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- Human genome Codon populations: Numbers and atomic weighs perfect balancing (2009)
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- **Proof of a Functional Human Chromosomes Meta-structure involving « Pi » and « Phi » Universal Constants.**
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Perez JC. Interdiscip Sci. 2010 Sep;2(3):228-40. Epub 2010 Jul 25.
Codon populations in single-stranded whole human genome DNA Are fractal and fine-tuned by the Golden Ratio 1.618.

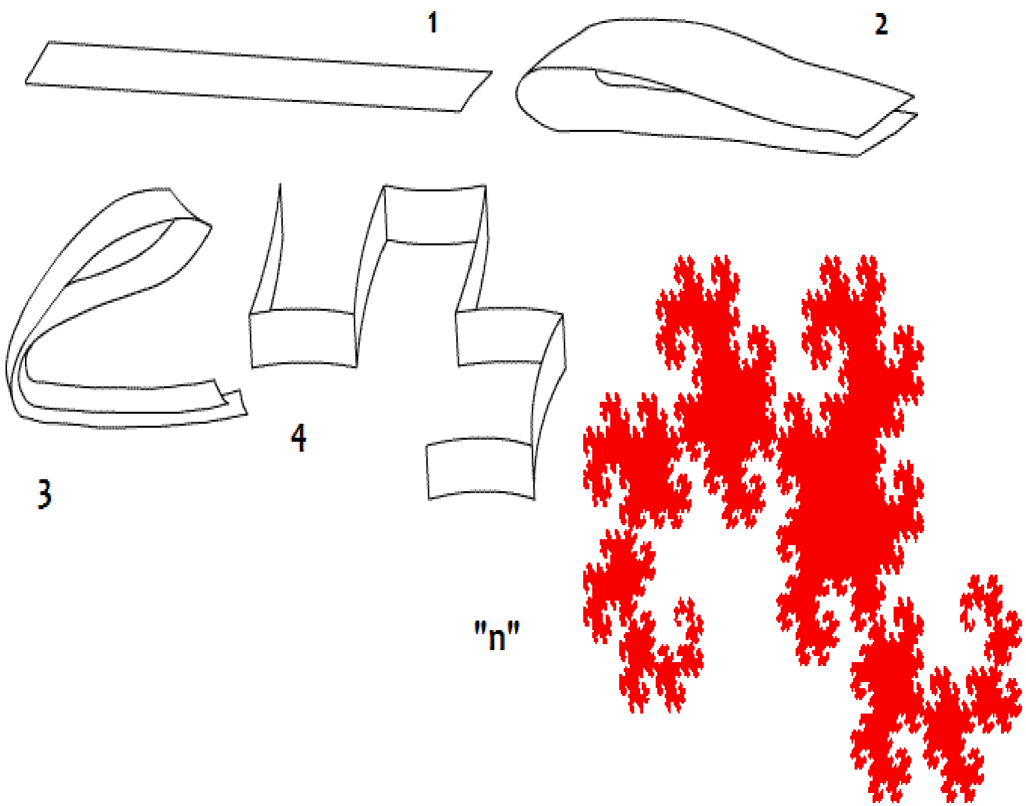
-I- ABSTRACT:

We propose a universal “Fractal Genome Code Law”: The frequency of each of the 64 codons across the entire human genome is controlled by the codon's position in the Universal Genetic Code table. We analyze the frequency of distribution of the 64 codons (codon usage) within single-stranded DNA sequences. Concatenating 24 Human chromosomes, we show that the entire human genome employs the well known universal genetic code table as a *macro* structural model. The position of each codon within this table precisely dictates its population. So the Universal Genetic Code Table not only maps codons to amino acids, but serves as a global checksum matrix. Frequencies of the 64 codons in the whole human genome scale are a self-similar fractal expansion of the universal genetic code. Particularly, the 6 folding steps of codon populations modeled by the binary divisions of the ***“Dragon fractal paper folding curve”*** show evidence of 2 attractors. The numerical relationship between the attractors is derived from the Golden Ratio. We demonstrate that:

1. The whole Human Genome Structure uses the Universal Genetic Code Table as a tuning model. It predetermines global codons proportions and populations. The Universal Genetic Code Table governs both micro and macro behavior of the genome.

2. We extend the *Chargaff*'s second rule from the domain of single TCAG nucleotides to the larger domain of codon triplets.

3. Codon frequencies in the human genome are clustered around 2 fractal-like attractors, strongly linked to the golden ratio 1.618.



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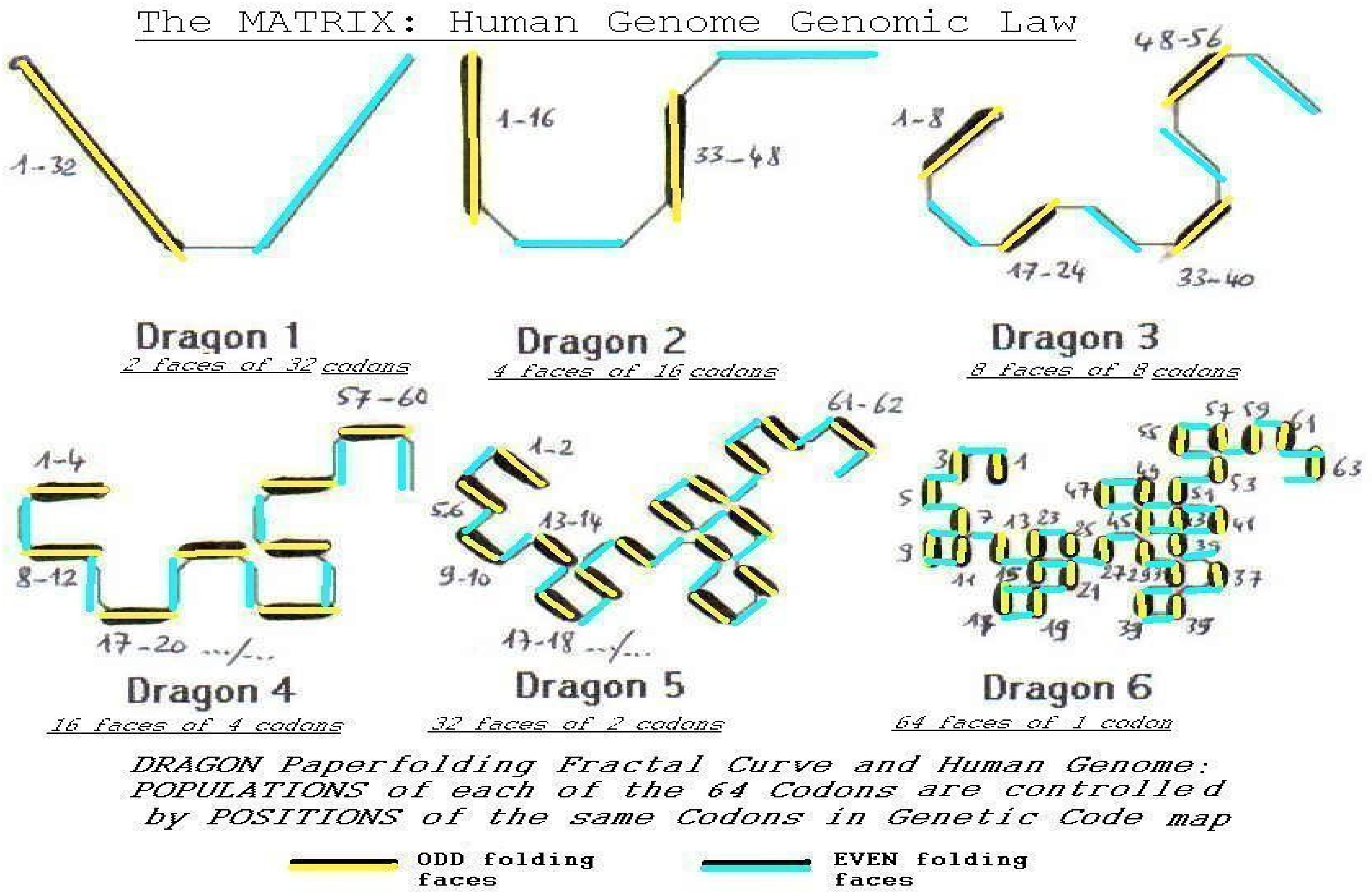
Codon populations in single-stranded whole human genome DNA Are fractal and fine-tuned by the Golden Ratio 1.618.

-II- RESHAPING THE GENETIC CODE TABLE BY FRACTAL DRAGON CURVE...



DRAGON Paperfolding Fractal Curve and Human Genome: POPULATIONS of each of the 64 Codons are controlled by POSITIONS of the same Codons in Genetic Code map

-III- Evidence of 2 « attractors »: « 1 » and « (3-Phi)/2 » where Phi = 1.618033 the Golden ratio

Table - Chessboard map summarizing major results, attractors and symmetries.

-I- 2 parts = 2*1 Dragon 1 2x32 Halves The ratio between the EVEN Half part and the ODD half part is

= 0.999247 = 1 (error=0.000753)

-II- 4 parts = 4*1 Dragon 2 4x16 Quartiles The ratio between EVEN Quartiles and ODD Quartiles is

= 0.691457 = (3 – Phi) / 2 (error=0.000474)

-III- 8 parts = 2*3 Dragon 3 8x8 Octants The ratio between EVEN Octants and ODD Octants is

= 0.999248 = 1 (error=0.000752)

-IV- 16 parts = 4*2 Dragon 4 16x4 Squares The ratio between EVEN Squares and ODD Squares is

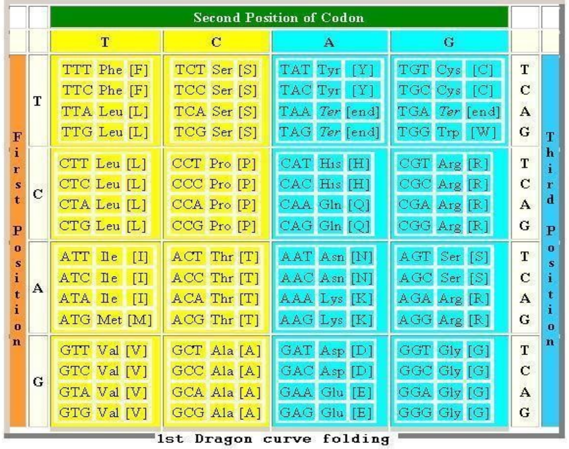
= 0.691458 = (3 – Phi) / 2 (error=0.000475)

