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The Optimal Multi-Isotopic Atomic Code of Life: Perspectives in Astrobiology

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Abstract

Background: At the starting of this research, we found it abnormal that life needed 3 different Biological languages to code the information of the living: DNA, RNA, and amino acids, language of proteins.

Results: The discovery of a simple numerical formula for the projection of all the atomic mass of life-sustaining CONHSP bio atoms leads to the emergence of a set of Nested CODES unifying all the biological, genetic and genomic components by unifying them from bio atoms 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.

Conclusion: The application of these embedded codes (particularly the Atomic Code of Life) to astrobiology field is illustrated here. Particularly: 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.

Keywords: Exobiology; Origins of life; Isotopes; Genetic code; Biomathematics; Atomic mass

Introduction

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, Everything simple is false, everything 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 [1,2] or small genomes such as mitochondrial DNA [3].

We were looking for a smaller common denominator for DNA, RNA, and amino acids; we have the intuition of the need of 3 "ingredients":

1. The atomic mass and the bioatoms C O N H S P are common to these 3 languages.
2. The 2 universal constants PI and Phi could play a role.
3. 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 [4,5] six "Russian doll-like" embedded CODES:

1. Atomic mass code.
2. Master code.
3. Binary code.
4. Undulatory code.
5. Cytogenetic code.
6. Standing waves meta-code.

This paper focus only on the first background code: -I-Atomic mass code.

In particular, generated from this code, 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.

Full details related to the remaining embedded codes are available in [4-8].

Material and Methods

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

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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 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 [5-15]. 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. Figures 1 and 2 illustrate this numerical projection of the atomic masses. The figure on the right in Figure 1 demonstrates that the diversity of 162 atomic masses of different Life bioatoms compounds is unified on a regular scale of only 9 numerical values, multiple integers of Pi / 10.

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:

$$\Pr ojPPI(m) = \left[1 - \left[P\Pi\right]\right]m$$

Where $P = 4.\sqrt{(\varphi)}.\varphi.\varphi^2$

Then P = 0.742340663...

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

Then consider the function:

$$Remainder(v) = \left|next\ whole\ integer\ \ just\ after\ whole\ number\ v\right| - \left|v\right|$$

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:

$$PPI(m) = Remainder\left[1 - \left[P\Pi\right]\right]m$$

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 Figure 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

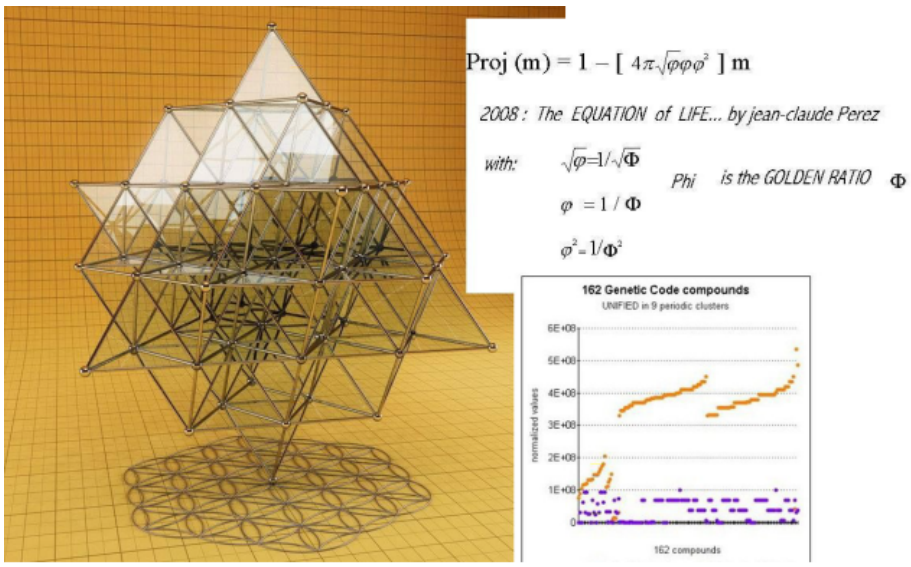

Figure 1: The numerical projection formula of the atomic masses of any biological component.

