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The Insulin Bio Intervals

By Lutvo Kurić
Centro Universitário Feevale

Abstract - The modern science mainly treats the biochemical basis of sequencing in bio-macromolecules and processes in medicine and biochemistry. One can ask weather the language of biochemistry is the adequate scientific language to explain the phenomenon in that science. Is there maybe some other language, out of biochemistry, that determines how the biochemical processes will function and what the structure and organization of life systems will be? The research results provide some answers to these questions. They reveal to us that the process of sequencing in bio-macromolecules is conditioned and determined not only through biochemical, but also through cybernetic and information principles. Many studies have indicated that analysis of protein sequence codes and various sequence-based prediction approaches, such as predicting drug-target interaction networks (He et al., 2010), predicting functions of proteins (Hu et al., 2011; Kannan et al., 2008), analysis and prediction of the metabolic stability of proteins (Huang et al., 2010), predicting the network of substrate-enzyme-product triads (Chen et al., 2010), membrane protein type prediction (Cai and Chou, 2006; Cai et al., 2003; Cai et al., 2004), protein structural class prediction (Cai et al., 2006; Ding et al., 2007), protein secondary structure prediction (Chen et al., 2009; Ding et al., 2009b), enzyme family class prediction (Cai et al., 2005; Ding et al., 2009a; Wang et al., 2010), identifying cyclin proteins (Mohabatkar, 2010), protein subcellular location prediction (Chou and Shen, 2010a; Chou and Shen, 2010b; Kandaswamy et al., 2010; Liu et al., 2010), among many others as summarized in a recent review (Chou, 2011), can timely provide very useful information and insights for both basic research and drug design and hence are widely welcome by science community. The present study is attempted to develop a novel sequence-based method for studying insulin in hopes that it may become a useful tool in the relevant areas.

Keywords : *human insulin, algorithm, insulin model, insulin code, bio interval.*

GJMR-B Classification : *NLMC Code: WK 820*

THE INSULIN BIO INTERVALS

Strictly as per the compliance and regulations of:

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Keywords : human insulin, algorithm, insulin model, insulin code, bio interval.

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.

II. Methods

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 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?

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III. 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.

R6 INSULIN HEXAMER (d1ai02)

The structure **1AI0** has in total **12** chains. Out of these **2** are sequence-unique

>1AI0:A		GIVEQCCTSICSLYQLENYCN
>1AI0:B		FVNQHLCGSHLVEALYLVCGERGFFYTPKT
>1AI0:C		GIVEQCCTSICSLYQLENYCN
>1AI0:D		FVNQHLCGSHLVEALYLVCGERGFFYTPKT
>1AI0:E		GIVEQCCTSICSLYQLENYCN
>1AI0:F		FVNQHLCGSHLVEALYLVCGERGFFYTPKT
>1AI0:G		GIVEQCCTSICSLYQLENYCN
>1AI0:H		FVNQHLCGSHLVEALYLVCGERGFFYTPKT
>1AI0:I		GIVEQCCTSICSLYQLENYCN
>1AI0:J		FVNQHLCGSHLVEALYLVCGERGFFYTPKT
>1AI0:K		GIVEQCCTSICSLYQLENYCN
>1AI0:L		FVNQHLCGSHLVEALYLVCGERGFFYTPKT

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

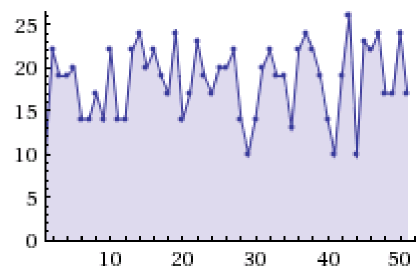
N	Y	C	N	F	V	N	Q	H	I	C	G	S	H	L	V	E
17	24	14	17	23	19	17	20	20	22	14	10	14	20	22	19	19
18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34

A	L	Y	L	V	C	G	E	R	G	F	I	Y	T	P	K	T
13	22	24	22	19	14	10	19	26	10	23	22	24	17	17	24	17
35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51

