# Fibonacci Numbers and Genetic Code

Initial data about genetic code

Among biological concepts, well formalized and having a level of the general scientific significance, the genetic code takes a special place. Let's use the data about genetic code given in the remarkable book "Biperiodical table of genetic code and number of protons" (2001), written by the well-known Russian scientist Sergey Petoukhov, working on the joint of biology and mathematics.
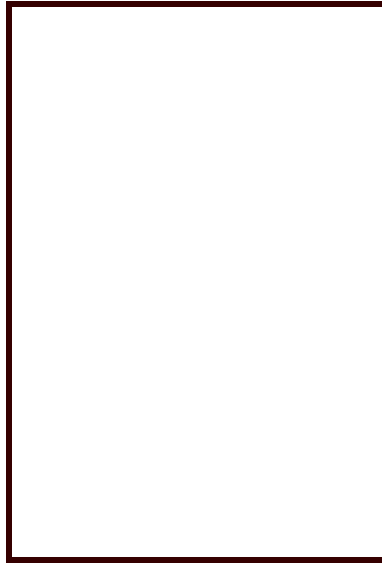
Petoukhov's book "Biperiodical table of genetic code and a number of protons" (2001).

A discovery of the well-known fact of a striking simplicity of basic principles of genetic coding falls into to number of major modern discoveries of mankind. This simplicity consists of the fact that the inheritable information is encoded by the texts from three-alphabetic words - *triplets* or *codonums* compounded on the basis of the alphabet consisted of four characters being the nitrogen bases: A (adenine), C (cytosine), G (guanine), T (thiamine). The given recording system is essentially unified for all boundless set of miscellaneous alive organisms and is called *genetic code*.

The well-known "double helix" of DNA-molecule consisting of two interdependent branch circuits is a saver of the genetic code triplets. The standardized links of these circuits are called as *nucleotides*. The mentioned above nitrogen bases A, C, G and T are arranged along each of circuits by one for each nucleotide. Here so-called condition of complementarity is executed: against the base A in one circuits always the base T stands in other, and against the base G always the base C stands in other.

Using three-alphabetic triplets or codonums we can code 20 amino acids. There exist $4^3 = 64$ different combinations from four on three basis's. In this connection some of 20 amino acids are encoded at once by several triplets. It is called as a *degeneracy of a code*. The finding of conformity between triplets and amino acids (or signs of the punctuation) is customary treated as *decryption of genetic code*.

The RNA plays a role of "intermediary" in synthesis of proteins from amino acids of the 20 kinds pursuant to sequence of triplets in DNA-circuits. A well-known difference of RNA from DNA is the fact that the standard set of nitrogen bases of its triplets contains instead of a thiamine (T) an uracil (U), which is very similar and related with it, that is why the four-alphabetic code alphabet for RNA consists of the set A, C, G, U.

The nitrogen bases in DNA and RNA fall into to two different chemical classes - pyramidin and purine. Cytosine C and uracil U (or thiamine T) are pyramidin bases and, and adenine A and guanine G are purine bases. Under operating of nitrous acid the objective mutations of RNA connected with base substitution are watched: A $\rightarrow$ G, C $\rightarrow$ U. Thus, basess A and C are *varied*, and G and U - *not varied*.

Proteins are main dense component of alive organism. Each of proteins executes only own, appropriate to it function. The proteins represent themselves large polymer molecules consisting of circuits of amino acids (polypeptides), irregularly alternated. All amino acids in proteins are paired one another by one-type chemical bond received a title of *peptide bond*. A molecule of protein often is compared to a train consisting of cars of twenty different kinds, which are spanned one another by the same way permitting to connect cars in any order.

Biperiodical Table of genetic code

The set from 64 triplets of a genetic code represents some structured system according to which the four nitrogen bases of genetic code (A, C, G, U) are subdivided, at first, into pairs of purine and pyramidine bases, at second, into complementary pairs and, thirdly, into pairs of bases of nitrous acid, mutating and not mutating under operating. On this cause each triplet is in some relation to all other triplets.

