Six Fractal Codes of Biological Life:
Perspectives in Astrobiology and Emergence of Binary Logics

"There's no sense in being precise when you don't even know what you're talking about".

John Von Neumann
"Where there is matter, there is geometry."
Johannes Kepler

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Abstract

The discovery of a simple numerical formula for the projection of all the atomic mass of life-sustaining CONHSP bioatoms leads to the emergence of a set of Nested CODES unifying all the biological, genetic and genomic components by unifying them from bioatoms up to whole genomes. In particular, we demonstrate the existence of a digital meta-code common to the three languages of biology that are RNA, DNA and amino acid sequences. Through this meta-code, genomic and proteomic images appear almost analogous and correlated. The analysis of the textures of these images then reveals a binary code as well as an undulatory code whose analysis on the human genome makes it possible to predict the alternating bands constituting the karyotypes of the chromosomes. The application of these codes to perspectives in astrobiology and the emergence of binary codes and regions of local stability (voting process), whose fractal nature we demonstrate is illustrated.

Introduction

Beyond its appearance, the major subject of this article will not concern biology, genetics or genomics, but rather the question of the emergence of COMPLEXITY, in the line of research like those of Ilya Prigogine, Benoit Mandelbrot or John Nash [1, 2, 3].

Indeed, the central question will be that of the emergence of "regularites" from an apparent disorder. The best illustration is that of the emergence of Benard's cells [1], putting organization emerging from the balance of billions of atoms, or the Mandelbrot's question "How Long Is the Coast of Britain?" [2] ...

Thus we will demonstrate how a binary code can emerge from the apparent disorder of DNA at the level of the entire human genome. We will also show how the living processes constituting the biosphere organize the proportions of the different atomic masses, including isotopes of the same atom (mono-isotopic masses of oxygen atom for example) then produce the "regularity" of the average atomic masses which prove to be optimal vis-a-vis of the code of the "atomic masses code" discovered here (§Methods Atomic code -I-).

Twenty years ago, in 1997, it was a kind of "scientific aesthetic sense" that motivated the following research: we found it abnormal that life needed 3 languages to code the information of the living: DNA, RNA, and amino acids, language of proteins ... this luxury of redundancy seemed illogical to us, if only because of this famous maxim *"All that is simple is false, all that is not is unusable "*. Others will say *"small is beautiful"* ... We could add *"all that is simple is beautiful"* . Alternatively quote by Paul Valery, *« Everithing simple is false, Everithing is complex is unusable »*... It is true that from 1990 we demonstrated how the Fibonacci numbers - key aesthetic of the nautilus, the pineapple or pine cones - structured the DNA sequences of genes (4, 5) or small genomes such as mitochondrial DNA [6] ...

We were looking for a smaller common denominator for DNA, RNA, and amino acids; we have the intuition of the need of 3 "ingredients":
-the atomic mass and the bioatoms C O N H S P are common to these 3 languages.
-the 2 universal constants PI and Phi could play a role.

-Finally, we imagine a kind of digital "projection" (such as those of the cosine or the sine in geometry), projection which would constitute a kind of "shadow" projecting on the 2D horizontal plane the image of a kind of complex "meta-code" common to these 3 languages …

Then we discovered and published [7, 8] six *"russian doll-like"* embedded CODES:
-I-Atomic mass code.
-II-Master code.
-III-Binary code.
-IV-Undulatory code.
-V-Cytogenetic code.
-VI- Standing waves meta-code.

Methods

We describe here the 6 embedded steps of 'Fractal Life Codes":
-I-Atomic mass code.
-II-Master code.
-III-Binary code.
-IV-Undulatory code.
-V-Cytogenetic code.
-VI-²Standing waves meta-code.

Their nature is fractal, each new code is based on entries on the previous code (s).


-I-Atomic mass code.
FUNCTION: Transform any atomic mass (real number) into an integer number between -3 and +7, corresponding to multiples of Pi / 10 (-3Pi / 10 ... / ... + 7Pi / 10).
INPUTS: a real number corresponding to any atomic mass mono-isotopic, average, or composed of one or more atoms
OUTPUTS: the « Pi-mass », an integer number between -3 and +7, corresponding to multiples of Pi / 10 (-3Pi / 10 ... / ... + 7Pi / 10).
SUMMARY :
A quick presentation of the formula for life: In [5,6,14,15] we introduced the law we call Formula for Life. This law unifies all of the components of living including bio-atoms, CONHSP and their various isotopes, to genes, RNA, DNA, amino acids, chromosomes and whole genomes. This law is the result of a simple non-linear projection formula of the atomic masses. The result of this projection is then organized in a linear scale of integer number based codes (e.g., -2, -1, 0, 1, 2, 3...) coding multiples Pi/10 regular values. These codes are called Pi-masses.
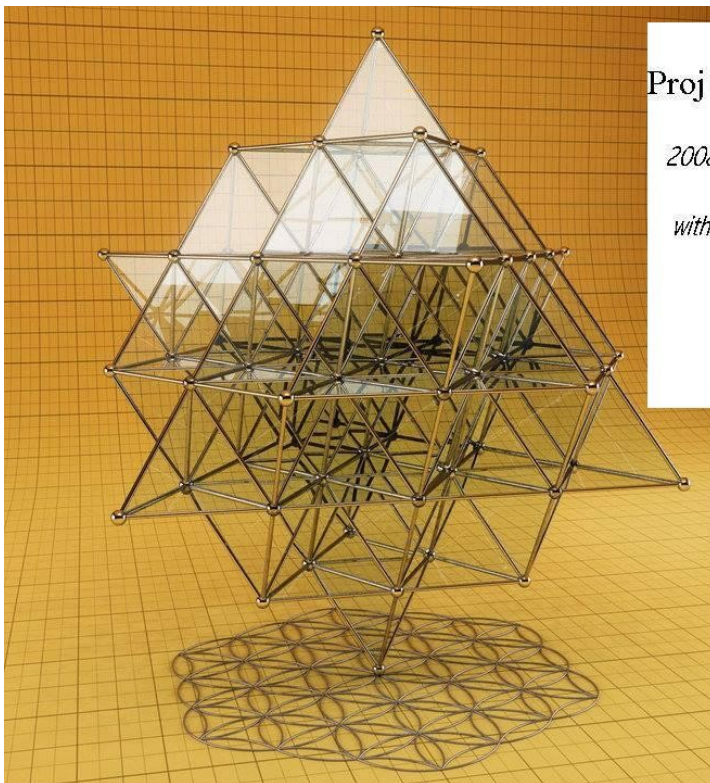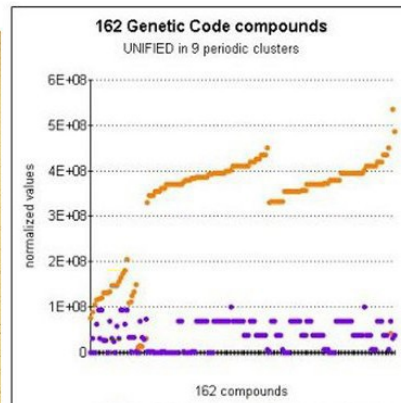
Figure 1 - The numerical projection formula of the atomic masses of any biological component.

Figure 2 - geometric meaning of the formula for life numerical projection

PROCESS :

Computing the "Formula for Life" associated with any atomic mass of Life components:

For atomic mass of any biological compound, we operate the "projection" of the atomic mass numerical value using the following operator:

$$\mathrm{Pr}_{oj}PPI(m) = \left[1 - [P\Pi]\right]m$$

where $P = 4.\sqrt{(\varphi)}.\varphi.\varphi2$

then P = 0.742340663...

Now, consider the "v" value, where v is always a negative or zero real number.

Then consider the function:

$$\mathrm{Re}mainder(v) = |nextwhole\,integer\,just\,after\,whole\,number\,v| - |v|$$

Where Abs (v) is the absolute value of v, and « remainder » or « residue » the decimal remainder of the numerical projection

For example: remainder (-27.85) = 28-27.85 = 0.15

We then defined PPI (m) such that:

$$PPI(m) = \mathrm{Re}mainder\left[1 - [P\Pi]\right]m$$

Note that (1-P.PI) is always negative because m is always positive, and (1-P.PI) is always negative.

As an example, consider the amino acid GLY:

We defined the average mass of GLY as: GLY = 75.067542

Then: (1-P.PI) . GLY = -99.99987286

Thus, PPI (GLY) = remainder [(1-P.PI) . GLY] = 0.0001271351803

Then finally, the result is a real number which we retain only the residues (decimal remainder),

PPI (GLY) = 0.0001271351803

Although no longer considered the decimal part, we note that, if we were interested in the set

(1-P.PI) . GLY = -99.99987286, this value is substantially equal to 100 = 10*2 ... which is not "just any number" ... So then, what is the geometric reality of this projection? As Fig 2 summarizes above, everything happens as if the atomic mass was "filtered" through the competitive interference of two projections: one through a cube of side = 1 and the second through of a sphere of radius = φ × 7/4.

More precisely, let's take an example, by extending the example already presented relating to Glycine (GLY):

We calculated PPI (GLY) = 0.0001271351803.

We can then calculate the 21 PPI (GLY) -R (N.PI / 10) deviations where R (N.PI / 10) is the rightmost column in the previous table of N.PI / 10.

The following 21 values are then obtained:

0.8582802112   0.1724394766   0.4865987419   0.8007580073   0.1149172727   0.429076538
0.7432358034
0.05739506874   0.3715543341   0.6857135995   0.0001271351803   0.3140321302   0.6281913955
0.9423506609
0.2565099263   0.5706691916   0.884828457   0.1989877223   0.5131469877   0.8273062531
0.1414655184

It can be seen that the minimum difference (underlined) corresponds to an angle of 0 °, so to N = 0.

So we'll say that "PI-MASS (GLY) = 0"

The successive stages characteristic having transformed the mass GLY in PI-MASS = 0 are:

Atomic mass GLY = 75.067542

PPI projection (GLY) = 0.0001271351803

Angle N.PI / 10 the nearest: 0.000000000 (N = 0)

Approximate error: EPI (GLY, 0) = 0.0001271351803

PI-MASS (GLY) = 0 either 0 ° or else 0.PI / 10

As a documentary, we will calculate the PI-MASSES relating to 10 sgnificant different genetic materials. Consider any atomic mass « m », which may be that of a bio-atom, of a nucleotide, a codon or an amino acid or any other genetic compound based on bio-atoms or even, any atoms from Mendeleiëv periodic table.

This process will work especially on the average masses (mix of various isotopes % proportions). But it may also be applied to a particular isotope or any derivative of specific atomic mass proportions of the various isotopes.

Table 1 - A set of Pi-mass projections for some main Life compounds.

Nature	Molecule or bioatom	Average atomic mass	Projection PPI(m)	Pi-mass NPI(m) = N.Pi/10	Angle	Error EPI(m,N)
Bioatom	C12 Carbon isotope 12	12.000000	0.01441631887	0 PI/10 (0°)	0°	0.01441631887
Bioatom	C (Carbon average mass)	12.0111	0.0003703460363	0 PI/10 (0°)	0°	0.0003703460363
Nucleotide	G (G nucleotide)	150.120453	0.01974469326	0 PI/10 (0°)	0°	0.01974469326
Codon	Codon TCA	369.324471	0.01106361166	0 PI/10 (0°)	0°	0.01106361166
Codon	Codon UCA	355.297477	0.6968708101	-1 PI/10 (-18°)	-18°	0.0110300755
Codon	Codon AGT (TCA complement)	409.349065	0.6930222208	-1 PI/10 (-18°)	-18°	0.0071814862
double-stranded DNA	DNA double strand : TCA+AGT	778.673536	0.7040858325	-1 PI/10 (-18°)	-18°	0.0182450978
Amino acid	PRO (Proline amino acid)	115.13263	0.6281423922	+2 PI/10 (+36°)	+36°	0.0001761385
Amino acid	LYS (Lysine amino acid)	146.190212	0.2553443926	+4 PI/10 (+72°)	+72°	0.0012926688
Peptide link	CONH Peptidic link	43.025224	0.6847234457	-1 PI/10 (-18°)	-18°	0.0011172889

Notes: Projections PPI(m) are multiples of Pi:10. Example: 0.314... = 1Pi/10, 0.628... = 2Pi/10, etc... But, symmetrically vs. 0Pi/10, it appears another regular scale of attractors in the negative region of Pi/10: -1Pi/10 = 1-0.314 = 0.685..., -2Pi/10 = 1-0.628...

Table 2 - Synoptic of PI-masses of different components of genetics.

	-3 PI/10 and less	-2 PI/10	-1 PI/10	0 PI/10	+1 PI/10	+2 PI/10	+3 PI/10	+4 PI/10	+5 and +7 PI/10
Bioatoms	P(-4pi/10)		H O	C	N			S	
Nucleotides				U G I	T C A				
Others compounds		Ph/ sugar RNA	CONH	H2O	CH2 Ph/ sugar DNA				
Amino acids			Asp	Asn Glu Gly Ser	Ala Gln His Thr	Pro Tyr Cys (+2)	Arg Phe Trp Val	Ile Leu Lys Met (+4)	Cys (+5) Met (+7)
Codons DNA	ggg	gtg gcg gag tgg cgg agg ggt ggc gga	ttg ctg atg gtt gtc gta tcg ccg acg gct gcc gca tag cag aag gat gac gaa tgt tgc tga cgt cgc cga agt agc aga	ttt ttc tta ctt ctc cta att atc ata tct tcc tca cct ccc cca act acc aca tat tac taa cat cac caa aat aac aaa					
Codons RNA	uuu uug guu gug ugu ugg ggu ggg	uuc uua cuu cug auu aug guc gua ucu ucg gcu gcg uau uag	cuc cua auc aua ucc uca ccu ccg acu acg gcc gca uac uaa	ccc cca acc aca cac caa aac aaa					

		gau	cau					
		gag	cag					
		ugc	aau					
		uga	aag					
		cgu	gac					
		cgg	gaa					
		agu	cgc					
		agg	cga					
		ggc	agc					
		gga	aga					

Table 3 – Sensitivity of "Formula for Life" vs atomic mass fine tuning.

Genetic compounds	Atomic mass m	PI-mass N PI/10	Error EPI(m,N)
Regular GLYCINE Amino acid. GLY=NH2-CH2-COOH HYDROGEN atom mass H=1.007947	75.067542	0 PI/10 (0°)	0.0001271351803
GLYCINE modified by the atomic mass of only one of the HYDROGEN atoms that becomes H*=1.0080424374 (the other H remain unchanged). GLY=NH2-CHH*-COOH	75.06763744	0 PI/10 (0°)	3.173283858 10*-11 soit 0.0000000000317…
Electron (à titre indicatif)	0.000549	0 PI/10 (0°)	0.0007313405

A startling observation opens the door to enormous opportunities in astrobiology: Table 4 and Figure 3 shows a very curious fact: the Pi-mass projection formula seems optimal only for the atomic masses of average atomic weights of basic life bioatoms C O N H. Instead of tiny perturbations on these atomic masses and atomic masses of the individual isotopes (example O16) of each of these atoms "destroy" the optimality and fine-tuning of these projections then, also, consequently all resulting master code perfect tuning. Example here (Table 4) for the Pi-mass projection of Oxygen isotopes and % average weighted atom mass. As shown in Figure 3, isotopes of oxygen lightest and heaviest O16 O18 both produce an error on the projections Pi-mass much higher than that of the average atomic mass of that atom of oxygen consisting of: 99,757% + 0.04% O16 O17 + 0.2% O18.

Table 4 – Example of Pi-mass fine-tuned projection selectivity for Oxygen average mass vs. individual isotopes

Atom	Isotope	Relative atomic mass	% isotopic composition	Pi projection residue and Pi mass value	Pi-mass NPI(m) = N.Pi/10	Error EPI(m,N)
Oxygen	Average % balance	15.9994(3)	-	0.686647751 0.685840735	-1	0.000807016
	O16	15.994 914 619 56(16)	0.997 57(16)	0.692662834 0.685840735	-1	0.006822099
	O17	16.999 131 70(12)	0.000 38(1)	0.354913152 0.371681469	-2	0.016768318

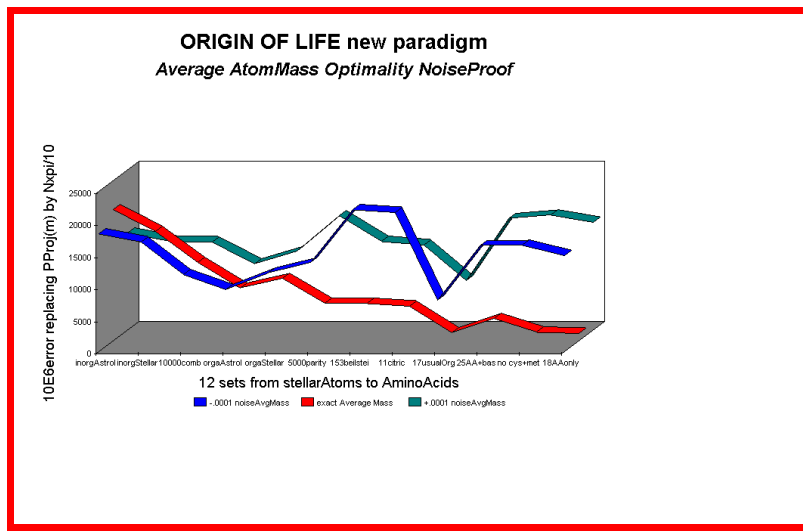| Atom	Isotope	Relative atomic mass	% isotopic composition	Pi projection residue and Pi mass value	Pi-mass NPI(m) = N.Pi/10	Error EPI(m,N)
	O18	17.999 161 0(7)	0.002 05(14)	0.022742056 0.000000000	0	0.022742056

Notes: $0.685840735 = 1 - Pi/10$, $0.371681469 = 1 - 2Pi/10$

Figure 3 - The OPTIMALITY of the average atomic mass is proved here on the PI-masses of ten primordial organic components.

-II-Master code.

FUNCTION: Global integration of Genomics and Proteomics Pi-mass codes at the whole sequence level.

INPUTS: DNA double stranded sequence by codons pairs producing Genomics (DNA) Pi-mass code and Proteomics (coresponding potential amino acid) Pi-mass code (an integer number for each codons pair)

OUTPUTS: 2 Genomic and Proteomic numerical vectors generating 2 patterned 2-D Genomic and Proteomic Images signatures.

SUMMARY :

Starting from the atomic masses constituting nucleotides and amino acids, a numerical scale of integers characterizing each bioatom, each TCAG DNA base, each UCAG RNA base, or each amino acid, an integer numbers scale code is obtained. Then, for each sequence of double - stranded DNA to be analyzed, the sequence of integers that characterizes it (genomics) is constructed as well as the sequence of amino acids that would encode this double strand if each of the strands was a potential protein (proteomics). The remarkable fact is that this proteomics image still exists, even for regions not translated into proteins (junk dna). The computational methodology of the Master code (3, 4) then produces 2 patterned images (2D curves, see Figures 4, 5, 6) which are very strongly correlated. This would mean that beyond the visible sequence of DNA there would be a kind of MASTER CODE being manifested by two supports of biological information: the sequences of DNA and of amino acids, the RNA image constituting a kind of neutral element like the zero of the mathematics (Figure 4). Our thousands of genes and genomes Master Code analyses (viruses, archaeas, bacteria, eucharyotes) demonstrated that the extremums (max and min) signify functional regions like proteins active sites, fragility points like chromosomes breakpoints).

PROCESS:

An overviev on the "Biology Master Code" Great Unification of DNA, RNA and Amino acids : this process run 3 sequential substeps :

a) The coding step

b) The globalization and integration step

c) The great Unification between Genomics and Proteomics Master Code images

It may seem surprising that such a fine tuned process like biology of Life requires the use of three languages as diverse and heterogeneous as DNA with its alphabet of four bases TCAG; RNA with its alphabet of four bases UCAG; and proteins with their language of 20 amino acids. Obviously, the main discoveries in biology were made by those who managed to unearth the respective areas and "bridges" between these three languages. However, any "aesthete" researcher will think the table of the universal genetic code seems rather "ad hoc" and heterogeneous.

Starting only from the double-stranded DNA sequence data, the "Master Code" is a digital language unifying DNA, RNA and proteins that provide a common alphabet (Pi-mass scale) to the three fundamental languages of Genetics, Biology and Genomics.

The construction method of "the Master Code" will be now fully described below. It will highlight a significant discovery we summarize as follows: "Above the 3 languages of Biology - DNA, RNA and amino acids, there is a universal common code that unifies, connects and contains all these three languages". We call this code the "Master Code of Biology."

Here is a brief description of our process for computing the Master Code:

a) The coding step: First, we apply it to any DNA sequence encoding a gene or any non-coding sequence (formerly mislabelled as junk DNA). So it may be either a gene, a contig of DNA, or an entire chromosome or genome. In this sequence, we always consider double-stranded DNA as we explore the following three codon reading frames and following the two possible directions of strand reading (3' ==> 5' or 5' ==> 3'). The base unit will always be the triplet codon consisting of three bases.

As shown in above sample, we calculate the Pi-mass related to double stranded triplets DNA bases, double stranded triplets RNA bases, and double-stranded pseudo amino acids. In fact, for each DNA single triplet codon, we deduce the complementary Crick Watson law bases pairing. We do the same work for RNA pseudo triplet codon pairs, then, similarly for amino acids translation of these DNA codon couples using the Universal Genetic Code table. Then we obtain 3 samples of pairs codes: DNA, RNA and amino acids and this, systematically even when this DNA region is gene-coding or junk-DNA.

A simple example: the starting region of Prion gene:

DNA image coding:

ATG CTG GTT CTC TTT...

-1 -1 -1 0 0...

Complement:

TAC GAC CAA GAG AAA...

0 -1 0 -2 0...

RNA image coding:

AUG CUG CUU CUC UUU...

-2 -2 -3 -1 -3...

Complement:

UAC GAC GAA GAG AAA...

-1 -1 0 -2 0...

Proteomics image coding:

MET LEU VAL LEU PHE

4 3 3 4 3...

Complement:

TYR ASP GLN GLU LYS

2 -1 1 0 4...

Pi-masses corresponding to two strands are then added for each triplet:

Double strand DNA image coding: -1 -2 -1 -2 0...

Double strand RNA image coding: -3 -3 -3 -3 -3...

Double strand Proteomics image coding: 6 2 4 4 7...

This produces three digital vectors relating to each of the 3 DNA, RNA, and proteomics coded images. At this point we already reach an absolutely remarkable result, as symbolized in Figure 1.

We will focus now – exclusively - on the DNA code (genomics) and amino acids code (proteomics).

b) The globalization and integration step: To these two numeric vectors we apply a simple globalization or integration linear operator. It will "spread" the code for each position triplet across a short, medium or long distance, producing an impact or "resonance" for each position and also on the most distant positions, reciprocally by feedback. This gives a new digital image where we retain not the values but the rankings by sorting them.

We run this process for each codon triplet position, for each of the three codon reading frames and for the two sequence reading directions (3' ==> 5' and 5' ==> 3').

For example, to summarize this method: on starting area of the GENOMICS (DNA) code of Prion above, the "radiation" of triplet codon number 1 would propagate well:

-1 -2 -1 -2 0... ==>

-1 -3 -4 -6 -6...then, we cumulate these values: -20

So we made a gradual accumulation of values.

The same operation from the codon number 2 produces:

-1 -2 -1 -2 0... ==>

-2 -3 -5 -5...then, we cumulate these values: -15

etc.

Similarly, the same process on starting area of the PROTEOMICS code of Prion above, the "radiation" of triplet codon number 1 would propagate well:

6 2 4 4 7... ==>

6 8 12 16 23...then, we cumulates these values: 65

So we made a gradual accumulation of values.