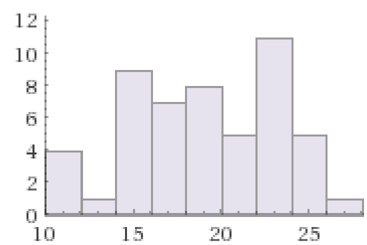
Input:

{10, 22, 19, 19, 20, 14, 14, 17, 14, 22, 14, 14, 22, 24, 20, 22, 19, 17, 24, 14, 17, 23, 19, 17, 20, 20, 22, 14, 10, 14, 20, 22, 19, 19, 13, 22, 24, 22, 19, 14, 10, 19, 26, 10, 23, 22, 24, 17, 17, 24, 17}

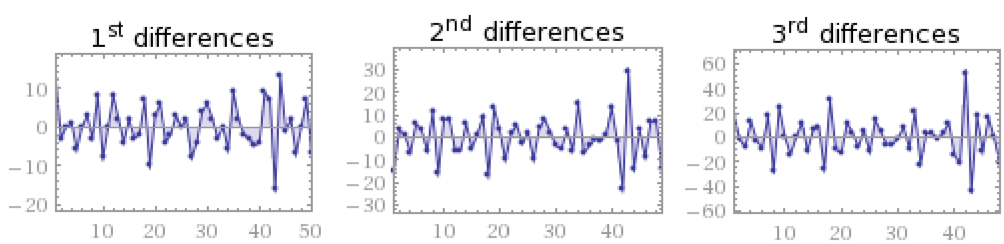
Plot:



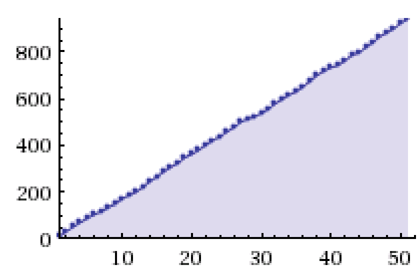
Histogram:



Differences:



Cumulative sums:



As wesee, the genetic information characterized only by biochemical, or also by cyberinformation principles

Fragment 1

From 1 to 102

G	I	V	E	Q	C	C		T
10	22	19	19	20	14	14	…	17
1	2	3	4	5	6	7		102

Fragment 2

From 103 to 204

G	I	V	E	Q	C	C		T
10	22	19	19	20	14	14	…	17
103	104	105	106	107	108	109		204

Fragment 3

From 205 to 306

G	I	V	E	Q	C	C		T
10	22	19	19	20	14	14	…	17
205	206	207	208	209	210	211		306

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. The first aminoacid in this example has 10 atoms, the second one 22, the third one 19, etc... Why do they have exactly this many atoms? It is because there are many codes in the molecule of insulin, analogue codes and other coded features. In fact, there is a program-cybernetic algorithm in which it is „recorded" that the firs amino acid has to have 10 atoms, the second one 22, the third one 19, etc... The first amino acid has its own biochemistry, the second and the third one also. The conclusion here has to be that there is a concrete relationship between quantitative ratios in the process of transfer of genetic information and qualitative appearance, i.e. the characteristics of organisms.

ALGORITHM

We shall now give some mathematical evidences that will prove that in the biochemistry of insulin 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.

Step 1 (From 1 to 306)

R1 = 10; R2 = 22; R3 = 19;... R306 = 17;

[R1 + (R1+R2) + (R1+R2+R3)..., + (R1+R2+R3..., + R306)] = S;

R1 = 10 atoms;

(R1+R2) = (10+22) = 32;
(R1+R2+R3) = (10+22+19) = 51;
(R1+R2+R3..., + R306) = 5640 atoms;
R1,2,3,n = Number of atoms in amino acids 1,2,3,n

[R1 + (R1+R2) + (R1+R2+R3)..., + (R1+R2+R3..., + R306)] =
= (10+32+51+70…, + 5640) = S;
S = 863 208;

Step 2 (From 306 to 1)

R306 = 17; R305 = 24; R304 = 17;... R1 = 10 atoms;

[R306 + (R306+R305) + (R306+R305+R304)..., + (R306+R305+R304..., + R1)] = S1;

