Algorithm of Insulin – Amino acid Gln

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Abstract: This paper discusses cyberinformation studies of the amino acid composition of insulin, **amino acid Gln**, in particular the identification of scientific terminology that could describe this phenomenon, ie, the study of genetic information, as well as the relationship between the genetic language of proteins and theoretical aspects of this system and ybernetics. The results of this research show that there is a matrix code for insulin. It also shows that the coding system within the amino acid language gives detailed information, not only on the amino acid "record", but also on its structure, configuration, and various shapes. The issue of the existence of an insulin code and coding of the individual structural elements of this protein are discussed. Answers to the following questions are sought. Does the matrix mechanism for biosynthesis of this protein function within the law of the general theory of information systems, and what is the significance of this for understanding the genetic language of insulin? What is the essence of existence and functioning of this language? Is the genetic information characterized only by biochemical principles or it is also characterized by cyberinformation principles? The potential effects of physical and chemical, as well as cybernetic and information principles, on the biochemical basis of insulin are also investigated. This paper discusses new methods for developing genetic technologies, in particular more advanced digital technology based on programming, cybernetics, and informational laws and systems, and how this new technology could be useful in medicine, bioinformatics, genetics, biochemistry, and other natural sciences.

Keywords
human insulin, insulin model, insulin code, genetics code, amino acid Gln

I.INTRODUCTION

The biologic role of any given protein in essential life processes, eg, insulin, depends on the positioning of its component amino acids, and is understood by the „positioning of letters forming words". Each of these words has its biochemical base. If this base is expressed by corresponding discrete numbers, it can be seen that any given base has its own program, along with its own unique cybernetics and information characteristics. Indeed, the sequencing of the molecule is determined not only by distin biochemical features, but also by cybernetic and information principles. For this reason, research in this field deals more with the quantitative rather than qualitative characteristcs of genetic information and its biochemical basis. For the purposes of this paper, specific physical and chemical factors have been selected in order to express the genetic information for insulin. Numerical values are them assigned to these factors, enabling them to be measured. In this way it is possible to determine oif a connection really exists between the quantitative ratios in the process of transfer of genetic information and the qualitative appearance of the insulin molecule. To select these factors, preference is given to classical physical and chemical parameters, including the number of atoms in the relevant amino acids, their analog values, the position in these amino acids in the peptide chain, and their frenquencies.There is a arge numbers of these parameters, and each of their gives important genetic information. Going through this process, it becomes clear that there is a mathematical relationship between quantitative ratios and the qualitative appearance of the biochemical „genetic processes" and that there is a measurement method that can be used to describe the biochemistry of insulin.

Insulin Model

The structure 1AI0 has in total 12 chains: A,B,C,D,E,F,G,H,I,J,K,L.

1AI0:A

G	I	V	E	Q	C	C	T	S	I	C	S	L	Y	Q	L	E	N	Y	C	N
10	22	19	19	20	14	14	17	14	22	14	14	22	24	20	22	19	17	24	14	17
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21

1AI0:B

F	V	N	Q	H	I	C	G	S	H	L	V	E	A	L
23	19	17	20	20	22	14	10	14	20	22	19	19	13	22
22	23	24	25	26	27	28	29	30	31	32	33	34	35	36
Y	L	V	C	G	E	R	G	F	I	Y	T	P	K	T
24	22	19	14	10	19	26	10	23	22	24	17	17	24	17
37	38	39	40	41	42	43	44	45	46	47	48	49	50	51

etc.

Figure 1. Group of chains A,B,C,D,E,F,G,H,I,J,K,L

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Notes: Aforementioned aminoacids are positioned from number 1 to 306. Numbers 1, 2, 3, n... present the position of a certain aminoacid. This positioning is of the key importance for understanding of programmatic, cybernetic and information principles in this protein. The scientific key for interpretation of bio chemical processes is the same for insulin and as well as for the other proteins and other sequences in biochemistry.

II.METHODS

Insulin can be represented by two different forms, ie, a discrete form and a sequential form. In the discrete form, a molecule of insulin is represented by a set of discrete codes or a multiple dimension vector. In the sequential form, an insulin molecule is represent by a series of amino acids according to the order of their position in the chains 1AI0.