The same operation from the codon number 2 produces:

6 2 4 4 7... ==>

2 6 10 17...then, we cumulate these values: 35

etc.

Finally, after computing by this method these "global signatures" for each codon position at Genomics and Proteomics levels, we sort each genomic and proteomic vector to obtain the codon positions ranking: example: as illustrated bellow, the Genomics ranking patterned signature is 2 1 4 3 5 for this Prion starting 5 codons mini subset sequence of 5 codons positions (arbitrary values). Then, to summarize the Master Code computing method on these 5 codon positions starting Prion protein sequence:

Genomics signature:

Codon 1:

Codon / Basic codes / Potentials (with circular closure) / circular complements:

!

-1 -2 -1 -2 0

-1 -3 -4 -6 -6

0

Cumulates: -20

Codon 2:

Codon / Basic codes / Potentials (with circular closure) / circular complements:

!

-1 -2 -1 -2 0

-2 -3 -5 -5

-6

Cumulates: -21

Codon 3:

Codon / Basic codes / Potentials (with circular closure) / circular complements:

!

-1 -2 -1 -2 0

-1 -3 -3

-4 -6

Cumulates: -17

Codon 4:

Codon / Basic codes / Potentials (with circular closure) / circular complements:

!

-1 -2 -1 -2 0

-2 -2

-3 -5 -6

Cumulates: -18

Codon 5:

Codon / Basic codes / Potentials (with circular closure) / circular complements:

!

-1 -2 -1 -2 0

0

-1 -3 -4 -6

Cumulates: -14

Final rankings:

Codon positions: 1 2 3 4 5

Potentials: -20 -21 -17 -18 -14

Rankings: 2 1 4 3 5

Then we run similar computing for Proteomics...

Codon 1:

Codon / Basic codes / Potentials (with circular closure) / circular complements:

!

6 2 4 4 7

6 8 12 16 23

0

Cumulates: 65

Codon 2:

Codon / Basic codes / Potentials (with circular closure) / circular complements:

!

6 2 4 4 7

2 6 10 17

23

Cumulates: 58

Codon 3:

Codon / Basic codes / Potentials (with circular closure) / circular complements:

!

6 2 4 4 7

4 8 15

21 23

Cumulates: 71

Codon 4:

Codon / Basic codes / Potentials (with circular closure) / circular complements:

!

6 2 4 4 7

4 11

17 19 23

Cumulates: 74

Codon 5:

Codon / Basic codes / Potentials (with circular closure) / circular complements:

!

6 2 4 4 7

7

13 15 19 23

Cumulates: 77

Final rankings:

Codon positions: 1 2 3 4 5

Potentials: 65 58 71 74 77

Rankings: 2 1 3 4 5

Then finally:

Codon position: 1 2 3 4 5

Genomics vector: 2 1 4 3 5

Proteomics vector: 2 1 3 4 5

To complete, the same work must be also operate on each codon reading frame...

Meanwhile, a more synthetic means to compute these "long range potentials" for each codon position is the following formula:

Cumulate potential of codon location "i"

$$P(i) = n.p(i) + \left[(n-1).p(i+1)\right] + \left[(n-2).p(i+2)\right]... + \left[\left(n-(n-1)\right).p\left(i+(n-1)\right)\right]$$

Then finally,

$$P(i) = FORj = \left[0,(n-1)\right] DOSIGMA\left[(n-j).p(i+j)\right]$$

Example for Genomics image of codon "i"

The initial computing method described above provides:

-1 -2 -1 -2 0... ==>

-1 -3 -4 -6 -6...then, we cumulate these values: -20

becomes, using this new generic formula:

(-1)x5 + (-2)x4 + (-1)x3 +(-2)x2 +(0)x1 = (-5) + (-8) + (-3) + (-4) + 0 = -20

c) The great Unification between Genomics and Proteomics Master Code images: When applying the process described above in any sequence – gene coding, DNA contig, junk-DNA, whole chromosome or genome - a second surprise appears just as stunning as that of RNA neutral element. We find that for one of the three reading frames of the codons given, the Genomics patterned signature and the Proteomics patterned signature are highly correlated.

Contrary to the three genomics signatures which are correlated in all cases, the proteomics signatures are correlated with genomics signatures only for one codon reading frame, and generally in dissonance for the two remaining codon reading frames. Also, there are perfect local areas matching's focusing on functional sites of proteins, hot-spots, chromosomes breaking points, etc.

In this global correlation, specific codon positions were a perfect match. This is remarkable when regions correspond to biologically functional areas: hot-spots, the active sites of proteins, breakpoints and chromosome fragility regions (i.e., Fragile X genetic disease), etc.
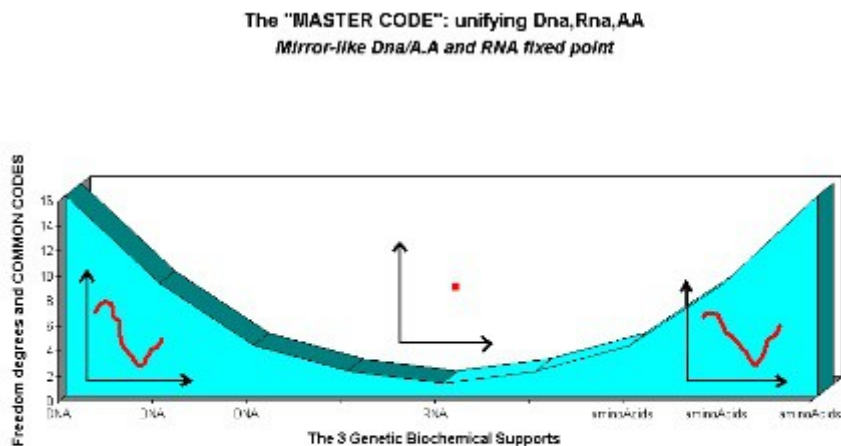
EXAMPLES:

Figure 4 – A symbolic representation of the 3 worlds of double stranded DNA (Genomics) highly corelated with potential double stranded amino acids (Proteomics) while RNA double stranded image is like a neutral element.
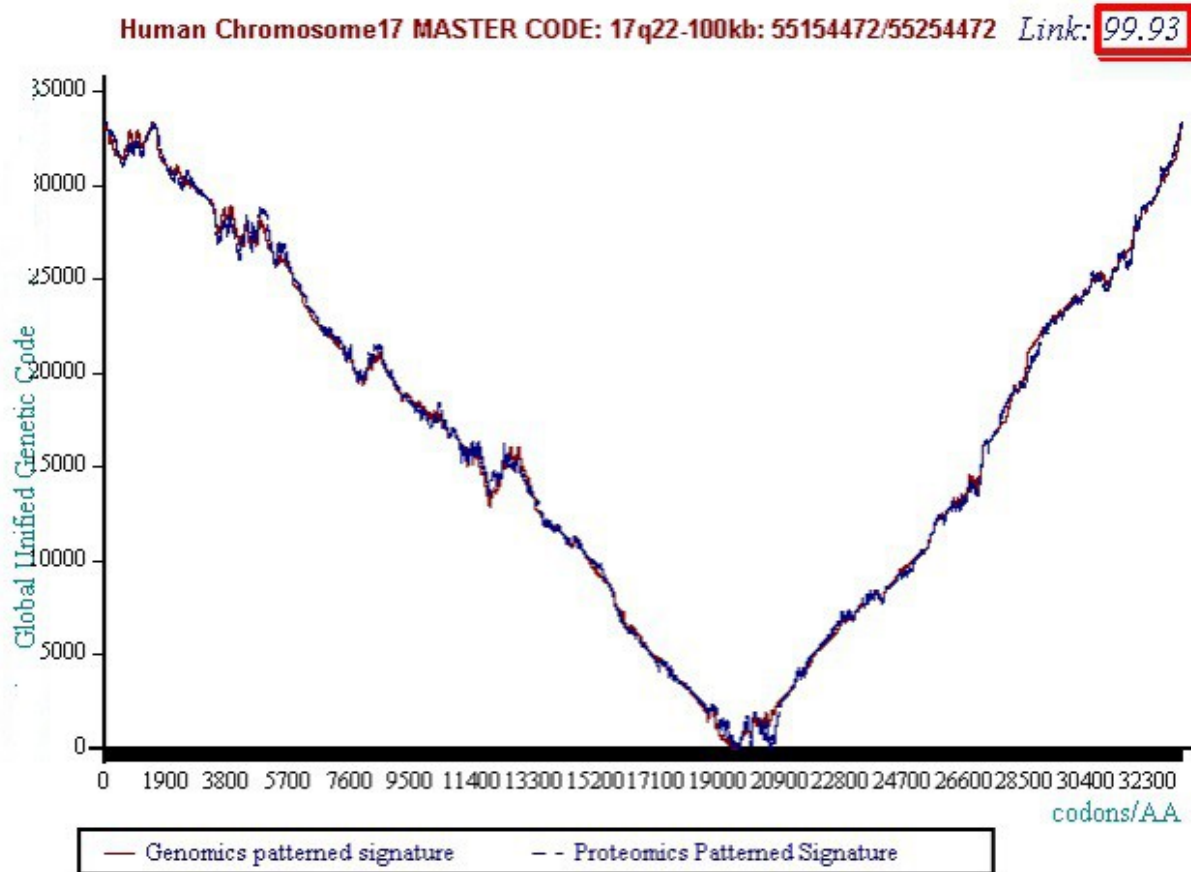
Figure 5 - illustration of the high correlation coupling between genomics and proteomics images of a 100kb stretch of chromosome 7 (99.93% correlation).
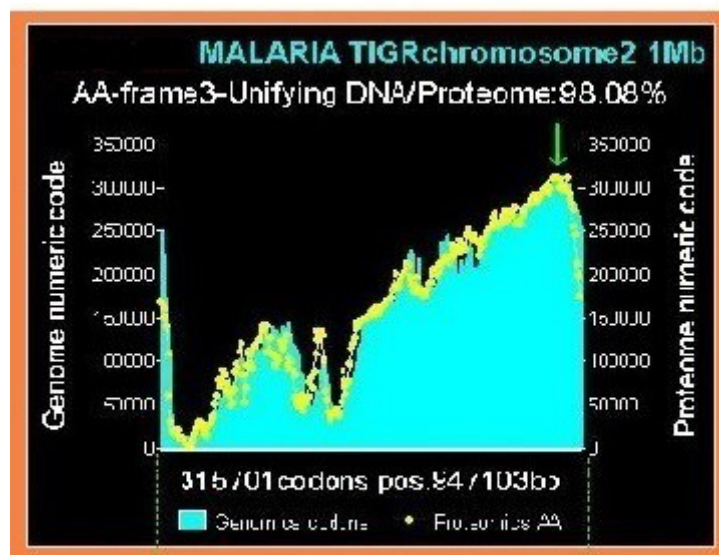

Figure 6 - illustration of the high correlation coupling between genomics and proteomics images of a complete MALARIA chromosome (98.08% correlation)..

-III-Binary code.
FUNCTION:
We compute first-order differential texture and roughness analysis (Leibniz) on Master Code
Genomics and Proteomics images.
INPUTS: Genomics and Proteomics images data from step -II- (2 numerical integer numbers
vectors).
OUTPUTS: 2 binary vectors (0/1) related Genomics and Proteomics textures analysis.
SUMMARY :
If this work is carried out for Genomic patterned pictures, we see that if this trend seems self-
organized around one attractor for DNA double strand (Genomics), it shows two levels, two
"attractors" for the second (Proteomics). A curious fact then emerges: although two genomics and
proteomics curves are still highly correlated in their respective forms and shapes, we discover that
their textures are radically different.

Thus the population of Genomics curves will be relatively dispersed around one single withdrawing
attractor in a kind of Gaussian dispersion, while the population of Proteomic curves will be
distributed around two attractors, bringing out a kind of binary frequency modulation.

We are witnessing the emergence, the "birth" of a Binary Code as demonstrated by Figures 8 , 9,
10, and particularly 3D!

Let us not forget that the initial information was the atomic mass of each bio-atom, which is... a real
(decimal) number! Then it is transformed into a code which is an integer number... and it now
emerges Binary Code, then 0/1 bits which are binary numbers!

Preliminary analysis shows that the average levels of these two attractors are around 0.61 (61%) and
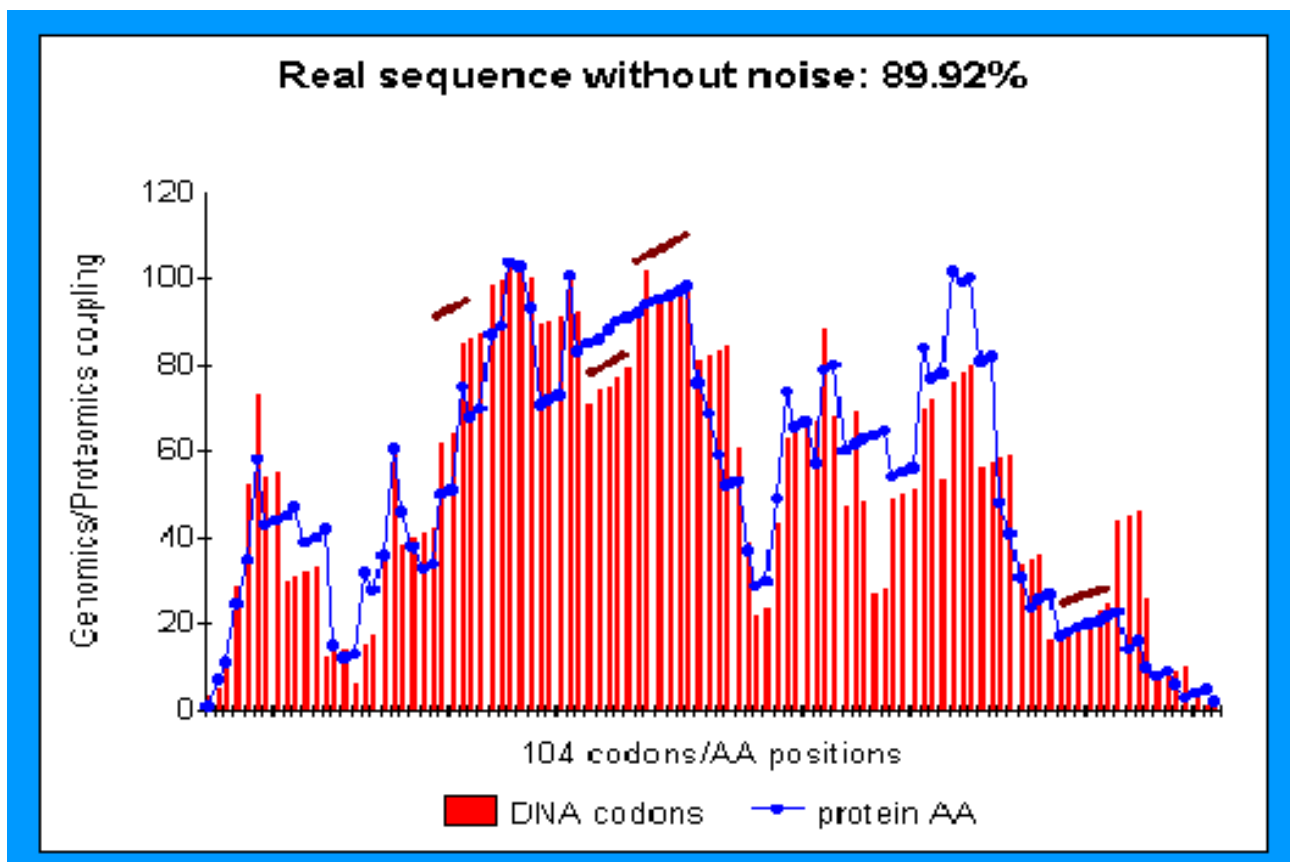0.30 (30%) then appear to be in a ratio of two. We will return to these two values bellow...

Figure 7 – Evidence of first-order differential texture and roughness analysis (Leibniz) on Master
Code Genomics and Proteomics images.

Here is a small example of a sequence of 312 bases where genomics (red) and proteomics (blue) signature (amino acids) are studied. Note the beauty of these mathematical structures which always increase and that some compare to artistic works by M.C. Escher or J.S. Bach.

PROCESS :

Towards discrete Waveforms and logic Biobits overlapping whole chromosomes and genomes

Here we analyze the texture, that is to say, the "roughness" of genomic and proteomic signatures provided by the Master Code. For this, we need only to analyze the slopes or mathematical differentiations from these patterned curves: slopes and gradients - in the sense of LEIBNIZ? - of order 1.

The curves of the Master Code are discontinuous (each point represents a position of triplet codon).

If we note M (i) the Master Code function as defined in -II-, then we agree that:

slope = 1 = "growing" i.e., "increase" if M (i + 1) > M (i)

and slope = 0 = "decreasing" i.e., "decrease" if M (i + 1) < M (i).

Biobits: The emergence of a "binary language" from the Proteomics Master Code of any DNA sequence:

A detailed analysis of the texture of Genomics and Proteomics curves reveals a strange phenomenon: as shown in Figures 8, 9and 10, a curious roughness or "sawtooth" usually characterizes these images. This somehow amounts to a search for the "derivative of order 1", that is to say the slope between two successive points. It becomes apparent that these slopes are mostly in the same direction: always growing or always decreasing.
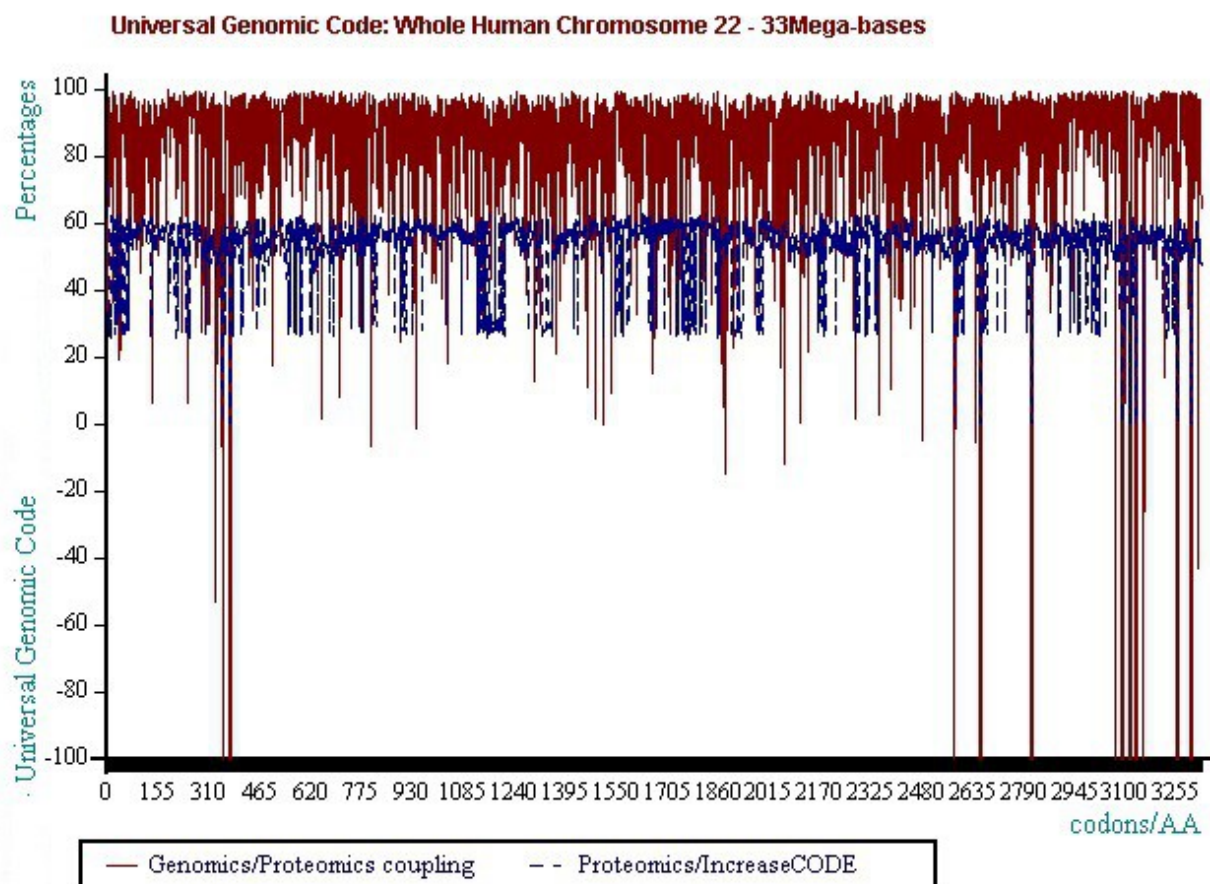
EXAMPLES:

Figure 8 – Clouds of points - In whole chromosome 22, population of Genomics curves will be relatively dispersed around one single withdrawing attractor in a kind of Gaussian dispersion (red), while the

population of Proteomic curves will be distributed around two binary attractors (blue).
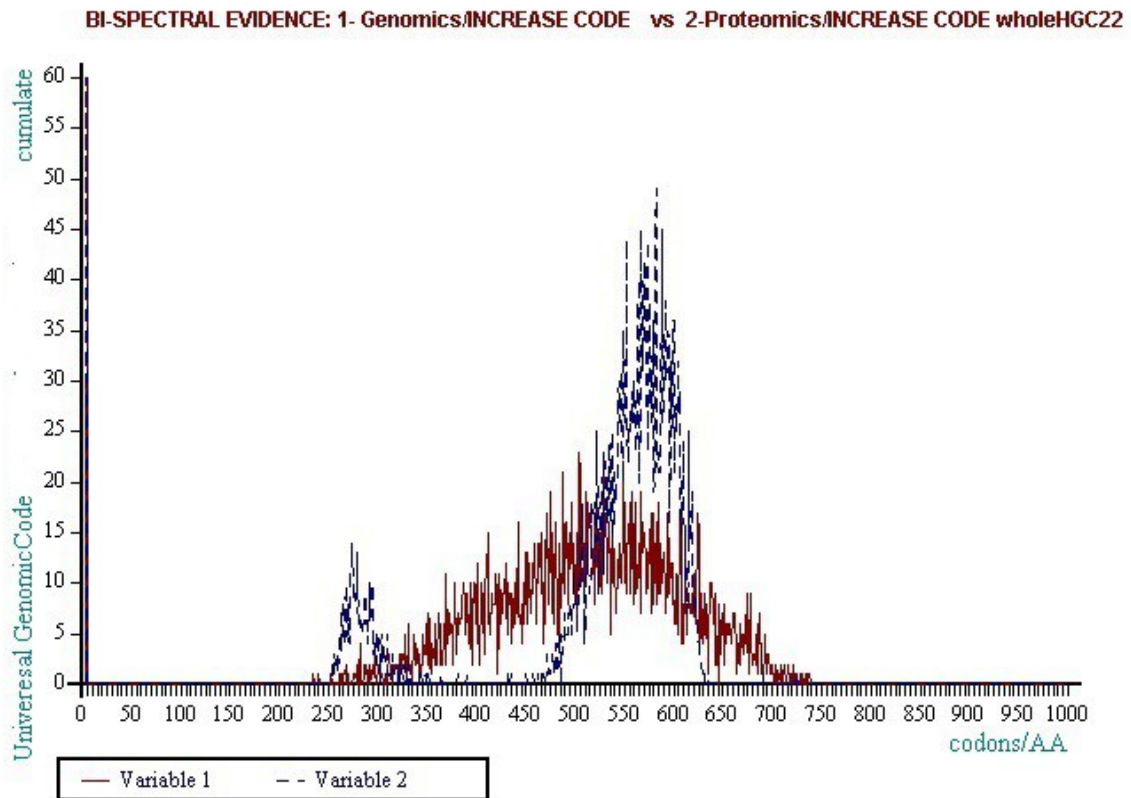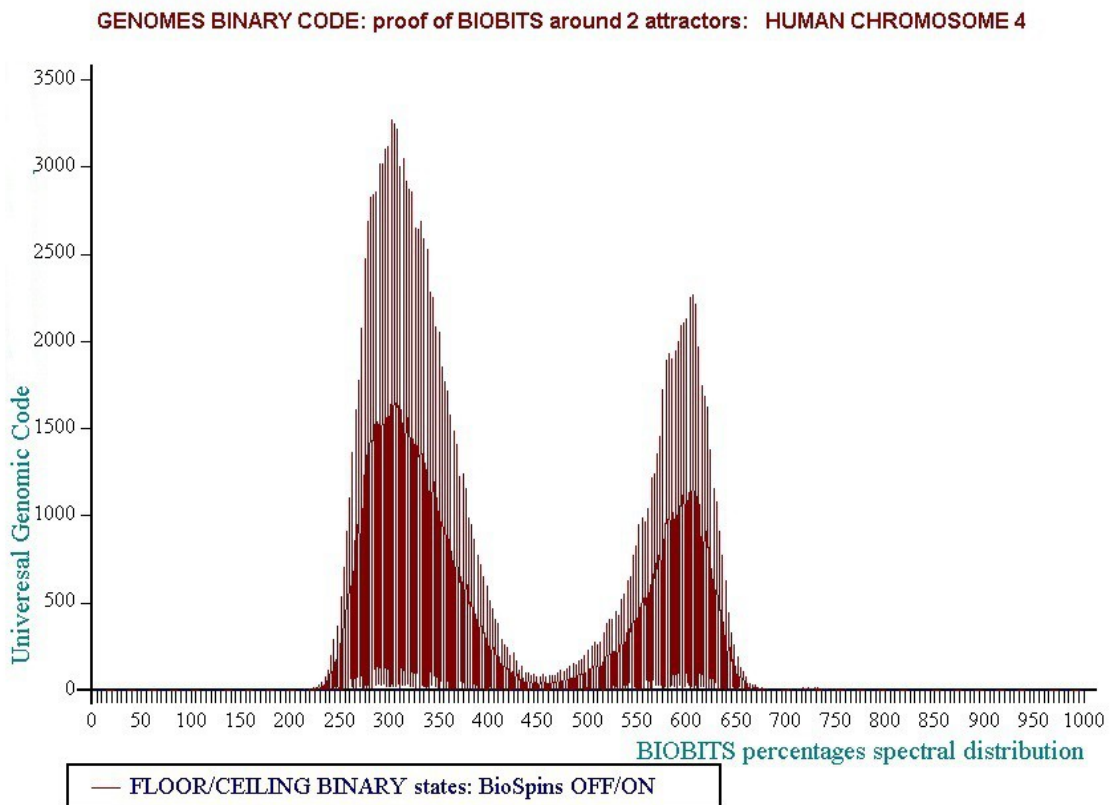

Figure 9 - Frequency distribution - In whole chromosome 22, population of Genomics curves will be relatively dispersed around one single withdrawing attractor in a kind of Gaussian dispersion (red), while the population of Proteomic curves will be distributed around two binary attractors (blue).