R306 = 17;
(R306+R305) = (17+24) = 41;
(R306+R305+R304) = (17+24+17) = 58;
(R306+R305+R304..., + R1) = (17+24+17..., + 10) = 5640;

R1,2,3,n = Number of atoms in amino acids 1,2,3,n

[R306 + (R306+R305) + (R306+R305+R304)..., + (R306+R305+R304..., + R1)] =
= (17+41+58+75..., + 5640) = S1;
S1 = 868 272;

From 1 to 102 and from 102 to 1

	G	I	V	E	Q	C	C	.	.	T	SUM
	10	22	19	19	20	14	14	.	.	17	1880
	1	2	3	4	5	6	7	.	.	102	5253
Step 1	10	32	51	70	90	104	118	.	.	1880	95976
Step 2	5640	5630	5608	5589	5570	5550	5536	.	.	3777	481184
											577160

(0+10) = 10; (10+22)=32; (10+22+19)=51; etc.
(17+24+17..., + 10) = 5640; (17+24+17..., + 22) = 5630; etc.
(95976 + 481184) = 577160:

From 103 to 204 and from 204 to 103

	G	I	V	E	Q	C	C	.	.	T	SUM
	10	22	19	19	20	14	14	.	.	17	1880
	103	104	105	106	107	108	109	.	.	204	15657
Step 1	1890	1912	1931	1950	1970	1984	1998	.	.	3760	287736
Step 2	3760	3750	3728	3709	3690	3670	3656	.	.	1897	289424
											577160

(287736 + 289424) = 577160;

From 205 to 306 and from 306 to 205

	G	I	V	E	Q	C	C	.	.	T	SUM
	10	22	19	19	20	14	14	.	.	17	1880
	205	206	207	208	209	210	211	.	.	306	26061
Step 1	3770	3792	3811	3830	3850	3864	3878	.	.	5640	479496
Step 2	1880	1870	1848	1829	1810	1790	1776	.	.	17	97664
											577160

(479496 + 97664) = 577160;

From 1 to 102		From 103 to 204		From 205 to 306
↓		↓		↓
577160		577160		577160
↘		↓		↙
		1.731.480		

1.731.480 = (5640+5640+5640... + 5640);

Number of atoms in Insulin = 5640;

Schematic representation of the bio intervals from 1 to 306 we will show in the fig.1 and 2.

In that group of chains there are three groups with 102 amino acids. Each of these three groups of amino acids has an identical number of atoms.

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.

BIO INTERVALS – AMINO ACIDS FROM 1 TO 306

Within the digital pictures in biochemistry, the physical and chemical parameters are in a strict compliance with programmatic, cybernetic and information principles. As an example, we will here give you the mathematical gravity forces. These forces determine the positioning of aminoacids in their molecules. 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.

Insulin Bio Intervals(1)

Step 1

Number of atoms	Bio intervals	Rank	Number of atoms	Bio intervals	Rank	Number of atoms	Bio intervals	Rank
199 From 1 to 12	199	78	1139 From 1 to 63	199	2016	2079 From 1 to 114	199	6555
323 From 1 to 18	124	171	1263 From 1 to 69	124	2415	2203 From 1 to 120	124	7260
361 From 1 to 20	38	210	1301 From 1 to 71	38	2556	2241 From 1 to 122	38	7503
579 From 1 to 32	218	528	1519 From 1 to 83	218	3486	2459 From 1 to 134	218	9045
617 From 1 to 34	38	595	1557 From 1 to 85	38	3655	2497 From 1 to 136	38	9316
741 From 1 to 41	124	861	1681 From 1 to 92	124	4278	2621 From 1 to 143	124	10296
940 From 1 to 51	199	1326	1880 From 1 to 102	199	5253	2820 From 1 to 153	199	11781
3760	940		10340	940		16920	940	

(199-0) = 199; (323-199) = 124; (361-323) = 38; (741-617) = 124;
(940-741) = 199; (1139-940) = 199; (1263-1139) = 124;
etc.

(Chain A + Chain B) = 940 atoms,
(Chain C + Chain D) = 940 atoms,
etc.