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 significant 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 Mendeleev's Periodic Table.

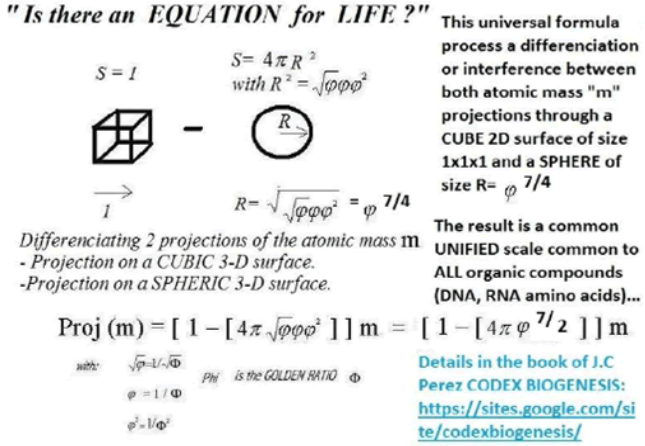

Figure 2: Geometric meaning of the formula for life numerical projection.

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 [16-22]. A set of Pi-mass projections for some main Life compounds has been explained in Table 1. Synoptic of PI-masses of different components of genetics has been explained in Table 2. Sensitivity of "Formula for Life" vs atomic mass fine tuning has been explained in Table 3.

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 O_{16}) 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 [22-26]. As shown in Figure 3, isotopes of oxygen lightest and heaviest O_{16}, O_{18} 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% O_{16} O_{17} + 0.2% O_{18} (Figure 3).

Results

"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?"

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

	-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 gau gag ugc uga cgu cgg agu agg ggc gga	cuc cua auc aua ucc uca ccu ccg acu acg gcc gca uac uaa cau cag aau aag gac gaa cgc cga agc aga	ccc cca acc aca cac caa aac aaa					

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

Genetic compounds	Atomic mass m	PI-mass N PI/10	Error EPI(m,N)
Regular GLYCINE Amino acid. $GLY=NH_2-CH_2-COOH$ 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). $GLY=NH_2-CHH^*-COOH$	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

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

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
	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						

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

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 (Figure 4), 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) [26-30].

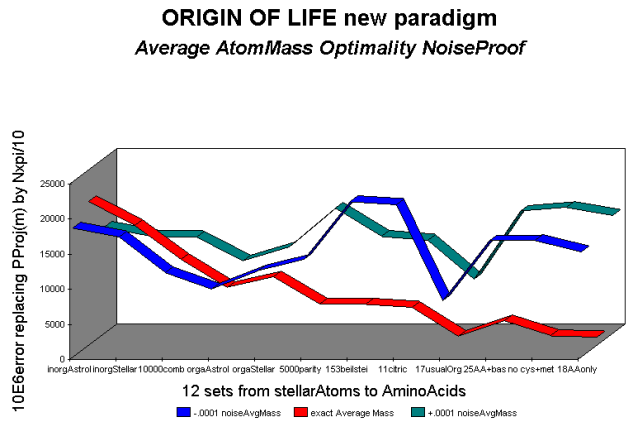

Figure 3: The optimality of the average atomic mass is proved here on the PI-masses of ten primordial organic components.

