and the chemical code (the periodic system of Mendeleev), and also on examples of literary classics (Homer, Dante, Shakespeare, Goethe, Pushkin, Njegoš, Tolstoy...) (works published in the journals Književnost (Literature), Srpski književni glasnik (Serbian Literary Gazette) etc. He has published several monographs: Genetičke informacije (Genetic Informations) (Stručna knjiga, Belgrade, 1988), Geni, molekuli, jezik (Genes, Molecules, Language) (Naučna knjiga, Belgrade, 1988), Logic of the Genetic Code (Naučna knjiga, Belgrade, 1994), Genetic Code as a Unique System (SKC, Niš, 1997), Njegošev iskonski logos (Njegoš's Ancient Logos) I and II (Interpres, Belgrade: I - 2000 and II - 2003), Vizionarstvom ka vrhu: stvaralački put Milana O. Raspopovića (By visionarity to the top: a creative way of Milan O. Raspopović) (Zavod za udžbenike, Beograd, 2012). He has also published a substantial number of scientific works, both in home and international journals (Journal of Theoretical Biology; Biosystems; Bulletin of Mathematical Biology). He is an expert in the field of genetic biochemistry and general chemistry at the national level, as well as in the field of "the initial genetic information" with the international foundation Origin-of-Life (Meryland, USA).


[^0]:    ${ }^{1}$ According to our hypothesis (and prediction), missing quantities (crossed out in the legends to illustrations) will be found during future researches; or will show that some of these cases represent a kind of jumps / falls, or even a „,veto".

[^1]:    ${ }^{1} \mathrm{Y}$ for pyrimidine, R for purine and N for all four types of nucleotides.

[^2]:    ${ }^{1}$ The pair S-R shows that the third position within the codon is also an encoding function, not just the first and the second. This fact also supports the hypothesis that the genetic code still in prebiotic conditions was complete.

[^3]:    ${ }^{2}$ The number 37 as „Prime Quantum 037" in determination of nucleon number within four-codon and non-fourcodon amino acids (Shcherbak, 1994).

[^4]:    ${ }^{3}$ The result corresponds with the number of nucleons within 20 canonical AAs ( 2550 vs 1255 ).
    ${ }_{5}^{4}$ A very significant number because it is a square of Prime Quantum 037 ( $37 \times 37=1369$ ).
    ${ }_{6}^{5}$ In the GCT, within two inner as well as two outer columns there are 3456 of atoms (see: Negadi, 2014).
    ${ }^{6}$ The number of nucleons within 20 canonical AAs.

[^5]:    ${ }^{7}$ The so-called "deviant codes" (Weaver, 2008) represent only a "degree of freedom" in deviation from the standard genetic code. In doing so, it remains only dilemma is whether, perhaps, the standard was preceded mitochondrial code, as more symmetrical (Dragovich, 2011), and then the standard, just because of its small asymmetry, took an evolutionary "course". [Weaver, 2008, pp. 568-569: "These deviant codes are still closely related to the standard one from which they probably evolved".]

[^6]:    ${ }^{1}$ With Roman numerals we denote the part of the work; hence, the Roman numeral II here refers to Part II.

[^7]:    ${ }^{2}$ Notice the difference $120-119=01$

[^8]:    ${ }^{3}$ Atom number in four bases is: $\mathrm{U}=12, \mathrm{C}=13, \mathrm{~A}=15, \mathrm{G}=16$ (cf. Table 2 in Rakočević, 1997, p. 647).
    ${ }^{4}$ Notice the difference $116-115=01$
    ${ }^{5}$ Hydrogen atom number in four bases is: $\mathrm{U}=4, \mathrm{C}=5, \mathrm{~A}=5, \mathrm{G}=5$. Notice the difference $76-76=00$.

[^9]:    ${ }^{1}$ The "Part I" as: "On the completeness of genetic code: some new examples" (viXra:1412.0274); "Part II" as: "On the completeness of genetic code: Part II" (viXra:1501.0117) etc., until the sixth part as: "On the completeness of genetic code: Part VI" (viXra:1502.0041).
    ${ }^{2}$ The nucleotides triplet table (TT) as Standard Genetic Code Table (GCT), valid for the so-called "Standard Genetic Code".
    ${ }^{3}$ The nucleotides doublet table (DT) as "Modified Rumer's Table", presented in Part II of this work as Table 2 (in other words: Table II/2).
    ${ }^{4}$ The ratio of the whole and its half boils down to the fact of "the symmetry in the simplest case" (Marcus, 1989).
    ${ }^{5}$ In modular formulation: $\pm 0$ and $\pm 1$.

[^10]:    ${ }^{6}$ For this reason, D and E have to go to into the second row. On the other hand, AAs that are located in two families of codons (L,S,R) appear only once in its first position each (in accordance with the principle of "all or nothing").

[^11]:    ${ }^{7}$ Tables VII / 3.1; 3.3; 3.4.
    ${ }^{8}$ Fig. I/1; Tables: I / 1.2 (a); 5 (a, b); II/5 (b, d); III/ 2;
    ${ }^{9}$ Tables VII / 3.2, 3.4, 3.5, 3.6.

[^12]:    ${ }^{10}$ Tables I / 3 (a).
    ${ }^{11}$ Tables: I/4(a); III/ 1(b); VII / 3.4; 3.5; 3.6.

[^13]:    ${ }^{12}$ „Britsh zoologist Richard Dawkins is best known for his popular science books. ... His most significant contribution to his field is his concept of the 'extended phenotype'. An organism's genotype is the sum of the instructions contained in its genetic code. Its phenotype is that which results from the expression of that code."

[^14]:    ${ }^{1}$ That natural numbers and decimal numbering system are valid for the genetic code, more than others has repeatedly demonstrated V. Shcherbak (1993, 1994, 2003, 2008); an alternative (or parallel?) aproach, based on the p-adic numbers, one can find in the works of Dragovich \& Dragovich (2006, 2007a,b).
    ${ }^{2}$ Cf. four diversity types with four stereochemical types (Popov, 1989; Rakočević \& Jokić, 1996). [Remark 2. In References all two (my) works on the same scientific problem are given together in two colors: first paper in red, and second one in blue color. Some references are not cited, but they stay in relation to cited ones.]
    ${ }^{3}$ Viewing such regularity (number of nucleons in a specific relation to amino acid classification), V. Shcherbak (1993) concluded: "The physical nature of such a phenomenon is so far not clear". After our opinion the answer, mutatis mutandis, lie in the title of the first Mendeleev work on the periodicity (see Appendix 1).

[^15]:    ${ }^{1}$ Notice that " 037 " is a quantum with the status of " 1 "; more precisely, it is a "Prime Quantum" [Shcherbak, 1994, p. 475: "The sums of nucleons ... are multiples of the Prime Quantum (PQ) 037".]