(3760 + 16920) = (10340 + 10340);
10340 = (940+940+940.., + 940);

3760 = (940+940+940+940)
10340 = (940+940+940..., + 940)
16920 = (940+940+940..., + 940)

(2079-1139) = (1139-199);
(2203-1263) = (1263-323);
(2241-1301) = (1031-361);
etc.

Correlation of bio intervals

Number of atoms	Bio intervals	Number of atoms	Bio Intervals	Number of atoms	Bio Intervals
199	199	1139	199	2079	199

[(199 + 2079) : 2] = 1139;

Number of atoms	Bio intervals	Number of atoms	Bio Intervals	Number of atoms	Bio Intervals
323	124	1263	124	2203	124

[(323 + 2203) : 2] = 1263;

Number of atoms	Bio intervals	Number of atoms	Bio Intervals	Number of atoms	Bio Intervals
361	38	1301	38	2241	38

[(361 + 2241): 2] = 1301;

Number of atoms	Bio intervals	Number of atoms	Bio Intervals	Number of atoms	Bio Intervals
579	218	1519	218	2459	218

[(579 + 2459) : 2] = 1519;

Number of atoms	Bio intervals	Number of atoms	Bio Intervals	Number of atoms	Bio Intervals
617	38	1557	38	2497	38

[(617 + 2497) : 2] = 1557;

Number of atoms	Bio intervals	Number of atoms	Bio Intervals	Number of atoms	Bio Intervals
741	124	1681	124	2621	124

[(741 + 2621) : 2] = 1681;

Number of atoms	Bio intervals	Number of atoms	Bio Intervals	Number of atoms	Bio Intervals
940	199	1880	199	2820	199

[(940 + 2820) : 2] = 1880;

Insulin Bio Intervals(2)

Number of atoms	Bio intervals	Rank	Number of atoms	Bio intervals	Rank	Number of atoms	Bio intervals	Rank
3019 From 1 to 165	199	13695	3959 From 1 to 216	199	23436	4899 From 1 to 267	199	35778
3143 From 1 to 171	124	14706	4083 From 1 to 222	124	24753	5023 From 1 to 273	124	37401
3181 From 1 to 173	38	15051	4121 From 1 to 224	38	25200	5061 From 1 to 275	38	37950
3399 From 1 to 185	218	17205	4339 From 1 to 236	218	27966	5279 From 1 to 287	218	41328
3437 From 1 to 187	38	17578	4377 From 1 to 238	38	28441	5317 From 1 to 289	38	41905
3561 From 1 to 194	124	18915	4501 From 1 to 245	124	30135	5441 From 1 to 296	124	43956
3760 From 1 to 204	199	20910	4700 From 1 to 255	199	32640	5640 From 1 to 306	199	46971
23500	940		30080	940		36660	940	

(3019-2820) = 199; (3143-3019) = 124; (3181-3143) = 38; etc.

Schematic representation of the bio intervals from 199 to 5640 we will show in the fig.3.

Correlation of bio intervals

Number of atoms	Number of atoms	Number of atoms
3019	3959	4899

(3019 + 4899) = (3959 x 2);

Number of atoms	Number of atoms	Number of atoms
3143	4083	5023

(3143 + 5023) = (4083 x 2);

Number of atoms	Number of atoms	Number of atoms
3181	4121	5061

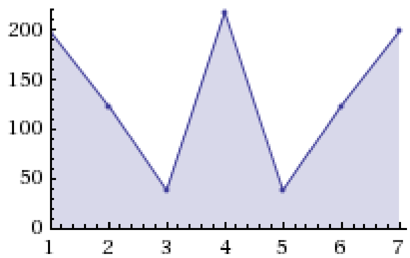
(3181 + 5061) = (4121 x 2); etc.

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.

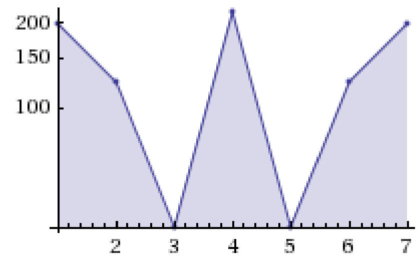
BIO INTERVALS(3)

Mathematica plaintext input:

Plot:



Long-linear plot:



ListLogPlot[{199, 124, 38, 218, 38, 124, 199}, Joined -> True, Mesh -> All, Filling -> Axis]

BIO INTERVAL – AMINO ACIDS-FROM 306 TO 1.