-V- 32 parts = 2*5 Dragon 5 32x2 Binomes The ratio between EVEN Binomes and ODD Binomes is

= 0.999247 =1 (error=0.000753)

-VI- 64 parts = 4*3 Dragon 6 64x1 codons The ratio between EVEN Codons and ODD Codons is

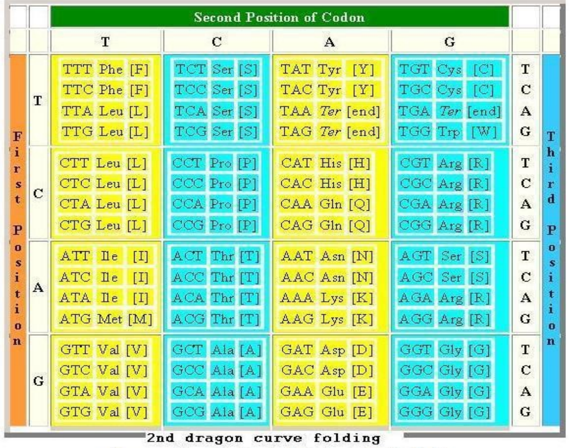
= 0.691458 = (3 – Phi) / 2 (error=0.000474)



		Second Position of Codon				
First Position		T	C	A	G	Third Position
	T	TTT Phe [F]	TCT Ser [S]	TAT Tyr [Y]	TGT Cys [C]	T
		TTC Phe [F]	TCC Ser [S]	TAC Tyr [Y]	TGC Cys [C]	C
		TTA Leu [L]	TCA Ser [S]	TAA Ter [end]	TGA Ter [end]	A
		TTG Leu [L]	TCG Ser [S]	TAG Ter [end]	TGG Trp [W]	G
	C	CTT Leu [L]	CCT Pro [P]	CAT His [H]	CGT Arg [R]	T
		CTC Leu [L]	CCC Pro [P]	CAC His [H]	CGC Arg [R]	C
		CTA Leu [L]	CCA Pro [P]	CAA Gln [Q]	CGA Arg [R]	A
		CTG Leu [L]	CCG Pro [P]	CAG Gln [Q]	CGG Arg [R]	G
	A	ATT Ile [I]	ACT Thr [T]	AAT Asn [N]	AGT Ser [S]	T
		ATC Ile [I]	ACC Thr [T]	AAC Asn [N]	AGC Ser [S]	C
		ATA Ile [I]	ACA Thr [T]	AAA Lys [K]	AGA Arg [R]	A
		ATG Met [M]	ACG Thr [T]	AAG Lys [K]	AGG Arg [R]	G
	G	GTT Val [V]	GCT Ala [A]	GAT Asp [D]	GGT Gly [G]	T
		GTC Val [V]	GCC Ala [A]	GAC Asp [D]	GGC Gly [G]	C
		GTA Val [V]	GCA Ala [A]	GAA Glu [E]	GGA Gly [G]	A
		GTG Val [V]	GCG Ala [A]	GAG Glu [E]	GGG Gly [G]	G

1st Dragon curve folding

Dragon 1: ratio Dark/Light = 1



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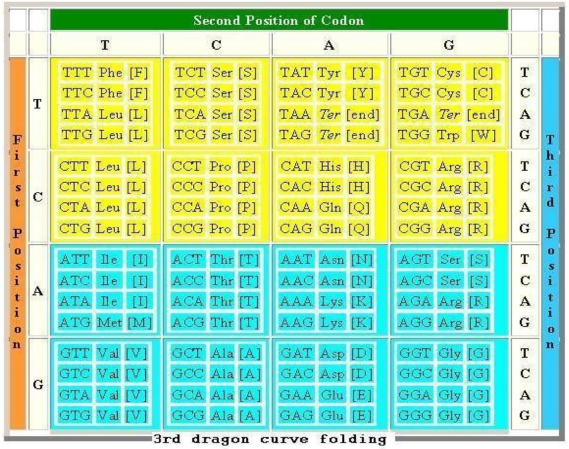
		TTA Leu [L]	TCA Ser [S]	TAA Ter [end]	TGA Ter [end]	A
		TTG Leu [L]	TCG Ser [S]	TAG Ter [end]	TGG Trp [W]	G
	C	CTT Leu [L]	CCT Pro [P]	CAT His [H]	CGT Arg [R]	T
		CTC Leu [L]	CCC Pro [P]	CAC His [H]	CGC Arg [R]	C
		CTA Leu [L]	CCA Pro [P]	CAA Gln [Q]	CGA Arg [R]	A
		CTG Leu [L]	CCG Pro [P]	CAG Gln [Q]	CGG Arg [R]	G
	A	ATT Ile [I]	ACT Thr [T]	AAT Asn [N]	AGT Ser [S]	T
		ATC Ile [I]	ACC Thr [T]	AAC Asn [N]	AGC Ser [S]	C
		ATA Ile [I]	ACA Thr [T]	AAA Lys [K]	AGA Arg [R]	A
		ATG Met [M]	ACG Thr [T]	AAG Lys [K]	AGG Arg [R]	G
	G	GTT Val [V]	GCT Ala [A]	GAT Asp [D]	GGT Gly [G]	T
		GTC Val [V]	GCC Ala [A]	GAC Asp [D]	GGC Gly [G]	C
		GTA Val [V]	GCA Ala [A]	GAA Glu [E]	GGA Gly [G]	A
		GTG Val [V]	GCG Ala [A]	GAG Glu [E]	GGG Gly [G]	G

2nd dragon curve folding

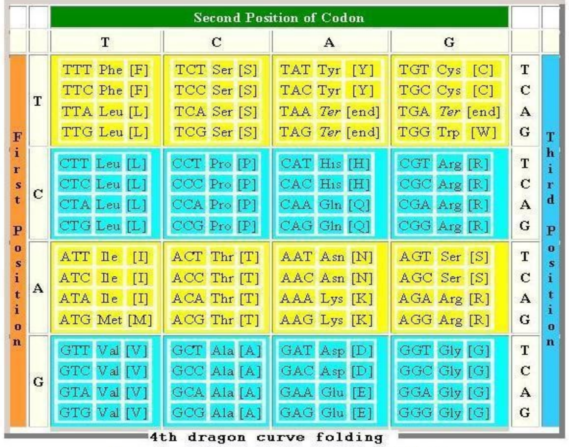
Dragon 2: ratio Dark/Light = (3 - Phi) / 2



		Second Position of Codon				
First Position		T	C	A	G	Third Position
	T	TTT Phe [F]	TCT Ser [S]	TAT Tyr [Y]	TGT Cys [C]	T
		TTC Phe [F]	TCC Ser [S]	TAC Tyr [Y]	TGC Cys [C]	C
		TTA Leu [L]	TCA Ser [S]	TAA Ter [end]	TGA Ter [end]	A
		TTG Leu [L]	TCG Ser [S]	TAG Ter [end]	TGG Trp [W]	G
	C	CTT Leu [L]	CCT Pro [P]	CAT His [H]	CGT Arg [R]	T
		CTC Leu [L]	CCC Pro [P]	CAC His [H]	CGC Arg [R]	C
		CTA Leu [L]	CCA Pro [P]	CAA Gln [Q]	CGA Arg [R]	A
		CTG Leu [L]	CCG Pro [P]	CAG Gln [Q]	CGG Arg [R]	G
	A	ATT Ile [I]	ACT Thr [T]	AAT Asn [N]	AGT Ser [S]	T
		ATC Ile [I]	ACC Thr [T]	AAC Asn [N]	AGC Ser [S]	C
		ATA Ile [I]	ACA Thr [T]	AAA Lys [K]	AGA Arg [R]	A
		ATG Met [M]	ACG Thr [T]	AAG Lys [K]	AGG Arg [R]	G
	G	GTT Val [V]	GCT Ala [A]	GAT Asp [D]	GGT Gly [G]	T
		GTC Val [V]	GCC Ala [A]	GAC Asp [D]	GGC Gly [G]	C
		GTA Val [V]	GCA Ala [A]	GAA Glu [E]	GGA Gly [G]	A
		GTG Val [V]	GCG Ala [A]	GAG Glu [E]	GGG Gly [G]	G

3rd dragon curve folding

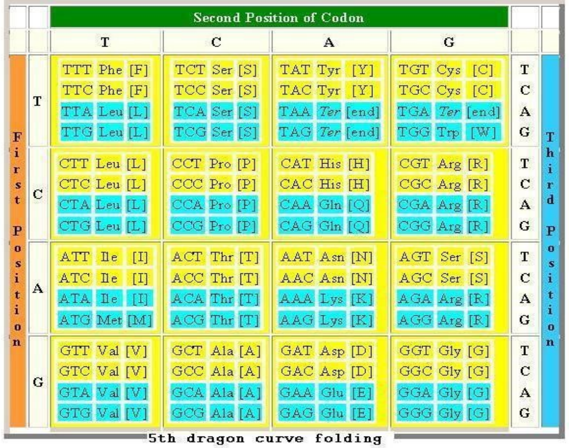
Dragon 3: ratio Dark/Light = 1



		Second Position of Codon				
First Position		T	C	A	G	Third Position
	T	TTT Phe [F]	TCT Ser [S]	TAT Tyr [Y]	TGT Cys [C]	T
		TTC Phe [F]	TCC Ser [S]	TAC Tyr [Y]	TGC Cys [C]	C
		TTA Leu [L]	TCA Ser [S]	TAA Ter [end]	TGA Ter [end]	A
		TTG Leu [L]	TCG Ser [S]	TAG Ter [end]	TGG Trp [W]	G
	C	CTT Leu [L]	CCT Pro [P]	CAT His [H]	CGT Arg [R]	T
		CTC Leu [L]	CCC Pro [P]	CAC His [H]	CGC Arg [R]	C
		CTA Leu [L]	CCA Pro [P]	CAA Gln [Q]	CGA Arg [R]	A
		CTG Leu [L]	CCG Pro [P]	CAG Gln [Q]	CGG Arg [R]	G
	A	ATT Ile [I]	ACT Thr [T]	AAT Asn [N]	AGT Ser [S]	T
		ATC Ile [I]	ACC Thr [T]	AAC Asn [N]	AGC Ser [S]	C
		ATA Ile [I]	ACA Thr [T]	AAA Lys [K]	AGA Arg [R]	A
		ATG Met [M]	ACG Thr [T]	AAG Lys [K]	AGG Arg [R]	G
	G	GTT Val [V]	GCT Ala [A]	GAT Asp [D]	GGT Gly [G]	T
		GTC Val [V]	GCC Ala [A]	GAC Asp [D]	GGC Gly [G]	C
		GTA Val [V]	GCA Ala [A]	GAA Glu [E]	GGA Gly [G]	A
		GTG Val [V]	GCG Ala [A]	GAG Glu [E]	GGG Gly [G]	G