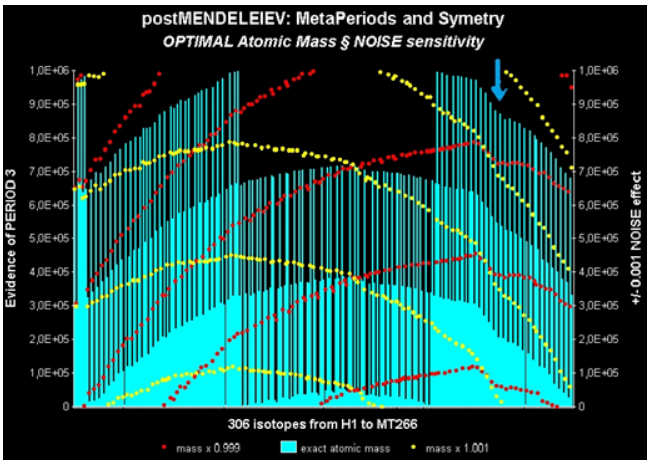

Figure 4: Symmetry of the PI-masses of the 306 successive isotopes of the Mendeleev Elements table. Figure 4 above illustrates very well the symmetry between the 306 isotopes revealed by the projection PI-masses. This symmetry is located on both sides of the Lanthanide element zone; the sudden break 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 5 and Table 5 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, N_2, H_2, H_2O (water), CO, CO_2 (carbon dioxide), CH_3OH, and NH_3. 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:

1. In the first test of N14 and H1 (the lightest isotopes of nitrogen and hydrogen).
2. In second test of N and H represented by their average atomic masses.

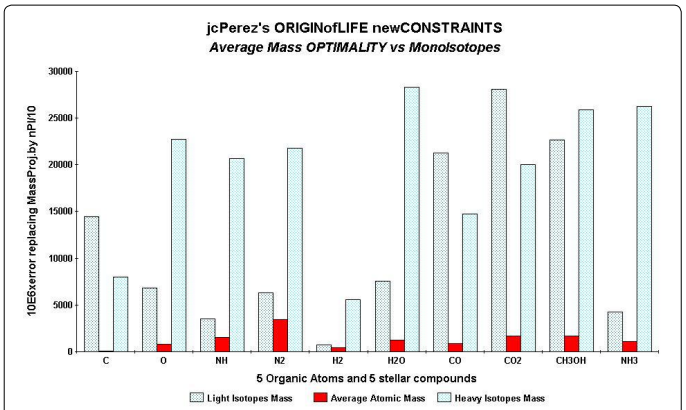

Figure 5: The optimality of the average atomic mass is proved here on the PI-masses of ten primordial organic components.

	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

Table 5: The detailed values of the PI-masses projections of the patchwork of 12 sets of compounds.

3. 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.

In Figure 6 and Figure 7 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. The concentrated comparison of lines 4, 6 and 12 are explained in Table 6.

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 7.

We compare the perturbations of the optimal PI-masses caused, on

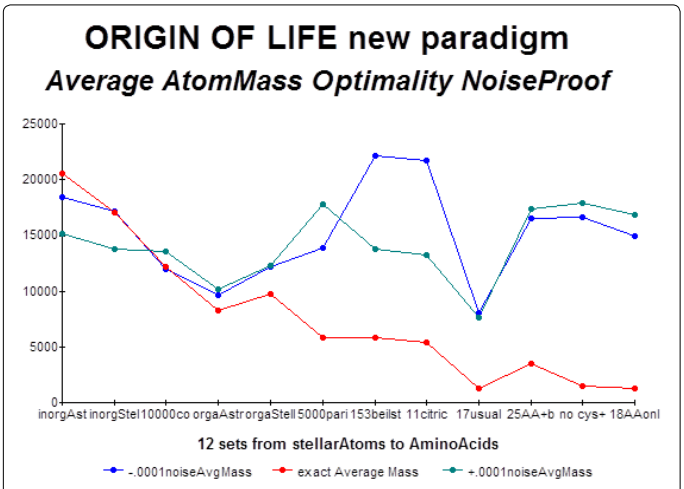

Figure 6: Evidence of noise sensitivity of average atomic masses for 12 sets of organic compounds essential to life.