Step 2

Number of atoms	Bio intervals	Rank	Number of atoms	Bio intervals	Rank	Number of atoms	Bio Intervals	Rank
199 From 306 to 297	199	3015	1139 From 306 to 246	199	16836	2079 From 306 to 195	199	28056
323 From 306 to 290	124	5066	1263 From 306 to 239	124	18530	2203 From 306 to 188	124	29393
361 From 306 to 288	38	5643	1301 From 306 to 237	38	19005	2241 From 306 to 186	38	29766
579 From 306 to 276	218	9021	1519 From 306 to 225	218	21771	2459 From 306 to 174	218	31920
617 From 306 to 274	38	9570	1557 From 306 to 223	38	22218	2497 From 306 to 172	38	32265
741 From 306 to 268	124	11193	1681 From 306 to 217	124	23535	2621 From 306 to 166	124	33276
940 From 306 to 256	199	14331	1880 From 306 to 205	199	26061	2820 From 306 to 154	199	35190
3760	940		10340	940		16920	940	

[(199 + 2079) : 2] = 1139; [(323 + 2203) : 2] = 1263; etc.

Schematic representation of the bio intervals from 306 to 1 we will show in the fig.4.

Step 2

199	199
323	124
361	38
579	218
617	38
741	124
940	199
3760	940

1139	199
1263	124
1301	38
1519	218
1557	38
1681	124
1880	199
10340	940

2079	199
2203	124
2241	38
2459	218
2497	38
2621	124
2820	199
16920	940

3019	199
3143	124
3181	38
3399	218
3437	38
3561	124
3760	199
23500	940

3959	199
4083	124
4121	38
4339	218
4377	38
4501	124
4700	199
30080	940

4899	199
5023	124
5061	38
5279	218
5317	38
5441	124
5640	199
36660	940

(323-199) = 124; (361-323) = 38; (579-361) = 218; etc.
(36660 + 3760) + (30080 + 10340) + (23500 + 16920) = (**940** x Y);
Y = 43;

Connection:

(36660 and 3760) > 36660 3760 = (940 x Y1);
(3760 and 36660) > 3760 36660 = (940 x Y2);
(30080 and 10340) > 30080 10340 = (940 x Y3);
(10340 30080) >10340 30080 = (940 x Y4);
(23500 and 16920) > 23500 16920 = (940 x Y5);
(16920 and 23500) > 16920 23500 = (940 x Y5);

In those examples there is an exact mathematical balance of groups of aminoacids from 1 to 102, 103 to 204, 205 to 306 and 199 to 5640.. This balance is one of important quantitative characteristics of all processes in biochemistry. How functioning of biochemistry is determined through cybernetic information principles, will be discussed further in Table 1.

BIO INTERVALS(4)

The result of the research that we have carried out clearly shows that there is a matrix code in insulin. It also shows that the coding system within the amino acidic language gives a full information, not only for the amino acid „record", but also for its structure, configuration and its various shapes. In the following text we shall discuss the issue of the existence of the insulin code, and also the issue of coding of individual structural levels in this protein.

BIO INTERVAL (+)199

Impulse 1 Impulse 2

G	I	V		S
10	22	19	…	14
1	2	3	…	12
10	32	51	…	199
5640	5630	5608	…	5455

(10+22+19…, + 14) = 199;

BIO INTERVAL (-)199

Impulse -2 Impulse -1

E		T	P	K	T
19	…	17	17	24	17
297	…	303	304	305	306
5460	…	5582	5599	5623	5640
199	…	75	58	41	17

BIO INTERVAL (+)323

Impulse 1				Impulse 3
G	I	V		N
10	22	19	…	17
1	2	3		18
10	32	51		323
5640	5630	5608		5334

BIO INTERVAL (-)323

Impulse -3					Impulse -1
A		T	P	K	T
13	…	17	17	24	17
290		303	304	305	306
5330		5582	5599	5623	5640
323		75	58	41	17

BIO INTERVAL (+)361

Impulse 1				Impulse 4
G	I	V		C
10	22	19	…	14
1	2	3		20
10	32	51		361
5640	5630	5608		5293

BIO INTERVAL (-)361

Impulse-4					Impulse –1
V		T	P	K	T
19	…	17	17	24	17
288		303	304	305	306
5298		5582	5599	5623	5640
361		75	58	41	17

etc.