4th dragon curve folding

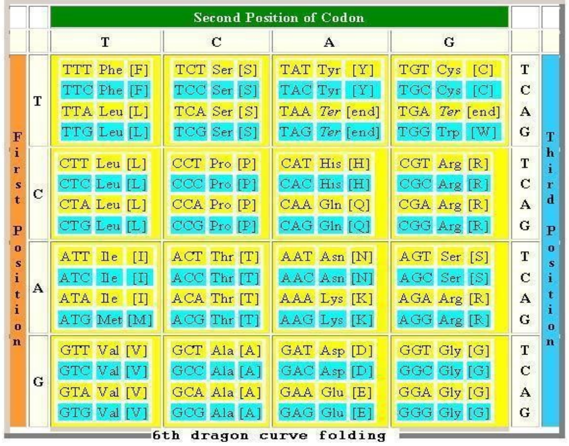
Dragon 4: ratio Dark/Light = (3 - Phi) / 2



		Second Position of Codon				
First Position		T	C	A	G	Third Position
	T	TTT Phe [F]	TCT Ser [S]	TAT Tyr [Y]	TGT Cys [C]	T
		TTC Phe [F]	TCC Ser [S]	TAC Tyr [Y]	TGC Cys [C]	C
		TTA Leu [L]	TCA Ser [S]	TAA Ter [end]	TGA Ter [end]	A
		TTG Leu [L]	TCG Ser [S]	TAG Ter [end]	TGG Trp [W]	G
	C	CTT Leu [L]	CCT Pro [P]	CAT His [H]	CGT Arg [R]	T
		CTC Leu [L]	CCC Pro [P]	CAC His [H]	CGC Arg [R]	C
		CTA Leu [L]	CCA Pro [P]	CAA Gln [Q]	CGA Arg [R]	A
		CTG Leu [L]	CCG Pro [P]	CAG Gln [Q]	CGG Arg [R]	G
	A	ATT Ile [I]	ACT Thr [T]	AAT Asn [N]	AGT Ser [S]	T
		ATC Ile [I]	ACC Thr [T]	AAC Asn [N]	AGC Ser [S]	C
		ATA Ile [I]	ACA Thr [T]	AAA Lys [K]	AGA Arg [R]	A
		ATG Met [M]	ACG Thr [T]	AAG Lys [K]	AGG Arg [R]	G
	G	GTT Val [V]	GCT Ala [A]	GAT Asp [D]	GGT Gly [G]	T
		GTC Val [V]	GCC Ala [A]	GAC Asp [D]	GGC Gly [G]	C
		GTA Val [V]	GCA Ala [A]	GAA Glu [E]	GGA Gly [G]	A
		GTG Val [V]	GCG Ala [A]	GAG Glu [E]	GGG Gly [G]	G

5th dragon curve folding

Dragon 5: ratio Dark/Light = 1



		Second Position of Codon				
First Position		T	C	A	G	Third Position
	T	TTT Phe [F]	TCT Ser [S]	TAT Tyr [Y]	TGT Cys [C]	T
		TTC Phe [F]	TCC Ser [S]	TAC Tyr [Y]	TGC Cys [C]	C
		TTA Leu [L]	TCA Ser [S]	TAA Ter [end]	TGA Ter [end]	A
		TTG Leu [L]	TCG Ser [S]	TAG Ter [end]	TGG Trp [W]	G
	C	CTT Leu [L]	CCT Pro [P]	CAT His [H]	CGT Arg [R]	T
		CTC Leu [L]	CCC Pro [P]	CAC His [H]	CGC Arg [R]	C
		CTA Leu [L]	CCA Pro [P]	CAA Gln [Q]	CGA Arg [R]	A
		CTG Leu [L]	CCG Pro [P]	CAG Gln [Q]	CGG Arg [R]	G
	A	ATT Ile [I]	ACT Thr [T]	AAT Asn [N]	AGT Ser [S]	T
		ATC Ile [I]	ACC Thr [T]	AAC Asn [N]	AGC Ser [S]	C
		ATA Ile [I]	ACA Thr [T]	AAA Lys [K]	AGA Arg [R]	A
		ATG Met [M]	ACG Thr [T]	AAG Lys [K]	AGG Arg [R]	G
	G	GTT Val [V]	GCT Ala [A]	GAT Asp [D]	GGT Gly [G]	T
		GTC Val [V]	GCC Ala [A]	GAC Asp [D]	GGC Gly [G]	C
		GTA Val [V]	GCA Ala [A]	GAA Glu [E]	GGA Gly [G]	A
		GTG Val [V]	GCG Ala [A]	GAG Glu [E]	GGG Gly [G]	G

6th dragon curve folding

Dragon 6: ratio Dark/Light = (3 - Phi) / 2

"1" Attractor: "Odd" Folding

"(3 - Phi) / 2" Attractor: "Even" Folding

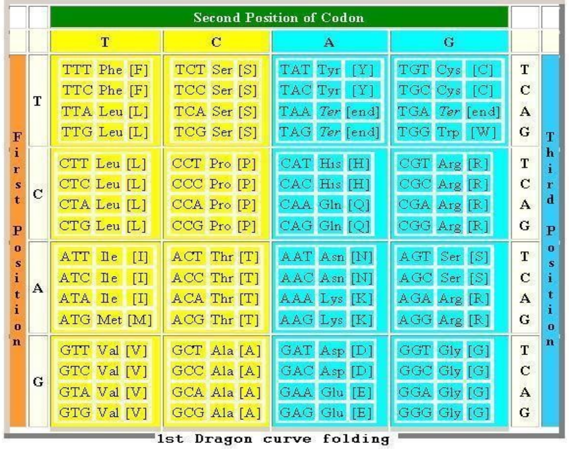
-IV- Extending 2 « attractors »: « 1 » and « (3-Phi)/2 »T+A and C+G nucleotides proportions

However, the most remarkable fact is the presence of both attractors «(3-Phi)/ 2» and «1» at the global T C A G nucleotide scale.

Effectively, attractor «1» corresponds to *Chargaff*'s second rule T=A and C=G which we have just demonstrated here.

The second attractor «(3-Phi)/2» is seen when we compute ratios T/C=1.447808424, A/G=1.444633555 and (T+A)/(C+G)=1.446220557.

When you compare these results with those of CODON POPULATIONS, they are extremely close to the ideal value 2 / (3-Phi) =1.447213595.



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	T	C	A	G	
T	TTT Phe [F]	TCT Ser [S]	TAT Tyr [Y]	TGT Cys [C]	T
	TTC Phe [F]	TCC Ser [S]	TAC Tyr [Y]	TGC Cys [C]	C
	TTA Leu [L]	TCA Ser [S]	TAA *Ter* [end]	TGA *Ter* [end]	A
	TTG Leu [L]	TCG Ser [S]	TAG *Ter* [end]	TGG Trp [W]	G
C	CTT Leu [L]	CCT Pro [P]	CAT His [H]	CGT Arg [R]	T
	CTC Leu [L]	CCC Pro [P]	CAC His [H]	CGC Arg [R]	C
	CTA Leu [L]	CCA Pro [P]	CAA Gln [Q]	CGA Arg [R]	A
	CTG Leu [L]	CCG Pro [P]	CAG Gln [Q]	CGG Arg [R]	G
A	ATT Ile [I]	ACT Thr [T]	AAT Asn [N]	AGT Ser [S]	T
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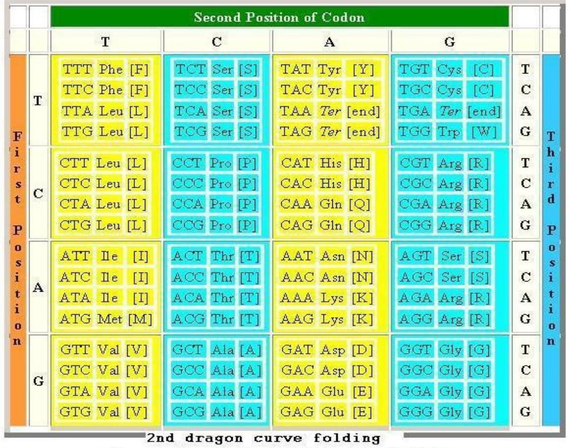
	ATA Ile [I]	ACA Thr [T]	AAA Lys [K]	AGA Arg [R]	A
	ATG Met [M]	ACG Thr [T]	AAG Lys [K]	AGG Arg [R]	G
G	GTT Val [V]	GCT Ala [A]	GAT Asp [D]	GGT Gly [G]	T
	GTC Val [V]	GCC Ala [A]	GAC Asp [D]	GGC Gly [G]	C
	GTA Val [V]	GCA Ala [A]	GAA Glu [E]	GGA Gly [G]	A
	GTG Val [V]	GCG Ala [A]	GAG Glu [E]	GGG Gly [G]	G

1st Dragon curve folding

Dragon 1: ratio Dark/Light = 1



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	TTA Leu [L]	TCA Ser [S]	TAA *Ter* [end]	TGA *Ter* [end]	A
	TTG Leu [L]	TCG Ser [S]	TAG *Ter* [end]	TGG Trp [W]	G
C	CTT Leu [L]	CCT Pro [P]	CAT His [H]	CGT Arg [R]	T
	CTC Leu [L]	CCC Pro [P]	CAC His [H]	CGC Arg [R]	C
	CTA Leu [L]	CCA Pro [P]	CAA Gln [Q]	CGA Arg [R]	A
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	ATC Ile [I]	ACC Thr [T]	AAC Asn [N]	AGC Ser [S]	C
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	ATG Met [M]	ACG Thr [T]	AAG Lys [K]	AGG Arg [R]	G
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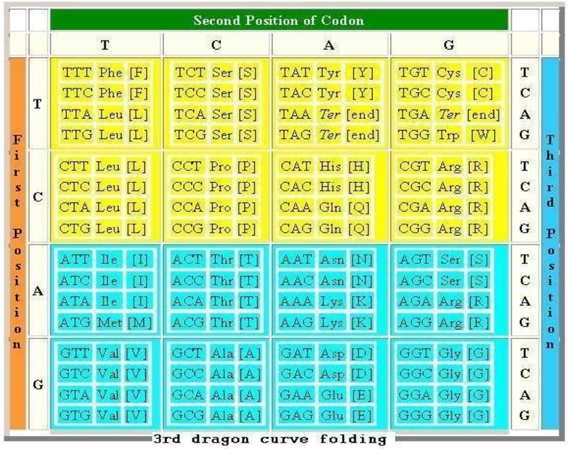
	GTC Val [V]	GCC Ala [A]	GAC Asp [D]	GGC Gly [G]	C
	GTA Val [V]	GCA Ala [A]	GAA Glu [E]	GGA Gly [G]	A
	GTG Val [V]	GCG Ala [A]	GAG Glu [E]	GGG Gly [G]	G