Figure 10 - whole chromosome 4 – evidence of the perfect Proteomics Binary Code.

-IV-Undulatory code.
FUNCTION: Building discrete waveforms from Genomic Master Code (-II-).
INPUTS: Genomics and Proteomics images data from step -II- (2 numerical integer numbers vectors).
OUTPUTS: descrete waveforms related Genomics textures analysis.
SUMMARY :
Discrete Waveforms: The emergence of "a modulated waveform code" from the Genomics Master Code of any DNA sequence: the generalization of previous gradient differentiations from second, third or nth gradient differentiation order now highlight "bits"… But waveforms, more precisely discrete waveforms of which we will measure periods: period of short-wave or 2 or 3 or even medium-wave wavelengths (greater than 10 times).

PROCESS:
Thus, we calculate exhaustively all successive gradients or slopes: S(i, i + 1), and S(i, i + 2), S(i, i + 3), ... S(i, i + n). From all these successive gradients periodicities emerge.

Figure 11 shows shortwave period = 4 codons, then 12 bases pairs in one million base pairs within human chromosome 3. Figure 12 shows long wave period = 12 codons, then 36 base pairs in the first 300000 base pairs within one of the largest human genes, the gene for the genetic disease Duchenne DMD.
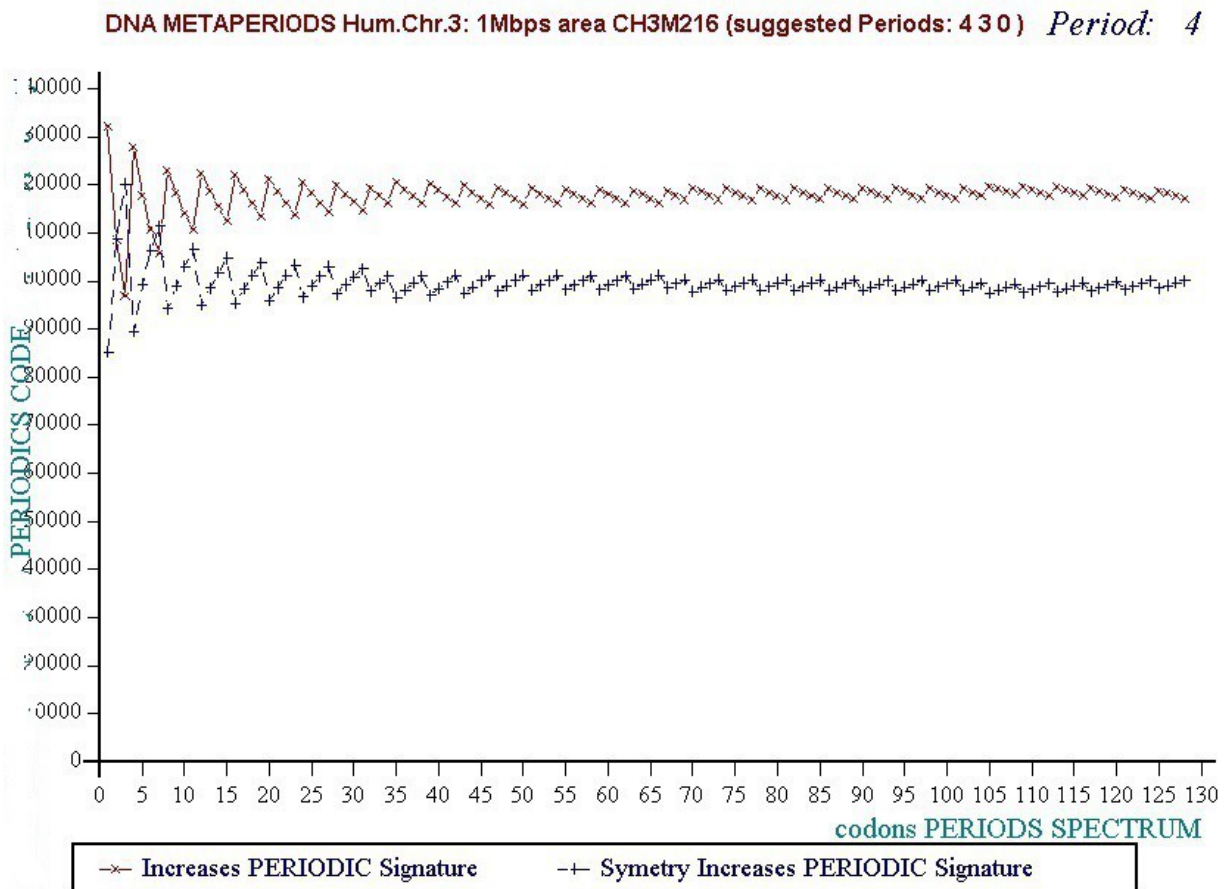
EXAMPLES:

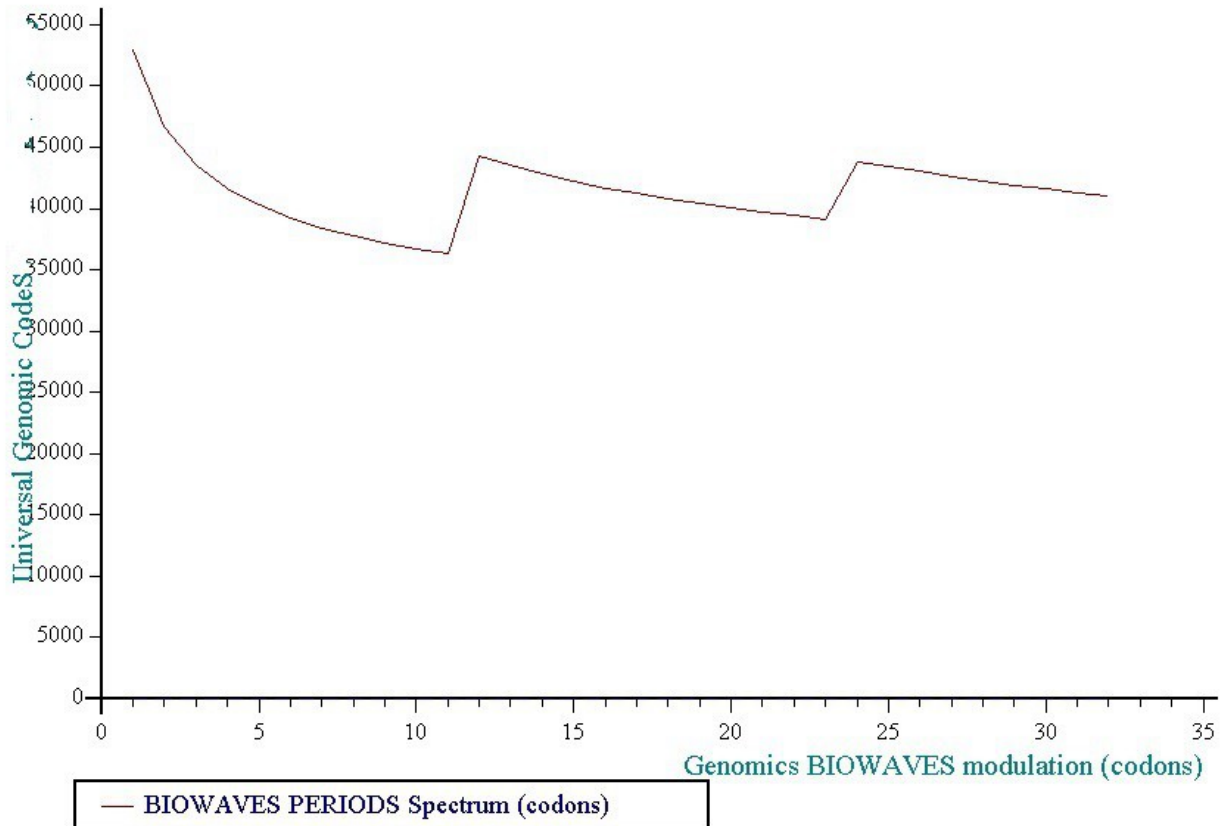Figure 11 – Short period 4 waves from Genomics master code images (1 million bases from chromosome 3)..

Figure 12 – Long waves from Genomics master code images (300000 bases from DMG gene (Duchenne Muscular Distrophy).

-V-Cytogenetic code.
FUNCTION: he combination of Proteomics binary code and Genomics undulatory code highlights the light / gray / dark bands characteristic of the kariotypes of each chromosome of the human genome.
INPUTS: Proteomics Binary code (-III-) and Genomics undulatory code (-IV-).
OUTPUTS: Kariotypes alternated bands of human chromosomes.
SUMMARY :
One of the experimental concrete chromosome representations is a universally known Karyotype image Figure 14). However, the synthesis of two earlier codes (binary code and waveforms) allows prediction throughout the whole human genome of alternating black/gray/white bands of karyotypes as demonstrated by Figure 13. This is the clearest proof of the functional reality of our Master Code discovery. We must recall here that karyotypes are obtained by interferometry, physical process of wave nature.

PROCESS:
Figures 13 and 14 show an illustration of the "calibration" in a portion of human chromosome 8 (30 first millions of bases)..
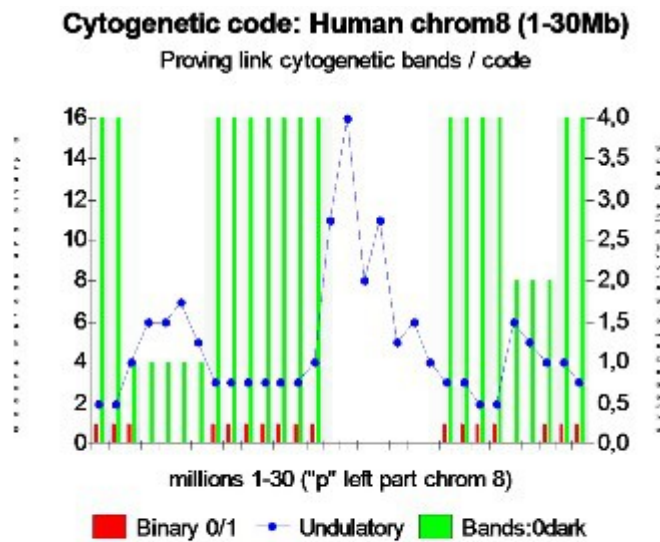
Figure 13 – Example of chromosome 8 bands evidence from Proteomics Binary code and Genomics undulatory code (30 first millions bases in human chromosome 8).
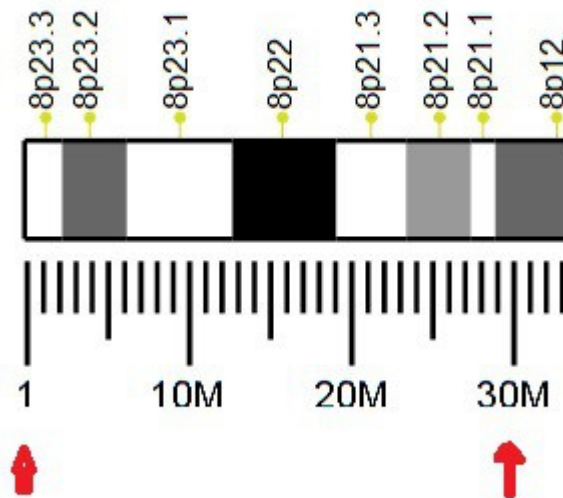

Figure 14 – Human chromosome 8 bands of the 30 first millions bases..

In Figure 13, the green bars represent the actual referenced colors of the karyotype bands for this region of human chromosome 8: 0 = black, 1 = dark gray, 2 = medium gray, light gray = 3, and 4 = white. Blue curve, modulation of waves is predicted by the textures of the "Master code": there is a fairly good correlation with the actual referenced colors of karyotypes, particularly, low wave period (2 or 3) for karyotypes clear (white), and waves heavy periods (in this case up to 16) for dark karyotypes (black).

Finally, Biobits, shown here in red, have a status = 1 = "increase" for karyotypes clear (white) and a status = 0 = "decrease" for dark karyotypes (black).

EXAMPLES :

Such predictive analysis was performed for 24 chromosomes representing the whole human genome. The results show a perfect correlation between the predictions from the textures of the Master Code and grayscale karyotypes as they have been highlighted by the global community of geneticists. Both Figures 6a and Figure 6b below show a graphical summary of texture modulations (Genomics) and Biobits (proteomics) throughout the whole human genome.
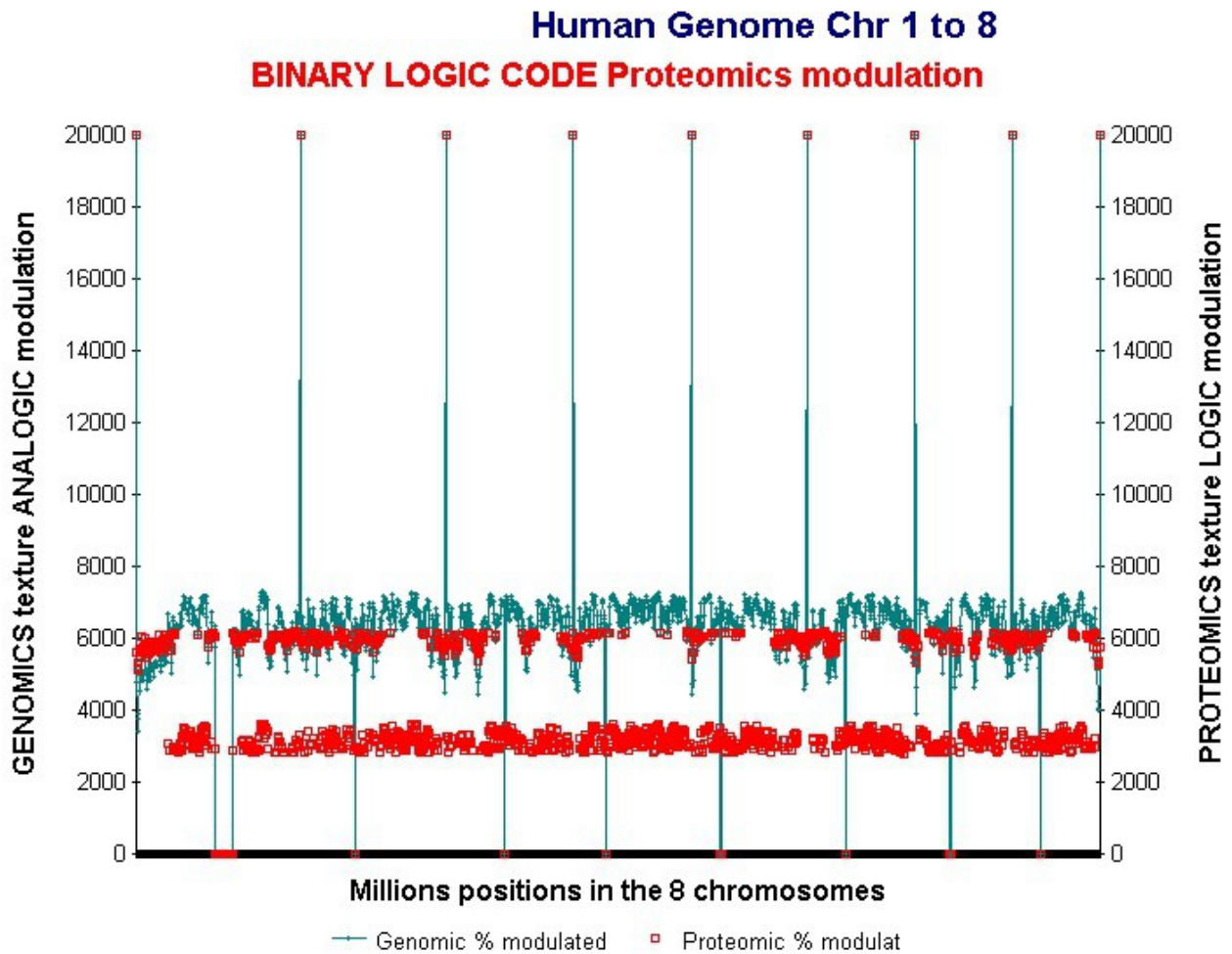

Figure 15 - The first 8 Chromosomes (1 to 8) of the whole HUMAN GENOME.
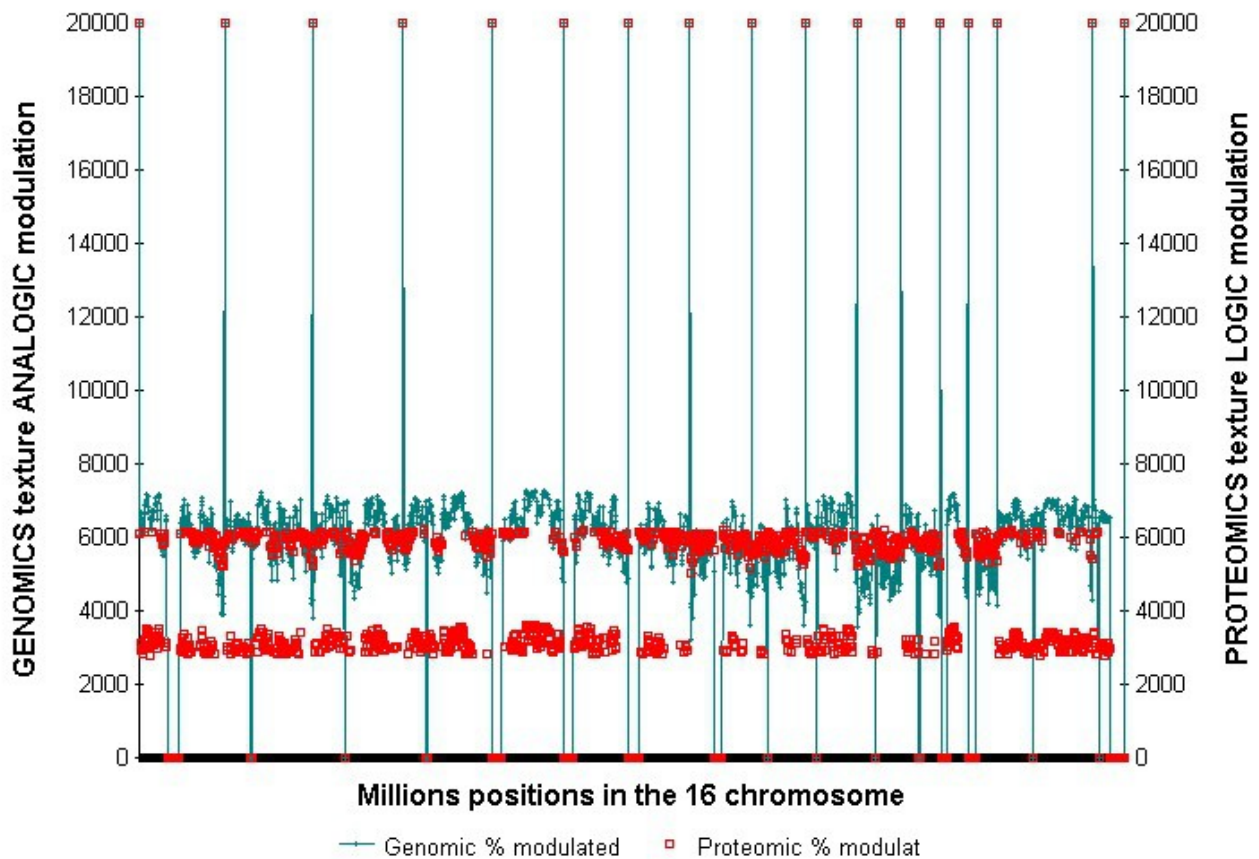
Figure 16 - The 16 other remaining Chromosomes (1 to 8) of the whole HUMAN GENOME.

Notes:

In each graph, the base unit analyzed in X (horizontally) is the million base pairs: 3266 units representing 3.266 billion bases. Of these, 3075 million bases are significant, while the remaining 191 million relate to GAPs (indeterminate "N" bases), especially the centromeric regions of chromosomes.

The vertical lines delimit the boundaries between chromosomes as well as their centromere regions.

The 2 variations represented correspond respectively to the DNA textures (Genomics) and the amino acid textures (Proteomics). They are calculated independently for each of the millions of bases analyzed, ie "one point" per million bases on the genomics curve and "one point" per million bases on the proteomics curve.

Although the two Genomics and Proteomics variation curves are very strongly correlated (96.63% on average throughout the genome), their respective "textures" are radically different!

In fact, the GENOMICS texture is "ANALOGIC modulated" around an average value close to 60% (graduation 6000) ... which would seem to be phi = 0.618.