Therefore, the sequential form can naturally reflect all the information about the sequence order and lenght of an insulin molecule. The key issue is whether we can develop a different discrete method of representing an insulin molecule that will allow accomodation of partial, if not all sequence order information? Because a protein sequence is usually represented by a series of amino acids should be assigned to these codes in order to optimally convert the sequence order information into a series of numbers for the discrete form representation

Expression of Insulin Code Matrix - 1AI0

The matrix mechanism of Insulin, the evolution of biomacromolecules and, especially, the biochemical evolution of Insulin language, have been analyzed by the application of cybernetic methods, information theory and system theory, respectively. The primary structure of a molecule of Insulin is the exact specification of its atomic composition and the chemical bonds connecting those atoms.

III ALGORITHM

We shall now give some mathematical evidences that will prove that in the biochemistry of insulin in there really is programmatic and cybernetic algorithm in which it is „recorded“, in the language of mathematics, how the molecule will be built and what will be the quantitative characteristics of the given genetic information.

Atomic progression

Step 1 (Amino acids from 1 to 306)

[AC1 + (AC1+ AC2) + (AC1+ AC2+ AC3)..., + (AC1+ AC2+ AC3..., + ACR)] = **S1**;
AC1 = APa1;
(AC1+ AC2) = APa2 ;
(AC1+ AC2+ AC3) = APa3;
(AC1+ AC2+ AC3..., + AC306) = APaR;
APa1,2,3,n = Atomic progression of amino acids 1,2,3,n
[APa1+APa2+APa3)..., + APaR)] = **S1**;

Step 2 (Amino acids from 306 to 1)

[ACR + (ACR+ AC(R-1)) + (ACR+ AC(R-1)+ Ac(R-2))..., + (ACR+AC(R-1)+AC(R-2)..., +AC1)] = **S2**;
ACR = APbR;
(ACR+ AC(R-1)) = APbR;
(ACR+ AC(R-1)+ AC(R-2)) = APb(R-2);
(ACR+ AC(R-1)+ AC(R-2)..., + AC1) = APb1;
APbR,(R-1),(R-2), …,n = Atomic progression of amino acids R,(R-1),(R-2),…n;
[APbR+APb(R-1)+APb1(R-2))..., + APb1)] = **S2**;

Within the digital pictures in biochemistry, the physical and chemical parameters are in a strict compliance with programmatic, cybernetic and information principles. Each bar in the protein chain attracts only the corresponding aminoacid, and only the relevant aminoacid can be positioned at certain place in the chain. Each peptide chain can have the exact number of aminoacids necessary to meet the strictly determined mathematical conditioning. It can have as many atoms as necessary to meet the mathematical balance of the biochemical phenomenon at certain mathematical level, etc. The digital language of biochemistry has a countless number of codes and analogue codes, as well as other information content. These pictures enable us to realize the very essence of functioning of biochemical processes. There are some examples:

Table 1. **Schematic representation of the atomic progression APa and APb (Amino acid Gln – position from 5 to 280 AA).**
The structure 1AI0 – Amino acid Gln

	Q	**Q**	**Q**	**Q**	**Q**	**Q**	**Q**	**Q**	**Q**
Number of atoms	**20**	**20**	**20**	**20**	**20**	**20**	**20**	**20**	**20**
Rank	**5**	**15**	**25**	**56**	**66**	**76**	**107**	**117**	**127**
APa	**90**	**265**	**457**	**1030**	**1205**	**1397**	**1970**	**2145**	**2337**
APb	**5570**	**5395**	**5203**	**4630**	**4455**	**4263**	**3690**	**3515**	**3323**
AP(a,b)	**5660**	**5660**	**5660**	**5660**	**5660**	**5660**	**5660**	**5660**	**5660**

	Q	**Q**	**Q**	**Q**	**Q**	**Q**	**Q**	**Q**	**Q**
Number of atoms	**20**	**20**	**20**	**20**	**20**	**20**	**20**	**20**	**20**
Rank	**158**	**168**	**178**	**209**	**219**	**229**	**260**	**270**	**280**
APa	**2910**	**3085**	**3277**	**3850**	**4025**	**4217**	**4790**	**4965**	**5157**
APb	**2750**	**2575**	**2383**	**1810**	**1635**	**1443**	**870**	**695**	**503**
AP(a,b)	**5660**	**5660**	**5660**	**5660**	**5660**	**5660**	**5660**	**5660**	**5660**

Number of atoms (Chains A,B) is **940**;

Notes: Namely, having mathematically analyzed the atomic preogression model of ***Insulin Model*** (Table 1) we have found out that the protein code is based on a periodic law. This being the only to „read“ the picture, the solution of the main problem (concering an arrangement where each amino acid takes only one, precisely determined position in the code), is quite manifest:

Table 2. Atomic progression APa and APb (Amino acid Gln – position from 5 to 280 AA)

