Fractal Self-similarity, Scale Invariance and Stationary waves Codes Architecture Human Chromosomes DNA sequences

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« A cloud is made of billows upon billows upon billows that look like clouds. As you come clother to a cloud you don’t get something smooth, but irregularities at a smaller scale. » Benoit Mandelbrot

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ABSTRACT
After demonstrating a method of numerical unification of DNA information at the level of each human chromosome, we have demonstrated the presence of periods and numerical “resonances” characterizing the DNA sequence of each human chromosome. We then analyze the fractal nature of these periods and numerical resonances by using a sample of reference human chromosomes in Sapiens and Neanderthal. In particular, we will demonstrate these properties of FRACTAL INVARIANCE by 3 types of results:
First proof: invariance of the periodic properties of chromosome 21 despite a random mixing of T C A G base-pairs.
Second proof: phenomena reminiscent of « discrete numerical waveforms » properties: resonances, dissonances, fractal periods, phase shifts, phase opposites. We will illustrate these properties by studying chromosomes 13 and 7 of Neanderthal and Sapiens HG38.
Third proof: invariance of the periodic properties of Sapiens HG38 chromosome 4 despite a regular sampling of the nucleotides (1 by 10 sampling then 1 by 100 sampling).
In this paper, we demonstrate the evidence of a robust INVARIANT at the global level of whole human chromosomes DNA sequences : « Law of chromosomal organization of the human genome », or " law of robustness of the chromosome ": Each chromosome (sapiens or neanderthal) is characterized by a spatial and fractal kind of "standing wave" (natural frequency) whose phase and period (in TCAG nucleotide number) appear to be determined not by the precise sequence but by the relative proportions of the TCAG base-pairs populations ".


INTRODUCTION
In research fields, it is sometimes necessary to "leave time to time"; indeed, the methods and premises of the research that has just been presented here took root as early as the end of the 1980s, so nearly 30 years ago. ..
Infinite Diversity of digital and fractal structures of DNA and genomes:
It was in 2009 that the fractal nature of the human genome was demonstrated [1].
Meanwhile, during our Artificial Intelligence research at IBM, based on our model "Fractal Chaos” [2, 3, 4], we
demonstrated the numerical hyper-sensitivity of an artificial neural network positioned in the vicinity of Phi and subjected to perturbations of Fibonacci number type [5].

The fractal architecture [6, 7], mathematics [8] and Phi the golden number are omnipresent in Nature, in humans, in DNA, and even on the atomic quantum scale [9] or also in RNA [10]. It is a serious mistake to fall into these simplistic thesis of an omnipresence of the golden number in the DNA as well as an omnipresence of waves in the DNA...

The reality that we have discovered for more than 25 years of biomathematic exploration of DNA is much more subtle:

Phi the golden ratio [11-14] and the Fibonacci numbers never appear in the same form according to the scale and level of genetic information studied:

In 1991 [11-13] we discovered sets of Fibonacci numbers structuring the proportions of bases TCAG within the genes sequences as well as small genomes dense in genes such as those of bacteria or, specifically, mtDNA ... but these proportions called "resonances" are absent in junk-DNA uncoding chromosome regions.

In 1997 [14] we discovered that a numerical law of projection of the atomic masses of the nucleotides, bioatoms and amino acids, law based on Pi and Phi, unifies the 3 languages of the genetics that are DNA, RNA, and amino acids.

In 2009 [14, 19] we demonstrate that the fractal texture of the above unified genomic and proteomic images is manifested in the form of periodic discrete waves.

Finally, from 2010 [15-19] we publish various articles demonstrating that the golden ratio controls and finely adjusts the proportions of triplets codons to the scale of the entire human genome. This multi-level diversity of Phi is as astonishing as it is radiant ...