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.

BIO INTERVAL – AMINO ACIDS-FROM 1 to 306 and 306 TO 1.

Bio intervals of insulin we will show in the table 1 and table 2.

Step 1

Table 1 : Bio intervals (from 1 to 306)

199	323	361	579	617	741	940
1139	1263	1301	1519	1557	1681	1880
2079	2203	2241	2459	2497	2621	2820
3019	3143	3181	3399	3437	3561	3760
3959	4083	4121	4339	4377	4501	4700
4899	5023	5061	5279	5317	5441	5640

(1139 -199) = (2079-1139) = (3019-2079); etc.

Step 2

Table 2 : Bio intervals (from 306 to 1)

940	741	617	579	361	323	199
1880	1681	1557	1519	1301	1263	1139
2820	2621	2497	2459	2241	2203	2079
3760	3561	3437	3399	3181	3143	3019
4700	4501	4377	4339	4121	4083	3959
5640	5441	5317	5279	5061	5023	4899

(1880-940) = 2820-1880); etc.

These tables contains an overview of all bio intervals. The bio intervals show some of the quantitative characteristics of the molecule of insulin.

Schematic representation of the bio intervals we will show in the fig.5, 6 and 7.

The Insulin Bio Signal Code

We shall now give some mathematical evidences that will prove that in the biochemistry of insulin 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.

	Signal +199	Signal -5441	
	S	L	Y
14	14	22	24
11	12	13	14
185	199	221	245
5469	5455	5441	5419

(199 + 5441) = 5640;

	Signal +323	Signal -5317	Signal +361	Signal -5279	
E	N	Y	C	N	F
19	17	24	14	17	23
17	18	19	20	21	22
306	323	347	361	378	401
5353	5334	5317	5293	5279	5262

(323+5317) = 5640; (361+5279) = 5640; (361-323) = (5317 – 5279)

	Signal +579	Signal -5061	Signal +617	Signal -5023	
H	L	V	E	A	L
20	22	19	19	13	22
31	32	33	34	35	36
557	579	598	617	630	652
5103	5083	5061	5042	5023	5010

(579+5061) = (617+5023) (617-579) = (5061 – 5023)

	Signal +741	Signal -4899	
C	G	E	R
14	10	19	26
40	41	42	43
731	741	760	786
4923	4909	4899	4880

(741 + 4899) = 5640;

	Signal +940	Signal -4700	
K	T	G	I
24	17	10	22
50	51	52	53
923	940	950	972
4741	4717	4700	4690

(4700 + 940) = 5640; etc.

Aforementioned bio-codes were calculated using of corresponding groups of aminoacids. These are unions with different number of aminoacids. There are different ways and methods of selecting these unions of amino acids. We hope that science will determine which method is most efficient for this selection. Some signals have a positive, and some have negative numeric value.

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 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 [34-40] 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.

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Awards

Gold medal for Bosnia and Herzegovina, in the name of your people and Bosnia and Herzegovina. Such individuals deserve recognition not only within their country of origin, but also worldwide. As such, the American Biographical Institute – a highly esteemed leader in the research of upstanding individuals around the globe – has selected you to receive one of its most internationally prominent honors, the GOLD MEDAL FOR BOSNIA AND HERZEGOVINA. –International health professional of the year 2010., -Man of the year in medicine and healthare designation for 2010.,-The international Hipocrates awards for medical achievement, -Cambridge certificate for outstanding medical achievement for 2011. – International health professional of the year 2012.-Cambridge certificate for Outstanding Medical Achievement, 2012., -ABI-Man of the year 2012. - Nomination for Great Minds of the 21st Century, a major reference directory including just 1.000 of the world's top thinkers and intellectuals. My contributions to the field of medicine and healthcare have waranted the high regard of nomination for Great Minds of the 21st Century.