APa

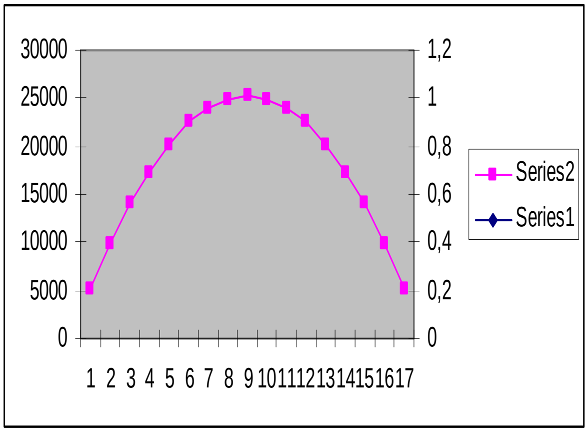
5157	5067	4892	4700	4127	3952	3760	3187	3012	2820	2247	2072	1880	1307	1132	940	367	192
4965	0	4875	4700	4508	3935	3760	3568	2995	2820	2628	2055	1880	1688	1115	940	748	175
4790	0	0	4700	4525	4333	3760	3585	3393	2820	2645	2453	1880	1705	1513	940	765	573
4217	0	0	0	4127	3952	3760	3187	3012	2820	2247	2072	1880	1307	1132	940	367	192
4025	0	0	0	0	3935	3760	3568	2995	2820	2628	2055	1880	1688	1115	940	748	175
3850	0	0	0	0	0	3760	3585	3393	2820	2645	2453	1880	1705	1513	940	765	573
3277	0	0	0	0	0	0	3187	3012	2820	2247	2072	1880	1307	1132	940	367	192
3085	0	0	0	0	0	0	0	2995	2820	2628	2055	1880	1688	1115	940	748	175
2910	0	0	0	0	0	0	0	0	2820	2645	2453	1880	1705	1513	940	765	573
2337	0	0	0	0	0	0	0	0	0	2247	2072	1880	1307	1132	940	367	192
2145	0	0	0	0	0	0	0	0	0	0	2055	1880	1688	1115	940	748	175
1970	0	0	0	0	0	0	0	0	0	0	0	1880	1705	1513	940	765	573
1397	0	0	0	0	0	0	0	0	0	0	0	0	1307	1132	940	367	192
1205	0	0	0	0	0	0	0	0	0	0	0	0	0	1115	940	748	175
1030	0	0	0	0	0	0	0	0	0	0	0	0	0	0	940	765	573
457	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	367	192
265	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	175
90	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Global balance	5067	9767	14100	17287	20107	22560	23867	24807	25380	24807	23867	22560	20107	17287	14100	9767	5067

APb

5570	5067	4875	4700	4127	3935	3760	3187	2995	2820	2247	2055	1880	1307	1115	940	367	175
5395	0	4892	4700	4525	3952	3760	3585	3012	2820	2645	2072	1880	1705	1132	940	765	192
5203	0	0	4700	4508	4333	3760	3568	3393	2820	2628	2453	1880	1688	1513	940	748	573
4630	0	0	0	4127	3935	3760	3187	2995	2820	2247	2055	1880	1307	1115	940	367	175
4455	0	0	0	0	3952	3760	3585	3012	2820	2645	2072	1880	1705	1132	940	765	192
4263	0	0	0	0	0	3760	3568	3393	2820	2628	2453	1880	1688	1513	940	748	573
3690	0	0	0	0	0	0	3187	2995	2820	2247	2055	1880	1307	1115	940	367	175
3515	0	0	0	0	0	0	0	3012	2820	2645	2072	1880	1705	1132	940	765	192
3323	0	0	0	0	0	0	0	0	2820	2628	2453	1880	1688	1513	940	748	573
2750	0	0	0	0	0	0	0	0	0	2247	2055	1880	1307	1115	940	367	175
2575	0	0	0	0	0	0	0	0	0	0	2072	1880	1705	1132	940	765	192
2383	0	0	0	0	0	0	0	0	0	0	0	1880	1688	1513	940	748	573
1810	0	0	0	0	0	0	0	0	0	0	0	0	1307	1115	940	367	175
1635	0	0	0	0	0	0	0	0	0	0	0	0	0	1132	940	765	192
1443	0	0	0	0	0	0	0	0	0	0	0	0	0	0	940	748	573
870	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	367	175
695	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	192
503	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Global balance	5067	9767	14100	17287	20107	22560	23867	24807	25380	24807	23867	22560	20107	17287	14100	9767	5067

↓

Global balance of the atomic progression



Schematic representation of the atomic progression APa, APb and global balance (Amino acid Gln –position from 5 to 280 AA).