On the other hand, the PROTEOMICS texture (although calculated in exactly the same way and on highly correlated curves), is "modulated according to a BINARY LOGIC", oscillating permanently between 2 attractors whose respective values are: Floor = FLOOR = 30% on average, or Ceiling = CEILING = 60% on average. The ratio between these 2 attractors is therefore very close to the number "TWO". The "clouds" of points perfectly illustrate the reality of these two 0/1 bit attractors or "FLOOR / CEILING".

-VI- Standing waves meta-code

FUNCTION:

The Genomics master code (-II-) is generalized to meta-codons that no longer have 3 nucleotides as a codon, but 4, 5, ... 377 nucleotides. Then we analyze the textures by the undulatory code (-IV-). It then appears dissonances and resonances that will reveal periods of discrete waves, resonances, and standing waves. The Genomics Binary code analysis (-III-) confirms these periods using a complementary independant method.

INPUTS: Double strand DNA sequence Pi-mass grouped by meta-codons (each Pi-mass is = -1 times number of « G » bases in meta-codon double strand or also = -1 times number of « C+G » bases in single strand meta-codon.

OUTPUTS: Peiod and resonance standing wave computed by two complementary methods.

SUMMARY :

We introduce here a method of global analysis of the roughness or fractal texture of the DNA sequences at the chromosome scale. To do this, we generalize the method of numerical analysis of the "Master Code" (-II-). Thus, we restructure the sequence into different generic sequences based on "meta codons", no longer triplets of 3 nucleotides, but values ranging from 17 to 377 nucleotides, ie 360 simulations. This method of analysis will then reveal, in most cases, discrete waves or interferences, most often dissonances (based on Genomics Undulatory waves described here in -IV-). However, sometimes there will emerge kinds of resonances where all scales of analysis appear to be in symbiosis.

PROCESS:

The discrete interferences fields resulting from the analysis of an entire chromosome are therefore a three- dimensional space: Dim y (vertical) restructuring in meta codons of lengths 17 to 377 nucleotides Dim x (horizontal) Leibnitz differentiations such that prmary 1/2 secondary 1/3... 1/4 ... 1 / n Dim z cumulated populations from the "Master code" operators. The + 1 / -1 derivatives will be of type increase, ie +1 if derivative increasing and will be of type decrease, ie -1 if derived decreasing. In this context we will explore these 3D spaces in 2 forms:

-Horizontally (IV- Undulatory code), meta codons dimension: curves for a given meta codon dimension, see in the example "resonances" below (see Figures 17 and 18).

-Vertically (-III- Genomics binary code), spectral differentiation: discrete series d2-d1 is +1 if increase and -1 if decrease (see Figure 19). We represent in top the +1 and in low the -1, (see Figure 19).

Table 5 – Computing the periodic standing waves and resonances for various metacodons Genomics Master code..

Dim x		d1	d2		…/... d100	
Dim y						
	0	1	2	3	4	5
	17	1298833	1181005	1133041	1103633	1087486
	18	1029171	1074033	960839	1000920	1028712
	19	1091521	982429	937709	912626	975473
	20	878537	903906	914801	922094	927631
	21	933380	834734	893561	848319	885361
	22	761233	774174	779102	783714	786854
	23	809977	837877	764596	791545	755377
	24	852758	779786	750287	735631	726226
	25	710190	727911	736109	742027	699579
…/... 377						

Horizontal scan : exp. meta codons of 22 bases : 22   761233 774174 779102 783714 786854 …/...

(see Figure 17)

Vertical scan example derivations of first order: 1 if d2>d1 and -1 if d2<d1 then : -1 1 -1 1 -1 1 1 -1 1 -1 1 1 …/...
(see Figures 18, 19).

HG38 Human Reference Chromosome21

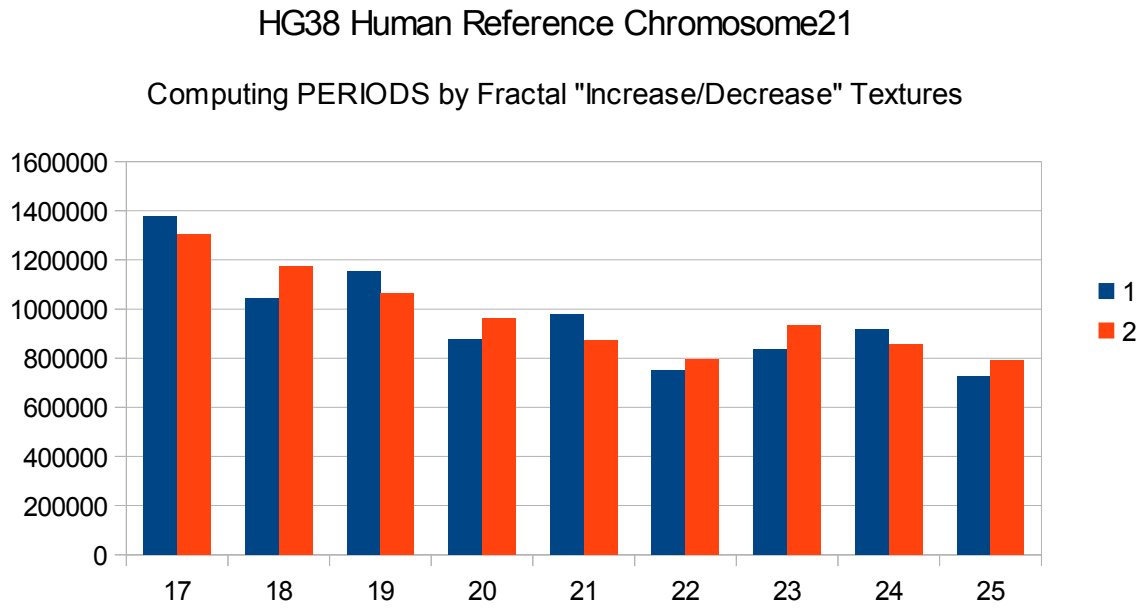### Computing PERIODS by Fractal "Increase/Decrease" Textures

Figure 17 - zoom on vertical scan method revealing PERIOD = 22 from HG38 reference chromosome21.

These two independent methods lead in all the cases analyzed to the same period value: here, for example, the period "horizontal scan" is a resonance of 22bp (Figure 18) and the period "vertical scan" is a period of repeatability of 22bp also (Figure 19).

CHR21 HG38 reference chromosome
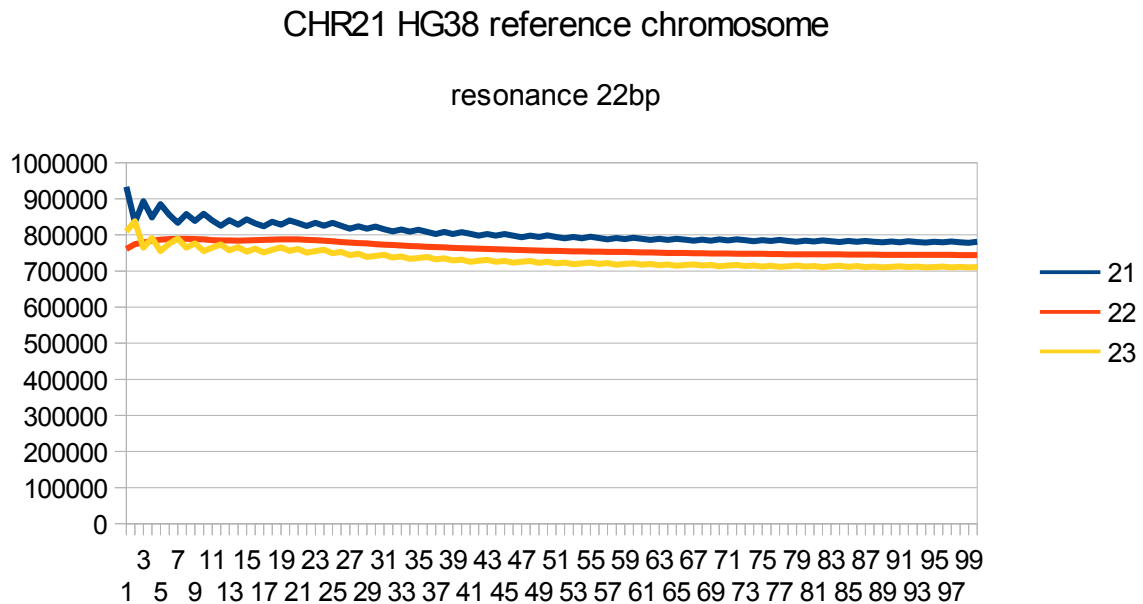
resonance 22bp

Figure 18 - Evidence of a resonance of 22bp period in the whole HG38 human reference chromosome21 (horizntal undulatory code -IV-).

Human Reference Chromosome 21 HG38

period 22 bases pairs
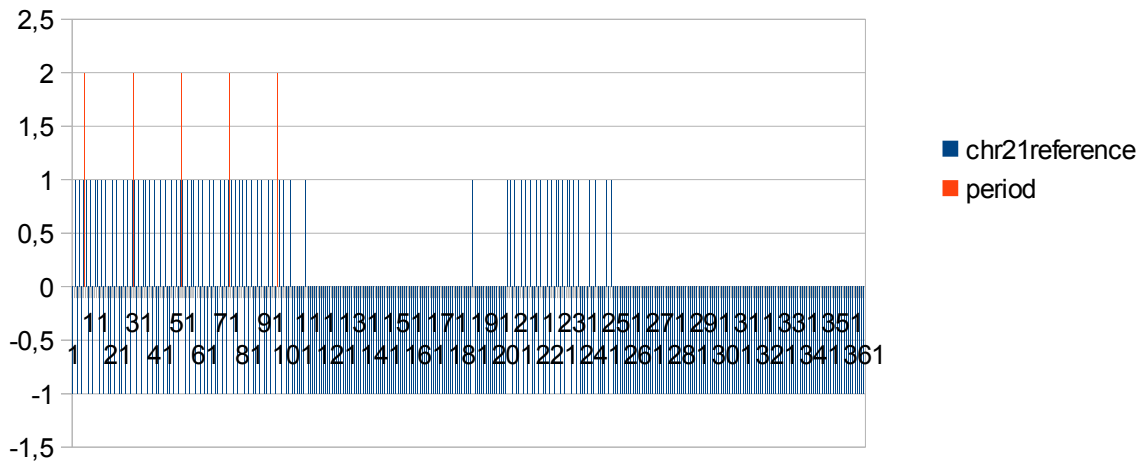
Figure 19 - Confirmation of a 22bp period in the whole HG38 human reference chromosome21 -vertical genomic binary code -III-).

A third complementary method is presented here: knowing the period determined and confirmed by the two previous methods, we segment the complete sequence of the chromosome by consecutive segments according to this period, for example here for the chromosome21, we will "cut" the entire sequence of the chromosome in successive sections of 22 bases, the length of the period discovered. Then we record for each segment the C + G populations on the one hand and T + A on the other hand. We then represent the cumulative distribution curve of these different CG and TA populations throughout the chromosome sequence.

Table 6 - This table shows a C+G top for 8 bases value within 22 bases segments distribution. segmented by 22 bases periods.

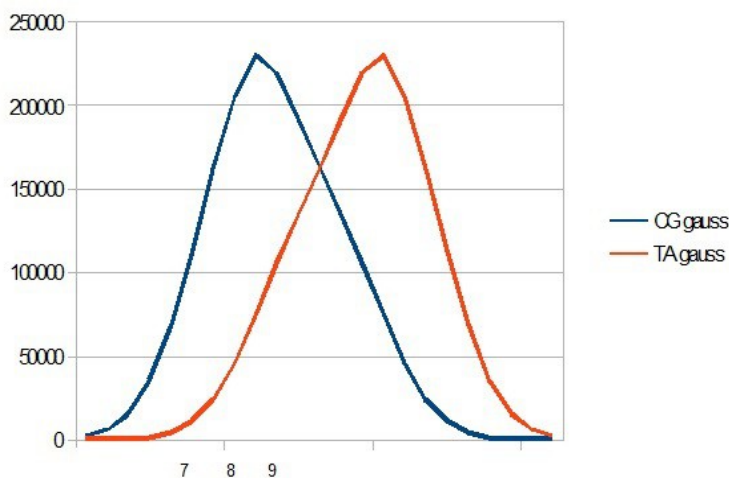| 7	8	9
205735	230173	219504
46083	75340	106183

Figure 20 - Gauss like CG / TA distribution within the whole human HG38 chromosome21

Results and Discussion:

First Experiment: "Natural Hierarchical Introspective Logics"

We revisit here "HIERARCHICAL INTROSPECTIVE LOGICS" The theories of John F. NASH [3] by highlighting the self-emergence of a bistable logic. structuring the entirety of the human genome (Logic code -III- in §Methods).
"There can exist no procedure for finding the set of all regularities of an entity. But classes of regularities can be identified. Finding regularities typically refers to taking the available data about the entity, processing it in some manner into, say, a bit string, and then dividing that string into parts in a particular way and looking for mutual AIC (Algorithmic Information Content) among the parts. If a string is divided into two parts, for example, the mutual AIC can be taken to be the sum of the AIC's of the parts minus the AIC of the whole. An amount of mutual algorithmic information content above a certain threshold can be considered diagnostic of a regularity. Given the identified regularities, the corresponding effective complexity is the AIC of a description of those regularities".

In one hand, in his unformal paper entitled "HIERARCHICAL INTROSPECTIVE LOGICS" [3], the Economy Nobel prize the mathematician Professor John F. Nash Jr. explores new approaches of Turing/Godel undecidability problems adding particularly the "EMBEDDABILITY" dimension.
In other hand, we report here mathematical CODES structuring all genomes and particularly the whole sequenced Draft Human Genome [9] released in 2001 (three billions base-pairs about distributed in the 24 Human chromosomes). This discovery describes particularly the evidence of a self-emerging embedded BINARY CODE structuring the whole human genome.

Then, analysing the texture (mathematical increase/decrease 1st degree derivates) of the Proteomics (code -III- in §Methods) associated curve patterned signature, we could associate with each codon position "biospins" as following:
If the local codon position derivate is in increase state ➜ then Biospin=1,
If the local codon derivate derivate is in decrease state ➜ then Biospin=0.
Now, for any analysed sequence, we could compute the related balancing increase/decriease percentage related to the whole analysed sequence. These percentage values are real numbers in the range 0-100. Normally, the distribution of biospins percentages must be random, like a Gauss-like distribution.
In fact, we obtain a very strange distribution as a "bath-tub"-like distribution: there appears, in ALL CASES, a binary distribution centered around two ATTRACTORS: one attractor, named "Floor-state attractor" is located around 29%.
The other second attractor, named "Ceiling-state attractor" is located about around 60%.

The following law is universal. We propose the following rule entitled "Genomic BINARY CODE law":
For any sequence " seq " of genomic DNA, whatever its length, its position, and its nature, one can always associate, by applying the numerical algorithm described in (code -III- in §Methods), a Binary Code status, called « BioBit » such as:
BioBit (seq) = 0 = « Floor » state = « FALSE » if %(seq) neighbouring attractor 29%.
BioBit (seq) = 1 = « Ceiling » state = « TRUE » if %(seq) neighbouring attractor 60%.
We validated and checked this universal law on the totality of the genomes known to date, and, more particularly, on the whole human genome which we studied independantly on three embedded scales: contiguous segments of 10000bases, 100000bases and 1million of bases from Build34 2003 Human genome release [10], see Figures 15 and 16 in §Methods.

We demonstrate now this Nash's sugested law "Natural Hierarchical Introspective Logics" on a randomly selected region within the Draft Human Genome sequence [9]. This genomic studied region is located between 130000000 and 131024000 positions within the human chromosome5.
Some regions are undefined ("N" undefined bases or "GAPS").

We run 11 independant embedded analyses:
-1024 contiguous DNA segments of 1000bases.
- 512 contiguous DNA segments of 2000bases.
- 256 contiguous DNA segments of 4000bases.
- 128 contiguous DNA segments of 8000bases.
- 64 contiguous DNA segments of 16000bases.
- 32 contiguous DNA segments of 32000bases.
- 16 contiguous DNA segments of 64000bases.
-   8 contiguous DNA segments of 128000bases.
-   4 contiguous DNA segments of 256000bases.
-   2 contiguous DNA segments of 512000bases.
-   1 unique DNA segment of 1024000bases.

In the following table, we resume, for the 11 independant analyses:

-the numbers of elementary BioBits decisions: exp in line 1: 468 "Floor states" and 409 "Ceiling states", the total correspond to 877 segments, the remaining are GAP segments.

-the average values of Floor and Ceiling percentages: exp in line 1: 31% for "Floor attractor" and 59% for "Ceiling attractor".

-the LOCAL LEVEL VOTE DECISION: exp in line1, the Floor state (468) is majority then the local level decision is "Floor"=FALSE.

Table 6 – Logica code "Biobits" from a randomly selected region within the Draft Human Genome sequence [9]. This genomic studied region is located between 130000000 and 131024000 positions within the human chromosome5.

11 Embedded levels	Floor/FALSE/0 states: Average Floor %	Ceiling/TRUE/1 states: Average Ceiling %	Level Vote Decision
First Level 1024 times 1000bases	468 floor level 31%	409 ceiling level 59%	Floor=FALSE
Second Level 512 times 2000bases	239 floor level 30%	201 ceiling level 60%	Floor=FALSE
Third Level 256 times 4000bases	123 floor level 29%	98 ceiling level 60%	Floor=FALSE
Fourth Level 128 times 8000bases	65 floor level 29%	47 ceiling level 61%	Floor=FALSE
Fifth Level 64 times 16000bases	34 floor level 29%	24 ceiling level 61%	Floor=FALSE
Sixth Level 32 times 32000bases	19 floor level 28%	11 ceiling level 61%	Floor=FALSE
Seventh Level 16 times 64000bases	8 (*) floor level 28%	8 (*) ceiling level 61%	UNDEFINED (*)
Eighth Level 8 times 128000bases	7 floor level 27%	1 ceiling level 60%	Floor=FALSE
Ninth Level 4 times 256000bases	3 floor level 27%	1 ceiling level 61%	Floor=FALSE
Tenth Level 2 times 512000bases	2 floor level 27%	0 ceiling level 0%	Floor=FALSE
Final Eleven Level 1 time 1024000bases	1 floor level 27%	0 ceiling level 0%	Floor=FALSE

(*) Nota: 4 Ceiling states are not significant (they include large gaps undefined DNA regions).

In the following couples of graphics we demonstrate the SCALE INVARIANCE and the EMBEDDED LOGICAL VOTE process.

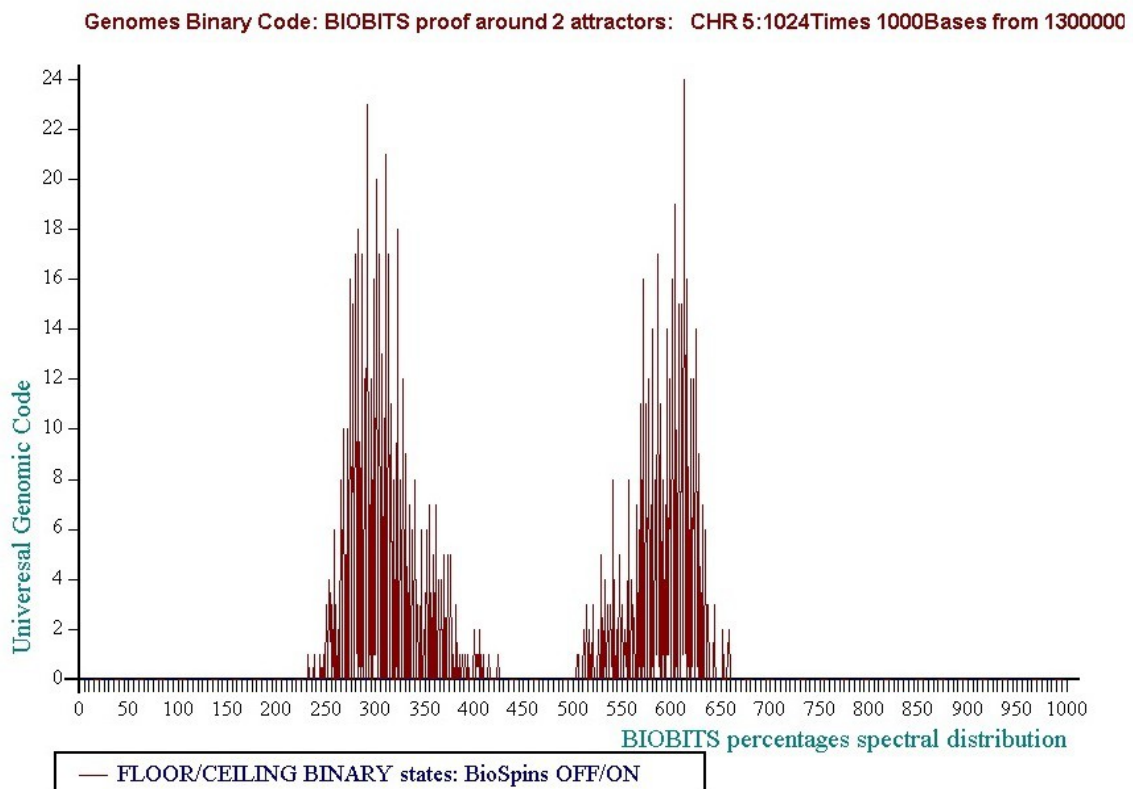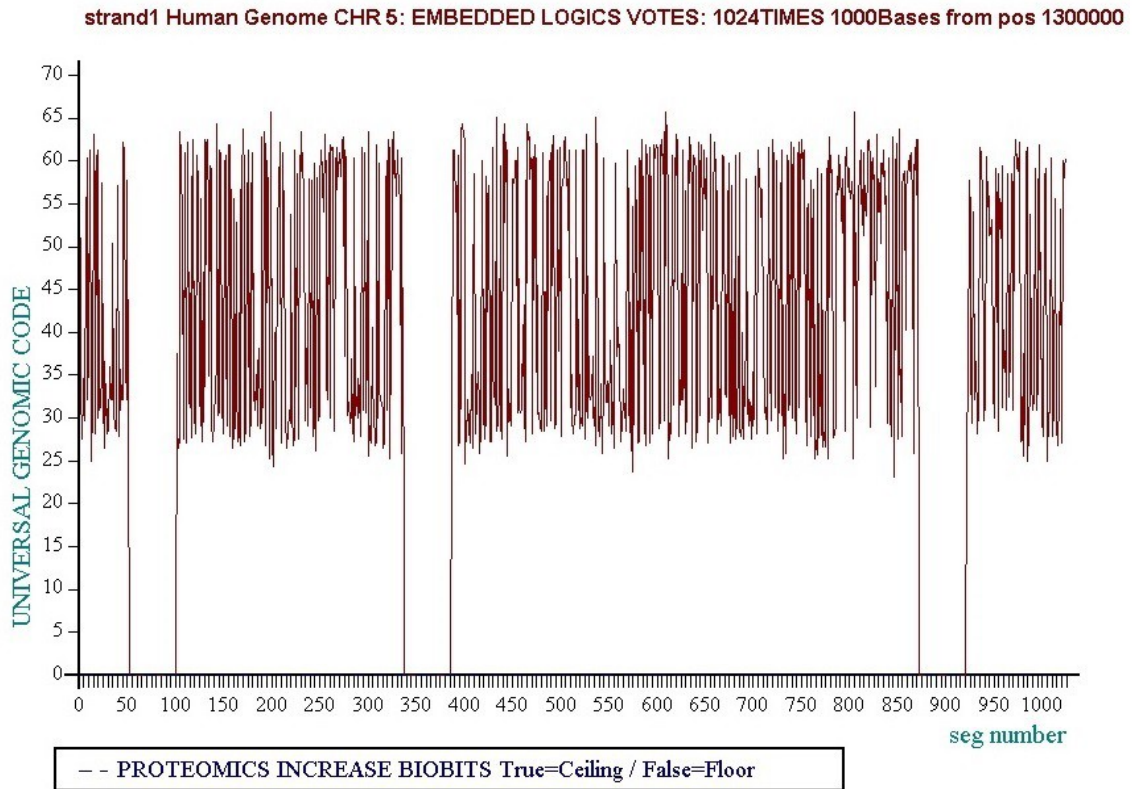→ Level 1: 1024 times 1000 bases... Concensus Decision "VOTE" = Floor = "False"