For example, facing the "cluster" formed by the six discoveries presented in this article on the one hand, in [20-24] on the other hand we can only remain amazed:

- In "The Human Genome Optimum: a numerical universal law control of all chromosomal deletions involved in human cancers" [23] we show that there is a sort of HGO [human genome optimum] uniting the entire human genome. This HGO will then allow the discovery of a universal law guiding all the LOH deletions implied in the cancers.
- In "Humans and Primates Chromosomes4 Fractal CODES: periodic stationary waveforms characterizing and differentiating Neanderthal and Sapiens whole chromosomes DNA sequences" [21] we show a sort of hierarchy classifying the 24 human chromosomes. One of them, the chromosome4 would be a kind of leader, "lighthouse" ... and this lighthouse vibrates to the proportions of Phi, the numbers of Lucas and Fibonacci.

- Finally, in [20] we discover more strange still: Phi and the numbers of Fibonacci and Lucas no longer appear explicitly. They hide behind a subtle interference, hiding behind a spectrum of numerical periods in the appearance of any numbers.

Our intuition is that there is a link, "dialogues" between these three heterogeneous but subtle disparate mechanisms that are mathematics, fractals, and the numbers of Fibonacci, Lucas, and Golden ratio.

Thus, in revisiting here the "supracode of DNA" discovered since the beginning of the 90s, as Professor Luc Montagnier baptized it [13], here we "rewind" this vast trip around digital structures of DNA and Genomes ...

Like the mtDNA genome, would the loop be "looped" ...!

However, it is only by deepening the notion of "fractal periodicity", outlined in [14, 19], and we will highlight in various articles in preparation [20-23] that we have re-discovered the major role that this GC / TA ratio at the whole chromosome and whole genome scales.

Here is the summary synopsis: comparing the three genomes of reference of Neanderthal [25], Sapiens BUILD34 of 2003 [26] and Sapiens HG38 of 2013 [27], we will demonstrate here then in [20-22] the evidence of "Fractals periods" and "resonance periods" characterizing each of the 24 human chromosomes. As illustrated
in Figure 1 below, these resonances make it possible to differentiate the respective genomes of Neanderthal and Sapiens on the global scale of the chromosome (here chromosome 4). Here a resonance of 34 nucleotides is common to both chromosomes 4 of Sapiens and Neanderthal, however, the respective forms of these resonance curves are radically different.

**Figure 1**: The 2 respective chromosomes 4 of Neanderthal and Sapiens HG38 share a “resonance” of 34 bp, however, these two radically different resonance curves illustrate a major differentiation between the two human species, at the GLOBAL chromosome 4 scale.

**MATERIALS AND METHODS**

**Analysed whole human genomes**:
We analyzed completely and systematically each of the 24 chromosomes of each of the following three reference genomes:

- Neanderthal genome

- Sapiens Build34 (2003) human reference genome ref [26]

- Sapiens HG38 (2013) human reference genome ref [27]

**Computing Fractal Periods and Resonances 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 of Biology" [14, 19]. 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, i.e., 360 simulations. This method of analysis will then reveal, in most cases, discrete waves or interferences, most often dissonances. However, sometimes there will emerge kinds of resonances where all scales of analysis appear to be in symbiosis.

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) derivatives mobile such that $1/2, 1/3, 1/4 \ldots 1/n$
Dim z cumulated populations from the "Master code" operators (14, 19).

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:

- Horizontal, meta codons dimension: curves for a dimension of meta codons given example 22 in the example "resonances" below (see Figure 7).
- Vertical, spectral differentiation: discrete series $d2-d1$ is +1 if increase and -1 if decrease (see Figure 8).

We represent in the top the +1 and in low the -1, (see all the other examples below).
Example of three-dimensional interference fields (chromosome21 Sapiens HG38 Figures 7 and 8).