[^16]:    ${ }^{2}$ Rakočević, 2004, p. 233: "... the existence of such a harmonic structure with unity of a determination with physical-chemical characteristics and atom and nucleon number at the same time appealed to Aristotle and to his idea of unity of form and essence".

[^17]:    ${ }^{1}$ About Gaussian algorithm see in: arXiv:q-bio/0610044v1 [q-bio.OT]) ("Genetic code as a harmonic system") (Rakočević, 2006).

[^18]:    ${ }^{2}$ Notice that this " X " is only and one possible solution (within the set of natural numbers) with such three addings ( Z ), where $\mathrm{Z}=\mathrm{Y} / 4$.

[^19]:    ${ }^{1}$ Two subsystems, each with two quadruplets; in total four quadruplets: two on the left as one-meaning (each nucleotide doublet codes for one AA) and two on the right as two-meaning (each nucleotide doublet codes for two AAs or for one AA and termination in the protein synthesis).
    ${ }^{2}$ Histidine $(\mathrm{H})$ is neutral in cloister energy with the value $\pm 0$ [4], but polar in hydropathy [5], polar requirement [6], [7] and in hydrophobicity [8], [9].
    ${ }^{3}$ Cloister energy is "a formal free energy (= cloister energy) of transfer of the amino acid from the outside of a protein to the inside ... I use cloister energy in preference to other measures of amino acid hydrophobicityphilicity because it is an in situ measure of the property of interest" [4].

[^20]:    ${ }^{4}$ Starting from diagonal ( $\mathrm{F}-\mathrm{G}$ ) together with two adjacent ones ( $\mathrm{S}-\mathrm{R}$ and $\mathrm{L}-\mathrm{E}$ ) we give a central space ("in" space) in a strict balance with the set of polar AAs, polar through hydropathy [5]: atom number in two and two sets ("in", "out" / polar, nonpolar) differs exactly for $\pm 1$ and $\pm 10$, respectively [Ref. 11, Tab. A.3, p. 840 in relation to equations $11-14$, p. 838].
    ${ }^{5}$ If we consider the set of " 61 " of AAs, then in two rows, YNR \& RNY, there are $\mathbf{8} \times \mathbf{3 3}$ and in two other, YNY $\& R N R, 10 \times 33$ atoms. On the other hand, in two pyrimidine columns, NYN, there are $(\mathbf{9} \times 33)-\mathbf{1}$ and in two

[^21]:    purine ones, NRN, $(\mathbf{9} \times \mathbf{3 3})+\mathbf{1}$ of atoms [Ref.12, Tab. 3a, p .224 ]. ( Y for pyrimidine, R for purine and N for all four types of nucleotides.)
    ${ }^{6}$ The full equation for "golden whole" can have the next form: $n^{2} \pm n=$ "WHOLE"; for $n=4$, the difference is 12 and the sum 20. In relation to genetic code there are self-similarities expressed through mathematical operations: $(4 \times 4)-4=\mathbf{1 2}$; $(4 \times 4)+4=\mathbf{2 0},(4 \times 4) \times 4=\mathbf{6 4}$. [Number 12, correspondent to $4+4+4$ doublets in sequence $\left[n_{1}-\left(n_{3}\right.\right.$ or $\left.n_{4}\right)-n_{2}$ ]; number 20 as 20 AAs ( $4 \times 4=16$ AAs of alanine stereochemical types and 4 of non-alanine stereochemical type); number 64 as 64 codons.] (About four stereochemical types see Ref. [13] \& [14].)
    ${ }^{7}$ By this one must notice that all these self-similarities are possible only for 4-letter alphabet and 3-letter words.

[^22]:    ${ }^{1}$ Two subsystems, each with two quadruplets; in total four quadruplets: two on the left as one-meaning (each nucleotide doublet codes for one AA) and two on the right as two-meaning (each nucleotide doublet codes for two AAs or for one AA and termination in the protein synthesis).
    ${ }^{2}$ Histidine $(\mathrm{H})$ is polar in hydropathy, polar requirement and hydrophobicity; nevertheless, in cloister energy it is neutral, because $\mathrm{H}= \pm 0$. [About parameters see in legend of Table 5.]
    ${ }^{3}$ Polarity / non-polarity here follows also by the second two parameters - hydropathy and polar requirement.
    ${ }^{4}$ Cloister energy is "a formal free energy of transfer of the amino acid from the outside of a protein to the inside ... I use cloister energy in preference to other measures of amino acid hydrophobicity-philicity because it is an in situ measure of the property of interest" (Swanson, 1984).

[^23]:    ${ }^{5}$ Starting from diagonal (F-G) together with two vicinal ones (S-R and L-E) we give a central space ("in" space) in a strict balance with the set of polar AAs, polar through hydropathy (Kyte and Doolittle, 1982): atom number in two and two sets ("in", "out" / polar, nonpolar) differs exactly for $\pm 1$ and $\pm 10$, respectively (Rakočević, 2011, Tab. A. 3 and equations 11-14).

[^24]:    ${ }^{6}$ "In correspondence with this, Complete Genetic Code must be based on several key principles. We are going to list only those considered to be the most important ...The principle of systemic self-related and self-similar organization. (The 'head' of an AA in relation to the first possible 'organic' molecule - methane; the functional groups within AAs side chains in relation to functional groups within the AA "head', and between themselves ...)." Here in the question is a non-fractal self-similarity, although genetic code is per se a fractal system at the same time. (Cf., for example, genetic code binary tree as fractal system (Swanson, 1984) and corresponding chapter in our book "GC as a unique system" on our web site: www.rakocevcode.rs) [Ref. 11]
    ${ }^{7}$ If we consider the set of " 61 " of AAs, then in two rows, YNR \& RNY, there are $8 \times 33$ and in two other, YNY $\& R N R, 10 \times 33$ atoms. On the other hand, in two pyrimidine columns, NYN, there are ( $9 \times 33$ ) - 1 and in two purine ones, NRN, ( $9 \times 33$ ) +1 of atoms [Ref. 13, Tab. 3a, p. 224]. (Y for pyrimidine, R for purine and N for all four types of nucleotides.)