Figure 21 - Level 1: 1024 times 1000 bases... Concensus Decision "VOTE" = Floor = "False"

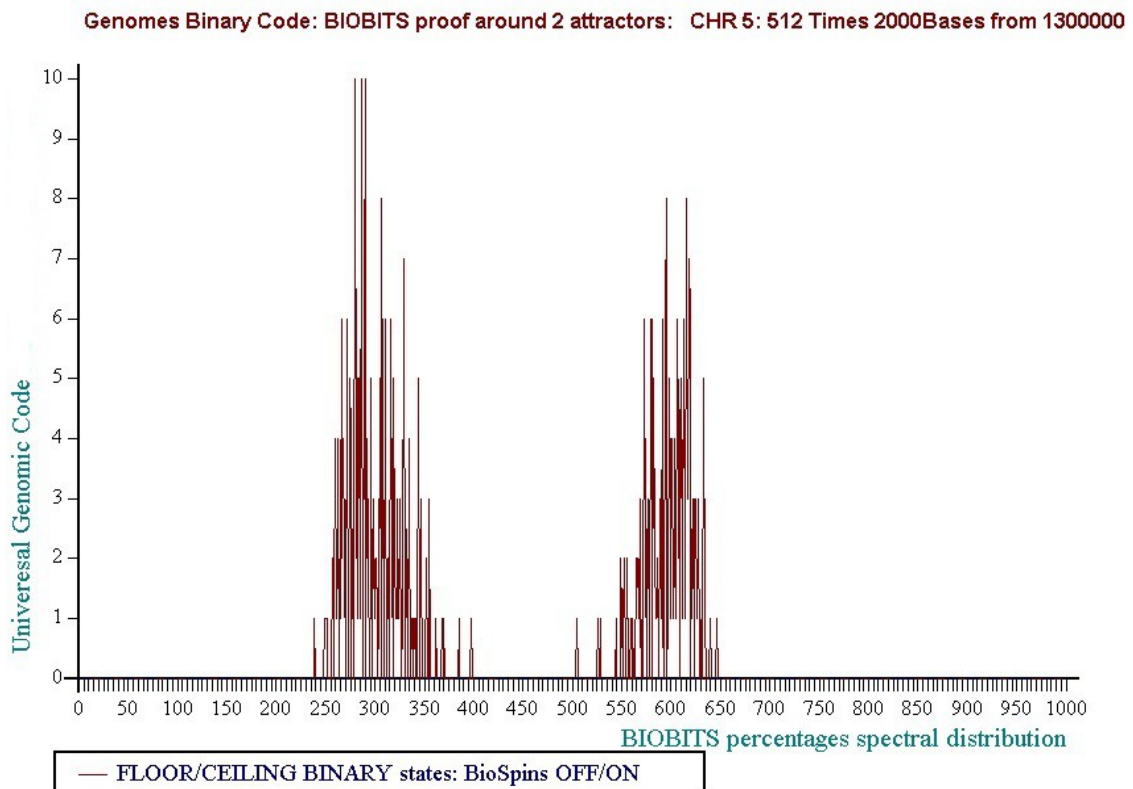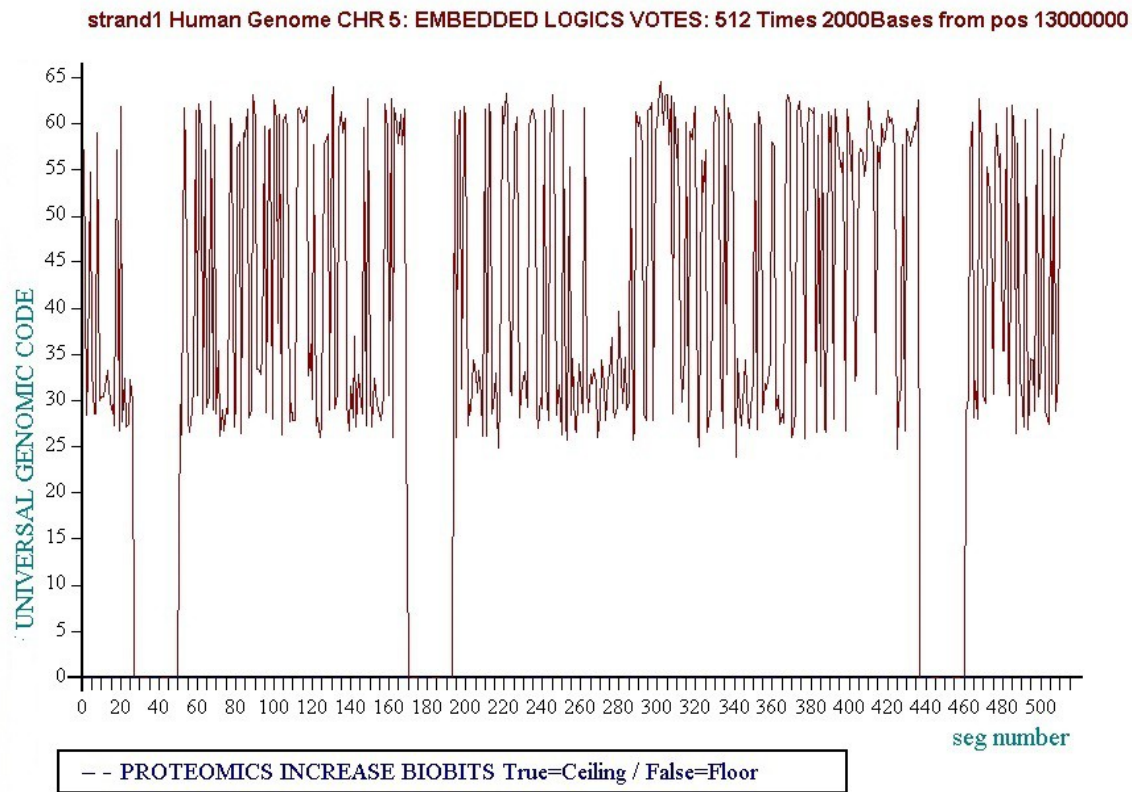➜ Level 2: 512 times 2000 bases... Concensus Decision "VOTE" = Floor = "False"

Figure 22 - Level 2: 512 times 2000 bases... Concensus Decision "VOTE" = Floor = "False"

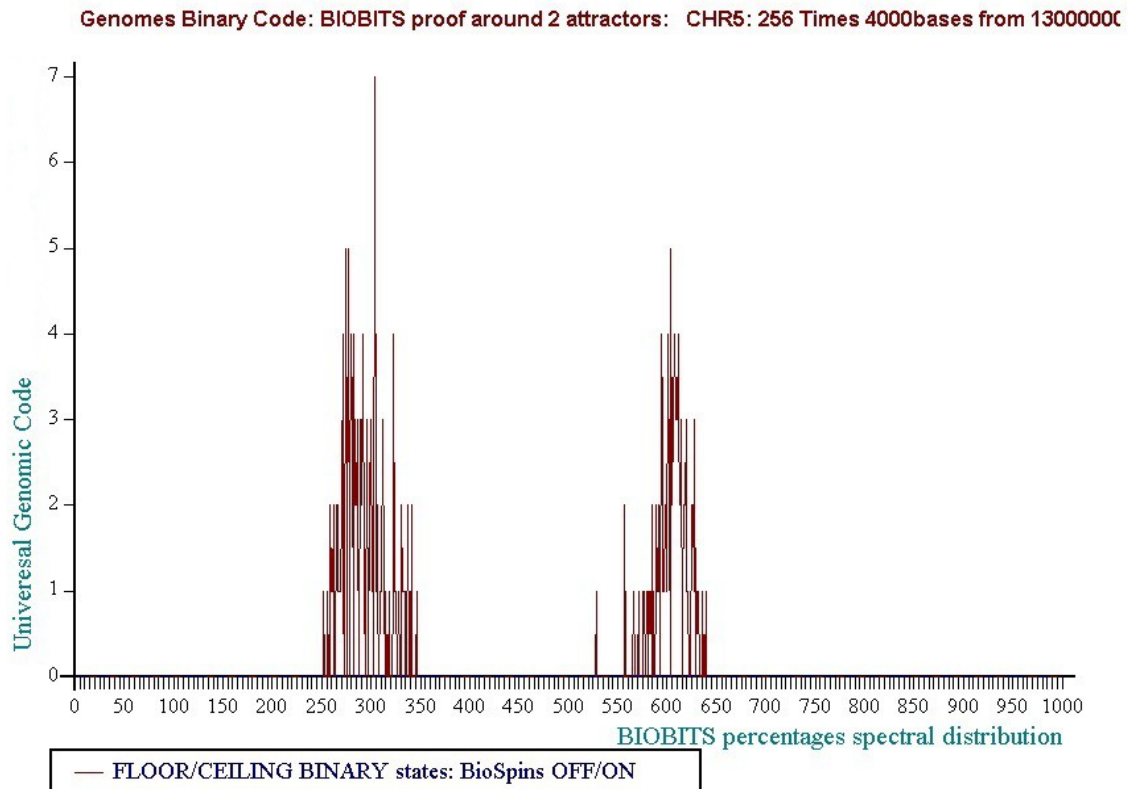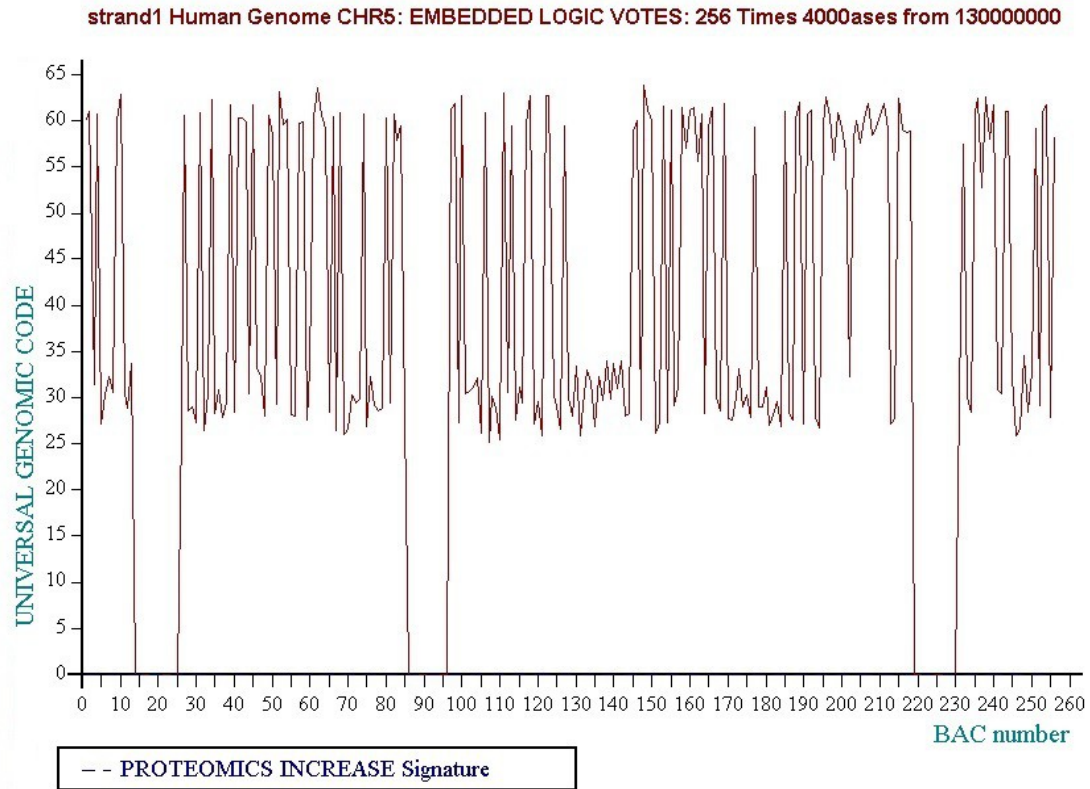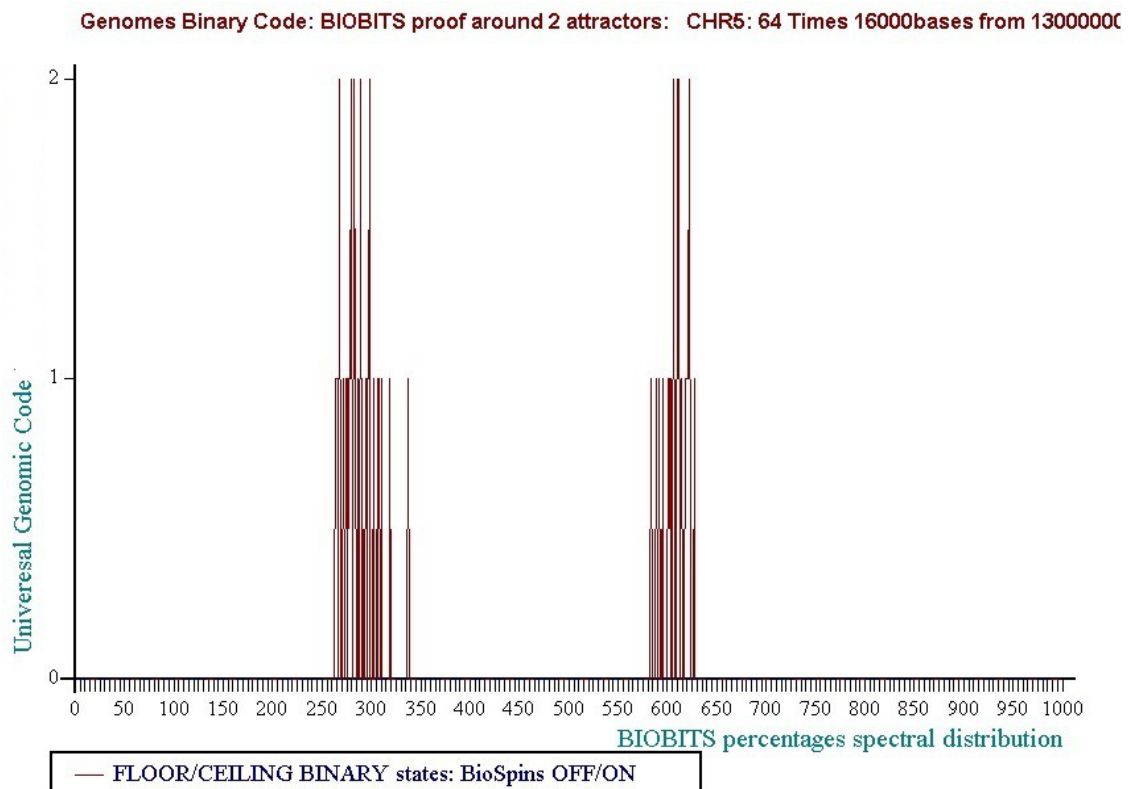➔ Level 3: 256 times 4000 bases... Concensus Decision "VOTE" = Floor = "False"

strand1 Human Genome CHR5: EMBEDDED LOGIC VOTES: 256 Times 4000ases from 130000000

– – PROTEOMICS INCREASE Signature

Genomes Binary Code: BIOBITS proof around 2 attractors: CHR5: 256 Times 4000bases from 1300000C

—— FLOOR/CEILING BINARY states: BioSpins OFF/ON

Figure 23 - Level 3: 256 times 4000 bases... Concensus Decision "VOTE" = Floor = "False"

➔ Level 4: 128 times 8000 bases... Concensus Decision "VOTE" = Floor = "False"
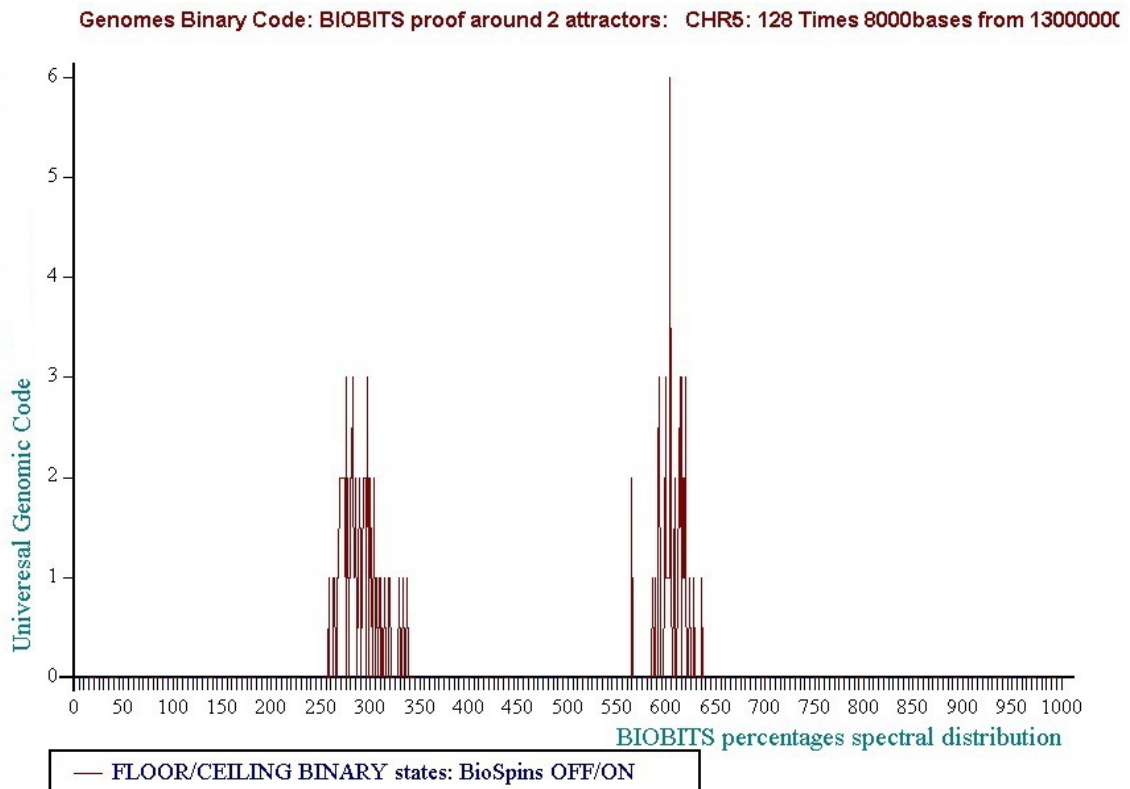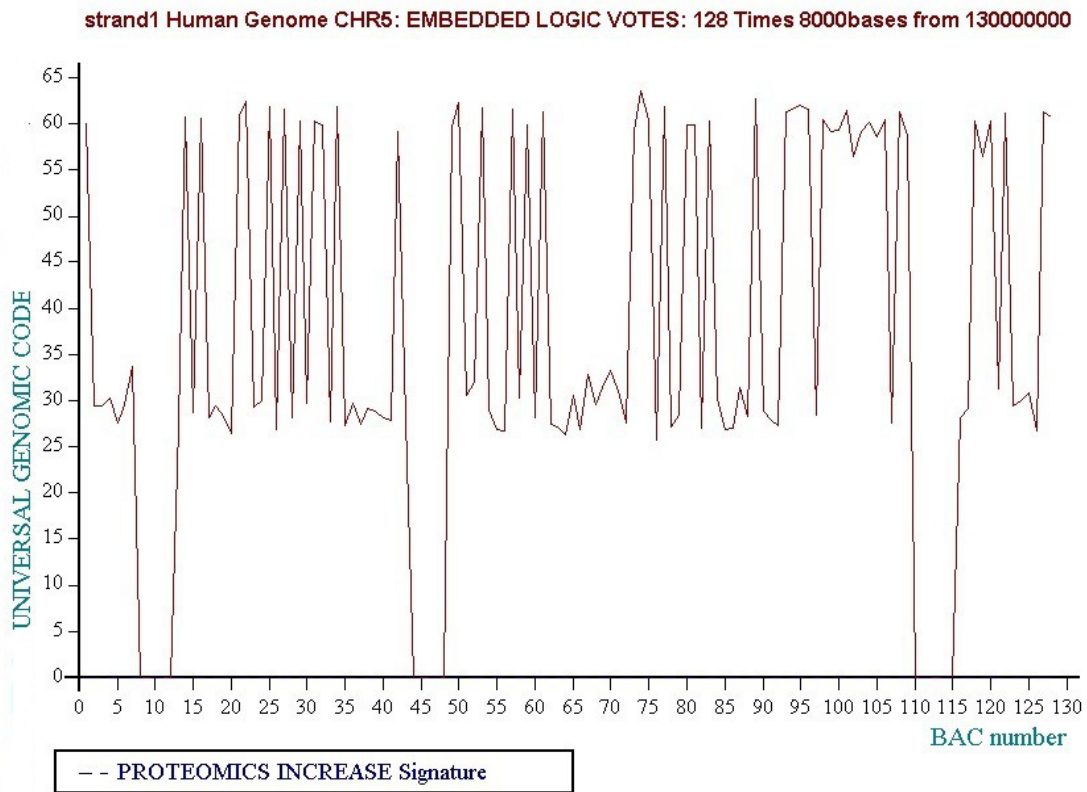
Figure 24 - Level 4: 128 times 8000 bases... Concensus Decision "VOTE" = Floor = "False"

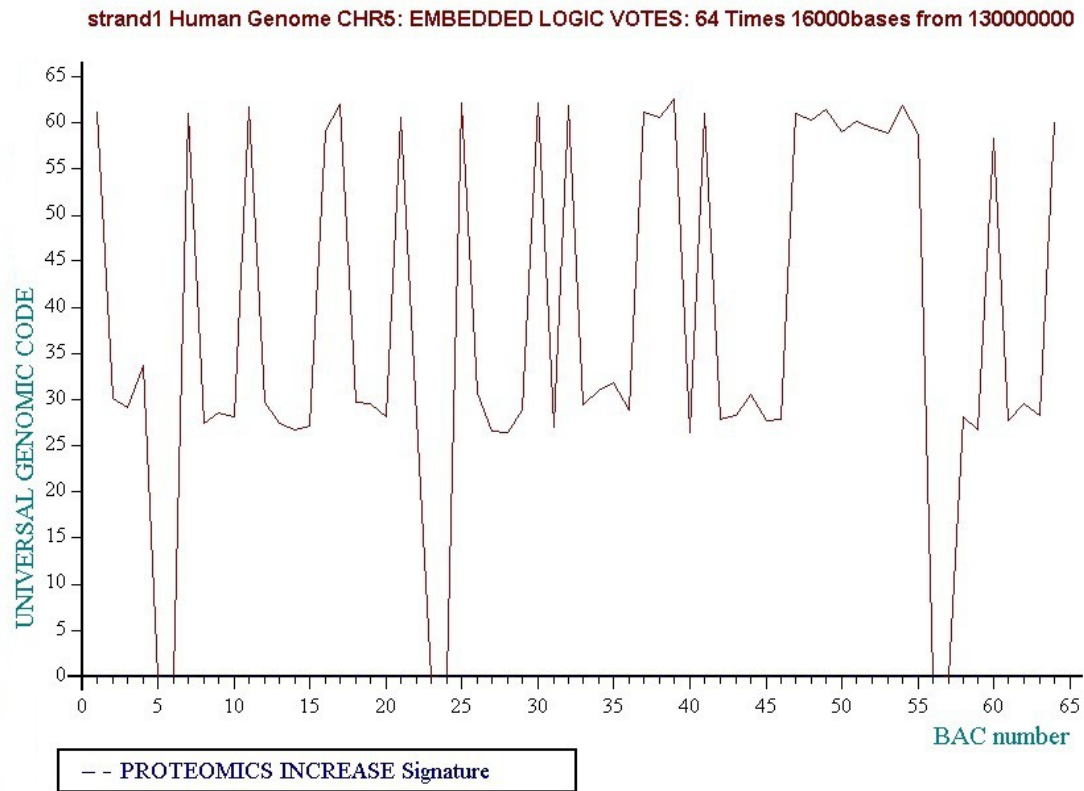➔ Level 5: 64 times 16000 bases... Concensus Decision "VOTE" = Floor = "False"