2nd dragon curve folding

Dragon 2: ratio Dark/Light = (3 - Phi) / 2



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	TTG Leu [L]	TCG Ser [S]	TAG *Ter* [end]	TGG Trp [W]	G
C	CTT Leu [L]	CCT Pro [P]	CAT His [H]	CGT Arg [R]	T
	CTC Leu [L]	CCC Pro [P]	CAC His [H]	CGC Arg [R]	C
	CTA Leu [L]	CCA Pro [P]	CAA Gln [Q]	CGA Arg [R]	A
	CTG Leu [L]	CCG Pro [P]	CAG Gln [Q]	CGG Arg [R]	G
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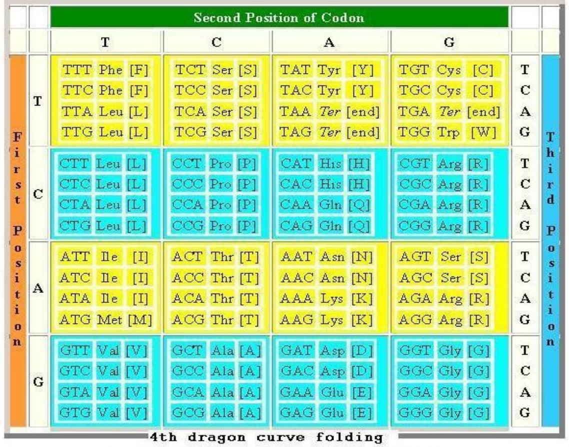
	ATC Ile [I]	ACC Thr [T]	AAC Asn [N]	AGC Ser [S]	C
	ATA Ile [I]	ACA Thr [T]	AAA Lys [K]	AGA Arg [R]	A
	ATG Met [M]	ACG Thr [T]	AAG Lys [K]	AGG Arg [R]	G
G	GTT Val [V]	GCT Ala [A]	GAT Asp [D]	GGT Gly [G]	T
	GTC Val [V]	GCC Ala [A]	GAC Asp [D]	GGC Gly [G]	C
	GTA Val [V]	GCA Ala [A]	GAA Glu [E]	GGA Gly [G]	A
	GTG Val [V]	GCG Ala [A]	GAG Glu [E]	GGG Gly [G]	G

3rd dragon curve folding

Dragon 3: ratio Dark/Light = 1



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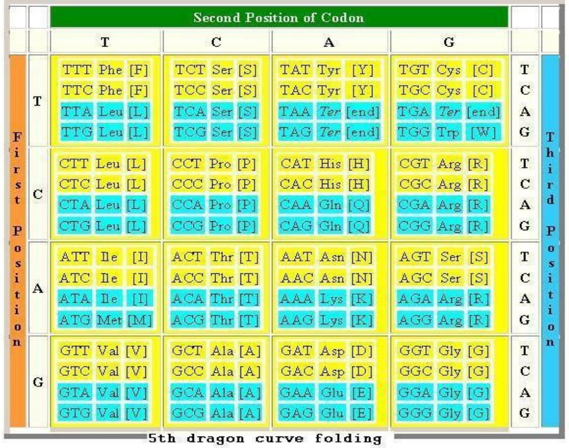
	TTA Leu [L]	TCA Ser [S]	TAA *Ter* [end]	TGA *Ter* [end]	A
	TTG Leu [L]	TCG Ser [S]	TAG *Ter* [end]	TGG Trp [W]	G
C	CTT Leu [L]	CCT Pro [P]	CAT His [H]	CGT Arg [R]	T
	CTC Leu [L]	CCC Pro [P]	CAC His [H]	CGC Arg [R]	C
	CTA Leu [L]	CCA Pro [P]	CAA Gln [Q]	CGA Arg [R]	A
	CTG Leu [L]	CCG Pro [P]	CAG Gln [Q]	CGG Arg [R]	G
A	ATT Ile [I]	ACT Thr [T]	AAT Asn [N]	AGT Ser [S]	T
	ATC Ile [I]	ACC Thr [T]	AAC Asn [N]	AGC Ser [S]	C
	ATA Ile [I]	ACA Thr [T]	AAA Lys [K]	AGA Arg [R]	A
	ATG Met [M]	ACG Thr [T]	AAG Lys [K]	AGG Arg [R]	G
G	GTT Val [V]	GCT Ala [A]	GAT Asp [D]	GGT Gly [G]	T
	GTC Val [V]	GCC Ala [A]	GAC Asp [D]	GGC Gly [G]	C
	GTA Val [V]	GCA Ala [A]	GAA Glu [E]	GGA Gly [G]	A
	GTG Val [V]	GCG Ala [A]	GAG Glu [E]	GGG Gly [G]	G

4th dragon curve folding

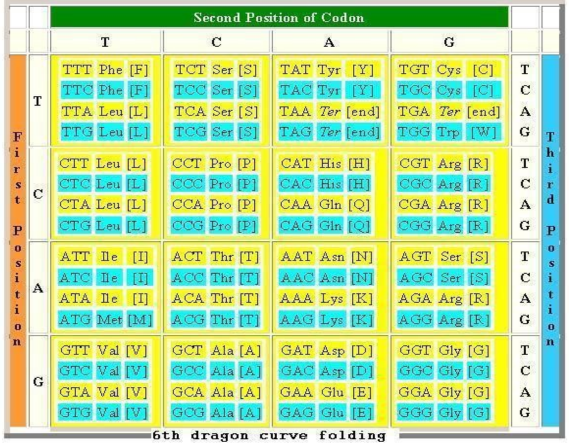
Dragon 4: ratio Dark/Light = (3 - Phi) / 2



First Position	Second Position of Codon				Third Position
	T	C	A	G	
T	TTT Phe [F]	TCT Ser [S]	TAT Tyr [Y]	TGT Cys [C]	T
	TTC Phe [F]	TCC Ser [S]	TAC Tyr [Y]	TGC Cys [C]	C
	TTA Leu [L]	TCA Ser [S]	TAA *Ter* [end]	TGA *Ter* [end]	A
	TTG Leu [L]	TCG Ser [S]	TAG *Ter* [end]	TGG Trp [W]	G
C	CTT Leu [L]	CCT Pro [P]	CAT His [H]	CGT Arg [R]	T
	CTC Leu [L]	CCC Pro [P]	CAC His [H]	CGC Arg [R]	C
	CTA Leu [L]	CCA Pro [P]	CAA Gln [Q]	CGA Arg [R]	A
	CTG Leu [L]	CCG Pro [P]	CAG Gln [Q]	CGG Arg [R]	G
A	ATT Ile [I]	ACT Thr [T]	AAT Asn [N]	AGT Ser [S]	T
	ATC Ile [I]	ACC Thr [T]	AAC Asn [N]	AGC Ser [S]	C
	ATA Ile [I]	ACA Thr [T]	AAA Lys [K]	AGA Arg [R]	A
	ATG Met [M]	ACG Thr [T]	AAG Lys [K]	AGG Arg [R]	G
G	GTT Val [V]	GCT Ala [A]	GAT Asp [D]	GGT Gly [G]	T
	GTC Val [V]	GCC Ala [A]	GAC Asp [D]	GGC Gly [G]	C
	GTA Val [V]	GCA Ala [A]	GAA Glu [E]	GGA Gly [G]	A
	GTG Val [V]	GCG Ala [A]	GAG Glu [E]	GGG Gly [G]	G

5th dragon curve folding

Dragon 5: ratio Dark/Light = 1



First Position	Second Position of Codon				Third Position
	T	C	A	G	
T	TTT Phe [F]	TCT Ser [S]	TAT Tyr [Y]	TGT Cys [C]	T
	TTC Phe [F]	TCC Ser [S]	TAC Tyr [Y]	TGC Cys [C]	C
	TTA Leu [L]	TCA Ser [S]	TAA *Ter* [end]	TGA *Ter* [end]	A
	TTG Leu [L]	TCG Ser [S]	TAG *Ter* [end]	TGG Trp [W]	G
C	CTT Leu [L]	CCT Pro [P]	CAT His [H]	CGT Arg [R]	T
	CTC Leu [L]	CCC Pro [P]	CAC His [H]	CGC Arg [R]	C
	CTA Leu [L]	CCA Pro [P]	CAA Gln [Q]	CGA Arg [R]	A
	CTG Leu [L]	CCG Pro [P]	CAG Gln [Q]	CGG Arg [R]	G
A	ATT Ile [I]	ACT Thr [T]	AAT Asn [N]	AGT Ser [S]	T
	ATC Ile [I]	ACC Thr [T]	AAC Asn [N]	AGC Ser [S]	C
	ATA Ile [I]	ACA Thr [T]	AAA Lys [K]	AGA Arg [R]	A
	ATG Met [M]	ACG Thr [T]	AAG Lys [K]	AGG Arg [R]	G
G	GTT Val [V]	GCT Ala [A]	GAT Asp [D]	GGT Gly [G]	T
	GTC Val [V]	GCC Ala [A]	GAC Asp [D]	GGC Gly [G]	C
	GTA Val [V]	GCA Ala [A]	GAA Glu [E]	GGA Gly [G]	A
	GTG Val [V]	GCG Ala [A]	GAG Glu [E]	GGG Gly [G]	G

6th dragon curve folding

Dragon 6: ratio Dark/Light = (3 - Phi) / 2

"1" Attractor: "Odd" Folding

"(3 - Phi) / 2" Attractor: "Even" Folding

-V- Towards a codon level generalization of *Chargaff*'s second rule.