[^25]:    ${ }^{8}$ The full equation for "golden whole" can have the next form: $n^{2} \pm n=$ "WHOLE"; for $n=4$, the difference is 12 and the sum 20. In relation to genetic code there are self-similarities expressed through mathematical operations: $(4 \times 4)-4=\mathbf{1 2} ;(4 \times 4)+4=\mathbf{2 0},(4 \times 4) \times 4=\mathbf{6 4}$. [Number 12, correspondent to $4+4+4$ doublets in

[^26]:    sequence " $n_{1}-\left(n_{3}\right.$ or $\left.n_{4}\right)-n_{2}$ "; number 20 as 20 AAs ( $4 \times 4=16$ AAs of alanine stereochemical types and 4 of non-alanine stereochemical type); number 64 as 64 codons.]
    ${ }^{9}$ By this one can notice that all these self-similarities are possible only for 4-letter alphabet and 3-letter words.
    ${ }^{10}$ Notice that Mendeleevian regularity (continuity and minimum change) is also valid for first two columns in Table 6: first half of Table is regular and the second one - irregular. (An analogy with two strands of DNA, one coding and one non-coding.) Notice also that the sums of molecules mass per columns in Table 7 (in both systems, SHS and SMT), are determined by multiples of shCherbak's "Prime quantum 37 ".
    ${ }^{11}$ Notice that AAs from the first and fourth type possess in their side chains the same aliphatic functional groups as in amino acid "head" (Gly H, Pro NH, Ser and Thr OH, Asp and Glu COOH, Asn and Gln $\mathrm{CONH}_{2}$, Lys and Arg $\mathrm{NH}_{2}$ ). (Aliphatic functional group in the sense of binding with an aliphatic molecule radical.) From this it is clear why two sulfur AAs belong to the third diversity type, together with aromatic AAs, and why there is an atom number balance between two and two diversity types (I \& IV vs. II \& III) [Ref. 14, Table 8, p. 830].

[^27]:    ${ }^{12}$ [Ref. 19, p. 162: "The only exception from the general structure of amino acids is provided by proline. It holds its own side chain with two bonds and has one less hydrogen inside the standard block."] As seen from proline formula one carbon atom, from total 3 in the side chain, exists in amino acid „head" (,standard block") at the same time.

[^28]:    ${ }^{13}$ All of these AAs are in standard as well as in mitochondrial GC. Thus, it remains an open question which of the two codes was at the beginning of evolution, and which is a "deviant" one. [Ref. 23, p. 568: "These deviant codes are still closely related to the standard one from which they probably evolved"].
    ${ }^{14}$ According to our hypothesis the pattern (127/112) we will find in further researches, but the pattern (137/102) we have in standard GCT within two and two columns as well as two and two rows.

[^29]:    15 "One important measure of amino acid similarity lies in the ability of one residue to replace another in a closely related protein molecule. Dayhoff (1978) has collected data on this subject, and using the method of ancestral sequences, has estimated the odds of any given amino acid remaining unchanged and its odds of being replaced by each of the other 19 in related protein sequences. Presumably, amino acids with high odds of replacing each other are more alike than amino acids with low odds. Dayhoff presents the data in a symmetric 20 x 20 matrix ..." [Ref. 21, p. 190].
    ${ }^{16}$ Space-3: 011. RCN $(\mathrm{T}, \mathrm{A})+001 . \mathrm{YCN}(\mathrm{S}, \mathrm{P})+010 . \mathrm{RUN}(\mathrm{I}, \mathrm{M}, \mathrm{V})+111 . \mathrm{RGN}(\mathrm{S}, \mathrm{R}, \mathrm{G})$, and Space-4: 100. YAN $(\mathrm{Y}, \mathrm{H}, \mathrm{Q})+000$. YUN $(\mathrm{F}, \mathrm{L})+101$. YGN $(\mathrm{C}, \mathrm{W}, \mathrm{R})+110$. RAN (N,K,D,E). (Note: Y for pyrimidine, R for purine and N for all four types of nucleotides.)

[^30]:    ${ }^{17}$ "We have used both the water-vapor transfer free energies and the interior-exterior distribution of amino acid side chain ... in assigned the final hydropathy values" [Ref. 7, p. 109-110] (cf. adequate relationship in cloister energy: footnote 3).

[^31]:    ${ }^{1}$ Shcherbak (1994, p. 475): "The cause of the regularity lies in the properties of three-digit number notations, multiples of 37 in the decimal additive-position system. The notations of the sums, the nucleon number of the amino acid standard box 074 and Prime Quantum 037 ... can be seen as a fragmentary pattern of the general regularity of Table 1" (here: Table A.2).

    2 "Such a strict regularity in a change ... exactly for a unit shall be specified (and defined) as the unit change law" (Rakočevič, 1994, p. 36).
    ${ }^{3}$ "... any two adjacent symbols [in Gray code] differ at only one bit" (Swanson, 1984, p. 188).
    4 "The binary-code tree [of the GC] corresponds per se with the Gray code model of the genetic code (Fig. 1 in Swanson, 1984 p. 188)" (Rakočević, 1998, p. 283).
    ${ }^{5}$ Is it just as a curiosity, or more than that, this can not be known, but the fact is that the number of verses in the 100 songs of Divine Comedy of Dante Aligierie corresponds with this sequence: the number of verses in any of the 100 songs is so large that the sum of the digits of the numeral record is $4,7,10$ or 13 , without any exception.
    ${ }^{6}$ We say "hidden relation," since from the aspect of valid paradigms in the current science it is not expected that "quantization" in positions in the decimal numbering records could in any way be analogous to quantization in quantum physics.

[^32]:    7 "The most important characteristic of a codon is whether it has a purine (most significant bit 1) or a pyrimidine (most significant bit 0) at the middle base position ...", etc (Swanson, 1984, p. 188).

[^33]:    ${ }^{8}$ There was, however, an attempt to "integrate" the lanthanides into the Periodic System, by Charles Janet (18491932), so each of them was in a separate group. Unfortunately, it was only in our time recognized that Charles Janet was "unrecognized genius of the Periodic System" (Stewart, 2010).
    9 "Such a surprisingly simple model at the same time represents the Logical-Informational and Geometrical-Homeomorphic-Topological model (LIGHT) of the cube-hypercube with an inscribed sphere-hypersphere." (Rakočević, 1991, p. 1).
    10 "... the chemical code, built on the very principles mentioned and in complete accordance with the genetic code. ... All the relations in the chemical code and the genetic code are in accordance with periodicity and cyclicity of the natural number system ..." (Rakočević, 1991, p. 1).
    ${ }^{11}$ In this paper, we will deal with only the standard genetic code, with the 20 canonical (protein) amino acids, and all other variants of the genetic codes will be considered as 'deviant codes' (Weaver, 2012, pp. 568-569). These codes, namely, do not change nothing on the fact, when it comes to the genetic code as "amino acid code" (Swanson, 1984), because they are represented in all variants with the same 20 protein amino acids. (The only exceptions are Pyrrolyisine and Selenocysteine, presented at some very few organisms.) [Knight at al., 2001, p. 49: "The genetic code evolved in two distinct phases. First, the 'canonical' code emerged before the last universal ancestor; subsequently, this code diverged in numerous nuclear and organelle lineages".]
    ${ }^{12}$ The chemical elements of $s \& p$ types we consider (within this paper) as "intransitive elements", then the elements of $d$ type as "the first transitive elements" and, finaly, the elemets of $f$ type as "the second transitive elements".