Figure 25 - Level 5: 64 times 16000 bases... Concensus Decision "VOTE" = Floor = "False"

➔ Level 6: 32 times 32000 bases... Concensus Decision "VOTE" = Floor = "False"
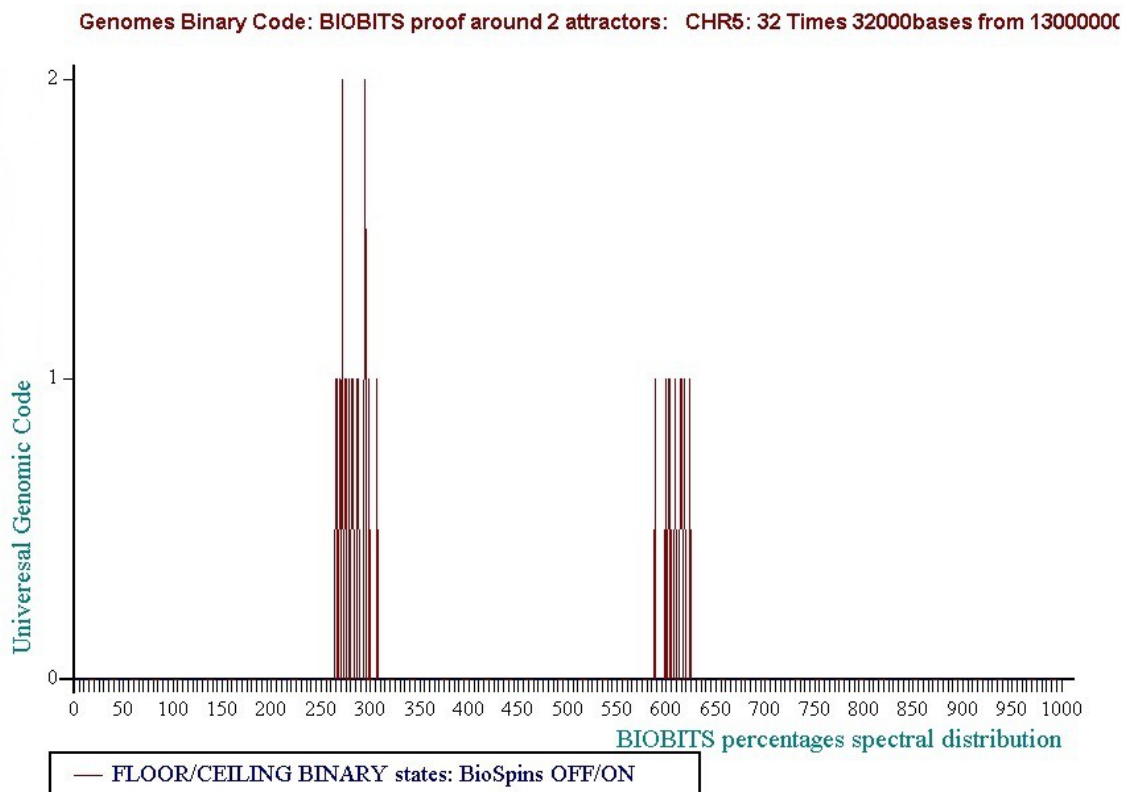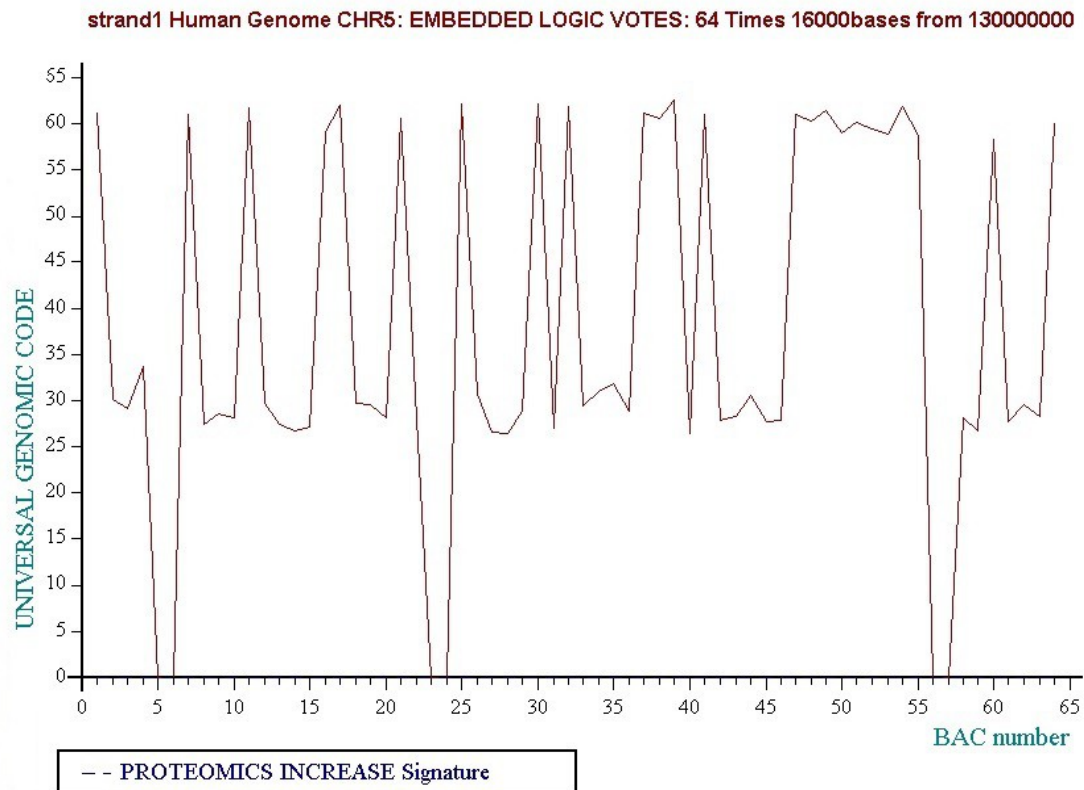

Figure 26 - Level 6: 32 times 32000 bases... Concensus Decision "VOTE" = Floor = "False"

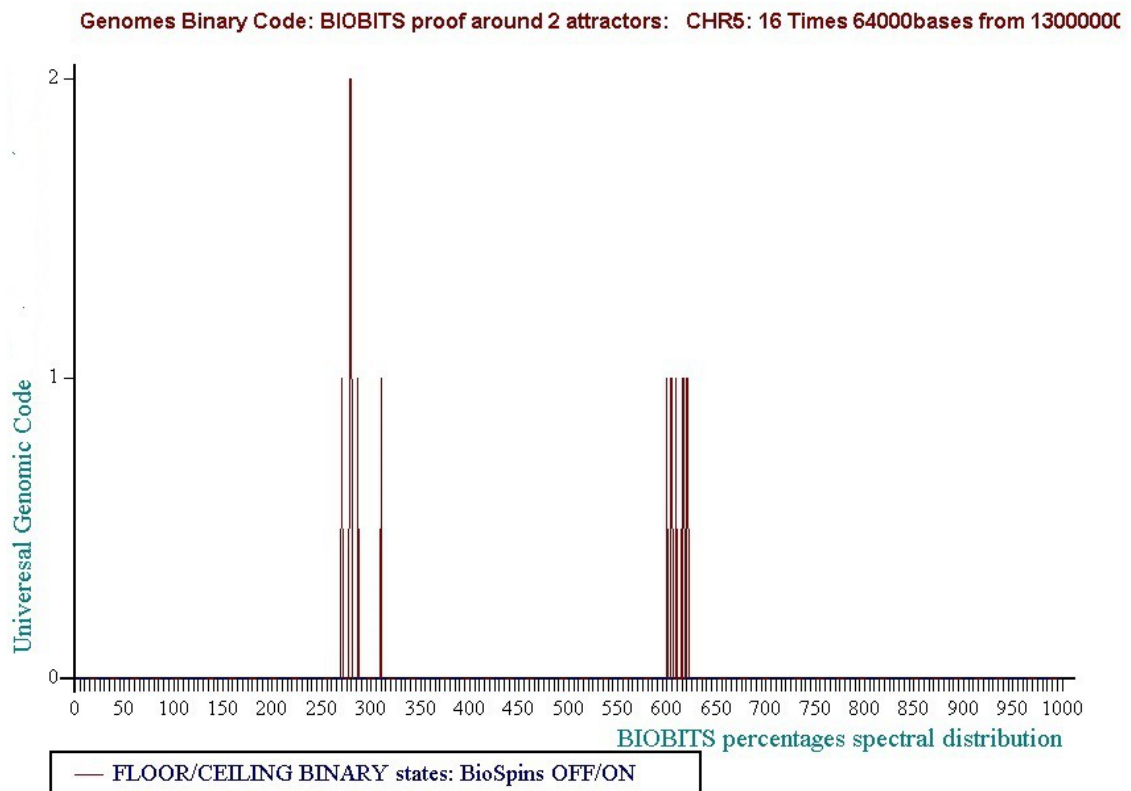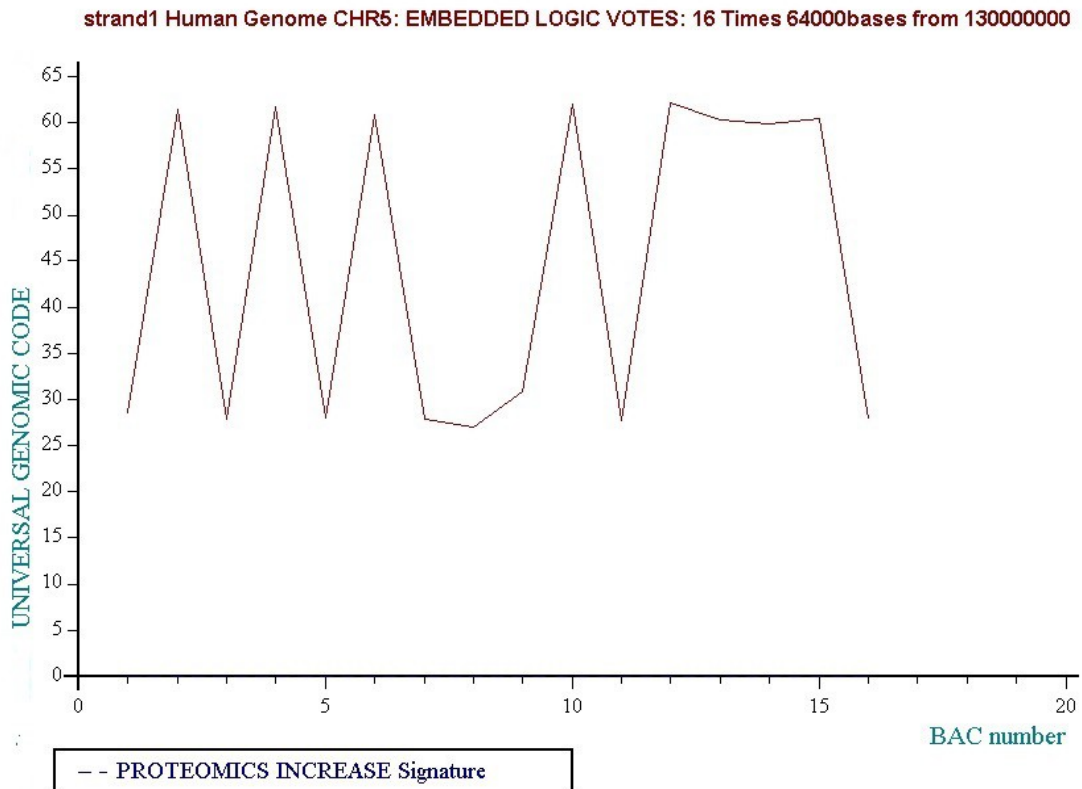➔ Level 7: 16 times 64000 bases... Concensus Decision "VOTE" = "Undefined"

strand1 Human Genome CHR5: EMBEDDED LOGIC VOTES: 16 Times 64000bases from 130000000

– – PROTEOMICS INCREASE Signature

Genomes Binary Code: BIOBITS proof around 2 attractors: CHR5: 16 Times 64000bases from 13000000

—— FLOOR/CEILING BINARY states: BioSpins OFF/ON

Figure 27 - Level 7: 16 times 64000 bases... Concensus Decision "VOTE" = "Undefined"

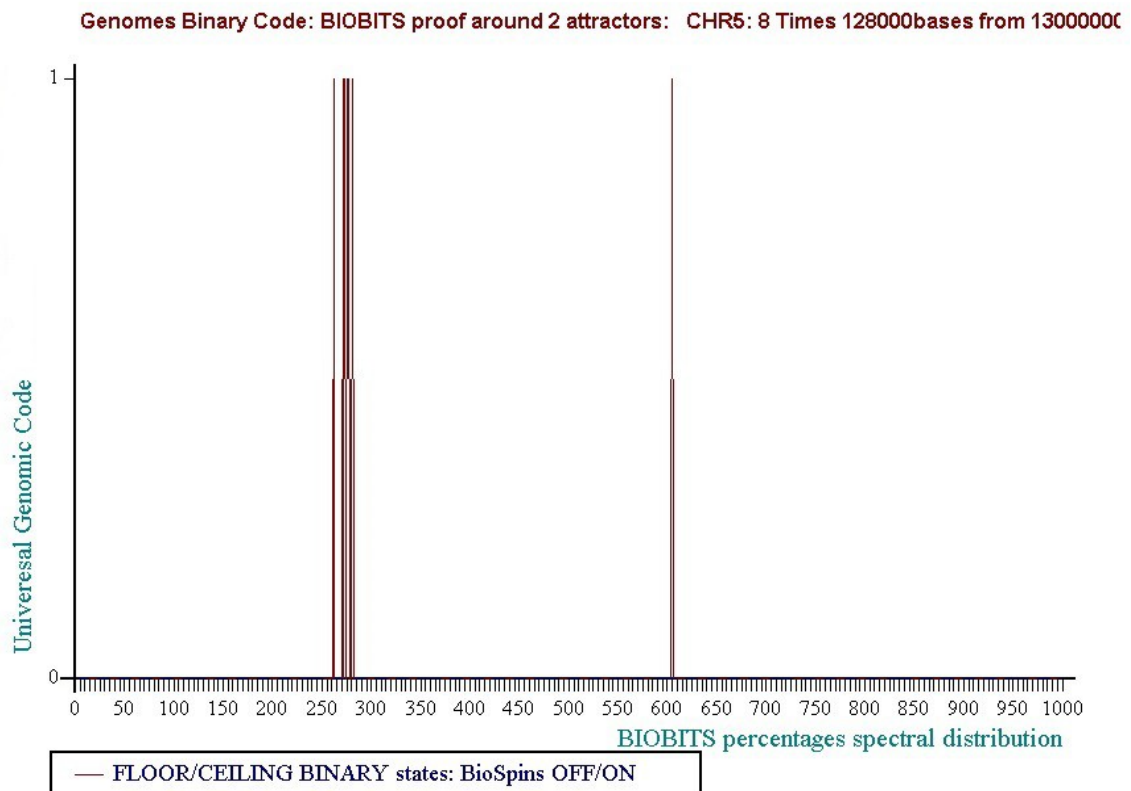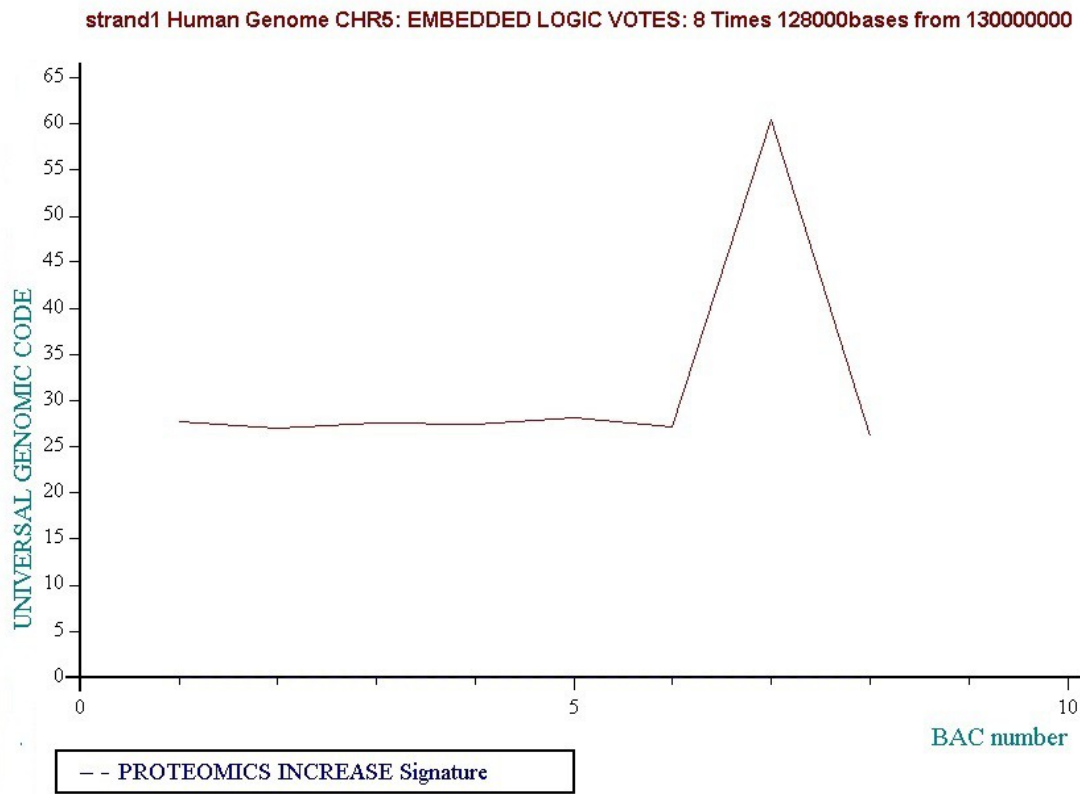➔ Level 8: 8 times 128000 bases... Concensus Decision "VOTE" = Floor = "False"

Figure 28 - Level 8: 8 times 128000 bases... Concensus Decision "VOTE" = Floor = "False"

➔ Level 9: 4 times 256000 bases... Concensus Decision "VOTE" = Floor = "False"
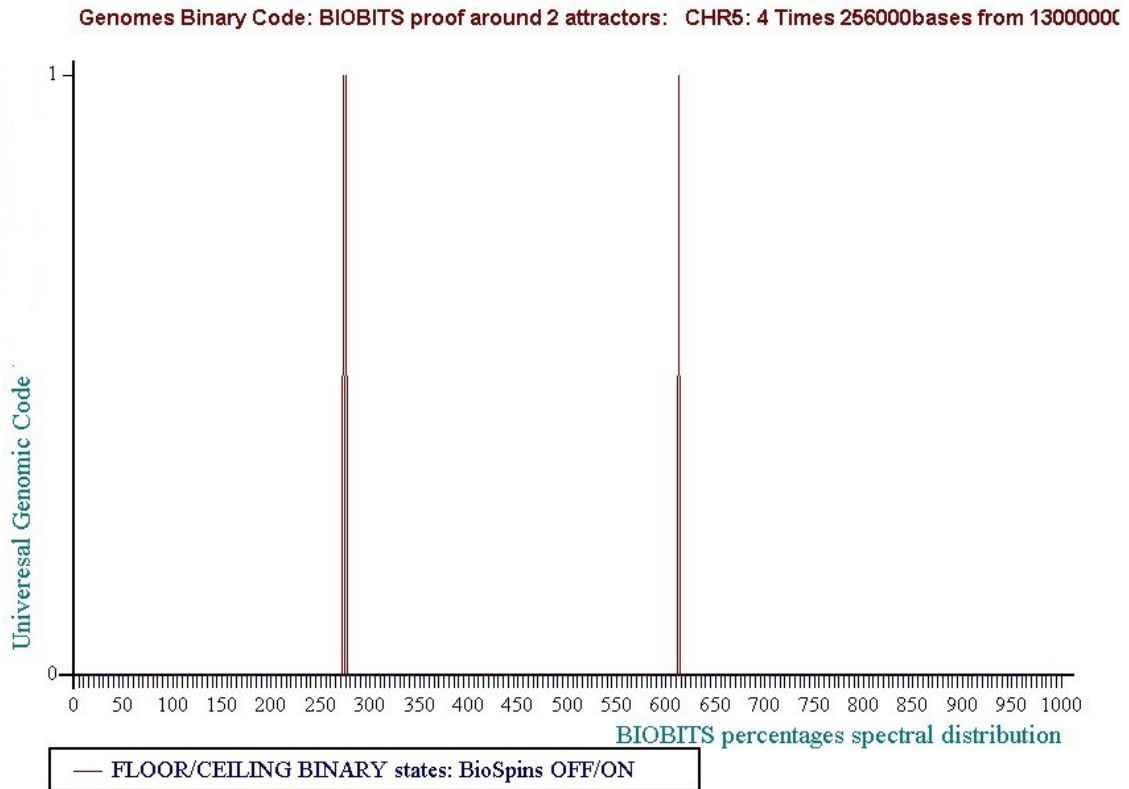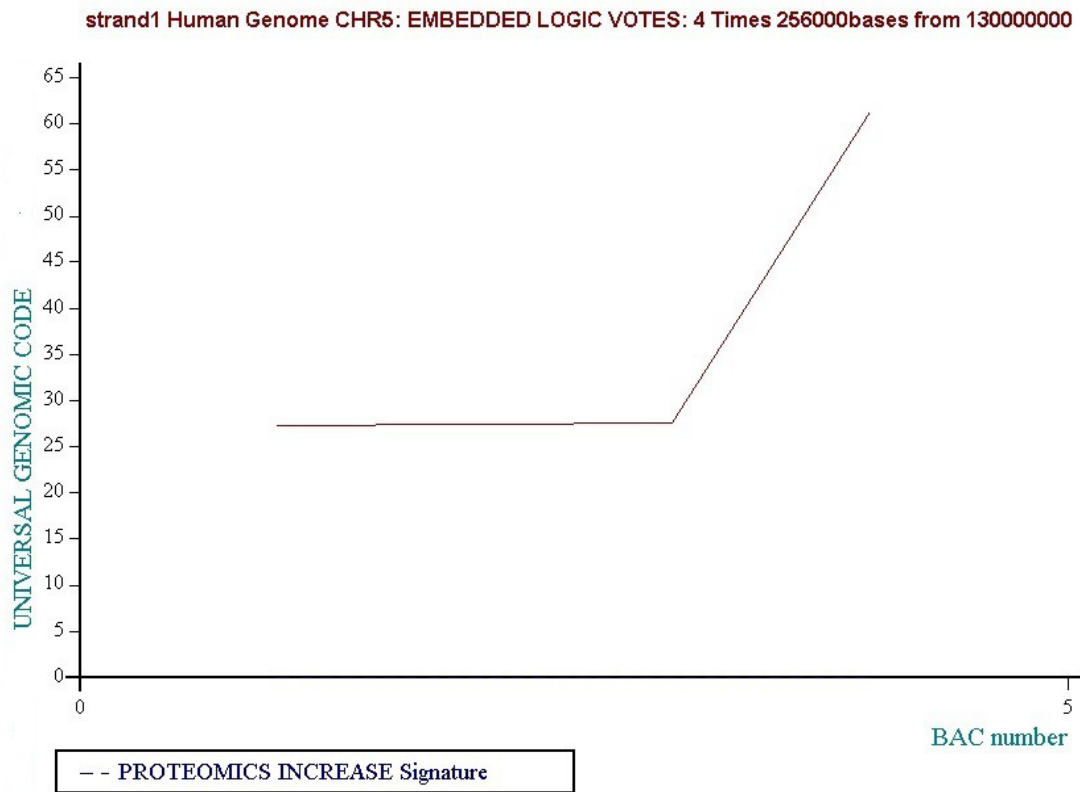