The problem of pithy ordering of all set from 64 triplets is put in the basis of research by Sergey Petoukhov who considers genetic code as an ensemble of binary subsystems. He describes a principle, according to which all triplets are regularly placed in a matrix (8 × 8), having double periodicity. Here all codonums by a natural mode are numbered by numbers from 0 up to 63, outgoing from biochemical symptoms of a binary type for nitrogen bases.

Biperiodical Table of genetic code

The principle of "doubly three-gram ordering" of the codonums set is put into the basis of Biperiodical Table (BT). He consists of two parts: the ordering subdivided 64 triplets on octets, and the ordering of Codonums inside all these octets. Both these principles have a steep biochemical substantiation. The former principle consists of fixation of numbers and sequence of purine and pyramidin bases in triplets. For example, let's consider a subset of triplets, for which the first base is pyramidin one (i.e. C or U), and the second one and the third one is purine base (i.e. A or G). It is easy to test, that the following eight of triplets (octets): CAA, CAG, CGA, UAA, CGG, UAG, UGA, UGG fit to this condition. If we designate now through "1" each pyramidin base and "0" each purine one, then each of the indicated triplets can put in conformity a three-digit binary number 100, called "three-gram character " (or simply by "trigram") of the given octet.

In the BT to each such octet there fits a separate column marked by personal "trigram". As there are the eight different "trigrams", to each of which there fits one of three-digit binary combinations (000, 001, 010, 011, 100, 101, 110, 111), then in the BT one may be selected the eight octets numbered (from left to right) by the binary numbers from 111 up to 000.

It is important to note, that the sequence of columns in the BT (from 111 to 000) is selected in such a manner that the octets of the left- and right half's of the BT are located are mirror-symmetrical about its center line so, that each trigram of the left-hand half (000, 001, 010, 011) meets the "antisymmetric" trigram (111, 110, 101, 100), occupying a mirror - symmetrical stand in the right-hand half.

Now let's analyze the BT by strings. It is easy to see, that here there is realized a principle of ordering of four nitrogen bases on the pair C and A (that corresponds to the binary digit "1") and the pair G and U (that corresponds to the binary digit "0"). It appears, that in such partitioning there is a steep biochemical sense from the point of view of property of mutagenicity, as the nucleotides C and A are maximum varied under operating of nitrous acid, and other two nucleotides G and U are not varied. Then by a three-digit binary code *111* (the first string of the BT) we can mark all the 8 triplets consisted only of the "varied" nucleotides: CCC, CCA, CAC, CAA, ACC, ACE, AAC, AAA.

Moving downwards on strings of the BT, we will get the triplets, all less sensing to operating the nitrous acid. Really, the three-digit binary code *110* (the second string of BT) will correspond to all triplets, in which the first two nucleotides correspond to "varied" nucleotides (the pair C and A), and the last nucleotide corresponds to the pair A and G. The last string of the BT consists of triplets conforming to the pair A and G ("not varied" nucleotides) and the binary three-digit code *000* corresponds to it.

At such way of triplets coding each codonum can be uniquely represented by a 6-digit binary code, which corresponds to some decimal number. Each such 6-digit code consists of two three-digit parts, and the left-hand part corresponds to the code of string where the triplet is, and the right-hand part corresponds to the trigram of the column where the codonum is. For example, the record *101* 110 corresponds to the codonum of CUA. If now the record *101* 110 to consider as the decimal 46, it means, that the codonum of CUA in the BT has the number of 46.

The genetic code analysis fulfilled by Sergey Petuokhov has resulted in discovery of new surprising system properties of genetic code and we refer everyone, who wants deeper to be acquainted with the problem, to the remarkable Petoukhov's book, which opens new outlooks of research of the genetic code problem. The additional information can be found on the site:
http://members.tripod.com/vismath/sg/petoukhov.htm

Some useful analogies between Fibonacci code and genetic code

Though "decryption" of genetic code was carried out in the beginning of the 60th years of the 20th century, but the researches in this area are intensively continued. Specially relevant one may be considered such applications of "gene engineering" as creation of "bio-computers" based on DNA. In this connection it is rather useful considering analogies between genetic code and code methods used in modern computer science, in particular, with Fibonacci code.