Chargaff's second parity rule appears to be extended from the nucleotide-level to populations of codon triplets, in the case of whole single-stranded Human genome DNA.
A kind of "codon-level second Chargaff's parity rule" is proposed as follows:

Codon populations where 1st base position is T are identical to codon populations where 3rd base position is A:
« % codons Twx ~ % codons yzA » (where Twx and yzA are mirror codons i.e TCG and CGA).
Codon populations where 1st base position is C are identical to codon populations where 3rd base position is G:
« % codons Cwx ~ % codons yzG » (where Cwx and yzG are mirror codons i.e CTA and TAG).
Codon populations where 2nd base position is T are identical to codon populations where 2nd base position is A:
« % codons wTx ~ % codons yAz » (where wTx and yAz are mirror codons i.e CTG and CAG).
Codon populations where 2nd base position is C are identical to codon populations where 2nd base position is G:
« % codons wCx ~ % codons yGz » (where wCx and yGz are mirror codons i.e TCT and AGA).
Codon populations where 3rd base position is T are identical to codon populations where 1st base position is A:
« % codons wxT ~ % codons Ayz » (where wxT and Ayz are mirror codons i.e CTT and AAG).
Codon populations where 3rd base position is C are identical to codon populations where 1st base position is G:
« % codons wxC ~ % codons Gyz » (where wxC and Gyz are mirror codons i.e GGC and GCC).

WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф…

-I- Summary:

- Now we run individually on the single stranded DNA of each human genome chromosome the same analysis described in *"DRAGON fractal paper folding curve"* fine-tuned around the ***"Golden ratio"*** (*"Codon Populations in single-stranded DNA Whole Human Genome Are fractal and fine-tuned by the Golden Ratio 1618"* , 2010, Interdisciplinary Science).
- We recall that ATTRACTOR « 1 » is provided by computing TC/AG bases populations.
- Exp: 1st codons reading frame:

T= 841214808   C=581026325 A=839827524 G=581342944

(T+A)÷(C+G)

1.446220557

(T+C)÷(A+G)

1.000753368

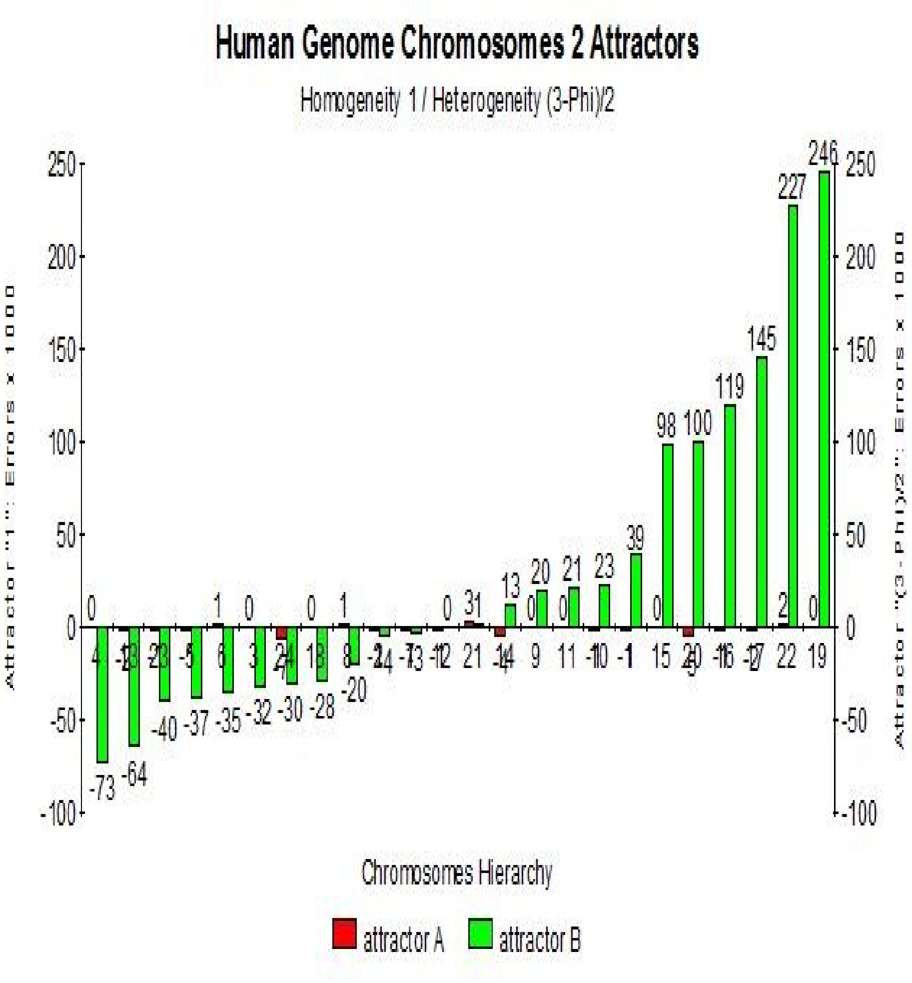
•And ATTRACTOR « (3-Phi)/2 » is provided by computing TA/CG bases populations.

•

•Curiously the « 1 » attractor is homogeneous and conserved in the case of the 24 chromosomes.

•

•Contrarly, the « (3-Phi)/2 » appears to be highly heterogeneous.



WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE

BASED ON л AND THE GOLDEN RATIO ф...

-II- Results:

ANALYSING CODON POPULATIONS – Generalizing Attractors « 1 » and « (3-Phi)/2 » from whole human génome to the 24 individual chromosomes:

CHROMOSOME / 6 cases: dragon1 to dragon6 / The 2 ERRORS vs attractors « 1 »(dragon1) and « (3-Phi)/ 2 » (dragon2)

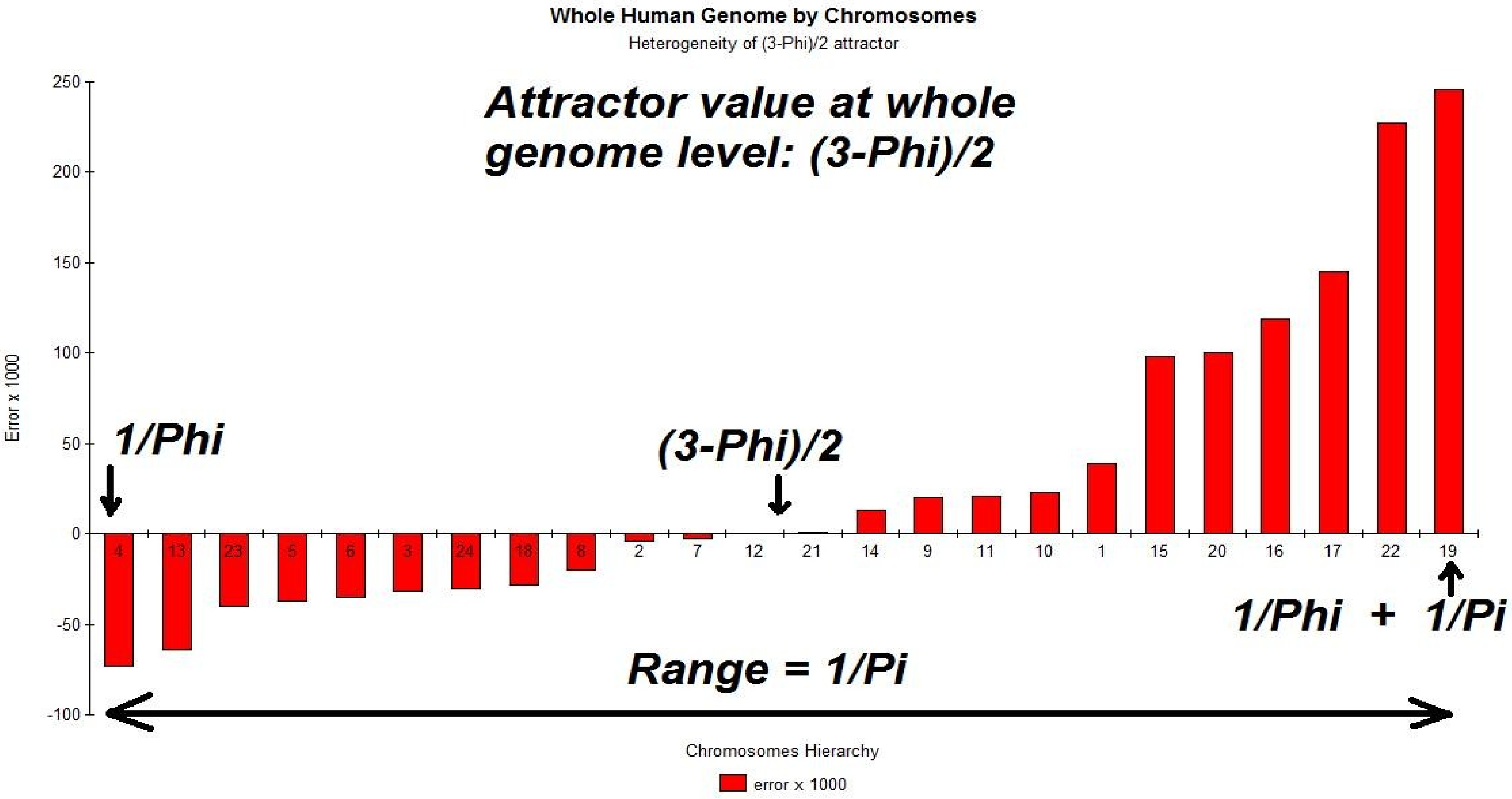
4	**0.9998414507**	**0.6182846465**	**0.9998417076**	0.6182848147	0.999841258	0.6182847866	**-0.0001585493105**	**-0.07269835919**
13	0.9982668844	0.6265479796	0.9982671351	0.6265483118	0.9982668008	0.6265479242	-0.001733115626	-0.06443502604
23	0.9985556692	0.6514329116	0.998556044	0.6514330944	0.9985553212	0.6514331675	-0.00144433077	-0.03955009401
5	0.9989193956	0.6538648891	0.9989195307	0.6538649353	0.9989193056	0.6538649507	-0.001080604355	-0.03711811656
6	1.000525858	0.6555684149	1.000526217	0.6555686115	1.000525762	0.6555683821	0.0005258577024	-0.03541459078
3	0.9997091032	0.6580066635	0.9997092677	0.65800672	0.9997090621	0.6580067483	-0.0002908967547	-0.03297634215
24	0.9931744751	0.6591081629	0.9931764092	0.6591089446	0.9931727023	0.6591088329	-0.00682552488	-0.03187484278
18	1.000012833	0.6607156383	1.000013101	0.66071586	1.000012833	0.6607156753	0.00001283261832	-0.03026736733
8	1.000720369	0.6709809502	1.00072065	0.670981166	1.000720116	0.6709810875	0.000720368643	-0.02000205546
2	0.9990576615	0.6729417129	0.9990578802	0.6729418778	0.9990572914	0.6729417246	-0.000942338463	-0.01804129279
7	0.9988696848	0.6866614322	0.9988699173	0.6866616713	0.9988693231	0.6866615793	-0.001130315215	-0.004321573483
12	**0.999372296**	**0.688058808**	**0.9993724808**	0.6880586324	0.9993719881	0.6880589617	**-0.000627703979**	**-0.002924197639**
21	1.003369337	0.6914042722	1.003369337	0.6914041879	1.003369337	0.6914045252	0.003369336504	0.0004212665743
14	0.9963855347	0.6915117446	0.9963856261	0.6915117118	0.996385489	0.6915116133	-0.00361446528	0.0005287389482
9	0.9999354134	0.7037292009	0.9999365895	0.7037303055	0.9999341334	0.7037302302	-0.00006458664014	0.01274619523
11	1.000343902	0.7112162565	1.000343993	0.7112164354	1.000343474	0.7112165025	0.0003439015863	0.02023325083
10	0.9992210126	0.7116203869	0.9992218353	0.7116209006	0.9992204032	0.71162099	-0.000778987353	0.02063738129
1	0.9988587539	0.7144457101	0.9988596375	0.714446307	0.998857708	0.7144462407	-0.001141246105	0.02346270441
15	1.000152264	0.7302638674	1.000152806	0.7302640148	1.000151624	0.7302641622	0.0001522643938	0.03928086178
20	0.994565246	0.7893931557	0.9945655138	0.7893936406	0.9945649782	0.7893933712	-0.005434753969	0.09841015006
16	0.9986619885	0.8100695879	0.9986625382	0.8100697109	0.9986616887	0.8100699568	-0.001338011494	0.1190865823
17	0.9980299988	0.8357433305	0.9980305641	0.8357437209	0.9980295363	0.8357436341	-0.001970001184	0.1447603248
22	1.002325596	0.917982601	1.002326646	0.9179838861	1.002324429	0.9179833506	0.002325595764	0.2269995954
19	**0.9997711858**	**0.9366474189**	**0.9997715443**	0.9366476878	0.9997710425	0.9366478223	**-0.0002288141751**	**0.2456644133**

WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф...

Analysing Attractor « (3-Phi)/ 2 » reveals HETEROGENEITY, SYMMETRY and NUMERICAL л and Φ STRUCTURES

<u>-III- Chromosomes numerical network classification scale:</u>

<u>Evidence of 2 limits: 1/ Phi (chr4) and (1/ Phi + 1/ Pi) chr19.</u>



Attractor value at whole genome level: (3-Phi)/2

1/Phi

(3-Phi)/2

1/Phi + 1/Pi

Range = 1/Pi

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Analysing Attractor « (3-Phi)/ 2 » reveals HETEROGENEITY, SYMMETRY and NUMERICAL л and Φ STRUCTURES

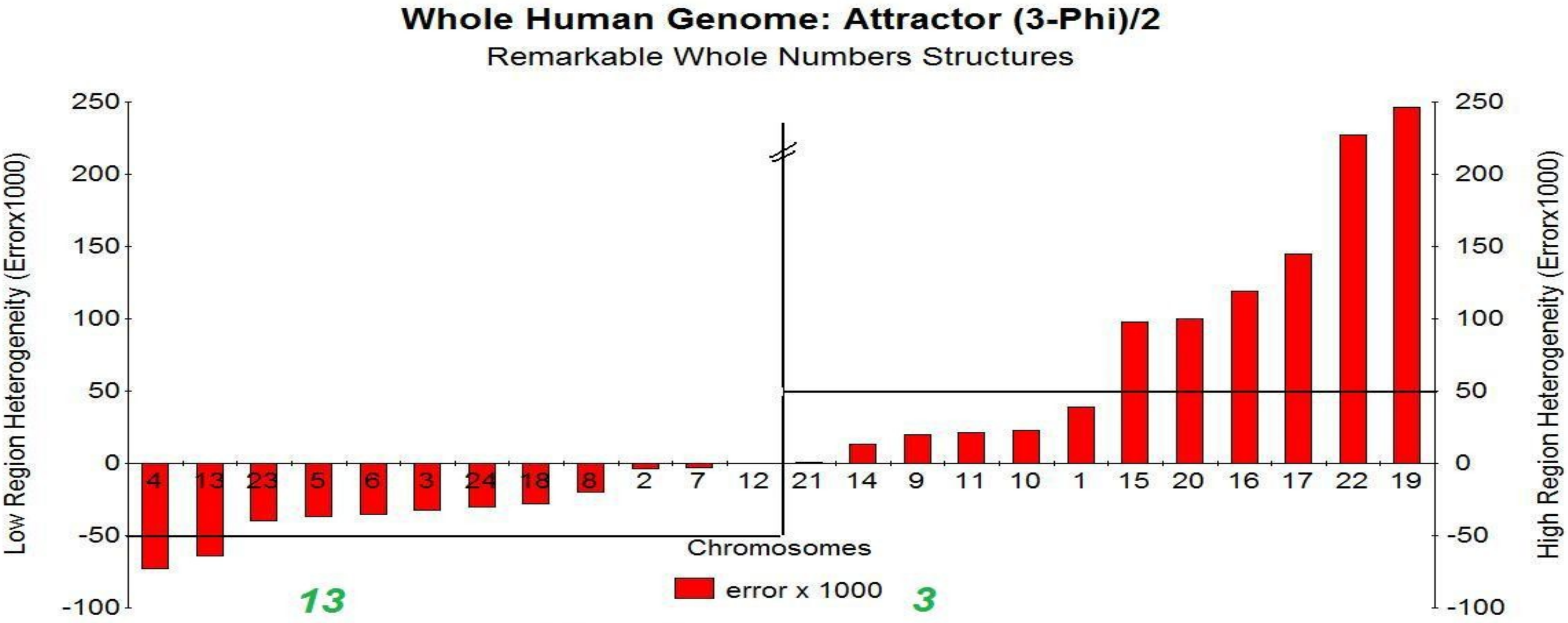
-III- Chromosomes numerical network classification scale: Evidence of 2 limits: 1/ Phi (chr4) and (1/ Phi + 1/ Pi) chr19.

Chromosome	Remarkable value	Ideal Real value	Measured Real value	Error
Low level: chromosome: 4	1/Phi	0.6180339887	0.6182846465	0.0002506578
Medium level chromosome 12	(3-Phi)/2	0.6909830056	0.6914042722	0.0004212666
WHOLE GENOME	(3-Phi)/2	0.6909830056	0.6914573163	0.0004743107
Medium level chromosome 21	(3-Phi)/2	0.6909830056	0.6915117446	0.000528739
High level: chromosome: 19	1/Phi + 1/Pi	0.9363438749	0.9366474189	¯ 0.000303544
Scope of variability	1/Pi	0.3183098862	0.3183627724	¯ 0.0000528862

WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф...

Analysing Attractor « (3-Phi)/ 2 » reveals HETEROGENEITY, SYMMETRY and NUMERICAL л and ɸ STRUCTURES

-IV- Chromosomes network classification scale: STRUCTURE CHARACTERIZATION.



13 3

12.99935 *Whole Genome* 2.99586

---

4 13 *2 low and 2 high* 3.00089 22 19

15.000021 *1/4 genome 6 high* 15 20 16 17 22 19

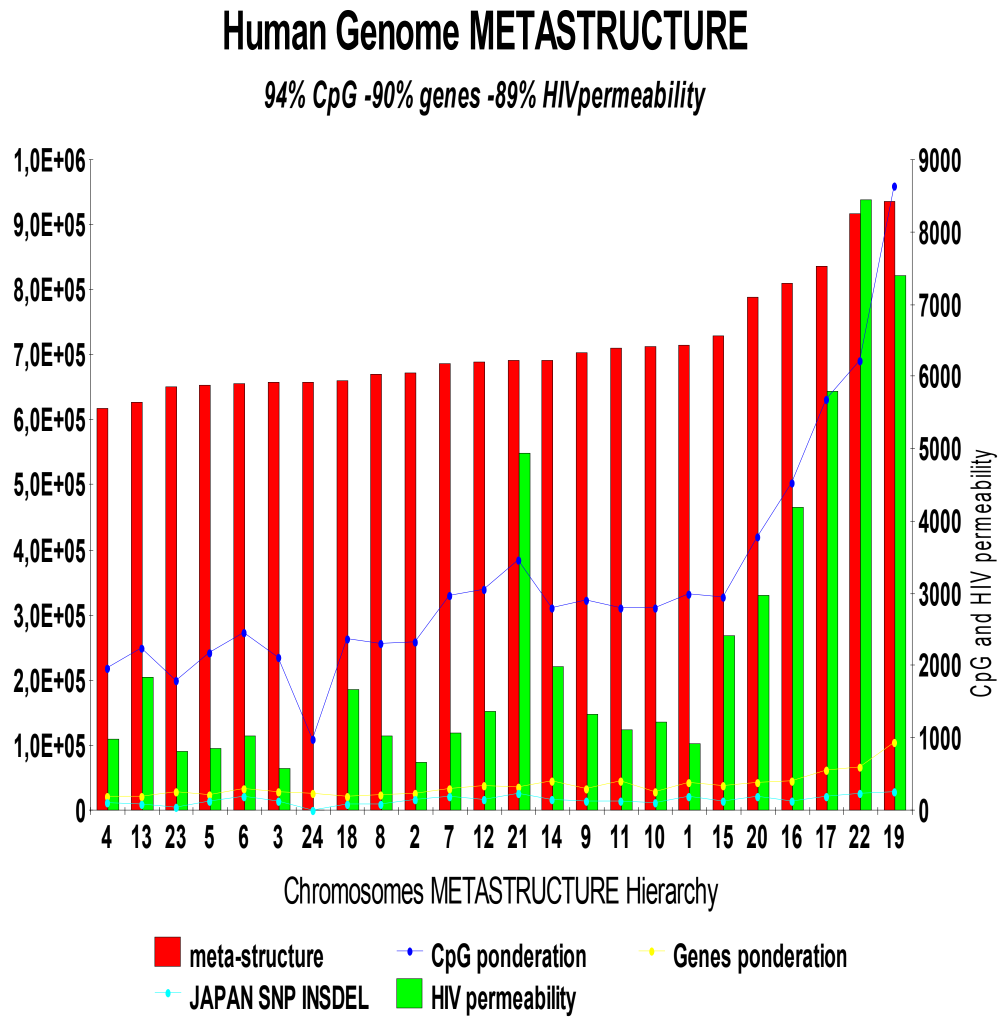
4 13 *1/3 genome* *2 low and 6 high* 2.90099 15 20 16 17 22 19