[^34]:    ${ }^{13}$ Through designated exponentiations from " m " follow nucleotide singlets and doublets in Survey 1, and triplets in Table 5, and from " n " the number of branches on the genetic code binary tree.
    ${ }^{14}$ From Eq. (1) it follows that the position of the hydrogen in the PSE can only be in the VII group, together with the halogen family, and neither in each other. (Lawrence Sacks, Foundations of Chemistry, 2006, 8, pp. 31-35: "A Coulombic model, in which all compounds of hydrogen are treated as hydrides, places hydrogen exclusively as the first member of the halogen family and forms the basis for reconsideration of fundamental concepts in bonding and structures. The model provides excellent descriptive and predictive ability for structures and reactivities of a wide range of substances.")

[^35]:    ${ }^{15}$ The block names (s, p, d, f) are derived from the spectroscopic notation for the associated atomic orbitals: sharp, principal, diffuse and $\underline{f} u n d a m e n t a l$.

[^36]:    ${ }^{16}$ In the standard GCT the amino acids L, S, R appear twice each; in an extremely nuance reading of the standard GCT the isoleucine appears also twice (Rakočević, 2007b, Table 7; Wohlin, 2015, Table 2); within the "doublettriplet" arrangement of protein AAs where reveals a link between AAs and their biosynthetic precursors, the four AAs from non-alanine stereochemical type (G,P,V,I) appear twice (Survey 1 and Table 1 in Rakočević and Jokić, 1996).

[^37]:    ${ }^{17}$ In front of the sign ' $\&$ ' are elements of the short periods, followed by elements of large periods.
    ${ }^{18}$ Under "unstable elements" we mean those elements, which in addition to the stable, also have unstable primordial isotopes one or more.

[^38]:    19 "Dec 2016 - Project update published in Chem. Int. Nov 2016, p. 25; https://doi.org/10.1515/ci-2016-0619 (Page last updated 11 Jan 2017)"

[^39]:    ${ }^{20}$ In IUPAC document - IUPAC Project 2007-038-3-200, "Development of an isotopic periodic table for the educational community" (October 1, 2013 www.ciaaw.org), for Europium was indicated the state ( $2+0$ ), what means that both its isotopes are stable. However, in "New interactive, electronic version of the IUPAC Periodic Table of the Elements and Isotopes" it is modified so that now it is EU $(1+1)$ because EU-151 is unstable and EU153 the stable isotope, as it is in our system in Survey 2 [Eu-63 (1+1)].

[^40]:    ${ }^{21}$ About Golden mean in periodic system, see in: Luchinskiy \& Trifonov, 1981; Rakočević, 1998a. About Golden mean in GC see in: Rakočević, 1998b, 2014.

[^41]:    ${ }^{1}$ A hypothesis on the determination of the genetic code with the perfect and friendly numbers we have presented in the book (Rakočević, 1997b). (www.rakocevcode.rs) [Perfect numbers: 6, 28, 496, 8128, etc; the pairs of the friendly numbers: (220-284), (1184-1210), (17296-18416) etc.]

[^42]:    2 "Systemic and systematically", that is, correspondent with the principles of continuity and minimum change (which, as we said, apply to both - genetic code and chemical code; cf. footnote 3). Practically, this means writing first the sequence $(0,1,2, \ldots, 9)$ as a vertical column, with the status of the first column. Then the results of the multiplication are written: the results of the multiplication by zero yield the zeroth column, to the left of the first column; the results of the multiplication by the unit give this same, start-up, t.e. the first column. Next, continuous columns of multiplication with 2,3 , etc

[^43]:    ${ }^{3}$ "... the chemical code, built on the very principles mentioned and in complete accordance with the genetic code. ... All the relations in the chemical code and the genetic code are in accordance with periodicity and cyclicity of the natural number system ..." (Rakočević, 1991, p. 1). (Cf. footnote 10.)
    4 "With insight into the results ... one is forced to propose a hypothesis (for further researches) that here, there really is a kind of intelligent design; not the original intelligent design, dealing with the question - intelligent design or evolution, which is rightly criticized .... Here, there could be such an intelligent design, which we could call 'Spontaneous Intelligent Design' SPID) that is consistent with that design which was presented by F. Castro-Chavez (2010), and is also in accordance with the Darwinism" (Rakočević, 2015, footnote 47) [Additional note: The evidence that Darwin tacitly advocates the idea of intelligent design, learns from the insight that his only illustration (Diagram) in Origin of Species is actually a strict mathematical program corresponding, directly and / or indirectly, to the structures currently known within Multiplication Table (TM) and within Table of Minimal Adding (TMA) [About Darwin's Diagram as a mathematical program one can see in (Rakočević, 1994; 2015).]
    ${ }^{5}$ These pairs are exceptions also in the basic chemical characteristic. The CM is the only pair in which both members, apart from atoms of the first and second periods of PT of chemical elements, possess one atom from the third period. On the other hand, the ST and CM pairs are chemically similar and constitute a set of halcogen AAs, over oxygen and sulfur, both from the sixth group of halcogen elements. With this insight, it is easier to understand why they are at the center of CIPS: they start counting from them and have an ordinal number 1.
    ${ }^{6}$ Doolittle (1985, p. 76) has shown that a possible replacement of amino acids during the evolution of proteins must be "based on the size of the amino acid's side chain and on the degree to which it is polarized".

[^44]:    ${ }^{7}$ Specificity is, among other things, in the fact that AAs of alanine stereochemical type are taken by once and of non-alanine type (GP-VI) by twice (cf. Remark 3). In addition, the specificity is that "specific amino acid arrangement" exists in a direct connection with the system of amino acids precursors, with their order of inclusion, thus confirming each other - the choice of AAs and their precursors.

[^45]:    8 "In correspondence with this, Complete Genetic Code must be based on several key principles. We are going to list only those considered to be the most important: 1. The principle of systemic self-related and self-similar organization. ..." (Rakočević, 2004, p. 231).
    9 "In determination of the genetic code, except two inherent alphabets - twenty amino acids and four amino bases (two pyrimidines \& two purines - is involved still one "hidden alphabet", the series of natural numbers, with all its regularities and laws" (Rakočević, 2011a, p. 4). (Cf. footnote 3.)

[^46]:    ${ }^{1}$ In fact, this is the third time. The first time, it was twenty-three (Rakočević, 1991), and the second time, it was 20 years ago (Rakočević, 1994). But both times it was only a pilot study, which was to serve as the initial "trigger" for a comprehensive analysis, the results of which are now presented. (Rakočević, 1991, p.4: „This diagram represents a specific coding system and the code program".) (Rakočević, 1994, p.16: as here in Box 1 and Box 2.)
    ${ }^{2}$ Primary branches go from the previous level (line) and they always reach the next level (and they are designated by letters). Secondary branches, however, fail to reach the next level, they are not finalized; they do not become a taxonomic category (a variety, species, and so on.)