<table>
<thead>
<tr>
<th>Dim x</th>
<th>d1</th>
<th>d2</th>
<th>…/… d100</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>1</td>
<td>2</td>
<td>3</td>
</tr>
<tr>
<td>17</td>
<td>1298833</td>
<td>1181005</td>
<td>1133041</td>
</tr>
<tr>
<td>18</td>
<td>1029171</td>
<td>1074033</td>
<td>960839</td>
</tr>
<tr>
<td>19</td>
<td>1091521</td>
<td>982429</td>
<td>937709</td>
</tr>
<tr>
<td>20</td>
<td>878537</td>
<td>903906</td>
<td>914801</td>
</tr>
<tr>
<td>21</td>
<td>933380</td>
<td>834734</td>
<td>893561</td>
</tr>
<tr>
<td>22</td>
<td>761233</td>
<td>774174</td>
<td>779102</td>
</tr>
<tr>
<td>23</td>
<td>809977</td>
<td>837877</td>
<td>764596</td>
</tr>
<tr>
<td>24</td>
<td>852758</td>
<td>779786</td>
<td>750287</td>
</tr>
<tr>
<td>25</td>
<td>710190</td>
<td>727911</td>
<td>736109</td>
</tr>
</tbody>
</table>

…/… 377

Horizontal scan example : 22 761233 774174 779102 783714 786854 …/… (see Figure 7)
Vertical scan example : 1 if $d2>d1$ and -1 if $d2<d1$ then : -1 1 -1 1 1 1 -1 1 1 …/… (see Figure 8).

**HG38 Human Reference Chromosome21**

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

![Figure 6: zoom on vertical scan method revealing PERIOD = 22 from HG38 reference chromosome21.](image)
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 (FIG. 7) and the period "vertical scan" is a period of repeatability of 22bp also (Figure 8).

RESULTS

In this study one fact is certain: there is indeed a hyper sensitivity, a fine tuning of the GC / TA ratios on the scale of the entire human genome.

The immediate underlying question then arises: between these two codes, which constitute, on the one hand, this ratio CG / TA, and on the other hand the DNA sequence itself, is there symbiosis, complementarity or even conflict?

Indeed if there exists a second level of code beyond the sequence this would introduce a multi-dimensional character of the chromosomes and the genome.

We will answer this question by illustrating 3 examples. All three will be based on the methods which will be described in the article [15] and which we have summarized briefly in § Methods.

First proof: invariance of the periodic properties of chromosome 21 despite a random mixing of T C A G base-pairs.

Second proof: phenomena reminiscent of « discrete numerical waveforms » properties: resonances, dissonances, fractal periods, phase shifts, phase opposites. We will illustrate these properties by studying chromosomes 13 and 7 of Neanderthal and Sapiens HG38.

Third proof: invariance of the periodic properties of chromosome 4 of Sapiens HG38 despite a regular sampling of the nucleotides (1 by 10 sampling then 1 by 100 sampling).

In all that follows, we will use the methods of analysis of the numerical periods and resonances of the chromosomes detailed in [15]. Let us emphasize, however, that the two types of analysis - which always lead to the same periods - are based on two INDEPENDENT methods, insofar as these methods derive their independence from their orthogonal nature (in the vector sense of mathematics).

Finally, on several human chromosomes such as chromosome 13 or here chromosome 21, we discover the invariance of periodic properties despite a random mixing of the bases T C A G:

First proof: invariance of the periodic properties of chromosome 21 despite a random mixing of T C A G base-pairs populations.

In this study we randomly shuffle the T C A G bases by moving them within the sequence while maintaining exactly the same relative proportions of each population of bases T, C, A and G.

This chromosome comprising 4008619 base pairs T C A G, the chromosome randomly stirred will also comprise 4008619 base pairs T C A G whose relative positions in the sequence will have been totally disrupted. The DNA sequence information will thus have been totally destroyed.

Here are 2 examples illustrating this mixing for regions 1 to 100 then 200000 to 200100 in the sequence.