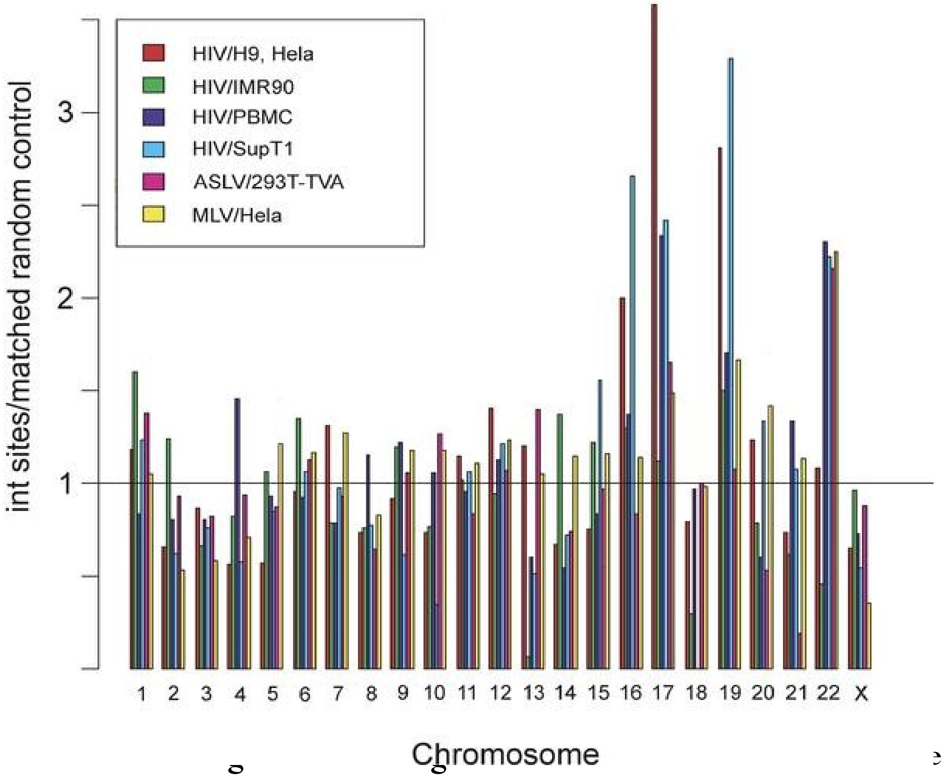
12.49995 *half genome 12 high* 21 14 9 11 10 1 15 20 16 17 22 19

WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф...

-V- CHROMOSOMES META-STRUCTURE IS 89% CORRELATED WITH CHROMOSOMES PERMEABILITY TO INTRUSION OF RETROVIRUSES...

A functionality of this fine-tuned structure appears: the structure is **90%** correlated with the density of genes per chromosome from the Human Genome project. <u>It is **89%** correlated with the chromosome's permeability to intrusion by retroviruses like HIV, **94%** with CpG density </u>Mitchell et al 1. Mitchell RS, Beitzel BF, Schroder AR, Shinn P, Chen H, et al. (2004) Retroviral DNA Integration :ASLV, HIV, and MLV Show Distinct Target Site Preferences. PLoS Biol 2(8) : e234.





WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф...

-VI- CHROMOSOMES META-STRUCTURE IS 90% CORRELATED WITH GENES DENSITY BY CHROMOSOMES (HUMAN GENOME PROJECT)..

A functionality of this fine-tuned

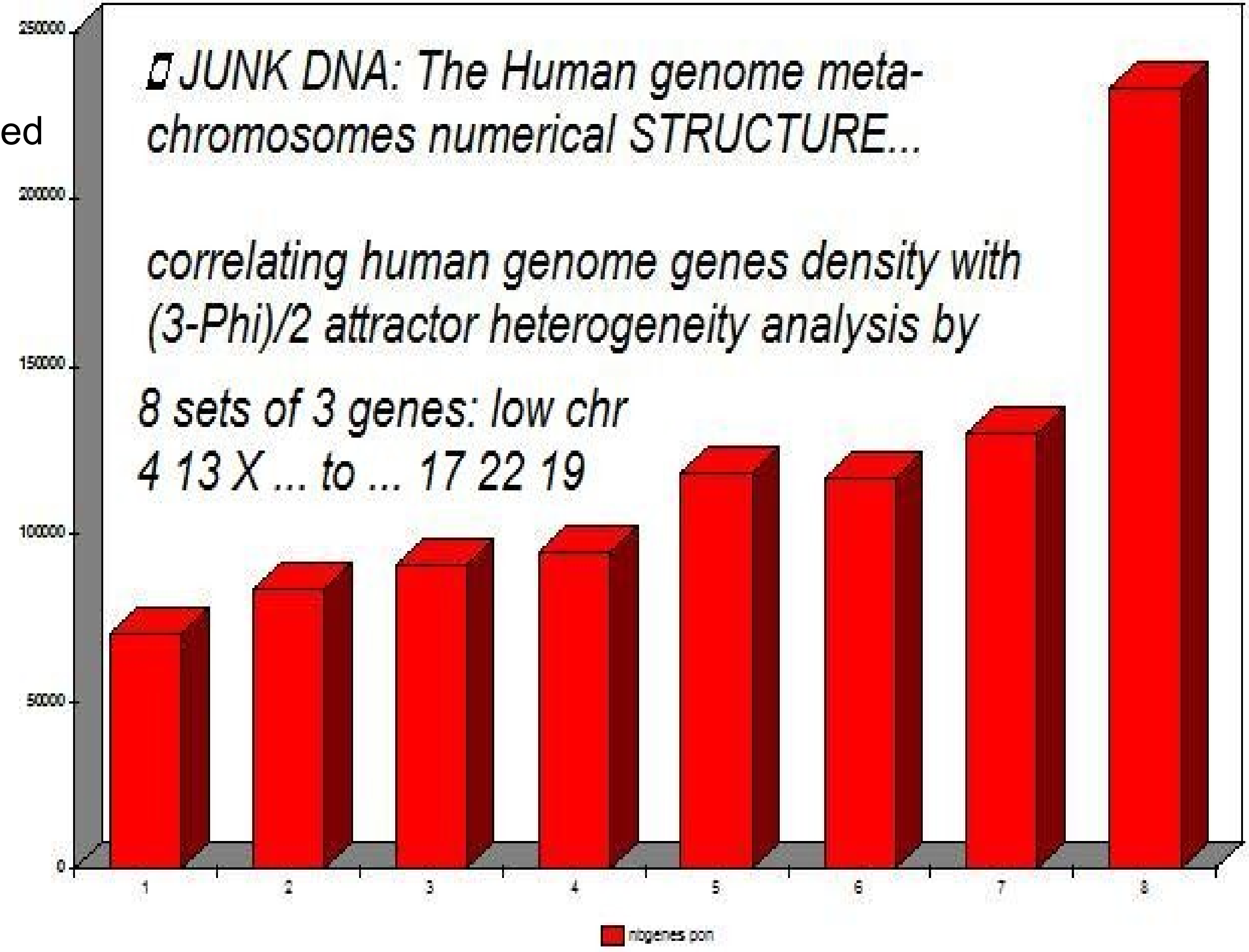
structure appears:

the structure is **90.91%** correlated

with the density of genes

per chromosome from the

Human Genome project.



◘ JUNK DNA: The Human genome meta-chromosomes numerical STRUCTURE...

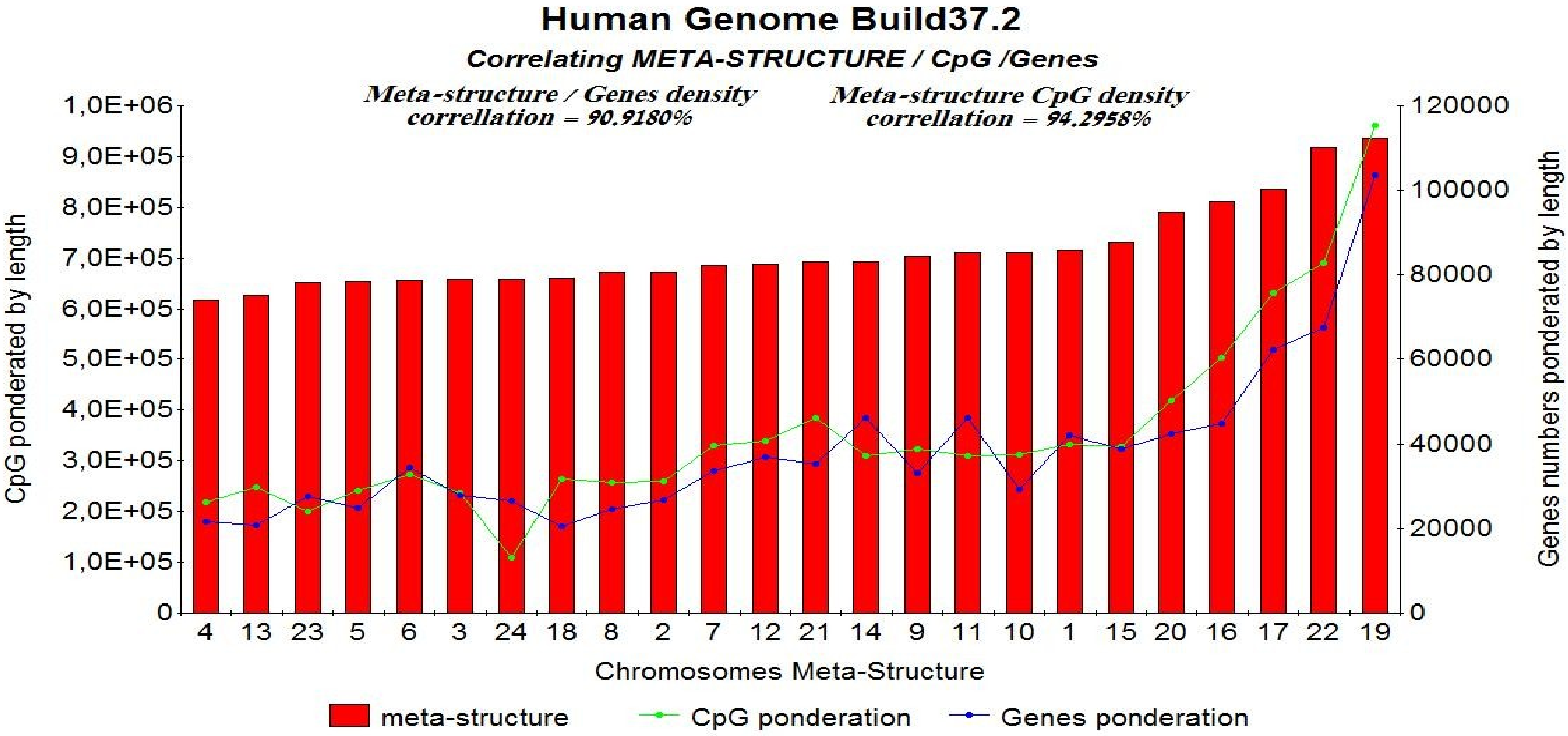
correlating human genome genes density with (3-Phi)/2 attractor heterogeneity analysis by

8 sets of 3 genes: low chr
4 13 X ... to ... 17 22 19

WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф...