[^47]:    3 "Surprisingly, the genetic code really privileges a number system and, even more unusual, the system is the decimal one" (Shcherbak, 2008, p. 157).
    ${ }^{4}$ Here we address the Mendeleev's principles of one element or one period change; But we also bear in mind the validity of these two principles in the genetic code (Swanson, 1984, p. 187).
    ${ }^{5}$ All of these copies, plus two tables, can be found on our website ("The Mendeleev's archive"). Those particularly significant are: a copy (copy I, p. 128) which demonstrates "the chemical patience (solitaire)"; copy IV, which presents the chemical elements in the even/odd positions, with a drawing which indicates the number of odd and even valences, and the atomic mass differences are presented using the Pythagorean method of determining the differences in tetraktis (by Mendeleev in $n$-aktis); and copy VIII with the diagonal relations drawn in the Periodic system table.

[^48]:    ${ }^{6}$ Positioning "from smaller to larger" in the genetic code is from the left to the right, and in Darwin's diagram it is from the right to the left.
    ${ }^{7}$ In Shcherbak's diagram the smaller part is in the upper part of the Diagram and the large part is down in the lower part of the Diagram, while in Darwin's diagram it is the opposite. However, as the first inversion (with respect to the genetic code) is essentially natural, the latter is completely random.
    ${ }^{8}$ This "first glance" refers to descendants that follow from the species "A" and "I", whereas for the remaining species (B, C, D, E, F on the left and G, H, K, L on the right), the situation is somewhat different, and that will be explained in the text which follows.
    ${ }^{9}$ All branches (the sum $60+216=276$ ) which are the descendants of all 11 species designated with large Latin letters at the bottom of the Diagram are included into this counting.

[^49]:    ${ }^{10}$ In Darwin's words: „The accompanying diagram will aid us in understanding this rather perplexing subject. Let A to $L$ represent the species of a genus large in its own country. These species are supposed to replase each other at unequal degrees, as is so generally the case in nature, and as is representes in the diagram by the letters standing at unequal distances" (The Origin of species, 1876, Chapter IV, p. 90).
    ${ }^{11}$ One might think that this omission is done because the two adjacent letters "I" and "J" are similar to each other, so that Darwin wanted to avoid confusion. We, however, believe that this is such a code, which requires the omission of only the $10^{\text {th }}$ letter, no matter how it looks.
    ${ }^{12}$ As if Darwin wanted to tell us something about these numbers; perhaps to present their uniqueness: [(11/11, $22 / 22,33 / 33, \ldots, 99 / 99),(12 / 21,24 / 42,36 / 63),(13 / 31,26 / 62,39 / 93)]$ (cf. Table A. 1 in Appendix A).
    ${ }^{13}$ This absence of branches should not be confused with the fact that at every level the branches (taxonomic entities) from the previous level are finalized, so thus, branches whose development started at the 9 th level are finalized at the tenth level.
    ${ }^{14}$ Future researches should show whether this self-similarity is of fractal and/or non-fractal nature. A significant fact with regard to this, is Darwin's insisting on the fact that the structure of the Diagram can also refer to various taxonomic categories. (The Origin of species, Chapter IV, p. 91: "When a dotted line reaches one of the horizontal lines, and is there marked by a small numbered letter, a sufficient amount of variation is supposed to have been accumulated to form it into a fairly well-marked variety, such as would be thought worthy of record in a systematic work"; Chapter XI, p. 303: "We may suppose that the numbered letters in italics represent genera, and the dotted

[^50]:    lines diverging from them the species in each genus. ... The horizontal lines may represent successive geological formations, and all the forms beneath the uppermost line may be considered as extinct.") As if the same fractal motif extended along the overall evolutionary lines.
    ${ }^{15}$ Is it just a curiosity, that number 28 is the second perfect number?
    ${ }^{16}$ The same or similar proportionalities exist for the number of nodes, as well as for the number of branchings, which will be discussed further.

[^51]:    ${ }^{17}$ The Origin of species, 1876, Chapter IV, p. 91: "In the diagram the process is represented up to the ten-thousandth generation, and under a condensed and simplified form up to the fourteen-thousandth generation."
    ${ }^{18}$ The Origin of species, 1876, Chapter IV, p. 94: "Hence very few of the original species will have transmitted offspring to the fourteen-thousandth generation. We may suppose that only one ( F ), of the two species which were least closely related to the other nine original species, has transmitted descendants to this late stage of descent. The new species in our diagram descended from the original eleven species, will now be fifteen in number.".
    ${ }^{19}$ Notice that square of $11\left(11^{2}=121\right)$ is zeroth case in logical-arithmetical arrangement presented in Table A.1; also, the tenth part of the fourth friendly number, 1210 [more exactly, the second member of the second pair (1184 $\& 1210)$ of friendly numbers].
    ${ }^{20}$ In addition, it is "arranged so" that the diagonal result changes, for $10 / 01$, respectively: The pattern $52 / 60$, valid for all primary branches (Table 2.1) was changed into the pattern 62/59 (Table 2.2), valid for secondary branches (cf. Section 4.6, first paragraph).
    ${ }^{21}$ More details on the determination of GC by perfect and friendly numbers see in Rakočević, 1997b, p. 60.

[^52]:    ${ }^{22}$ Table 4.5 presents the missing 88 (all branches on the second tree, for the "A" and "I" species, in $3 \times 5$ arrangement, $0-14$ level), and again Table 7.5 (primary branches in all 11 species, $0-9$ level); in Table 5 there is the number 99 , also missing in this sequence.
    ${ }^{23}$ In relation to Table 6.1 there are Tables 6.2, 6.3, 6.4 and 6.5 , in relation to Table 7.1 there are Tables 7.2, 7.3, 7.4 and 7.5.

[^53]:    ${ }^{24} \mathrm{~A}$ second manner in which we write this formula is $\mathrm{N}=2(2 \mathrm{n}+1)(\mathrm{n}=0,1,2,3)$. A "half" of this formula, in the form $\mathrm{N}=(2 \mathrm{n}+1)(\mathrm{n}=0,1,2,3)$ is just a formula for calculation of the odd numbers and the number of atom orbitals: 1s, 3p, 5d, 7f ...
    ${ }^{25}$ In addition to what was written 20 years ago, now some refinements are given. It is obvious that Darwin in several different ways makes distinctions corresponding to the Hückel's rule. Two ways are explicit, one in a set of letters, and another in the set of the branches. First, we present solutions in the set of letters. So, the case for $\mathrm{n}=0$, and $\mathrm{N}=$ 2 refers to the second letter of the alphabet (B), which begins the second set of species. [In the first set there are (A, I), while in the second set there are (B, C, D, E, F, G, H, K, L).] The case for $\mathrm{n}=1$ and $\mathrm{N}=6$, refers to the 6th letter (F), which separates the left tree from the right tree in the Diagram. The case for $\mathrm{n}=2$ and $\mathrm{N}=10$ refers to the 10th letter (J), which is excluded. The case for $\mathrm{n}=3$ and $\mathrm{N}=14$, refers to the 14th letter ( n ), which for the first and for the last time appears on the 14th level. [Letter $n$ as $13^{\text {th }}$, the middle letter reading backwards.] The solutions in the set of branches are these: on the $2^{\text {nd }}$ level, a first fixed branch appears ( $s 2$ ); after the $6^{\text {th }}$ level there is no branching; on the $10^{\text {th }}$ level there is the finalization of the branches from the lower part of the Diagram, and on the $14^{\text {th }}$ level there is the finalization of the branches from the upper part of the Diagram.
    ${ }^{26}$ Two linear equations whose unknown quantities are linked with a plus sign and two are associated with a minus sign.