CHR21HG38[1 to100]
GATCCCCGCCTTGGCCTTCTAAAGTGTGCTGTAATAGGCAGGTTAGGGCCACCACGTCCAGCTGGTTAA
TTTTATATTTAATGAAGTAATGTTAATGATTTTATGTTTGGCTCGG
CTTAGCTGGCGAGTTTTTTCTTTACTACAG

CHR21HG38H[1 to 100]
ACTCCGTAATCTACTACAATGAGTAATCTACAGGCTGATATCTATATAGTTTTTGGCTCGG
CTTAGCTGGCGAGTTTTTTCTTTACTACAG

CHR21HG38[200000 to 200100]
TTTTATACAAAGATTTTTATATTAAGCTTCTTCAATCAGTCTTGAATTTTTTTTTTTTTTTTTTATATGA
TGGAAAAAGGGGTCCAGCTCAATCTCC
CHR21HG38H[200000 to 200100]
AAAGCTGAGGGGTGGTACATTGATAGGGAGAAGGTTAATATTACAGGCAATTTGTTTATAAAGTCTGAAC
TAATTATCGAAGTTCTCGTTTCTGATTGTTT
Figure 7: Evidence of a resonance of 22bp period in the whole HG38 human reference chromosome 21.

Figure 8: Confirmation of a 22bp period in the whole HG38 human reference chromosome 21.
Figure 9: Evidence of a resonance of 22bp period in the whole HG38 human chromosome 21 where T C A G bases are randomly swapped.

Figure 10: Confirmation of a 22bp period in the whole HG38 human chromosome 21 where T C A G bases are randomly swapped.

Although strictly different sequences, the 2 reference chromosomes 21 and then its randomly shuffled version would be structured by strictly identical periods (22 base-pairs)².

² We will note, however, by comparing Figures 8 and 10, that, although all confirming the same 22bp period, there would appear to be a notable difference: in the periods of the reference chromosome (Figure 8) there appears a kind of "cut-off" after 4 regular periods. On the contrary, in the version of chromosome 21 randomly stirred (Figure 10), this period propagates throughout the spectrum analyzed. Our interpretation would be that the fractal range of this periodic regularity remains limited in the real chromosome, whereas, due to the regularity of the random mixing of the bases throughout the chromosome, this periodic phenomenon would have a scope extending to the entirety of the chromosome.
Thus, this highlighting of “periods”, “resonances” or even “phase shifts” (see below) characterizing on a global scale each of the human chromosomes constitutes an absolutely remarkable phenomenon.

Thus, if in this chromosome 21 we “disrupt” the DNA sequence while maintaining strictly the same T, C, A and G nucleotide ratios, these same phenomena of periods and resonances are preserved!

Thus, we could write now : ”Law of chromosomal organization of the human genome, or” law of robustness of the chromosome ”

Each chromosome (sapiens or neanderthal) is characterized by a spatial and fractal kind of “standing wave” (natural frequency) whose phase and period (in TCAG nucleotide number) appear to be determined not by the precise sequence but by the proportions Relative to the TCAG bases ”.

This surprising property, which has been verified on chromosomes 13 and 21, must be validated and then generalized on each of the 24 human chromosomes.

Second proof: phenomena reminiscent of « discrete numerical waveforms » properties: resonances, dissonances, fractal periods, phase shifts, phase opposites. We will illustrate these properties here by studying chromosomes 13 of Neanderthal and Sapiens HG38:

When analysing by the same methods described in Methods both Neanderthal and Sapiens chromosomes13, we obtain the same 13bp period resonance characterizing each of these 2 chromosomes (Figures 11 and 12).

Figure 11 : We show here a “resonance” of 13bp structuring the chromosome13 of Neanderthal, while periods 12 and 14bp illustrate “dissonances”.
Figure 12: We show here a “resonance” of 13bp structuring the chromosome13 of Sapiens HG38, while periods 12 and 14bp illustrate “dissonances”.

This period 13 is confirmed - independently - by the second type of analysis below (FIG. 13).

FIG. 13: the red vertical bars show a repeatability of the 13bp period structuring the chromosome13 of Sapiens HG38, confirming the resonance of the same period previously demonstrated using a totally different method.
In this Figure 13 we propose a notation where a high line [+1] will be marked "+" and a low line [-1] will be written "-". We will then identify the characteristic patterns "++ - + - ++ ", which we will symbolize by a kind of letter" W ". Thus, in this figure of periods illustrating Sapiens HG38, there is a sequence of 3 successive patterns "W". Then, these types of figures are reversed, switching to the negative region of this sort of "bar code" causing "reversed" occurrences of "M" sorts in the lower region, then returning to the High region with 5 occurrences of "W", etc ...