For consideration of these analogies let's consider the 6-digit Fibonacci code used Fibonacci numbers 1, 1, 2, 3, 5, 8 as digit weights:

$$N = a_6 \times 8 + a_5 \times 5 + a_4 \times 3 + a_3 \times 2 + a_2 \times 1 + a_1 \times 1. \tag{1}$$

Note the following analogies between the 6-digit Fibonacci code and genetic code:

1. *The first analogy.* For representation of numbers the 6-digit binary Fibonacci code uses $2^6 = 64$ binary code combinations from 000000 up to 111111, that coincides with number of triplets of genetic code: $4^3 = 64$.
2. *The second analogy.* Using the 6-digit Fibonacci code it is possible to represent 21 integers starting since the number of 0 encoded with the 6-digit binary combination 00000 and finishing with the maximum number 20 encoded with the 6-digit code combination 111111. Note that using triplet's coding we can represent also 21 objects including 20 amino acids and one additional object using for coding of the stop-codonum (a sign of the punctuation) carrying in itself the information about termination of protein synthesis.
3. *The third analogy.* The main feature of Fibonacci code is the multiplicity of number representation. Except of the minimum number of 0 and the maximum number of 20, which have in Fibonacci code alone code representations (accordingly 000000 and 111111), all remaining numbers from 1 up to 19 have in Fibonacci code multiple representations, that is, they use not less than two code combinations for their representation. It is necessary to note that in genetic code property of multiplicity of representation also is used and it is called called as *"degeneracy"* of genetic code.

Thus, between the 6-digit Fibonacci code and genetic code, based on triplet's representation of amino acids, there are rather interesting analogies, which allow to select Fibonacci code in special class of redundant codes among other ways of redundant coding. One may express assumption that just a study of Fibonacci code can promote finding new features of genetic code. It is possible to state the supposition, that similar analogies can become rather useful at a solution of a problem of the DNA-based bio-computers design.

Biperiodical Table for Fibonacci code

Let's consider a code table of the 6-digit Fibonacci code. It gives all the binary code combinations (CC) from the code combination $A_0 = 000000$ up to the code combination $A_{63} = 111111$ and each code combination puts in conformity to any integer N, which is expressed by this CC I according to the Fibonacci code (7).

CC	8	5	3	2	1	1	N	CC	8	5	3	2	1	1	N
A_0	0	0	0	0	0	0	0	A_{32}	1	0	0	0	0	0	8
A_1	0	0	0	0	0	1	1	A_{33}	1	0	0	0	0	1	9
A_2	0	0	0	0	1	0	1	A_{34}	1	0	0	0	1	0	9
A_3	0	0	0	0	1	1	2	A_{35}	1	0	0	0	1	1	10
A_4	0	0	0	1	0	0	2	A_{36}	1	0	0	1	0	0	10
A_5	0	0	0	1	0	1	3	A_{37}	1	0	0	1	0	1	11
A_6	0	0	0	1	1	0	3	A_{38}	1	0	0	1	1	0	11
A_7	0	0	0	1	1	1	4	A_{39}	1	0	0	1	1	1	12
A_8	0	0	1	0	0	0	3	A_{40}	1	0	1	0	0	0	11
A_9	0	0	1	0	0	1	4	A_{41}	1	0	1	0	0	1	12
A_{10}	0	0	1	0	1	0	4	A_{42}	1	0	1	0	1	0	12
A_{11}	0	0	1	0	1	1	5	A_{43}	1	0	1	0	1	1	13
A_{12}	0	0	1	1	0	0	5	A_{44}	1	0	1	1	0	0	13
A_{13}	0	0	1	1	0	1	6	A_{45}	1	0	1	1	0	1	14