[^54]:    27 "According to Mendel, such system is determined by the four entities, $1^{n}-2^{n}-3^{n}-4^{n}(n=1,2,3 \ldots)$ : Stammarten - Konstante Formen - Glieder - Individuen ... Note that Mendel only uses the term Stammarten, i.e. Stammpflanzen for the first entity but not the mathematical expression $1^{\text {n }}$ which we use for the explanation of the Mendel's idea" (Rakočević, 1994, p. 176).
    ${ }^{28}$ However, by branching, not only levels are classified into $7+3$, but that was also done through the distribution of branchings on the left and the right tree; on the left tree the 7 of them, and on the right 3 branchings.

[^55]:    ${ }^{29} \mathrm{Cf}$. Section 4.1, paragraph 6, the first to the last.

[^56]:    ${ }^{30}$ As a result of splitting the arrangement $5+5$ into $7+3$, a specific self-similarity also appears through the patterns (46/44 versus 66/64) in Tables 4.1 and 4.2, respectively.
    ${ }^{31}$ The change of $\pm 02$ is in relation to the diagonal result 80/97 in Table 4.2.

[^57]:    ${ }^{32}$ L.N. Tolstoy (by Pierre Bezukhov in "War and Peace"): "Today my benefactor revealed me a part of the secret. He spoke about a large outer space square and he told me that the third and the seventh number are the basis of everything".
    ${ }^{33}$ Cf. the result 66 in the upper part and 037 in the lower part in Table 4.3 with the same pattern $(66 / 037)$, also 66 in the upper part and 037 in the lower part, in Survey B.1.
    ${ }^{34}$ Kedrov, 1977, p. 128, photocopy X. Having found the result where Mendeleev allegedly made a mistake in two out of three cases (!?), Kedrov concluded that even the greatest can make a mistake. In our opinion, Mendeleev did not make a mistake, he actually made his (hidden) code, which strictly corresponds to the Darwin's. (cf. Survey B.4).
    ${ }^{35}$ The results shown in Tables 6.1-6.5 refer to the "other nine species", while the results for the "all 11 species" are shown in Tables 7.1-7.5; in all of these tables, the letters on the two final branches, instead of the previous designation with small letters " a " and " z " now have the designations â and $\hat{\mathrm{z}}$, with circumflex accent.

[^58]:    ${ }^{36}$ Cf. this result $\mathbf{0 7}$ for the total number of secondary branches (at 0-6 level, i.e. at1-7. level), in „other nine species", with 07 primary finalized and fixed branches in „first two species" ("A" and "I", in Table 1.4) at 0-7 level, i.e. at 1-8 level.
    ${ }^{37}$ As we see, Darwin's splitting into $7+3$ levels is given not only in the logic of branching (the nodes for the "first two" species "A" and "I"), but also in the logic of the secondary branches layout (in levels) for the "other nine species." Moreover, this logic is given for the third time as well, in the right part of the Diagram, for the "other four species" (G-H and K-L) not any branch, neither primary nor secondary, is present at the levels after the sixth. [Notice that "nine other species" are splitting into five on the left, and four on the right.]
    ${ }^{38} \mathrm{Cf} .39$ all branches in "other nine species" (Tab.6.5) with all 49 primary, finalized non-fixed branches in the "first two species" ("A" and "I") (Table 1.4).
    ${ }^{39}$ In the Preliminaries we have presented that here, there is also the relation between the "final" result in the genetic code ( 60 of "Prime Quantum 037" and $5^{\wedge} 2 \times 037$ ) and the "final" result in Darwin's diagram ( 60 of "First Quantum $01 "$ and $1 \times 6^{\wedge} 3$ ). And the relation between the numbers 2220 and 925 in the GC is obvious (in fact it is both times determined by Pythagorean Law) while in Darwin's diagram the relation between 60 and 216 is almost unnoticeable. In the absence of a more obvious insight, we now present a possible regularity: $60=5 \times(6+6)$ and $216=6 \times(6 \times 6)$.

[^59]:    ${ }^{40}$ One-meaning AAs are decoded by the codons from one codon family, but two-meaning AAs are decoded by codons from two codon families (L,S, R).

[^60]:    ${ }^{41}$ In one of his first works in which he presented that the physico-chemical classification of the constituents of the genetic code is followed by arithmetical patterns and the balance of the number of particles (nucleons), V. Shcherbak concluded that "The physical nature of such a phenomenon is so far not clear" (Shcherbak 1993, last sentence).
    ${ }^{42}$ The number 276 as the total number of branches within Darwin's diagram. Anyway, here within the set of "possible cases" there are all two-digit, three-digit and four-digit numbers, provided that the zeroth case $(1,12,12)$ is excluded; because, if it was involved, then single-digit numbers would be included as well, and the combinations would be - the combinations with repetition, so the probability would be even less.

[^61]:    ${ }^{43}$ The result $52+60=112$ as the number of primary branches within species "A" and "I" (Table 2.1). Anyway, within the set of "possible cases" there are all two-digit, three-digit and four-digit numbers, provided that the zeroth case $(0,12,12)$ is excluded; because, if it was involved, single-digit numbers would be included as well, and the combinations would be - the combinations with repetition, so the probability would be even less.
    ${ }^{44}$ Notice that arithmetical system in Figure 5 is a derivative of the system in Figure 4, of its first row.
    ${ }^{45}$ Having realized that this triple is an element of another system, as well (Table C.2), which is in a strict connection with the system in Table C.1, and which is a direct determinant of the genetic code (the determinant of assignment of codons to amino acids, classified into four types of diversity), the calculation of probability practically loses its point; it becomes immediately obvious that intentions, and not coincidences are present here. At the same time, it becomes clear how and why the structure of Darwin's diagram corresponds with the structure of the genetic code, although, in the time when he lived, Darwin could not know anything about the genetic code. Simply, Darwin understood relations in arithmetical systems, presented in Tables C. 1 and C.2, based on which, as we now know, the genetic code was also built.
    46 " ... and in the systems of distant celestial spheres ... changes, similar to those which happen in front of us during the chemical reactions of particles, have been happening up to now. A future Newton will discover the laws of these changes, as well. And, although the chemical changes are unique, they are, however, just variations on the general theme of harmony which regins in the nature" (Mendeleev, 1958, p. 554).