(24807-5067) = (940 x Y1); (23867-9767) = (940 x Y2); (22560-14100) = (940 x Y3); (20107-17287) = (940 x Y4);
25380 = (940 x Y5);

Number of atoms (Chains A,B) is 940;
Number of atoms (chains A,B,C,D,E,F,G,H,I,J,K,L.) is 5640 = (940+940+940…+ 940);
Discret code of atomic progression is 940; (Amino acid Gln – position from 5 to 280 AA);

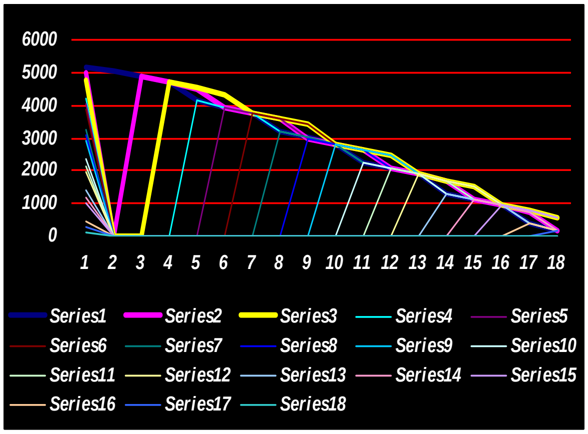


Figure 2. A schematic diagram to show of the atomic progression APa (Amino acid Gln – position from 5 to 280 AA).

This diagram contain an overview of all atomic progression APa amino acid Gln. The values show some of the quantitative characteristics of the molecule of insulin. Actually, they show that there is an exact mathematical balance between atomic progression.

Matrix 5157 – APa

5157	**5067**	**4892**	**4700**	**4127**	**3952**	**3760**	**3187**	**3012**	**2820**	**2247**	**2072**	**1880**	**1307**	**1132**	**940**	**367**	**192**
4217	**0**	**0**	**0**	**4127**	**3952**	**3760**	**3187**	**3012**	**2820**	**2247**	**2072**	**1880**	**1307**	**1132**	**940**	**367**	**192**
3277	**0**	**0**	**0**	**0**	**0**	**0**	**3187**	**3012**	**2820**	**2247**	**2072**	**1880**	**1307**	**1132**	**940**	**367**	**192**
2337	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2247**	**2072**	**1880**	**1307**	**1132**	**940**	**367**	**192**
1397	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1307**	**1132**	**940**	**367**	**192**
457	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**367**	**192**

Matrix 5570 – APb

5570	**5067**	**4875**	**4700**	**4127**	**3935**	**3760**	**3187**	**2995**	**2820**	**2247**	**2055**	**1880**	**1307**	**1115**	**940**	**367**	**175**
4630	**0**	**0**	**0**	**4127**	**3935**	**3760**	**3187**	**2995**	**2820**	**2247**	**2055**	**1880**	**1307**	**1115**	**940**	**367**	**175**
3690	**0**	**0**	**0**	**0**	**0**	**0**	**3187**	**2995**	**2820**	**2247**	**2055**	**1880**	**1307**	**1115**	**940**	**367**	**175**
2750	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2247**	**2055**	**1880**	**1307**	**1115**	**940**	**367**	**175**
1810	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1307**	**1115**	**940**	**367**	**175**
870	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**367**	**175**

Figure 3. Schematic representation of the atomic progression-matrix 5157 and 5570. (Amino acid Gln)

(5157-4217) = (4217-3277) = (3277-2337) = (2337-1397) = (1397-457) = 940;
(5067-367) = (940 x Y1); (4892-192) = (940xY1); (4127-367) = (940 x Y); etc.

Number of atoms (Chains A,B) is 940;

Discret code of amino acid Gln is 940;

Insulin should be „remodelled“ into a periodic system

The molecule of insulin we can understand as words built from letters, i.e. aminoacids. The meaning of words is determined by positioning of letters. Each of these words has its biochemical base. If this base is expressed by corresponding discrete numbers, we find out that the base has its own program, cybernetic and information characteristics. In fact, we will find out that the sequencing of the molecule is conditioned and determined not only by biochemical, but also by cybernetic and information principles.

Atomic progression model of *insulin* should, in fact, be „remodelled“ into a periodic system.

Schematic representation of the amino acid Gln and atomic progression we will show in the fig. 3 – 18.