A_{14}	0	0	1	1	1	0	6	A_{46}	1	0	1	1	1	0	14
A_{15}	0	0	1	1	1	1	7	A_{47}	1	0	1	1	1	1	15
A_{16}	0	1	0	0	0	0	5	A_{48}	1	1	0	0	0	0	13
A_{17}	0	1	0	0	0	1	6	A_{49}	1	1	0	0	0	1	14
A_{18}	0	1	0	0	1	0	6	A_{50}	1	1	0	0	1	0	14
A_{19}	0	1	0	0	1	1	7	A_{51}	1	1	0	0	1	1	15
A_{20}	0	1	0	1	0	0	7	A_{52}	1	1	0	1	0	0	15
A_{21}	0	1	0	1	0	1	8	A_{53}	1	1	0	1	0	1	16
A_{22}	0	1	0	1	1	0	8	A_{54}	1	1	0	1	1	0	16
A_{23}	0	1	0	1	1	1	9	A_{55}	1	1	0	1	1	1	17
A_{24}	0	1	1	0	0	0	8	A_{56}	1	1	1	0	0	0	16
A_{25}	0	1	1	0	0	1	9	A_{57}	1	1	1	0	0	1	17
A_{26}	0	1	1	0	1	0	9	A_{58}	1	1	1	0	1	0	17
A_{27}	0	1	1	0	1	1	10	A_{59}	1	1	1	0	1	1	18
A_{28}	0	1	1	1	0	0	10	A_{60}	1	1	1	1	0	0	18
A_{29}	0	1	1	1	0	1	11	A_{61}	1	1	1	1	0	1	19
A_{30}	0	1	1	1	1	0	11	A_{62}	1	1	1	1	1	0	19
A_{31}	0	1	1	1	1	1	12	A_{63}	1	1	1	1	1	1	20

If now to select subsets of all CC's corresponding to the same number, we will get the following picture:

N	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
CC	A_0	A_1 A_2	A_3 A_4	A_5 A_6 A_8	A_7 A_9 A_{10}	A_{11} A_{12} A_{16}	A_{13} A_{14} A_{17} A_{18}	A_{15} A_{19} A_{20}	A_{21} A_{22} A_{24} A_{32}	A_{23} A_{25} A_{26} A_{33} A_{34}	A_{27} A_{28} A_{35} A_{36}	A_{29} A_{30} A_{37} A_{38} A_{40}	A_{31} A_{39} A_{41} A_{42}	A_{43} A_{44} A_{48}	A_{45} A_{46} A_{49} A_{50}	A_{47} A_{51} A_{52}	A_{53} A_{54} A_{56}	A_{55} A_{57} A_{58}	A_{59} A_{60}	A_{61} A_{62}	A_{63}
M	1	2	2	3	3	3	4	3	4	5	4	5	4	3	4	3	3	3	2	2	1

This table sets mapping all integers in range from 0 up to 20 on the set of all the 6-digit CC's. This mapping has a stringent regularity. To each number N in range 0-20 there corresponds anti-number $\bar{N}$ connected by the following relations:

1. $N + \bar{N} = 20$ (for instance, $9 + 11 = 20$);
2. A number of CC's, representing the number of N, coincides with a number of CC's, representing the anti-number of $\bar{N}$. And here to each CC representing the number of N corresponds some CC representing the anti-number of $\bar{N}$, which is "inversion" of the initial CC representing the number of N. For example, to the number of 9 there corresponds the anti-number of 11, and here CC A_{23} = 010111, representing the number of $9 = 5 + 2 + 1 + 1$, corresponds to CC A_{40} = 101000, which is the representation of the number $11 = 8 + 3$ and the latter CC can be obtained from the CC A_{23} by inverting of its binary digits. Note also that the number 23, being the number of the CC of A_{23}, is connected to the number of 40, being the number of the CC of A_{40}, by the following relation: $23 + 40 = 63$ (this rule is fair for all CC of such kind).
3. The number of 10, being simultaneously also its anti-number ($10 + 10 = 20$), is the only exception of the rule, indicated in the point of 2; here to each of four CC's, representing the number of 10, corresponds the CC being "inverse" to the initial one (for example, the CC A_{27} is connected to the CC A_{36} with the relation: $27 + 36 = 63$, and the CC of A_{28} is connected to the CC of A_{35} with the relation: $28 + 35 = 63$).