[^62]:    ${ }^{47}$ Rakočević, 2013, p. 10: "With insight into the results ... one is forced to propose a hypothesis (for further researches) that here, there really is a kind of intelligent design; not the original intelligent design, dealing with the question - intelligent design or evolution (Pullen, 2005), which is rightly criticized by F.S. Collins (2006). Here, there could be such an intelligent design, which we could call "Spontaneous Intelligent Design" (SPID) that is consistent with that design which was presented by F. Castro-Chavez (2010), and is also in accordance with the Darwinism. [F. Castro-Chavez (2010, p. 718): "We can conclude that the genetic code is an intelligent design that maximizes variation while minimizing harmful mutations."] Actually, it can be expected that the hypothetical SPID, contained in the results ..., is in accordance with an identical (or similar?) SPID, presented in the only diagram, in Darwin's book "Origin of Species" (Darwin, 1996), as we have shown through an analysis of that diagram in one of our books (Rakočević, 1994; www.rakocevcode.rs). [In the case of the statement that spontaneity and intelligent design are mutually opposite, one must ask the question: isn't it true that human intelligence is the result of a spontaneous evolutionary process?]"
    ${ }^{48}$ Kaufman, 2014, p. 1: "As Gabora points out, ideas and artifacts get put to new uses and combined with one another in new ways for new functionalities, and this is what underlies technological, cultural and political evolution. None of this is captured or even approachable by way of a Darwinian theory of culture. Gabora does two things in this paper. First, she levels a reasoned and devastating attack on the adequacy of a Darwinian theory of cultural evolution, showing that cultural evolution violates virtually all prerequisites to be encompassed by Darwin's standard theory. Second, she advances the central concept that it is whole world views that evolve."

[^63]:    ${ }^{49}$ The connection with the number 276 through the relation: $\varphi(276)=88(088+188=276)$
    ${ }^{50}$ The connection with the number 60 and 56 through the relation: $\varphi(116)=56(56+60=116)$; the $\mathbf{5 6}$ as all primary branches at 1-10 levels as well as at 11-14 levels, for two species A and I (Tab. 2.1); the 60 as total number of all branches in upper part of Darwin Diagram (DD): the 56 as said, plus 4 branches in second set of species ( 9 species) as it is shown in (Table 6.1). [Note: in Table 6.1 see above the levels $10-14$ with only 4 branches.]; the 116 as complement of 216 (footnotes 55 and 58).
    ${ }^{51}$ The 233, as all branches (prim. + second.) for two species, "A" and "I" into ( $3 \times 5$ ) levels (Tab. 4.5). Here: $111+$ 122 equals 233. In DD: 112 as all primary branches +121 as all secondary branches equals 233 .

[^64]:    ${ }^{52}$ The $\mathbf{1 1 2}$ as the number of all primary branches for two species, "A" and "I" into ( $3 \times 5$ ) levels (Tab. 2.1).
    ${ }^{53}$ The $\mathbf{1 2 1}$ as all secondary branches for two species, "A" and "I", into (1-10) levels (Table 2.2).
    ${ }^{54}$ The $\mathbf{1 7 7}$ as all branches (primary + secondary) for two species, "A" and "I" into (1-10) levels (Tab. 4.1). xxx
    ${ }^{55}$ The 216 as all branches (primary + secondary) for all 11 species at $1-10$ levels (Table 7.2). xxx
    ${ }^{56}$ The $\mathbf{3 8 4}$ as total number of atoms in 20 amino acid molecules, within their "bodies" and "heads".
    ${ }^{57}$ Cf. with the starting 777 in Table B.2.
    ${ }^{58}$ The $\mathbf{2 1 6}$ as in footnote 55; then the $\mathbf{1 1 6}$ contains all other quantitatives to the sum of 332 (Table 5) "branch" quantitatives: 60 branches at 11-14 levels into all 11 species, plus 46 nodes (Table 3.1), plus 10 branchings (Table 3.2) [Note: the nodes and branchings exist only in species, "A" and "I".]
    ${ }^{59}$ The $\mathbf{8 8}$ as all primary branches for all 11 species at $1-10$ levels (Table 7.5). The $\mathbf{1 8 8}$ as the sum of all other branches to the total sum of $\mathbf{2 7 6}$.
    ${ }^{60}$ The 39 as all branches (primary + secondary) for 9 species (B, C, D, E, F on the left and G, H, K, L on the right) at 0-9, i.e. 1-10 levels (Table 6.5).
    ${ }^{61}$ The $\mathbf{4 3}$ as all branches (primary + secondary) for 9 species (B, C, D, E, F on the left and G, H, K, L on the right) at $0-14$ levels (Table 6.4).
    ${ }^{62}$ The $\mathbf{4 3}$ as in footnote 61.

[^65]:    ${ }^{78}$ Appendices labeled with the letters "I" and "J" in this paper do not exist.

[^66]:    research situations. With them, from the early nineties of the twentieth century, there is still a model of intelligent design, what will be discussed further in a following paper.
    ${ }^{2}$ By this, the words are arranged in quartets, quintets, sixth, and so on, respectively. That's because this is the first, the simplest n -tet, in which each letter of the alphabet used at least once.
    ${ }^{3}$ Božidar Knežević (1862-1905), a famous Serbian philosopher of history („The Serbian Montaigne"): "One of the basic laws that are the same for the whole nature and all human things is the law of order. With one and the same order are going the things in all external nature, and in the process of individual and social life of a human, in the matter, and in the process of soul and spirit" [14].
    ${ }^{4}$ Bearing in mind the relation $\left(2^{6} \rho 6^{2}\right)$ it becomes clear why from the 64 coding words (codons) in the genetic code to encode the amino acids are used $61\left(36+25=6^{2}+5^{2}=61\right)$, and three codons have a "stop" function (encode the end of protein synthesis) (cf. legend to Figure 3).
    ${ }^{5}$ Why the decimal numbering system is the best possible in the coding processes, see our paper [15].
    ${ }^{6}$ The first Njegoš's triptych make: Glas kamenštaka (The Stone Man's Voice), Svobodijada (Voices of Freedom) and Ogledalo srpsko (The Serbian Mirror); the second triptych: Luča mikrokozma (The Ray of the Microcosm), Gorski vijenac (The Mountain Wreath) and Lažni car Šćepan Mali (The False Tsar Stephan the Small) [18].

[^67]:    ${ }^{12}$ On the four diversity types of AAs $(2+4+6+8)$ as it is presented in linear model of Figure 2, about a strict chemical hierarchy within and between them, the reader can see in Ref. [15].
    ${ }^{13}$ The only exception is valine, which is understandable enough when we know that valine and isoleucine belong to the same stereochemical type, the valine type. That sequence should, therefore, be understood as follows: two AAs of the alanine stereochemical type ( $\mathrm{N}, \mathrm{Q}$ ) are followed by two AAs of the valine stereochemical type (V, I).