Schematic representation of the matrix 5157

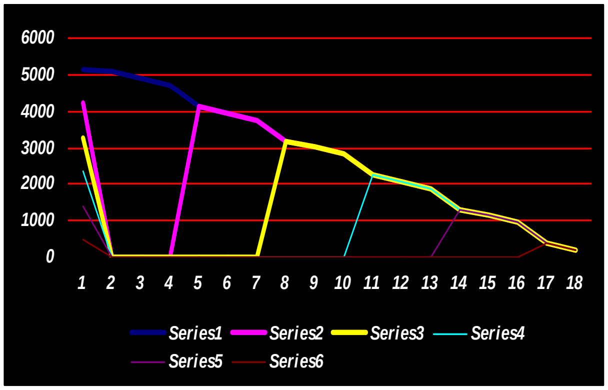


Figure 4. A schematic diagram to show of the atomic progression APa (Amino acid Gln – matrix 5157).

Matrix 4965 – APa

4965	0	4875	4700	4508	3935	3760	3568	2995	2820	2628	2055	1880	1688	1115	940	748	175
4025	0	0	0	0	3935	3760	3568	2995	2820	2628	2055	1880	1688	1115	940	748	175
3085	0	0	0	0	0	0	0	2995	2820	2628	2055	1880	1688	1115	940	748	175
2145	0	0	0	0	0	0	0	0	0	0	2055	1880	1688	1115	940	748	175
1205	0	0	0	0	0	0	0	0	0	0	0	0	0	1115	940	748	175
265	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	175

Matrix 5395 - APb

5395	0	4892	4700	4525	3952	3760	3585	3012	2820	2645	2072	1880	1705	1132	940	765	192
4455	0	0	0	0	3952	3760	3585	3012	2820	2645	2072	1880	1705	1132	940	765	192
3515	0	0	0	0	0	0	0	3012	2820	2645	2072	1880	1705	1132	940	765	192
2575	0	0	0	0	0	0	0	0	0	0	2072	1880	1705	1132	940	765	192
1635	0	0	0	0	0	0	0	0	0	0	0	0	0	1132	940	765	192
695	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	192

Figure 5. Schematic representation of the atomic progression-matrix 4965 and 5395. (Amino acid Gln)

(4965-4025) = (4025-3085) = (3085-2145) = (2145-1205) = **940**;
(4875-175) = (**940**xY); 4700 = (**940**xY); (4508-748) = (**940**xY1); etc.

Schematic representation of the matrix 4965

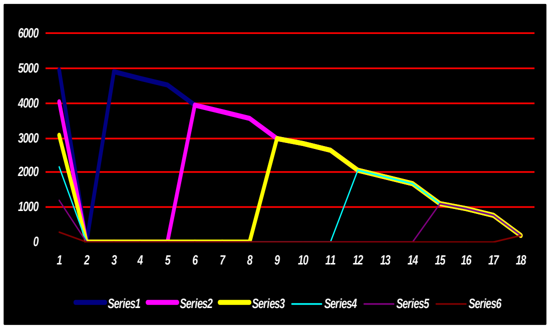


Figure 6. A schematic diagram to show of the atomic progression APa (Amino acid Gln –matrix 4965).

Schematic representation of the matrix 4790

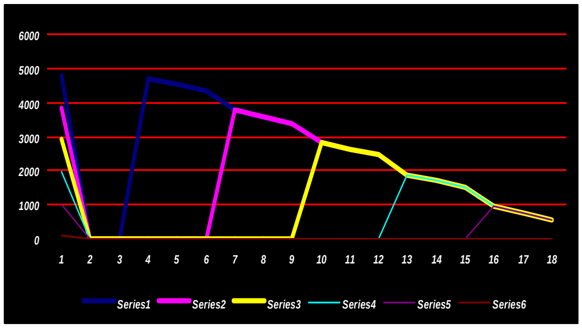


Figure 8. A schematic diagram to show of the atomic progression APa (Amino acid Gln – matrix 4790).