We will now compare these patterns in the "bar codes" associated with the 2 respective chromosomes of Neanderthal and Sapiens: Figures 14 and 15 below will illustrate a sort of "phase shift" phenomenon between these two chromosomes 13 ...

Schematically, this could be symbolized by:

Néanderthal :
WWWW  WWWWW  WWWWW...
    MMMMM  MMMMM...

Sapiens :
WWW  WWWWW  WWWWW...
    MMMMM  MMMMM...

Figure 14 : In these "bar codes" structuring the chromosome 13 of Neandertal, four successive "W" patterns are counted in the beginning of the upper region, namely: "W W W W"
Figure 15: In these “barcodes” structuring the chromosome 13 of Sapiens HG38, only three "W" patterns in the beginning of the upper region are now counted, namely: “W W W”.

In these two figures, in addition to the “phase shift”, the FRACTAL nature of these periodic patterns is also shown: indeed, above the local patterns of the "W" or "M" type, a fractal meta-structure is drawn “WWWWWMMMMM”, Of which one can even calculate the period: 13x10 = 130.

Figure 16: Human Sapiens HG38 chromosome 7 reveals a period of 27bp.
Although strictly identical (13bp) periods, the two chromosomes 13 of Neanderthal and Sapiens HG38 differentiate themselves by what it would seem advisable to call a “phase shift”. Thus, this highlighting of "periods", "resonances" or even "phase shifts" characterizing on a global scale each of the human chromosomes constitutes an absolutely remarkable phenomenon. However, if in these chromosomes 13 we “disrupt” the DNA sequences while strictly maintaining the same T, C, A and G nucleotide ratios, these same phenomena of periods and resonances are preserved!

In order to confirm this strange analogy with the theory of waves, we will briefly illustrate the cases of the chromosomes 7 of Sapiens and Neanderthal whose period patterns are ... in “phase opposition”!

**Third proof: invariance of the periodic properties of chromosome 4 of Sapiens HG38 despite a regular sampling of the nucleotides (1 by 10 sampling then 1 by 100 sampling):**

In (23) Table 9 recall:

<table>
<thead>
<tr>
<th>Chr</th>
<th>C+G</th>
<th>T+A</th>
<th>CG / TA</th>
</tr>
</thead>
<tbody>
<tr>
<td>4</td>
<td>72568001</td>
<td>117184666</td>
<td><strong>0.6192619178</strong></td>
</tr>
</tbody>
</table>

We note that the CG/TA ratio of chromosome 4 is very close to 1/Phi = 0618 ... where Phi is the "Golden Ratio" with Phi = 1.618 ... (27).

Indeed:

\[
\frac{1}{\Phi} = 0.6180339887 \\
(1/\Phi) - 0.6192619178 = -0.00122792905
\]

There will be an absolutely remarkable phenomenon: for this chromosome 4, a major resonance will be 34, but secondary resonances will also appear for periods 21, 55, 89 ... (which are, with 34, Fibonacci numbers) As well as for periods 29, 47, 76 ... which are Lucas numbers.

It is known that in these two sequences of Lucas and Fibonacci the ratio of 2 consecutive numbers (examples 34 and 21) tends towards Phi the Golden Ratio.
We shall now study the invariance or the modulations of these resonances and periods by successively comparing the following four cases:

- The reference chromosome4 HG38.
- A chromosome4 sampling at the rate of 1 base every 10 bases.
- A chromosome 4 sampling at the rate of 1 base every 34 bases.
- A chromosome 4 sampling at the rate of 1 base every 100 bases.

The chromosome 4 HG38 of reference:

Figure 18: The main resonance of 34bp characterizing the HG38 reference Chromosome 4.