Using the approach stated in the above mentioned book by Petoukhov, it is possible to construct Biperiodical Table (BT) of the 6-digit Fibonacci code. BT represents a square arrangement by the size 8×8. To each cell of BT there corresponds some the 6-digit CC consisting of two three-digit parts, low and high. The low part of the CC encodes corresponding table column, and the high one does its string. Then the CC is in the corresponding BT cell located on the intersection of the corresponding string and column; here the three-digit codes of the string and column form total code of the given 6-digit CC. For example, the CC A_{51} = 110 011 is in the BT cell being on intersection of the string encoded as 110 and the column encoded as 011. According to the code table considered above in the Fibonacci code each CC corresponds to some number. For example, the CC of A_{51} = 110 011 corresponds to the number of 15. Then we should record to the corresponding cell of BT the CC together with the number corresponding to it.

	111	110	101	100	011	010	001	000	Σ
111	A_{63} = 20	A_{62} = 19	A_{61} = 19	A_{60} = 18	A_{59} = 18	A_{58} = 17	A_{57} = 17	A_{56} = 16	$144 = 8 \times 18$

	111	110	101	100	011	010	001	000	
111	$A_{63}=20$	$A_{62}=19$	$A_{61}=19$	$A_{60}=18$	$A_{59}=18$	$A_{58}=17$	$A_{57}=17$	$A_{56}=16$	$144=8\times18$
110	$A_{55}=17$	$A_{54}=16$	$A_{53}=16$	$A_{52}=15$	$A_{51}=15$	$A_{50}=14$	$A_{49}=14$	$A_{48}=13$	$120=8\times15$
101	$A_{47}=15$	$A_{46}=14$	$A_{45}=14$	$A_{44}=13$	$A_{43}=13$	$A_{42}=12$	$A_{41}=12$	$A_{40}=11$	$104=8\times13$
100	$A_{39}=12$	$A_{38}=11$	$A_{37}=11$	$A_{36}=10$	$A_{35}=10$	$A_{34}=9$	$A_{33}=9$	$A_{32}=8$	$80=8\times10$
011	$A_{31}=12$	$A_{30}=11$	$A_{29}=11$	$A_{28}=10$	$A_{27}=10$	$A_{26}=9$	$A_{25}=9$	$A_{24}=8$	$80=8\times10$
010	$A_{23}=9$	$A_{22}=8$	$A_{21}=8$	$A_{20}=7$	$A_{19}=7$	$A_{18}=6$	$A_{17}=6$	$A_{16}=5$	$56=8\times7$
001	$A_{15}=7$	$A_{14}=6$	$A_{13}=6$	$A_{12}=5$	$A_{11}=5$	$A_{10}=4$	$A_9=4$	$A_8=3$	$40=8\times5$
000	$A_7=4$	$A_6=3$	$A_5=3$	$A_4=2$	$A_3=2$	$A_2=1$	$A_1=1$	$A_0=0$	$16=8\times2$
	$96=8\times12$	$88=8\times11$	$88=8\times11$	$80=8\times10$	$80=8\times10$	$72=8\times9$	$72=8\times9$	$64=8\times8$	640

Below it is given the same BT of the Fibonacci code, in which in cells of the BT the values of numbers represented by the corresponding CC's are left only.