Matrix 4790 – APa

4790	0	0	4700	4525	4333	3760	3585	3393	2820	2645	2453	1880	1705	1513	940	765	573
3850	0	0	0	0	0	3760	3585	3393	2820	2645	2453	1880	1705	1513	940	765	573
2910	0	0	0	0	0	0	0	0	2820	2645	2453	1880	1705	1513	940	765	573
1970	0	0	0	0	0	0	0	0	0	0	0	1880	1705	1513	940	765	573
1030	0	0	0	0	0	0	0	0	0	0	0	0	0	0	940	765	573
90	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Matrix 5203 -APb

5203	0	0	4700	4508	4333	3760	3568	3393	2820	2628	2453	1880	1688	1513	940	748	573
4263	0	0	0	0	0	3760	3568	3393	2820	2628	2453	1880	1688	1513	940	748	573
3323	0	0	0	0	0	0	0	0	2820	2628	2453	1880	1688	1513	940	748	573
2383	0	0	0	0	0	0	0	0	0	0	0	1880	1688	1513	940	748	573
1443	0	0	0	0	0	0	0	0	0	0	0	0	0	0	940	748	573
503	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Figure 7. Schematic representation of the atomic progression-matrix 4790 and 5203. (Amino acid Gln)

(4790-3850) = (3850-2910) = (2910-1970) = (1970-1030) = (1030-90) = **940**;
4700 = (**940**xY); (4525-765) = (**940**xY1); (4333-573) = (**940**xY1); etc.

Matrix 4217 – APa

4217	0	0	0	4127	3952	3760	3187	3012	2820	2247	2072	1880	1307	1132	940	367	192
3277	0	0	0	0	0	0	3187	3012	2820	2247	2072	1880	1307	1132	940	367	192
2337	0	0	0	0	0	0	0	0	0	2247	2072	1880	1307	1132	940	367	192
1397	0	0	0	0	0	0	0	0	0	0	0	0	1307	1132	940	367	192
457	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	367	192

Matrix 4630 – APb

4630	0	0	0	4127	3935	3760	3187	2995	2820	2247	2055	1880	1307	1115	940	367	175
3690	0	0	0	0	0	0	3187	2995	2820	2247	2055	1880	1307	1115	940	367	175
2750	0	0	0	0	0	0	0	0	0	2247	2055	1880	1307	1115	940	367	175
1810	0	0	0	0	0	0	0	0	0	0	0	0	1307	1115	940	367	175
870	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	367	175

Figure 9. Schematic representation of the atomic progression-matrix 4217 and 4630. (Amino acid Gln)

(4217-3277) = (3277-2337) = (2337-1397) = (1397-457) = **940**;
(4127-367) = (**940**xY); (3952-192) = (**940**xY); 3760 = (**940**xY); etc.

Schematic representation of the matrix 4217

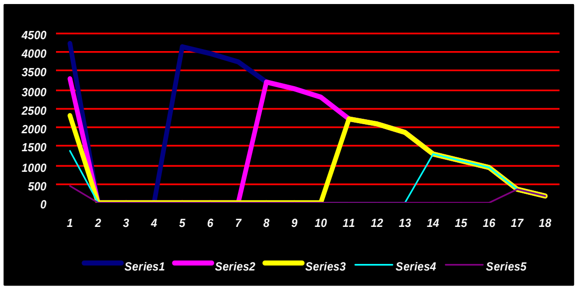


Figure 10. A schematic diagram to show of the atomic progression APa (Amino acid Gln – matrix 4217).

Schematic representation of the matrix 4205

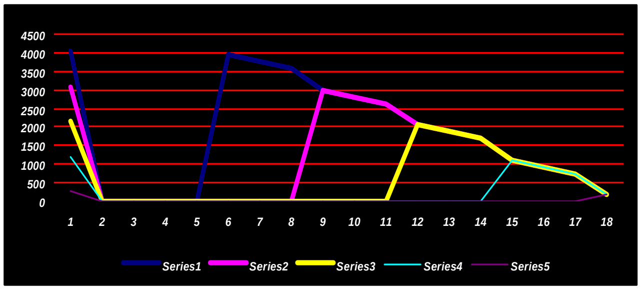


Figure 12. A schematic diagram to show of the atomic progression APa (Amino acid Gln– matrix 4205).

Matrix 4025 – APa

4025	0	0	0	0	3935	3760	3568	2995	2820	2628	2055	1880	1688	1115	940	748	175
3085	0	0	0	0	0	0	0	2995	2820	2628	2055	1880	1688	1115	940	748	175
2145	0	0	0	0	0	0	0	0	0	0	2055	1880	1688	1115	940	748	175
1205	0	0	0	0	0	0	0	0	0	0	0	0	0	1115	940	748	175
265	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	175

Matrix 4455 - APb

4455	0	0	0	0	3952	3760	3585	3012	2820	2645	2072	1880	1705	1132	940	765	192
3515	0	0	0	0	0	0	0	3012	2820	2645	2072	1880	1705	1132	940	765	192
2575	0	0	0	0	0	0	0	0	0	0	2072	1880	1705	1132	940	765	192
1635	0	0	0	0	0	0	0	0	0	0	0	0	0	1132	940	765	192
695	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	192

Figure 11. Schematic representation of the atomic progression-matrix 4025 and 4455. (Amino acid Gln)
(4025-3085) = (3085-2145) = (2145-1205) = (1205-265) = **940**;
(3935-175) = (**940**xY); 3760 = (**940**xY); (3568-748) = (940xY1); etc.