Figure 19: The main period of 34bp characterizing the HG38 reference Chromosome 4.
In Figure 20 below, we show the distribution spectrum of T + A and C + G populations throughout chromosome 4. This analysis is obtained by segmenting the whole sequence of the chromosome in sections of 34bp, and then counting in each of these sections the numbers of T + A on the one hand and the numbers of C + G on the other hand. The values can therefore vary from 0 to 34 for each of the segments. It is found that the respective peaks are at 13 and 21, which are with three consecutive Fibonacci numbers: 13 21 34.

![Figure 20: The spectral analysis of TA vs CG distribution within HG38 Chromosome 4.](image)

The following figures illustrate the ”secondary resonances” of 21, 55, and 47 which organize at a second degree this chromosome 4.

![Figure 21: The secondary resonance of 21bp (Fibonacci) characterizing the HG38 reference Chromosome 4.](image)
Figure 22: The secondary resonance of 47bp (Lucas) characterizing the HG38 reference Chromosome 4.

Figure 23: The secondary resonance of 55bp (Fibonacci) characterizing the HG38 reference Chromosome 4.

On the one hand, the period 34bp is obtained by the 2 complementary methods (FIGS. 18 and 19), and on the other hand the cases corresponding to numbers of Fibonacci or Lucas close to 34 lead to secondary resonances, We should rather say "harmonics".

Chromosome 4 sampling 1 by 10:

We will now perform a first sampling by selecting, in a regular way throughout the chromosome, only a single nucleotide every 10 nucleotides. This operation, although regular, should normally totally destroy the sequence of the chromosome. Because of the fractal nature of the chromosome, we risk having pleasant surprises!
Figure 24: The main resonance of 34bp characterizing the 1 by 10bp sampling Chromosome4.

Figure 25: The secondary resonance of 21bp characterizing the 1 by 10bp sampling Chromosome4.
Figure 26: The secondary resonance of 55bp characterizing the 1 by 10bp sampling Chromosome4.

Figure 27: The secondary resonance of 47bp characterizing the 1 by 10bp sampling Chromosome4.
It is found that this chromosome4 sampling at the rate of 1 nucleotide every 10 nucleotides retains simultaneously the main resonance of 34, the period of 34 and the harmonic resonances of 21, 47 and 55. This extraordinary fact reveals the high level of redundancy and the FRACTAL nature of the whole sequence of chromosome 4.

**chromosome4 sampling 1 by 34:**
We will then perform a second sampling by retaining, in a regular way throughout the chromosome, only a single nucleotide every 34 nucleotides. Our idea is to find out what happens if the value of sampling is precisely the main resonance period of 34bp. This operation, although regular, should normally totally destroy the sequence of the chromosome.
Figure 30: The secondary resonance of 21bp characterizing the 1 by 34bp sampling Chromosome4.

Figure 31: The secondary resonance of 55bp characterizing the 1 by 34bp sampling Chromosome4.
Figure 32: The secondary resonance of 47bp characterizing the 1 by 34bp sampling Chromosome4.

Figure 33: The main period of 34bp characterizing the 1 by 34bp sampling Chromosome4.

Although the resonances continue to be unaffected by this sampling of 34, Figure 33 above shows some modulations at the time curve. However, the period of 34 remains, on the other hand, the upper part of the barcodes shows a phase shift, whereas in the lower part of the barcode, the same phase-shifted patterns of a half-period appear very clearly (this phenomenon already existed in the Figure 28 of 1 by 10 sampling).
Chromosome4 sampling 1 by 100:
Finally, we will perform a sampling by retaining only one nucleotide every 100 nucleotides in a regular way throughout the chromosome. This operation, although regular, should normally totally destroy the sequence of the chromosome.

Figure 34: The main resonance of 34bp characterizing the 1 by 100bp sampling Chromosome4.

Figure 35: The secondary resonance of 21bp characterizing the 1 by 100bp sampling Chromosome4.
Figure 36: The secondary resonance of 55bp characterizing the 1 by 100bp sampling Chromosome 4.