|	111	110	101	100	011	010	001	000	
111	20	19	19	18	18	17	17	16	$144=8\times18$
111	20	19	19	18	18	17	17	16	$144=8\times18$
110	17	16	16	15	15	14	14	13	$120=8\times15$
101	15	14	14	13	13	12	12	11	$104=8\times13$
100	12	11	11	10	10	9	9	8	$80=8\times10$
011	12	11	11	10	10	9	9	8	$80=8\times10$
010	9	8	8	7	7	6	6	5	$56=8\times7$
001	7	6	6	5	5	4	4	3	$40=8\times5$
000	4	3	3	2	2	1	1	0	$16=8\times2$
	$96=8\times12$	$88=8\times11$	$88=8\times11$	$80=8\times10$	$80=8\times10$	$72=8\times9$	$72=8\times9$	$64=8\times8$	$640=8\times80$

We can see the following regularities in the indicated table:

1. The sum of numbers by columns and strings always is a number multiple to 8. Let's remind, that the number of 8 is characteristic for the sums of protons in amino acids. In particular, there are 12 amino acids (see page 125 of Petoukhov's book), having the octal base of 8.

2. The Biperiodical Table of the Fibonacci code has an exceptional regularity. In it the following property of the "mirror symmetry " is seen. If to divide the table into two equal parts in the horizontal direction and the vertical one, the strings located from above and from below from the horizontal line or to the right and to the left of the vertical one consist of identical numbers (12, 11, 11, 10, 10, 9, 9, 8 - in the horizontal direction and 18, 15, 13, 10, 10, 7, 5, 2 - in the vertical direction). It is curious, that the number of 10, which is simultaneously and its anti-number, is in center of the table. To each number in a top of a vertical column corresponds mirror-symmetrically a number in bottom of the vertical column, such, that these numbers by the sum give constant number for each column (24 - for the 1st column, 22 for the 2nd and 3rd columns, 20 - for the 4th and 5th columns, 18 - for the 6th and 7th columns, 16 - for the 8th column).We can see the same regularity for the "mirror - symmetrical" numbers arranged in the table strings. If we will consider the first string from above, then the sums of the "mirror - symmetrical" numbers by strings give the following values (36 - for the 1st string, 30 - for the 2nd string, 26 - for the 3rd string, 20 - for the 4th and 5th strings, 14-for the 6th string, 10- for the 7th string, 4 - for the 8th string). Also note that the sums of the numbers arranged on diagonals of the table, are equal $80 = 20 + 16 + 14 + 10 + 10 + 6 + 4 + 0 = 4 + 6 + 10 + 8 + 10 + 12 + 14 + 16$.

3. Note that the same property of "mirror symmetry" is watched and in each of the table quadrants. Really, for the 1st quadrant (the left-hand above) we have the following regularities for the sums of the "mirror-symmetrical numbers (32, 30, 30, 28 by columns, 38, 32, 28, 22 by strings); for the 2nd (the right-hand above) quadrant we have the following sums of the "mirror-symmetrical numbers (38, 36, 36, 34 by columns and 34, 28, 24, 18 by strings); for the 3rd (the left-hand from below) quadrant we have the following sums of the "mirror-symmetrical numbers (16, 14, 14, 12 by columns, 22, 16, 12, 6 by strings); for the 4th (the right-hand from below) quadrant we have the following sums of the "mirror-symmetrical numbers (12,10, 10, 8 by columns, 18, 12, 8, 2 by strings). Also note that the sum of the numbers arranged on diagonals of the 1st quadrant is equal $60 = 20 + 16 + 14 + 10 = 12 + 14 + 16 + 18$; for the 2nd quadrant does $52 = 18 + 14 + 12 + 8 = 10 + 12 + 14 + 16$; for the 3rd quadrant does $28 = 12 + 8 + 6 + 2 = 4 + 6 + 10 + 8$; for the 4th quadrant does $20 = 10 + 6 + 4 + 0 = 2 + 4 + 6 + 8$.

4. If now we divide each of quadrants into 4 new 2 ×2 quadrants we can see in them the same regularity (all diagonal sums are equal among themselves).