Matrix 3850 – APa

3850	**0**	**0**	**0**	**0**	**0**	**3760**	**3585**	**3393**	**2820**	**2645**	**2453**	**1880**	**1705**	**1513**	**940**	**765**	**573**
2910	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2820**	**2645**	**2453**	**1880**	**1705**	**1513**	**940**	**765**	**573**
1970	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1880**	**1705**	**1513**	**940**	**765**	**573**
1030	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**940**	**765**	**573**
90	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Matrix 4263 - APb

4263	**0**	**0**	**0**	**0**	**0**	**3760**	**3568**	**3393**	**2820**	**2628**	**2453**	**1880**	**1688**	**1513**	**940**	**748**	**573**
3323	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**2820**	**2628**	**2453**	**1880**	**1688**	**1513**	**940**	**748**	**573**
2383	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1880**	**1688**	**1513**	**940**	**748**	**573**
1443	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**940**	**748**	**573**
503	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

Figure 13. Schematic representation of the atomic progression-matrix 3850. (Amino acid Gln)
(3850-2910) = (2910-1970) = (1970-1030) = (1030-90) = **940**;
3760 = (940xY); (3585-765) = (**940**xY1); (3393-573) = (940xY1); etc.

Schematic representation of the matrix 3850

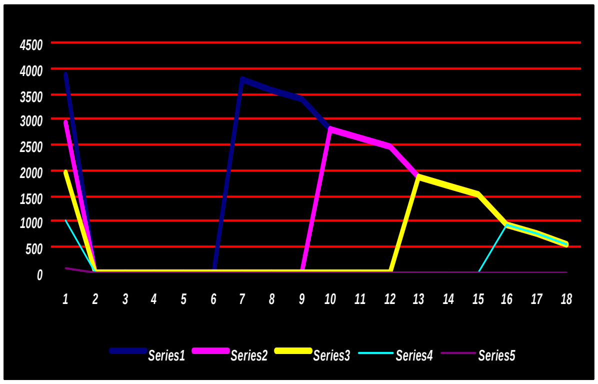


Figure 14. A schematic diagram to show of the atomic progression APa (Amino acid Gln – matrix 3850).

Schematic representation of the matrix 3277

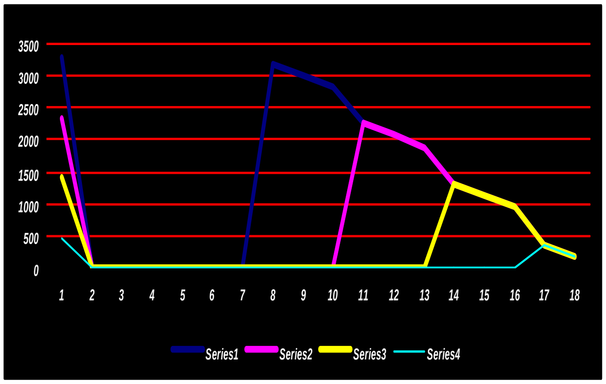


Figure 16. A schematic diagram to show of the atomic progression APa (Amino acid Gln –matrix 3277).

Matrix 3277 – APa

3277	0	0	0	0	0	0	3187	3012	2820	2247	2072	1880	1307	1132	940	367	192
2337	0	0	0	0	0	0	0	0	0	2247	2072	1880	1307	1132	940	367	192
1397	0	0	0	0	0	0	0	0	0	0	0	0	1307	1132	940	367	192
457	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	367	192

Matrix 3690 - APb

3690	0	0	0	0	0	0	3187	2995	2820	2247	2055	1880	1307	1115	940	367	175
2750	0	0	0	0	0	0	0	0	0	2247	2055	1880	1307	1115	940	367	175
1810	0	0	0	0	0	0	0	0	0	0	0	0	1307	1115	940	367	175
870	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	367	175

Figure 15. Schematic representation of the atomic progression-matrix 3277 and 3690. (Amino acid Gln)
(3277-2337) = (2337-1397) = (1397-457) = **940**;
(3187-367) = (**940**xY); (3012-367) = 2820 = (**940**xY); etc.