Figure 29 - Level 9: 4 times 256000 bases... Concensus Decision "VOTE" = Floor = "False"

➔ Level 10: 2 times 512000 bases... Concensus Decision "VOTE" = Floor = "False"
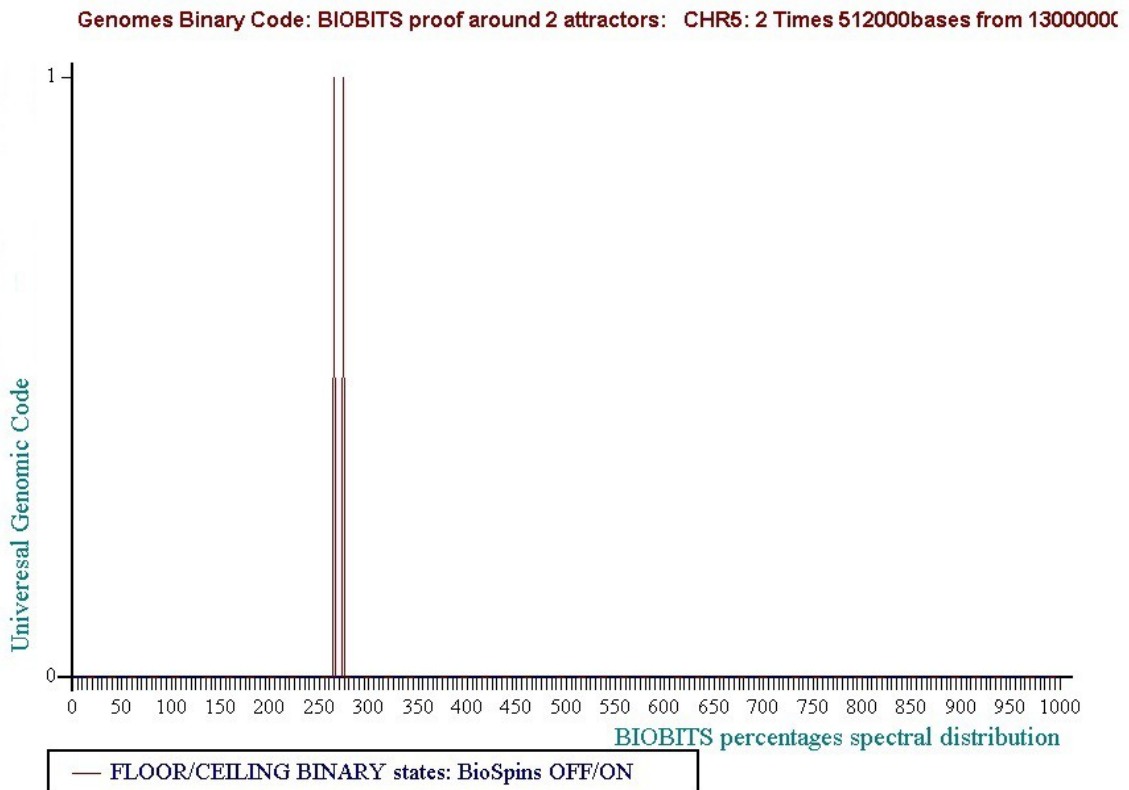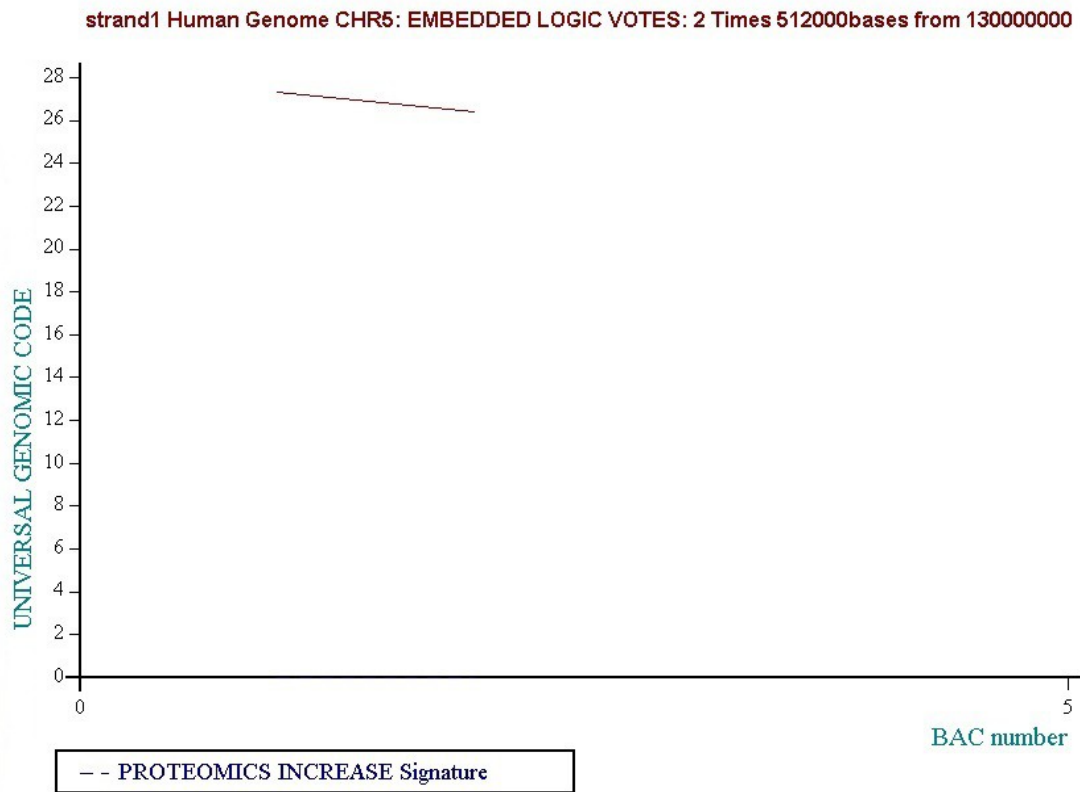

Figure 30 - Level 10: 2 times 512000 bases... Concensus Decision "VOTE" = Floor = "False"

In the following graphic, we summarize the genomic area around the 1024000bases DNA sequence analysed. This 10 millions lenght sequence was analysed spliting it in 10 "ONE MILLION regions". The red arrow localizes the studied 1024000 studied region. Then, the area is globally at "Floor" state, with a "Ceiling" state transition at the end (see on the right).
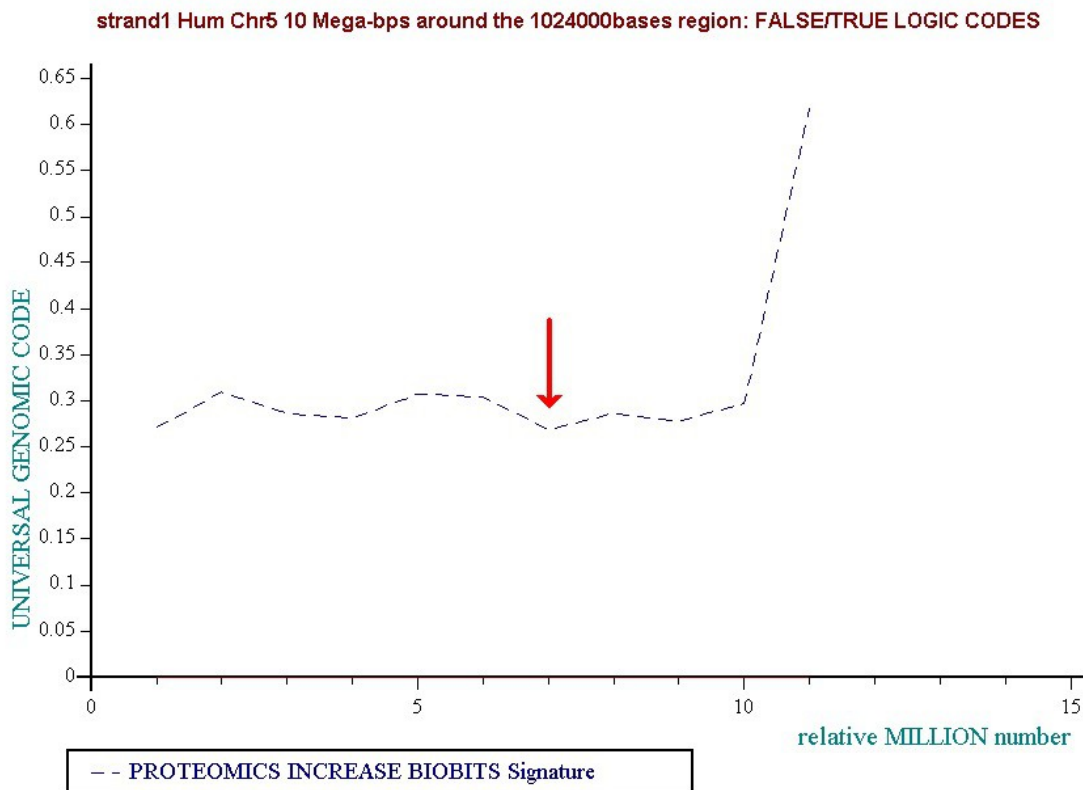

Figure 31 – 10 illions bases genomic region around the 1024000 bases analysed region is globally also in "floor" binary state.

As Professor NASH in " Hierarchical Introspective Logics "proposes it:
On the one hand, the concept of incompleteness will be able to evolve with the levels of human knowledge. In addition, the discovery of new natural laws will be able to make evolve the approach of this problem *".../... But the history of human progress in science and mathematics reveals that observation of the phenomena of Nature has always played a large rôle.../..."* (by J. F. NASH in the above paper).

In other hand, the concept of LOGIC suggested here is radically new because it acts of a self-emerging logic, output of a self-organized multi-levels embedded process of which the roots (" ground level ") are at the basic level of the "average atomic masses of the 6 DNA CONHSP bio-atoms", therefore in a world of real numbers (atomic mass code -I-)..

Lastly, the concept of hierarchy is not discrete but completely continue in an infinity of embedded levels. Thus, the choice of 11 levels in the example suggested is arbitrary, one could also have chosen thousands of others embedded levels... We show thus that the human genome (as all the other genomes) is the source of an omnipresent logical binary language which appears to be invariant on all the scales. This code is not explicit and formal but self-emergent as the " output " of a complex genetic system. This code is embedded in a self-referred infinity of VOTE-like level. Perhaps it could give new ways and tracks to understand the "Natural Hierarchical Introspective Logics" decision making process.

Second Experiment: "Proof of the optimality of the Life isotopes atomic masses proportions fine tuned balance"

Thus, the totality of the average atomic masses of all basic materials of genetics, bioatoms, UTCAG bases, amino acids, codons, DNA RNA and proteins are unified as soon as they are mathematically projected in the space of PIs. masses (Atomic mass code -I-).

But why their average atomic masses rather than the atomic masses of individual isotopes?
Does this property extend to the isotopes constituting their bioatoms?

The meta-structure of isotopes:

A new question naturally arises:
"Would the projection of the PI-masses be" reserved "and exclusive to the atoms of the living? "
"What would happen if we applied this same projection to all the other atoms of nature? "

We therefore apply the law of projection of PI-masses to all known stable isotopes. This list is then extended after the isotope Bi209 which follows the radioactive isotopes of the following elements. We then discover two remarkable phenomena:
on the one hand, a periodicity = 3.
on the other hand, a symmetry which would be located on both sides of the Lanthanides region (more precisely towards the element CE140.

Finally, it should be noted that these meta-structures are destroyed by a deliberate random disturbance of the atomic masses of all these elements of the order of 1/1000).
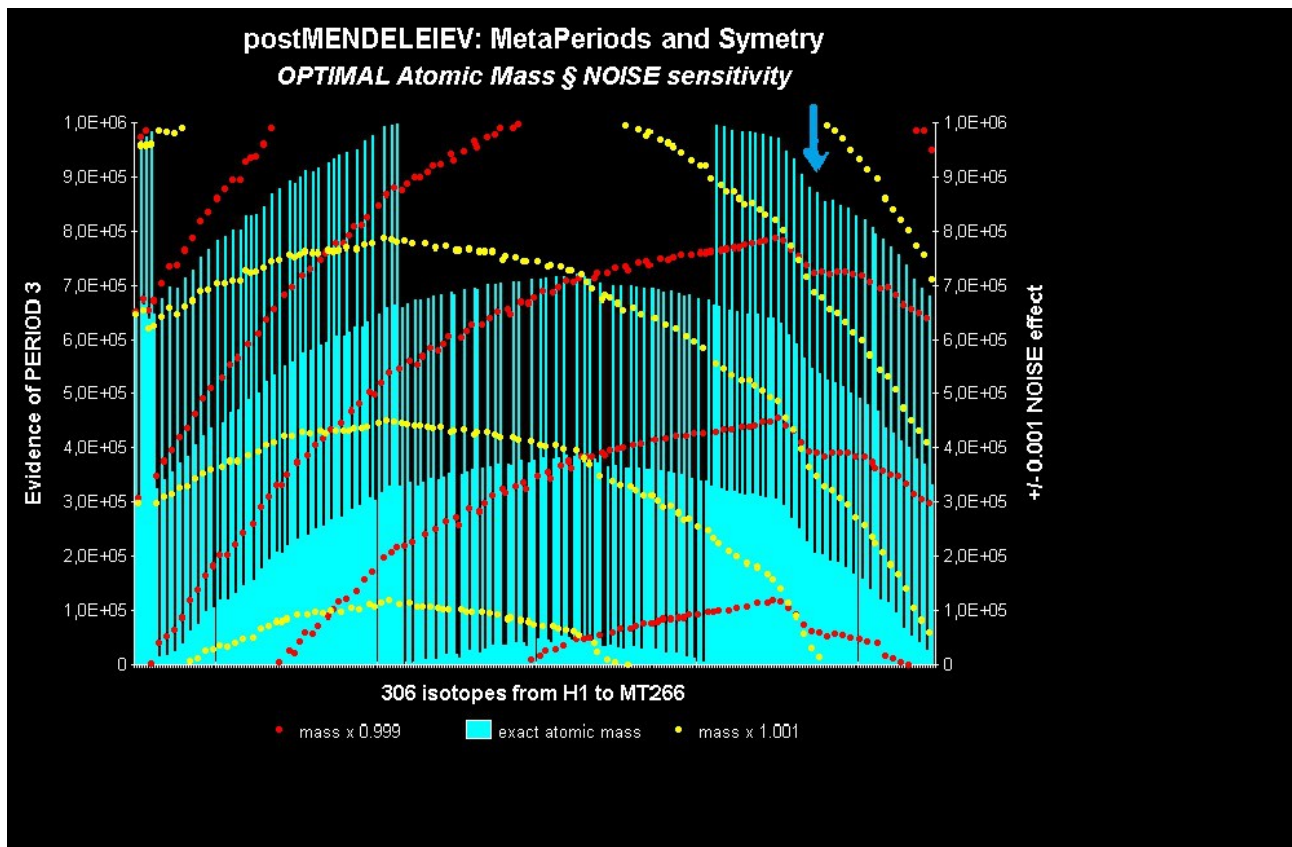

Figure 32 - Symmetry of the PI-masses of the 306 successive isotopes of the Mendeleev Elements table.
Figure 32 above illustrates very well the symmetry between the 306 isotopes revealed by the

projection PI-masses. This symmetry is located on both sides of the Lanthanide element zone; the sudden break between regular elements and radioactive elements (inflection of the graph, see blue arrow) located on the right of the graph corresponds to the transition between regular elements and elements (towards element Bi209).

Proof of the optimality of the average atomic masses:

In figure 33 below, we study the PI-masses in the case of bioatoms or most basic molecules. Those who are the origin of life and who maintain life on earth. But also those that can be encountered in outer space: clouds of interstellar dust, atmosphere of TITAN etc ...

We will analyze here among others carbon C, oxygen O, primitive molecules NH, N2, H2, H2O (water), CO, CO2 (carbon dioxide), CH3OH, and NH3. Let 5 organic atoms and 5 interstellar molecules. In each of these 10 cases, we will analyze the PI-masses of the molecule formed by the lightest isotopes, the average atomic masses, and the heavier isotopes. Thus, NH will be formed:

-in the first test of N14 and H1 (the lightest isotopes of nitrogen and hydrogen).

In second test of N and H represented by their average atomic masses.

-in the third test of N15 and H3 (heavier isotopes of nitrogen and hydrogen).

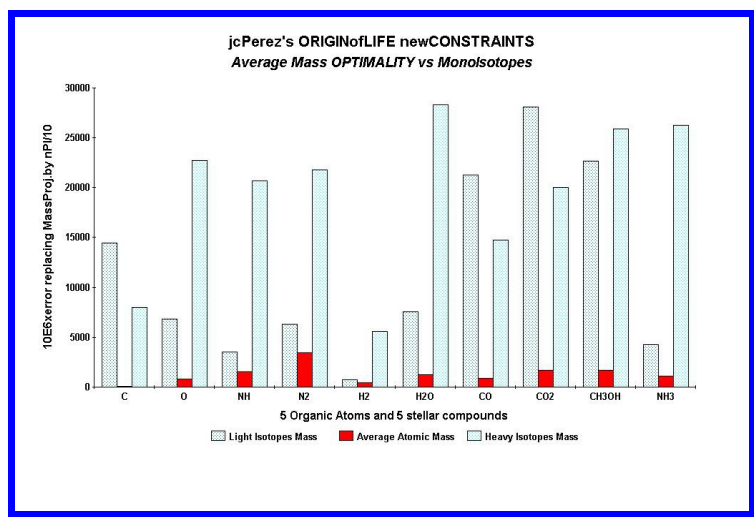And so on for each of the 10 tests of molecules analyzed.

Figure 33 -The OPTIMALITY of the average atomic mass is proved here on the PI-masses of ten primordial organic components.

In Figures 34 and 35, we now study in a similar way a patchwork of several thousand bio-molecules essential for life, from the most primitive bioatoms, to the amino acids, and through the 11 bio-molecules citric metabolic control, all are essential organic compounds for life. All these molecules are derived, on the one hand, from primitive compounds such as can be found in interstellar clouds, and on the other hand, from basic organic compounds extracted from the famous BEILSTEIN [11] ranging from compounds simple to more complex compounds (bases and amino acids).

In this first type of simulation, we submit 12 test sets of "more or less" organic molecules to a set of 3 tests: in the middle, the actual and exact average atomic mass, and, on both sides, on the left. , this same value weakened by a ten thousandth, and on the right, the same value, increased by a ten thousandth. The compared values measure the error observed when adjusting the PI-masses of these various atomic masses by the associated PI-mass integer (multiple of Pi/10). As a result, the higher these values, the poorer the PI-mass optimality. It is therefore concluded that these minute random "noises" applied to the atomic masses destroy the optimality of the PI-mass nPi/10 image value, hence, consequently, the optimality of the atomic mass as well.

Table 7 - The detailed values of the PI-masses projections of the patchwork of 12 sets of compounds.

	Average atomic mass decreased by 0.0001	Real average atomic mass	Average atomic mass increased by 0.0001
Inorganic astrobiologic isotopes	18439	20536	15109
Stellar Inorganic compounds	17124	17067	13819
10000 organic compounds	12040	12218	13662
Inorganic astrobiologic isotopes	9721	8312	10212
Organiques stellaires	12273	9836	12319
5000 combinations with parity N + H	13922	5879	17813
153 combinations extracted from Beilstein	22179	5865	13847
11 "citric metabolic control" compounds	21669	5428	13259
17 common organic compounds	8044	1320	7679
25 amino acids + UTCAG nucleotids	16515	3500	17371
Same without sulfur amino acids Cys and Met	16646	1465	17900
18 amino acids alone (without cys and met)	14967	1238	16758

ORIGIN OF LIFE new paradigm
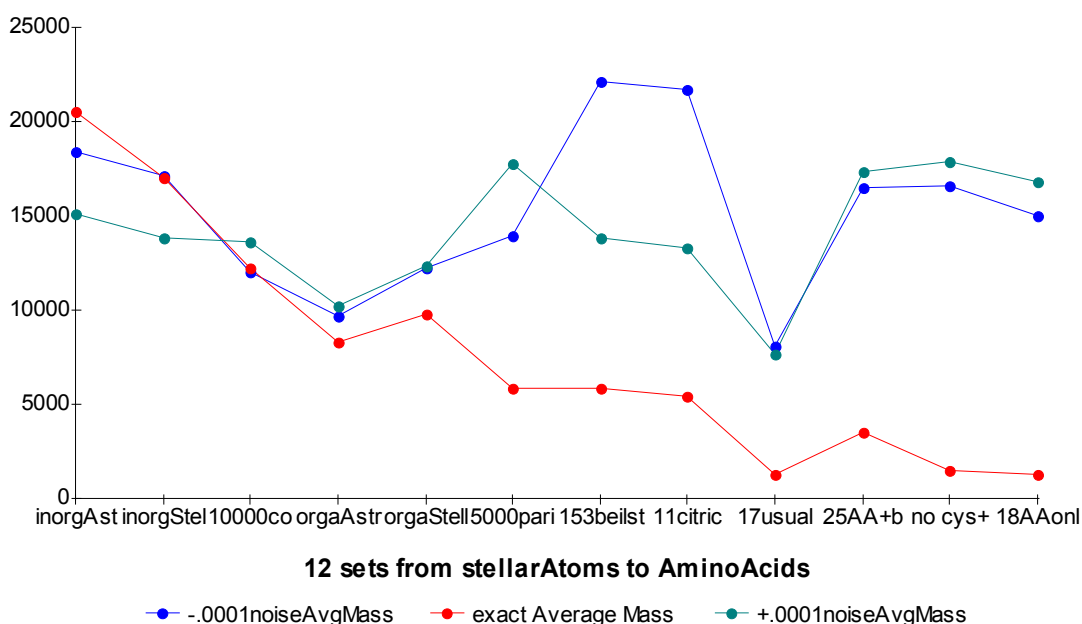## *Average AtomMass Optimality NoiseProof*

Figure 34 - Evidence of noise sensitivity of average atomic masses for 12 sets of organic compounds essential to life.
.

On the other hand, the more the organic compounds are to the right, the lower the PI-mass error (average atomic mass), and the more this error becomes hypersensitive to perturbations of its atomic mass. Thus, compounds such as amino acids would be more optimal than interstellar organic compounds, themselves more optimal than non-organic interstellar compounds ...

Would the whole path and path of evolution be "trapped" by our discovery of the digital projection of PI-masses?

Finally, a final confirmation of this meta-order revealed by PI-masses is visualized by the analysis of Figure 35 below.