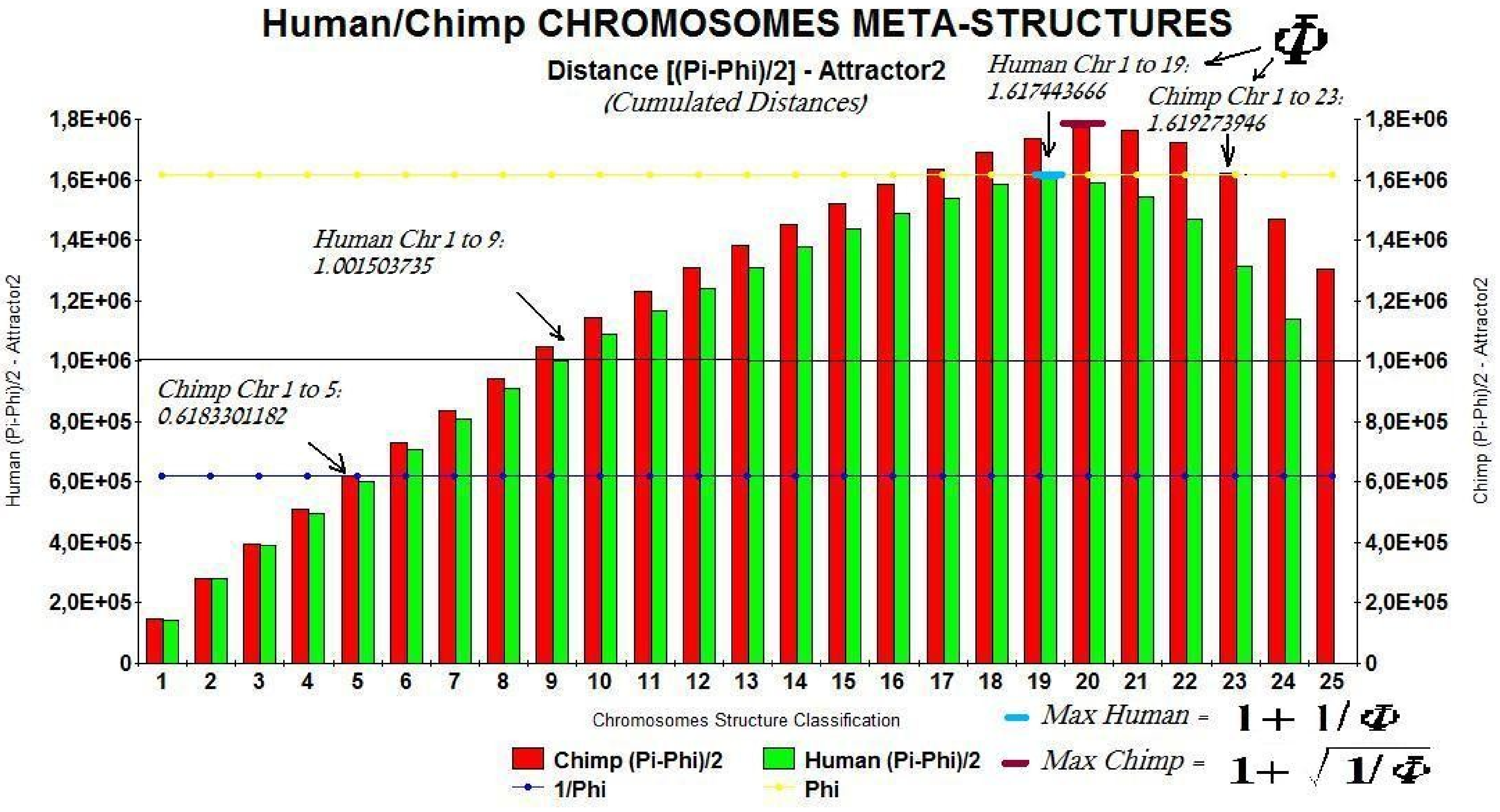
-VII- CHROMOSOMES META-STRUCTURE IS 94% CORRELATED WITH CpG DENSITY BY CHROMOSOMES ...

A functionality of this fine-tuned structure appears: the structure is **90%** correlated with the density of genes per chromosome from the Human Genome project. It is **89%** correlated with the chromosome's permeability to intrusion by retroviruses like HIV, **94%** with CpG density



WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф...

-VIII- « INTEGRATING » the meta strucure (cumulating distances) reveals a maximum=Phi (1.618)... in both cases of HUMAN and CHIMP genomes!



Human/Chimp CHROMOSOMES META-STRUCTURES

Distance [(Pi-Phi)/2] - Attractor2

(Cumulated Distances)

Human Chr 1 to 19: 1.617443666

Chimp Chr 1 to 23: 1.619273946

Human Chr 1 to 9: 1.001503735

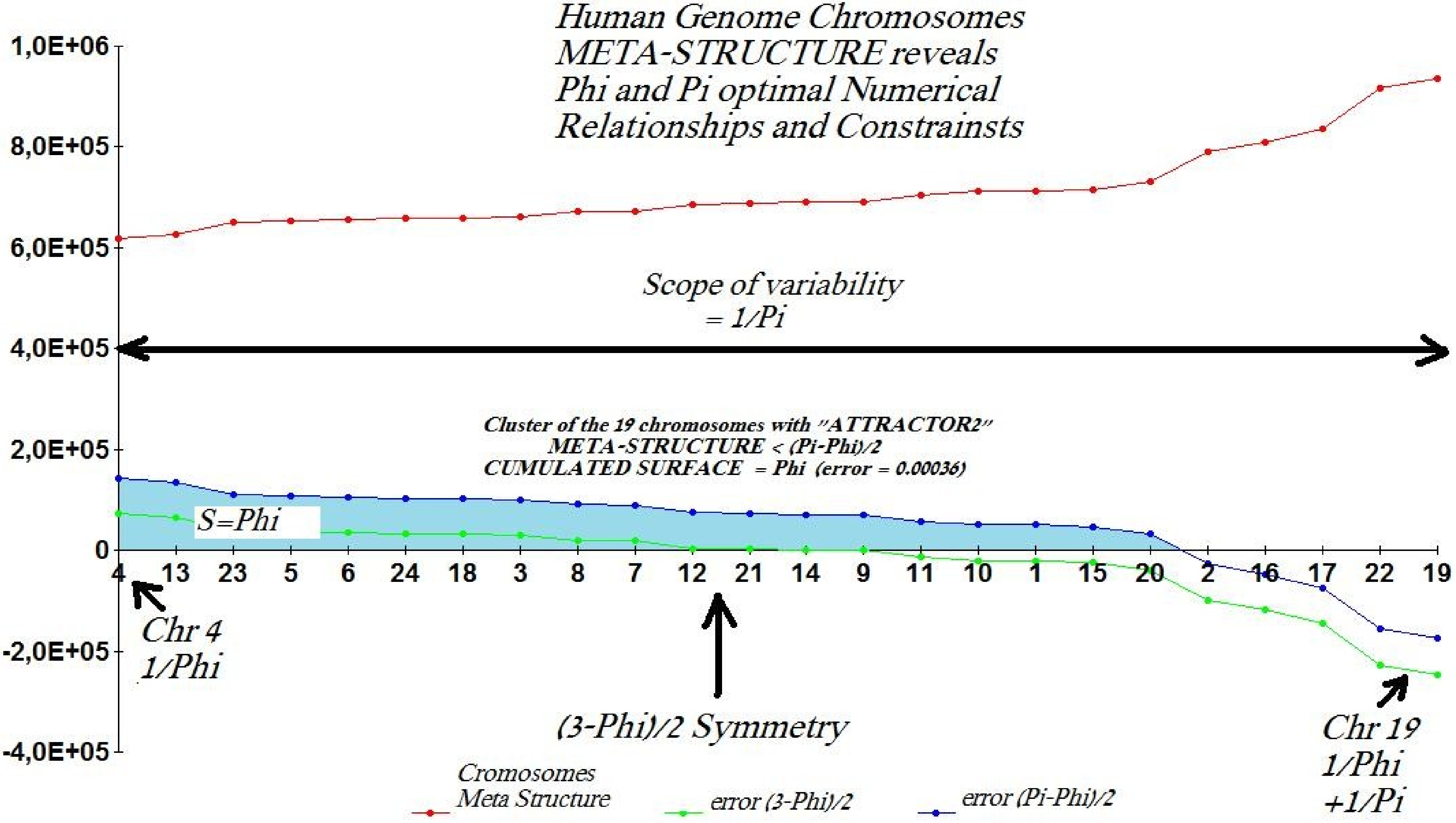
Chimp Chr 1 to 5: 0.6183301182

Max Human = $1 + 1/\Phi$

Max Chimp = $1 + \sqrt{1/\Phi}$

WHOLE HUMAN GENOME DECODING NONCODING DNA CODES REVEALS A META-CHROMOSOMES ARCHITECTURE BASED ON л AND THE GOLDEN RATIO ф...

-IX- « 2 order INTEGRATION » of the meta strucure (re-cumulating cumulated distances) reveals a Surface of integration=Phi (1.618)...



Human Genome Chromosomes META-STRUCTURE reveals Phi and Pi optimal Numerical Relationships and Constrainsts

Scope of variability = 1/Pi

Cluster of the 19 chromosomes with "ATTRACTOR2" META-STRUCTURE < (Pi-Phi)/2 CUMULATED SURFACE = Phi (error = 0.00036)

Chr 4 1/Phi

(3-Phi)/2 Symmetry

Chr 19 1/Phi +1/Pi