Matrix 3085 – APa

3085	0	0	0	0	0	0	0	2995	2820	2628	2055	1880	1688	1115	940	748	175
2145	0	0	0	0	0	0	0	0	0	0	2055	1880	1688	1115	940	748	175
1205	0	0	0	0	0	0	0	0	0	0	0	0	0	1115	940	748	175
265	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	175

Figure 17. Schematic representation of the atomic progression-matrix 3085. (Amino acid Gln)

(3085-2145) = (2145-1205) = (1205-265) = **940**;
(2995-175) = (**940**xY); 2820 = (**940**xY); (2628-748) = (**940**xY1); etc.

Schematic representation of the matrix 3085

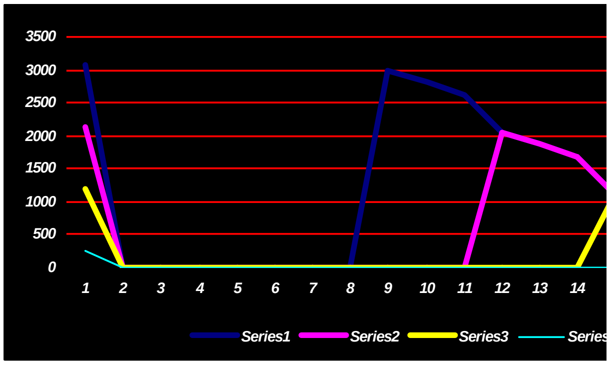


Figure 18. A schematic diagram to show of the atomic progression APa (Amino acid Gln – matrix 3085).
etc.

AS we see, atomic progression model of *insulin* – amino acid Gln, should, in fact, be „remodelled" into a periodic system.

In those examples we translated the physical and chemical parameters from the language of biochemistry into the digital language of programmatic, cybernetic and information principles. This we did by using the adequate mathematical algorithms. By using chemical-information procedures, we calculated the numerical value for the information content of Insulin What we got this way is the digital pictures of insulin. These digital pictures reveal to us a whole new dimension of this protein. They reveal to us that the biochemical process is strictly conditioned and determined by programmatic, cybernetic and information principles.

The conclusion here has to be that there is a concrete relationship between number of atoms and discret code 940.

Atomic progression presented in previous figures are calculated using the relationship between corresponding groups of those progressions. These are groups with different progression. There are different ways and methods of selecting these groups of progressions, which method is most efficient some We hope that science will determine which method is most efficient for this selection.

From the previous examples we can see that this protein really has its quantitative characteristics. It can be concluded that there is a connection between quantitative characteristics in the process of transfer of genetic information and the qualitative appearance of given genetic processes.

IV. DISCUSSION

The results of our research show that the processes of sequencing the molecules are conditioned and arranged not only with chemical and biochemical lawfulness, but also with program, cybernetic and informational lawfulness too. At the first stage of our research we replaced nucleotides from the Amino Acid Code Matrix with numbers of the atoms and atomic numbers in those nucleotides. Translation of the biochemical language of these amino acids into a digital language may be very useful for developing new methods of predicting protein sub-cellular localization, membrane protein type, protein structure secondary prediction or any other protein attributes. Since the concept of Chou's pseudo amino acid composition was proposed [1-2], there have been many efforts to try to use various digital numbers to represent the 20 native amino acids in order to better reflect the sequence-order effects through the vehicle of pseudo amino acid composition. Some investigators used complexity measure factor [3], some used the values derived from the cellular automata [4-7], some used hydrophobic and/or hydrophilic values [8-16], some were through Fourier transform [17-18], and some used the physicochemical distance [19]. The author [34-46] is devoted to provide a digital code for each of 20 native amino acids. These digital codes should more complete and better reflect the essence of each of the 20 amino acids. Therefore, it might stimulate a series of future work by using the author's digital codes to formulate the pseudo amino acid composition for predicting protein structure class [20-22], subcellular location [23,24], membrane protein type [9,25], enzyme family class [26,27], GPCR type [28, 29], protease type [30], protein-protein interaction [31], metabolic pathways [32], protein quaternary structure [33], and other protein attributes. It is going to be possible to use a completely new strategy of research in genetics in the future. However, close observation of all these relationships, which are the outcomes of periodic laws (more specifically the law of binary coding), stereo-chemical and digital structure of proteins.

V.CONCLUSIONS

The process of sequencing in bio-macromolecules is conditioned and determined not only through biochemical, but also through cybernetic and information principles. The digital pictures of biochemistry provide us with cybernetic and information interpretation of the scientific facts. Now we have the exact scientific proofs that there is a genetic language that can be described by the theory of systems and cybernetics, and which functions in accordance with certain principles.

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