DNA SUPRA-code
(Jean-Claude Perez's discovery)

In 1990. Jean-Clode Perez, the scientific employee of IBM, has made rather unexpected discovery in the field of genetic code. He has discovered the mathematical law controlling by self-organizing of the basis T, C, A, G inside of DNA. He has found out, that the consecutive sets of DNA nucleotides are organized in frames of the distant order called as "RESONANCES". Here "Resonance" represents the special proportion ensuring division of DNA parts pursuant to the Fibonacci numbers (1, 2, 3, 5, 8, 13, 21, 34, 55, 89, 144, ...). As already repeatedly was emphasized in our Museum, it is the same proportion, which controls by morphology of natural organisms such, as a pinecone, cactus, pineapple, etc. For example, let's consider 144 adjacent nucleotides of DNA formed from 55 basis of T and 89 basis of A, C or G; then the proportion (55-89-144) represents itself the "Resonance".
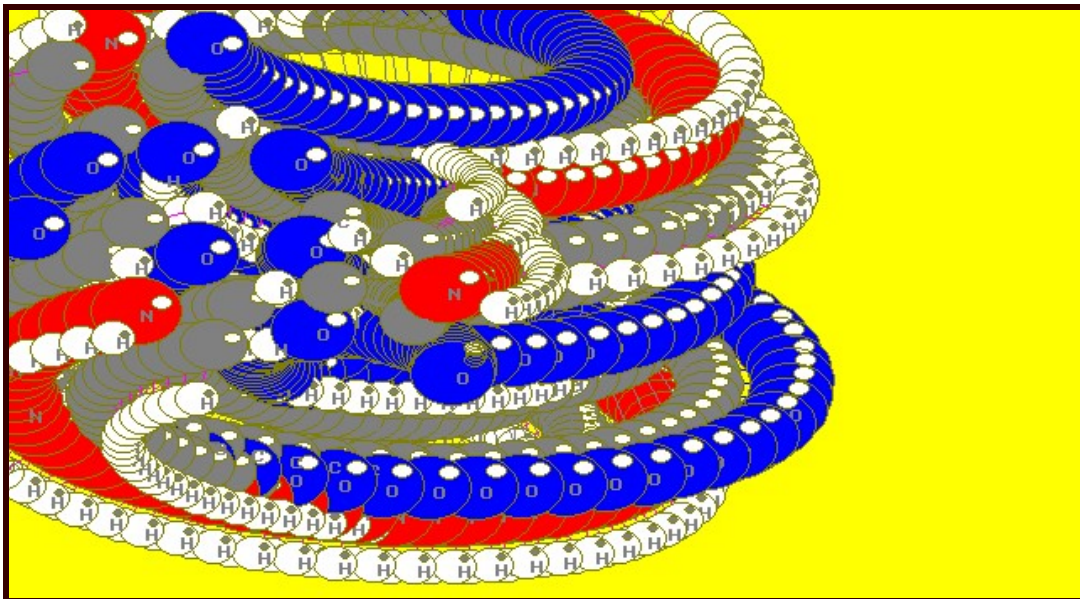
An Artistic Image of Dynamic Molecular-Genetic Structure (from Zenkin's WEB site **http://www.com2com.ru/alexzen/**).

Just this Fibonacci's proportion is a key idea of Jean-Clode Perez's discovery called DNA SUPRA-code. The essence of the DNA SUPRA-code consists of the following. Let's consider any section of a genetic code consisting of the T, C, A, G bases, and let the length of this section is equal to the Fibonacci number, for example, 144. If the number of the T-bases in the considered DNA section is equal 55 (Fibonacci number) and the general number of the C, A, G bases is equal to 89 (Fibonacci number), then the considered section of a genetic code represents a "resonance", that is, the "resonance" is the proportion between three adjacent Fibonacci numbers (55-89-144). Here it is permissible any combinations of the bases, that is, C against AGT, A against TCG, or G against TCA. The discovering consists of the fact that DNA consists of the set of "resonances" of the considered kind, that is, as a rule, sections of the genetic code of the length, equal Fibonacci number F_n are divided by the golden section into the set of the T-bases, which number in the considered section of the genetic code is equal to F_{n-2}, and the general set of the remaining bases, which number is equal to F_{n-1}. If to make systematic research all the possible Fibonacci's sections of the genetic code, then we will get some set of the "resonances" and this set is called SUPRA-code of DNA.