We compare the perturbations of the optimal PI-masses caused, on the one hand, by the substitution of average atomic masses by mono-isotopic atomic masses, and, on the other hand, the substitution of average atomic masses by noisy atomic masses by a tiny random noise. The first disturbance is real and natural whereas the second disturbance is artificial and the virtual order of the simulation.
In all these cases, the reference is the slight thin horizontal line annotated 100%.
We then observe that the more we move to the right of the graph, hence from the inorganic to the organic, and the more the effect of real (isotopic) or artificial (random) perturbations will then increase, become showing strong overtaking above the 100% mark horizontal line.
We conclude the optimality of the average atomic masses vis-à-vis both mono-isotopic atomic masses that atomic masses whose precise value would be very slightly disturbed.

ORIGIN OF LIFE new paradigm
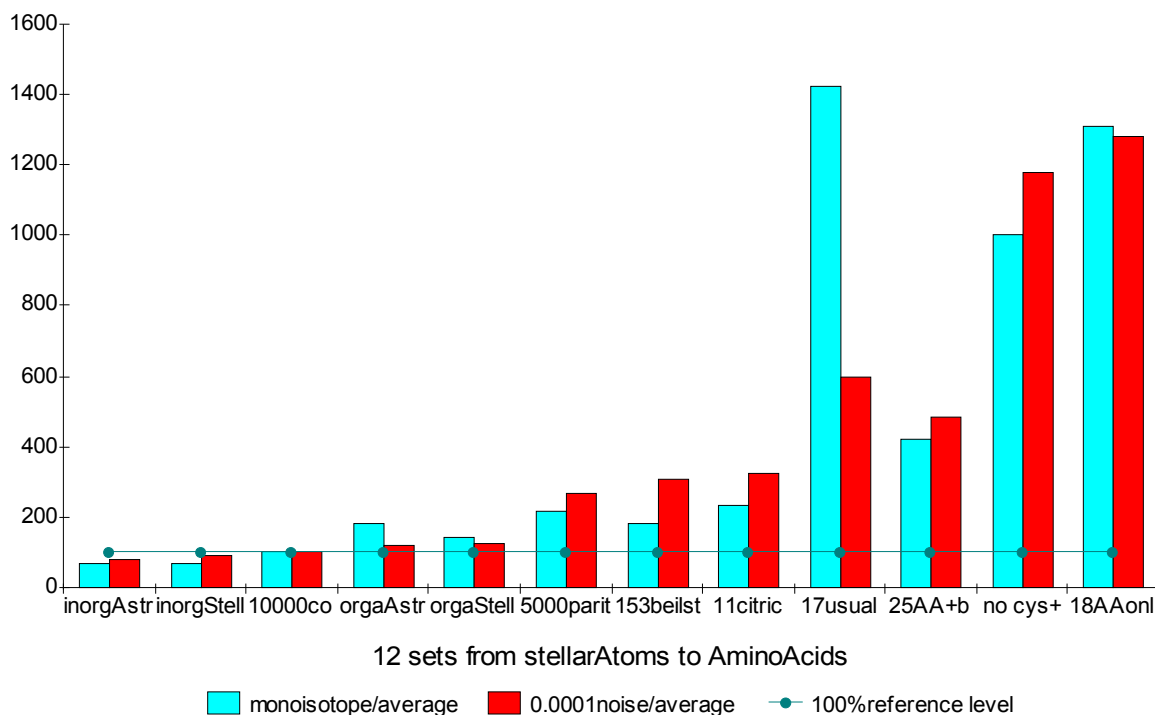## *monoisotope/average§noise/averageRatios*

Figure 35 - The comparison of the ratios "monoisotopic mass / average mass" between real cases and noisy cases.

Perspectives in Exobiology:

Concentrated information and meaning represented by the 3 figures 34 35 36, it will emerge remarkable information: more organic compounds are moving towards more evolution, from small molecules premisses of life, until Amino acids, bricks of all life, and more the selectivity, the optimality of the atomic masses becomes pointed and adjusted, the work of a grandiose "tuning" ...
And it is from this PI-mass - perfect - that go animate whole life "codes": PI-masses (atomic mass code -I-)!
Indeed, it is thanks to this hyper-adjustment of PI-masses that will emerge codes and even real languages that will organize and unify ALL genetic information despite its apparent diversity - bioatoms, DNA, RNA, amino acids proteins and genomes - to lead and induce a high organization up to the scale of whole genomes: from the atom to the genome (code -I- to code -VI-) ...
A mystery however is that these optimal values of the masses atomic ones are those of the average atomic masses and not those of the mono-isotopic atomic masses ... However, let us remember that the average atomic mass is only ... average. That is to say that not a single molecule, not a single nucleotide, not a single amino acid has this keystone value from which come alive the "codes" in whole numbers of life: the PIs -masses! But the reality is that this ideal PI-mass

is only a deception, a kind of "Omega Point" Teilhard Chardin that no molecule can ever achieve, at best only some will approach. Thus, we discover an ideal law, which can only exist in a mass universe, probabilistic, a universe of means, a universe of large numbers. In fact, you will never meet a carbon atom whose mass is exactly 12.01114727 (its Carbon average atomic mass). On the contrary, you will encounter a multiplicity of individualized, mono-isotopic atoms: billions of C12 isotopes, other billions - albeit a little less - of C13 isotopes ... In the same way, you will never come across an Oxygen atom of which the mass is exactly 15.99929706 (its Oxygen average atomic mass). On the contrary, you will find a multiplicity of individualized, mono-isotopic atoms: billions of O16 isotopes, other billions - albeit a little less - of O18 isotopes ... or even more rarely, billions of isotopes O17 Here is the famous curve in "V" that we will call by analogy *"Sergeant Major curve"* ...

Table 8 - The concentrated comparison of lines 4, 6 and 12 of Table 7.

	Average atomic mass decreased by 0.0001	Real average atomic mass	Average atomic mass increased by 0.0001
18 amino acids alone, without cys and met (line 12)	14967	1238	16758
5000 combinations with parity N + H (line 6)	13922	5879	17813
Inorganic astrobiologic isotopes (line 4)	9721	8312	10212

ORIGIN OF LIFE paradigm:"Life route"
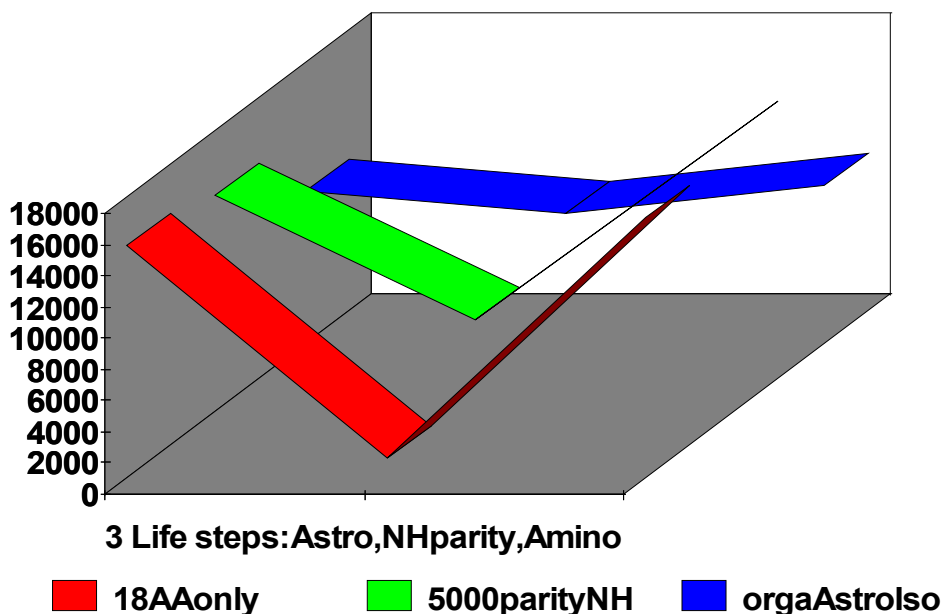## *Average AtomMass Optimality NoiseProof*

Figure 36 - The triple curve in "V", concentrated comparison of lines 4, 6 and 12 of Table 8.

We are therefore faced with an enigmatic situation:
On the one hand, we discover a generic law organizing the entirety of living molecules - the PI-masses code (atomic mass code -I-).
on the other hand, this law is optimal only in the case of the average atomic masses.
But the real world of biology is not a world of average atomic masses but a world of atomic masses

mono-isotopes.

This would mean that this optimal law is only a kind of "inaccessible star" as Cervantes would have written ...

But, nevertheless, the average atomic masses exist on earth since they constitute the weighted average of the billions of isotopes constituting each one of the populations of atoms.

Then would it mean that life implies, by the very nature of its laws, that its molecules and atoms rely on diversity and multiplicity, perhaps even on the equilibrium and collective co-operation between these billions of atoms?

Life through the optimal search for the average PI-masses would imply in every way spaces of life and permanently a kind of permanent dynamic equilibrium - Piaget spoke of "mobile equilibrium" - taking its roots and feeding on the multiplicity and diversity of the different isotopes (C12 / C13, N14 / N15, H1 / H2, O16 / O17 / O18, etc.) forming each bioatom. It will be noted that the complexity of advanced molecules such as amino acids already favors this diversity, the same amino acid can be heterogeneous and consists of different isotopes of the same atom, which will already approach some of the PI-mass ideal average mass (for example the amino acid glycine (Gly) which is written NH2 CH2 COOH may for example consist of an atom O16 and an atom O18, likewise for its carbon atoms which may be 2xC12 or 2xC13 or C12C13 ...

It will also be noted that this multiplicity of isotopes can be topological (3-dimensional space) but also temporal.

Topological diversity and we then think of the GAIA [12] hypothesis of James Lovelock, about which we wrote :

« He is to science what Gandhi was in politics. His central idea, that the planet behaves like a living organism, is as radical, profound, and vast in its consequences as any of Gandhi's ideas. »

According to Lovelock, everything that lives on our planet would contribute more or less to the balance, maintenance and continuity of life on earth. But it turns out that Lovelock as we reach by taking two radically different paths ...

Immediate consequences of this requirement of multiplicity of isotopes are multiple:

the loss of bio-diversity destroys this balance of average atomic masses required by life.

-the discourse on global warming must climate change revisited according to this new angle of the requirement of isotopic equilibrium. We will think of cancers whose hidden causes are more and more due to the industrial pollution of modern life and agro-industrial mass supply.

-the economic arguments of certain lobbies according to which the methane released into the atmosphere by the cows of our campaigns would pollute almost as much (1/5) as the methane rejected by the industries of our cities will suddenly fall: indeed we will have to consider seriously the hypothesis that the isotopes constituting CH4 (methane) released by our cows are very different from the isotopes of CH4 released by our polluting industries!

The other level of isotope multiplicity of the same atom is the temporal and dynamic aspect.

This inspires us with two ideas:

On the one hand, this could partly explain the natural and permanent need for renewal and regeneration of living cells. Nature would thus seek to maintain permanently the isotopic equilibrium of the respective proportions of the billions of isotopes of bioatoms forming the living cells.

- on the other hand - it may seem bold as a thesis - the dynamic equilibrium of the average atomic masses can also be reached by temporal alternations of the various isotopes constituting the same atom. It would then be a kind of "quantum dance" with a kind of temporal alternation between isotopes of the same atom ... We would then be very close to the wave or quantum theories of matter ... The real but invisible atom would have as mass the mass atomic average while we perceive in the universe palpable and visible that different "views" with distinct masses, the different isotopes of the same atom ...

A bold thesis, of course, but why not?

One thing is certain when exobiologists will look for traces of life on other planets, on TITAN, on

MARS or EUROPA ... They will not only have to look for the presence of carbon, nitrogen oxygen or hydrogen, but also the existence of isotopes of these atoms in proportions comparable to those which constitute the average atomic masses on the earth biosphere.

Thus, it is in 2010 that a probe went to analyze with precision the reports isotopic C12 / C13 or N14 / N15 on TITAN ...
Have we discovered proportions comparable to those of our planet?
Only in such a case that our discoveries could allow to predict the isotopic ratios that it should find there ... Then, the projections PI-masses of the code of the atomic masses will be able to measure these traces of extra-terrestrial life ...
We will indeed affirm that:

"The emergence of life in the Universe requires a DIVERSITY and an ISOTOPIC BALANCE of bioatoms C O N H identical to those observed on Earth"

or…

"A necessary but not sufficient condition for the emergence in the universe of life-forms similar to earthly life requires that we find, in these regions of the universe, and in MARS in particular, the different isotopes of organic CONH atoms in proportions identical to those observed on Earth "...

Conclusions

We will conclude here by interesting the different following themes that emerge from the reflexions raised by these 6 codes:

The diversity:
The law of numerical projection atomic mass code (-I-) behaves like a kind of ideal law, objective in the sense defined by Jacques Monod [13]. Because it is optimal for the average atomic masses of bioatoms, it is inaccessible in the real universe which is only individual isotopes. Thus this law, if the nature of the living "seeks" to approach it in search of better equilibrium and stability, will compel to seek more DIVERSITY. Diversity of isotopes of the same atom, diversity of isotope changes over time. We can make an analogy with the electron layers of atoms: they are only densities of probability, an individual electron only reaching by chance this ideal value. Here it is the same: this optimal ideal code for the average atomic mass that never exists in the real world of isotopes will force them to diversify and self-organize for more stability ... as if the forced plan of evolution towards more complexity (molecules, RNA, DNA, amino acids) was already a necessity, an implication, in the sense dear to Nobel prizewinner Jacques Monod ...

The unification:
Contrary to the appearances established by the "Central Dogma of Biology", there would not exist 3 distinct and heterogeneous types of genetic information (DNA, RNA and amino acid sequence) but only one "meta-information" such that, to any double-stranded DNA sequence (coding or junk-DNA), we can ALWAYS, after projection according to the atomic mass code (-I-), associate 3 unified images named respectively: genomic signature, proteomic signature and RNA signature, such than:
-the RNA image is always empty and zero.
-the 2 genomic and proteomic images are always almost identical and correlated more than 99%.
Everything happens as if an inaccessible unique and virtual information, "implied" in the sense of the physicist David Bohm [14], "unfolded" materially according to the 3 physical media or respective languages of the DNA , RNA and amino acids, so that one of the 3 images is "empty" (RNA) and the other 2 similar and equivalent (DNA and amino acids).

The fractal textures:

A fine analysis of the "texture" of these curves Genomics and Proteomics will now reveal a strange phenomenon: a curious roughness "sawtooth" (Figure 7) characterizes most of these images. It is a kind of search for the "derivative of order 1", that is to say the "slope" between 2 successive points. We then note that these slopes are mainly of the same direction: always increasing or always decreasing.

After successive applications of the first and second codes (-I- and -II-) to any genomic double stranded DNA sequence, the texture analysis (roughness) of the genomic and proteomic images highlights:

-a modulation in the form of a ANALOGIC distribution (Figure 9) for the Genomic code.

-a modulation in the form of a 0/1 BINARY distribution (Figure 10) for the Proteomic code.

Everything happens as if: two different languages (genomics and proteomics) produced two very similar images but radically different roughnesses: the first (genomics) would be analogous to an amplitude modulation, while the second one (proteomics) would be analogous to a frequency modulation (to use the analogy of radio sounds and waves). We can even say that the second would correspond to a coding of these sounds in binary form as we find them in compact disk or in the current laser based digital coding of information …

A second analogy: suppose that a same sequence of information is coded and transmitted according to two radically different languages (for example in French and in English), These 2 encodings will produce the same "meaning", the same "comprehension", the same mental representation of the transmitted message. However, the "roughness", (% of vowels of each of the 2 languages for example) will be radically different ...

Numbers and Codes of Life:
One of the most fascinating questions of mathematics is the relation between these two universes of numbers, so different as real numbers and integers. One models the universes of the continuum while the other represents the discrete, quantum universes. .. Here, with these 6 successive nested codes we went from a continuous universe of real numbers of atomic masses to the discrete universe of integers encoding Pi-masses. Then, with the Master code we continue in a universe of integers producing these 2D Genomics and Proteomics images. Then, with the biobits of the binary logic code of the proteomic textures, we comets the universe of the integers in a binary universe with only 2 states, those of the logic. Then, with discrete waves, standing waves and resonances, it is again in a continuous world that we come back: the wave universe ... Thus, over these 6 codes, the 3 digital worlds of the continuous, the discrete and binary have always been ubiquitous. We think that biology and genetics are inseparable from the world of numbers!

Geometry and Codes of Life:
Phi = 1.618033 ... the "golden number" is omnipresent in Nature, often in the form of proportions according to Fibonacci numbers (1 1 2 3 5 8 13 21 34 55 89 ...), as in the pinecone or pineapple [15] …

From the 80s, in our research in Artificial Intelligence, we demonstrated with our neural model "Fractal Chaos" a natural link between fractals [16] and the golden ratio [17, 18, 19].

In this paper, the analysis of the genetic information (proteomic image) of the entire human genome highlights a binary modulation (Figures 15 and 16) throughout the genome.This binary modulation is distributed statistically around 2 binary attractors whose ratio is equal to TWO and whose respective values are phi (level "high" = 1) and phi / 2 (level "low" = 0) With phi = 0.618 ... = 1 / Phi the Golden ratio (Phi = 1.618. ..).

More generally, since 1991, we have described the presence of Phi the Golden ratio and that of Fibonacci numbers in DNA, genes, chromosomes and genomes in many forms [20, 21, 22, 23, 24, 25, 26, 27, 28].

Finally, Golden ratio and Fibonacci numbers are an evidence in DNA numerical structure, see by example these « 34 » scale invariance fractal occurrences of Fibonacci number 34 :

Recently published, in [29], in « DNA as an Electromagnetic Fractal Cavity Resonator: Its Universal Sensing and Fractal Antenna Behavior », P. Singh et al. Simulated the DNA geometry using biomaterials, they write : « then, they

demonstate that 3D-A-DNA structure behaves as a fractal antenna, which can interact with the electromagnetic fields over a wide range of frequencies. Using the lattice details of human DNA, we have modeled radiation of DNA as a

helical antenna. The DNA structure resonates with the electromagnetic waves at 34 GHz ».
Thus, the reader can now reflect on this strange trilogy:
- Each DNA helix rises about **34 angstroms** during each complete turn.
- We have also demonstrated that the chromosomes 4 of Sapiens and Neanderthal have a standing wave of **34 nucleotides** [30].
- Singh et al. demonstrate in 2017 that a standingwave of **34 Giga Hertz** would organize DNA molecules [29]...:

Finally, DNA, mathematics [31] and stationary waves [32, 33] form a rich intersection, which many publications affirm.
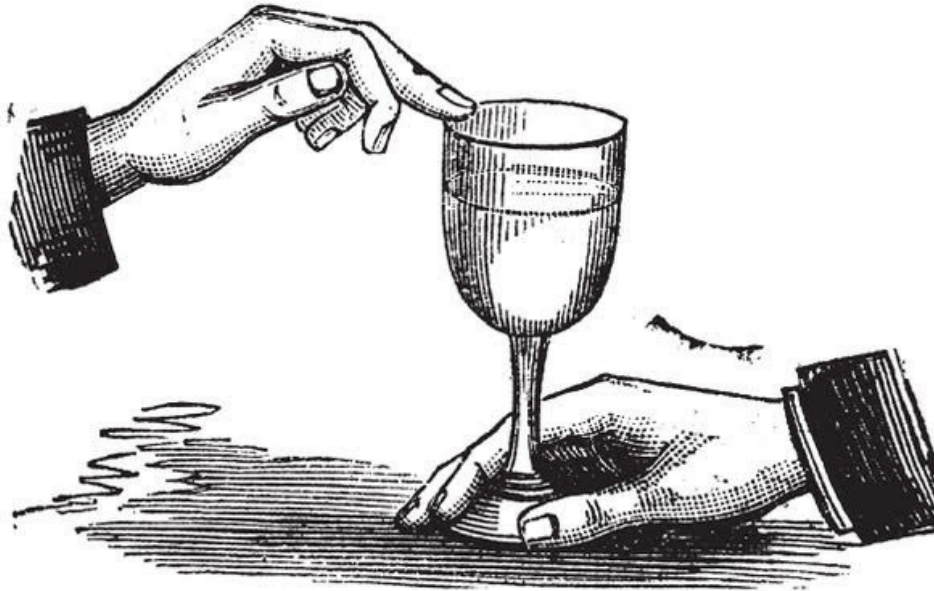
Figure 37: « physical harmonic resonance » analogy scenarii (thanks picture from Dr Robert Friedman).
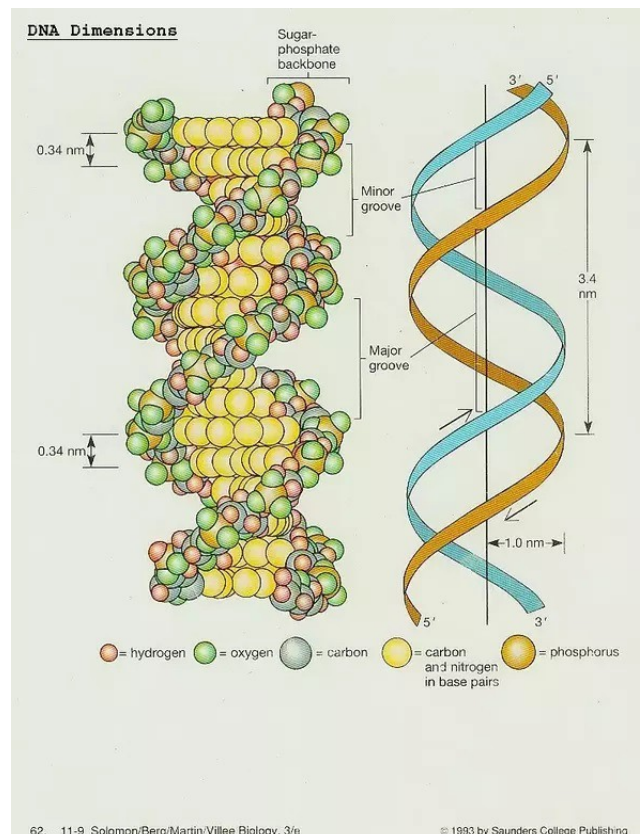
Figure 38: Each DNA helix rises about 34 angstroms during each complete turn
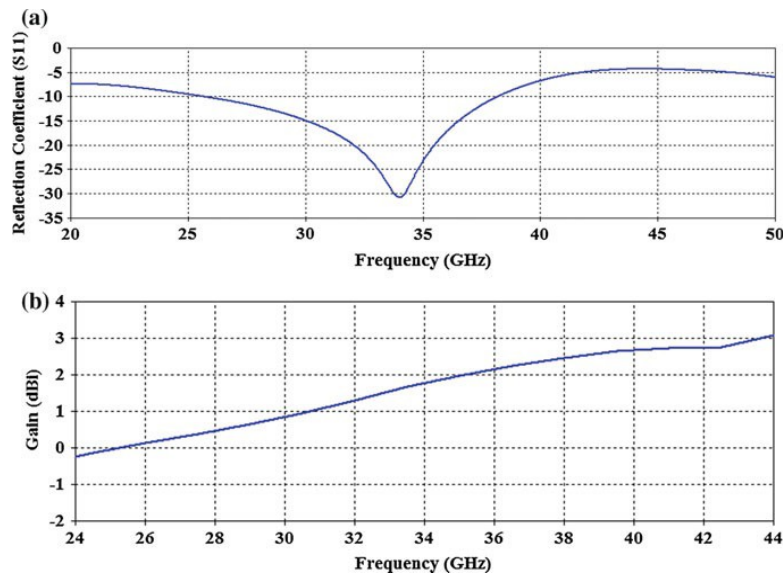
Figure 39 – Evidence of a standing wave of 34 Giga Hertz in a modelized DNA molecule using biomaterials (source publication [47]

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