[^68]:    ${ }^{14}$ The dilemma whether before N or P is resolved by the following pairs: N is followed by a smaller pair $\mathrm{V}(10)-\mathrm{I}(13)$, while $P$ by a larger one $\mathrm{L}(13)-\mathrm{K}(15)$.

[^69]:    ${ }^{15}$ There are, however, the authors with a point of view, that the mathematical essence birth the matter as such. Similar view had a great Serbian poet, and philosopher in addition, Laza Kostić; the 127 years ago he wrote: "The twins of the cross principle, fertilized by pure crossing, symmetry and harmony, were able to conceive the universe and then born it, developed, and populated with eternal life." ("Bliznakinje načela krsta, oplođene čistim ukrštajem, simetrija i harmonija su uspele da začnu vaseljenu i da je rode, razviju i nasele večnim životom") [20].

[^70]:    ${ }^{16}$ In the case of the system of the constituents of the genetic code, this activity refers to the possibility of generating the life.
    ${ }^{17}$ This issue is important from the aspect of interpretation that the genetic code from the beginning was complete or not; whether it was possible that life arises only with the $7-8$ amino acids - what is the prevailing view of the current science - or the genetic code from the very beginning must be a complete system of molecules [21]?

[^71]:    ${ }^{1}$ "All together, they favor the recognition that the chemical reactions that determine the GC are not only the reactions in a "test tube", but these reactions are associated with a specific balance of the number of particles (atoms and nucleons); balance, determinated by unique arithmetic and algebraic regularities and expressed in the form of specific (nonfractal) selfsimilarity ("a harmonized chemistry"). From this it follows further that presented facts also support the hypothesis that the genetic code was from very beginning, in prebiotic times and conditions, a complete code. On the other hand, the knowledge that "the chemistry of living" is actually a harmonized chemistry requires great care in medicine, agriculture and natural environment, taking into account the fact that this harmonization is strictly immanent to the living as such, mediated by genetic code as such" [24c].

[^72]:    ${ }^{1}$ The 16 photocopies are placed between 128 and 129 pages of Kedrov's book. In addition, we add them here two tables; Table 13 from page 183 and Table 16 from page 188.

[^73]:    ${ }^{1}$ The whole paragraph in the letter reads: "Ants, brought to life by the Creator build their artistic anthills, and bees, their majestic palaces. And I, as the intellectual substance of the Creator, must needs follow the general accord. "
    ${ }^{2}$ The first triptych: The Voice of Mountaineers, The Song of Freedom, The Serbian Mirror, and the second triptych: The Ray of Microcosm, The Mountain Wreath and The False Tsar Stephen the Small.
    ${ }^{3}$ M. Rakocevic Njegosh's Primordial Logos (in Serbian), Volume I in 2000. and Volume II in 2003. (Interpres, Belgrade). This book will soon be available on the website: www.rakocevcode.rs

[^74]:    ${ }^{4}$ The best possible harmony (coherence) implies relations of the best possible symmetry, reduced to division of the segment line into two equal parts; as well as the relations of the best possible harmony, presented with the harmonic mean of the system (seen as a unit segment line) and the golden mean, which represents the relations of the best possible proportion, as well.
    ${ }^{5}$ The Ray, III 148-150: "Steps are mine Devine, / Yet I may name it the space".

[^75]:    ${ }^{6}$ M. Schonberger, The I Ching and Genetic Code ( ASI, New York, 1980).
    ${ }^{7}$ M.M. Rakočević, The genetic code as a Golden mean determined system, BioSystems, 46 (1998).
    ${ }^{8}$ B.M. Kedrov, Prognozy D.I. Mendelyeva v atomistike - neizvestnie elementi, Atomizdat, Moskva, 1977.

[^76]:    ${ }^{9}$ See the following works: 1. M.M. Rakocevic, Univerzalna svest i univerzalni kod, in: Consciousness - Scientific Challenge of the 21st Century, Symposium (ECPD, Belgrade, 1996); 2. M.M. Rakocevic, The Universal Consciousness and The Universal Code. In: Consciousness - Scientific Challenge of the 21st Century (ECPD, Belgrade, 1995), 3. M.M. Rakocevic, The Universal Consciousness as a Universal Comprehension of the Universal Code. In: Brain and Consciousness (ECPD, Belgrade, 1997). The second, hereby suggested paper can be found in the book: M.M. Rakocevic, Genetic Code as a Unique System (SKC, Beograd, 1997), which is also available on our website ( www.rakocevcode.rs ). The same illustrations can be found in Annex. No. 7 in the second volume of our book "Njegosh's Primordial Logos."

[^77]:    ${ }^{10}$ In relation to this, 2013th year, it has been exactly 60 years since in 1953., Francise Crick and James Watson revealed the structure of the gene (nucleic acid, DNA), and 50 years, since in 1963. experimental studies (which showed that the triplet molecular aggregations of DNA (more exactly, of RNA) are coded for 20 amino acid molecules in their building of proteins) were finished.
    ${ }^{11}$ That is also stated in my book, Genetic Code as a Unique System (SKC Nis; Bina, Belgrade, p. 60, also available on the website: www.rakocevcode.rs).
    ${ }^{12}$ There are six songs in the Ray; then 'Kolo' six times in The Wreath; there also are $6+1$ Montenegrins in The Wreath as Vuk (six active persons and one silent character: Vuk Borilović), there are also $6+1$ Turks (six Turkish chiefs and one Turkish wedding guest).
    ${ }^{13}$ See "Explanations with The Ray of Microcosm" in: P. P. Njegoš, Celokupna dela, Prosveta-Beograd and Obod-Cetinje, seventh edition, Book III, p. 351, where it is said that Nikola Banašević in 1954. proposed such a hypothesis.
    ${ }^{14}$ Aurelius Augustine, God's Country, (CID, Podgorica, 2004, p. 473).
    ${ }^{15}$ Alvager et al, 1989, Biosystems, 22, p. 191: „The number of all distributions in the set of 64 codons is 1741630."

[^78]:    ${ }^{16}$ Permutation cyclicity in two steps is achieved by each (read in three positions) two-digit number, whereas in the third step cyclicity, i.e. conservation of the three figures altogether, is achieved solely by number 037 .However, the next number, number 038, cannot achieve that. Namely, $1 \times 038=038$ and $10 \times 038=380$, but already in the next modular cycle the three figures disappear because $19 \times 038=722$, and not 803 as expected according to the rules.
    ${ }^{17}$ V.I. Shcherbak, Sixty-four triplets and 20 canonical amino acids of the genetic code: the arithmetical regularities. Part II. J Theor. Biol. 166 (1994), pp. 475-477.

[^79]:    ${ }^{18}$ L. de Freitas, 515 - a symmetric number in Dante, Computers Math. Applic. 17 (1989), pp. 887-897.

[^80]:    ${ }^{19}$ The numbers are written in the decimal numeral system digits. The result of " 48 " in the octal system is written as " 60 ". It should be noted that the simple / composite number positions are different from the situation in the decimal numeral system.