Since 1990 the indicated regularity multiply was tested and confirmed by many outstanding biologists, in particular, by professors Montagnier and Chermann, studied the DNA of the AIDS virus.

What underlies the biological substantiation of the indicated law? The writer of the discovery Jean-Clode Perez gives a following explanation to this phenomenon. The analysis of sensitivity of DNA to noise and minor alterations demonstrates that such principle of DNA construction is super sensing to minor change. In outcome there arises a paradoxical conformity between STABILITY and SENSITIVITY.

It is doubtless, that the considered discovery falls into to category of outstanding one's in DNA area determining development of gene engineering. In opinion of the discovery author Jean-Clode Perez the SUPRA-code of DNA is the universal bio-mathematical law indicating the highest level of self-organizing of nucleotides in DNA according to the principle of the "golden section".

Testing Jean-Clode Perez's Law

In the mentioned above Petoukhov's book (hages165-166) the sequences of triplets in the synthetic genes for α- and β-circuits of insulin are given. For the β-circuit this sequence has the following form:

ATG-TTG-GTC-AAT-CAG-CAC-CTT-TGT-GGT-TCT-CAC-CTC-GTT-GAA-GCT-TTG-

TAC-CTT-GTT-TGC-GGT-GAA-CGT-GGT-TTC-TTC-TAC-ACT-CCT-AAG-ACT

Note that all T-bases in the indicated sequence are marked by red color.

Testing Jean-Clode Perez's Law for the example of the β-circuit of the insulin molecule (see above) resulted in the following outcome. The total number of triplets in β-circuit is equal to 30, that is, the molecule contains 90 bases (the nearest Fibonacci number is 89). If we calculate a number of the T-bases in the β-circuit we will find that it is equal to 34 (note that 34 is Fibonacci number), then the number of the remaining bases is equal to 90-34 = 56 (the nearest Fibonacci number is 55). Thus, there exists the following proportion between the T-bases and the remaining bases in the β-circuit: 90-56-34. This proportion is very close to the "resonance": 89-55-34. It follows from this analysis that Jean-Clode Perez's Law for the insulin β-circuit is fulfilled with accuracy sufficient for practice. If now we take the initial segment of the β-circuit consisting of the first 18 triplets, that is, of 54 bases, (the nearest Fibonacci number is 55) and calculate a number of the T-bases in this segment we will find that it is equal 22 (the nearest Fibonacci number is 21). This means that we have the following proportion in the first segment of the β-circuit: 54-32-22, that also is close to the "resonance": 55-34-21. Thus, Jean-Clode Perez's Law also is fulfilled in the first segment. If we take the segment consisting of the rest 12 triplets (of 36 bases), then a number of the T bases in this segment is equal to 12 (the nearest Fibonacci number is 13). Thus we have for this case a proportion: 36-24-12 that is close to the "resonance": 34-21-13. Thus, both for the β-circuit of the insulin molecule as a whole, and for its separate segments Jean-Clode Perez's Law is fulfilled with accuracy sufficient for practice. Also it is possible to see, that practically in any segment of β-circuit the tendency to the golden section is saved.

The surprising discovery by Jean-Clode Perez allows to make an interesting conclusion regarding to analogy between music, poetry, market processes ("Elliott Waves") and genetic code. It is clear that "harmony" of Shopen's etudes, Pushkin's poetry or "Elliott Waves", in which the "golden section" is watched multiply, is similar to "harmony" of the genetic code, in which Fibonacci's "resonance's ", underlying the SUPRA-code, are watched multiply both in all the DNA molecule and in its every separate part.