Figure 37: The secondary resonance of 47bp characterizing the 1 by 100bp sampling Chromosome 4.
Here again, the resonances continue not to be affected by this 100 sampling. The period of 34 remains, the upper part of the barcodes shows an unchanged phase agreement with the reference whole chromosome (Figure 19). Thus, for a reference chromosome4 comprising 190214555 bp, reducing this length in a ratio of 100 to 1902145 bp by retaining only one base pair every 100 base pairs, maintains and retains these remarkable properties of resonances and of periodicities that characterize this chromosome on its global scale. We believe here to bring the best evidence of the FRACTAL nature of the chromosome.

CONCLUSION

We still have a lot to discover on this fascinating CODE that is DNA ...
In this study we have just raised a new corner of sail on DNA and the human genome ...
A breakthrough was the discovery of the fractal nature of DNA (1, 7) then of certain structures of the brain (28) ...
Thus, mathematics has become imbedded in genetics. Other mathematical approaches to genomes, which are equally original, are to be noted with approaches to matrix (29) or mathematical topology (8).

Then it is frankly the wave theory that invites itself into DNA with the current research of the co-discoverer of the HIV virus Luc Montagnier (30).
And, of course, there is this famous number of gold and its Fibonacci sequence; Do not find them in the rhythms of the heart or the arborescence of our arteries (31), but also in the RNA (10) or in quantum physics (9).

Finally, like these different researchers, we have just demonstrated how the "CODES" (14) are at the heart of the mechanisms of Nature ... "Codes" real today ... "Codes" artificial tomorrow (32). ..

But we will mainly have to continue to reflect on this notion of "standing waves" at the scale of the entire chromosome ...
A possible track of investigations is the scenarii of "physical harmonic resonance" as sugested Dr Robert Friedman « Do you think that whole human chromosome DNA sequence with the right number of Fibonacci resonance points could act like a singing wine glass? 

When you rub a finger around the rim of the glass, harmonic energy, tones or information are produced. This could be a mechanism that mitochondria and cells use to communicate with each other... ».

This scenarii could play a rôle in chromosomal DNA genome epigenetics then in genes expression tuning.
The point that seems to be the most important remains however the discovery of this INVARIANT: "how can the same relative proportion of TCAG bases on the scale of an entire chromosome several tens of millions of bases always lead to the same characteristic invariant Regardless of the sequence of its nucleotides?"

Here it appears incredible phenomenon: the discovery of an invariant independent of the chromosome DNA sequence (example of the chromosome21 above).

It seemed useful to propose some analogies in order to better understand the nature of this phenomenon of organization of genetic information:

1 / Musical Analogy: the stationary waves of a musical instrument: on a string of guitar or violin, the note remains unchanged whatever the point where it is pinched ...

2/ The Fractal analogy: in a line drawn with a pencil, two neighboring points in time will also be in space. On the contrary, in a fractal this is no longer the case ... yet radically different initial conditions end up drawing the same image of the fractal. Example of the famous Mandelbrot's Fractal zn = c2 + z2.

The analogy here becomes clearer: different sequences of DNA produce the same period of resonance if exactly the same relative proportions of bases T A C G are preserved ther (example of chromosome 21 randomly stirred).

3 / Analogy of the attractor: Let us suppose a three-dimensional container of some form containing no local minima, as one finds it in mathematical optimization. The fact of launching by multiple ways a same bead in this container (initial conditions) All the cases this ball towards the single and even deepest point of the three-dimensional container (optimum or minimum principal).

Rather than a heavy ball, now launch a light feather: after a long sequence of numerical twists, it will also fall back into optimum ...

This will remind the reader of this famous SYRACUSE conjecture (33) where any integer leads to the attractor
"1' after bouncing thousands of times in a sequence of integers …
In the face of these emerging CODES structuring and architecturing DNA and genomes, the question which fascinated Nobel co-discoverer of DNA structure Francis Crick about « panspermia » remains an open question (34, 35).

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