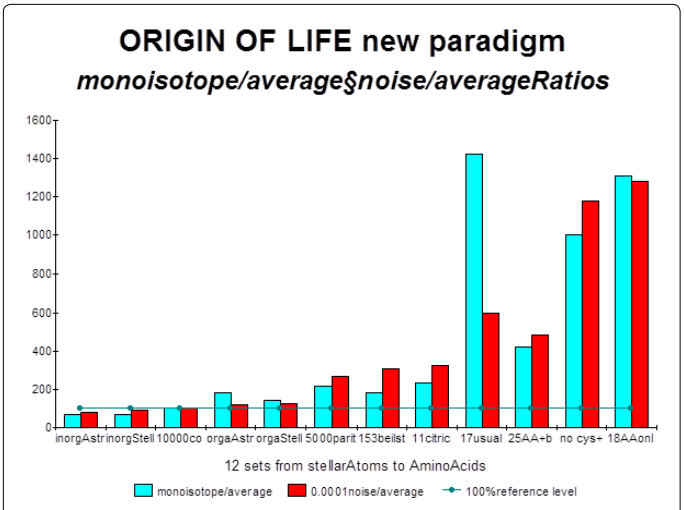

Figure 7: The comparison of the ratios "monoisotopic mass/average mass" between real cases and noisy cases.

	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

Table 6: The concentrated comparison of lines 4, 6 and 12 of Table 6.

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.

Conclusions

Perspectives in exobiology

Concentrated information and meaning represented by the 3 graphs Figures 6-8, it will emerge remarkable information: more organic compounds are moving towards more evolution, from small molecules premises 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 C_{12} isotopes, other

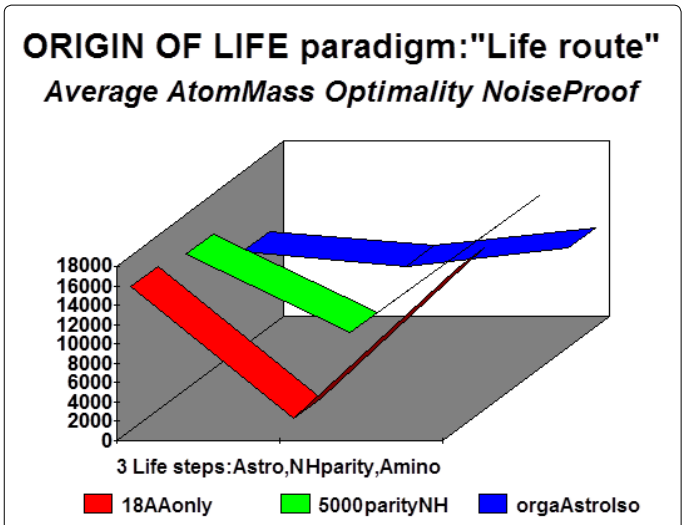

Figure 8: The triple curve in "V", concentrated comparison of lines 4, 6 and 12.

billions - albeit a little less - of C_{13} 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 O_{16} isotopes, other billions - albeit a little less - of O_{18} isotopes or even more rarely, billions of isotopes O_{17} Here is the famous curve in "V" that we will call by analogy "Sergeant Major curve" [31,32].

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 (C_{12} / C_{13}, N_{14} / N_{15}, H_1 / H_2, O_{16} / O_{17} / O_{18}, 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 NH_2 CH_2 COOH may for example consist of an atom O_{16} and an atom O_{18}, likewise for its carbon atoms which may be $2xC_{12}$ or $2xC_{13}$ or $C_{12}C_{13}$.

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:

1. The loss of bio-diversity destroys this balance of average atomic masses required by life.
2. 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.
3. 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 CH_4 (methane) released by our cows are very different from the isotopes of CH_4 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:

1. 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.
2. 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 C_{12} / C_{13} or N_{14} / N_{15} on Titan.

Have we discovered proportions comparable to those of our planet?

Only in such a case that our discoveries could allow predicting 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".

Reflexions on the diversity

The law of numerical projection atomic mass code 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.

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