

Research Staff

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Research Associates and PhD or Master students in our group during the last years

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Alexandros Klimopoulos

Giannis Tsiagkas

Research Interests – general description

Probabilistic and statistical aspects in genome organization – Non-randomness at several length scales.

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Deviations from randomness at the level of nucleotide n -tuplets. Patterns related to the functionality of genomic regions and to global genome structure.

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Deviations from randomness at the “middle” length scale, expressed mainly through clustering of similar nucleotides. Distinction between protein-coding and non-coding functionalities.

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Long range correlations and Zipf laws in the genome structure. Power-laws in the distribution of exons and of other genomic functional localizations. Entropic scaling in the study of genomic sequences as an indication of long range order and fractality.

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DNA sequences seen as genomic text – Linguistic features in the genome: redundancy, multiple coding, polarity and asymmetry etc.

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“Conservation laws” at the genome structure. The case of “Chargaff’s 2nd parity rule”. The use

of deviations from this law in the study of genomic dynamics and evolution.

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Evolution at the genomic level. Formulation of minimal evolutionary scenarios compatible with the observed probabilistic features of genomes. Interpretation of the above mentioned probabilistic features either by selectionist or mutationist causality.

Pattern formation in biological systems – Self-organization and evolution.

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Early development – Left-right asymmetries – Mechanisms of activation of Hox genes during limb development.

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Reaction-diffusion systems – Spontaneous symmetry breaking and pattern-formation in systems with feedbacks and non-linear dynamics

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Prebiotic and early evolution as a complex self-organization procedure.

Findings in the field of Computational Genomics

“Word” preference in the genomic text and genome evolution

C

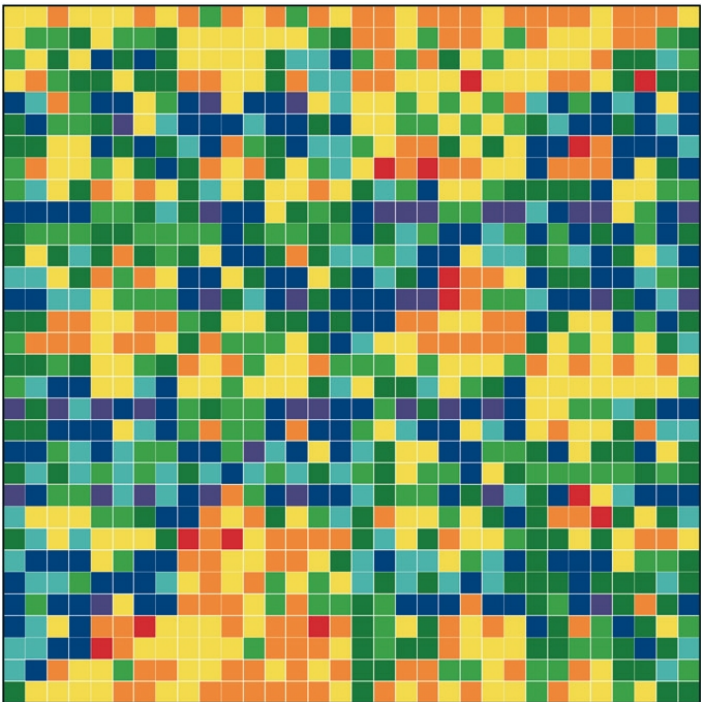
(b)

(a)

G

G

C



TTTAA (dG)

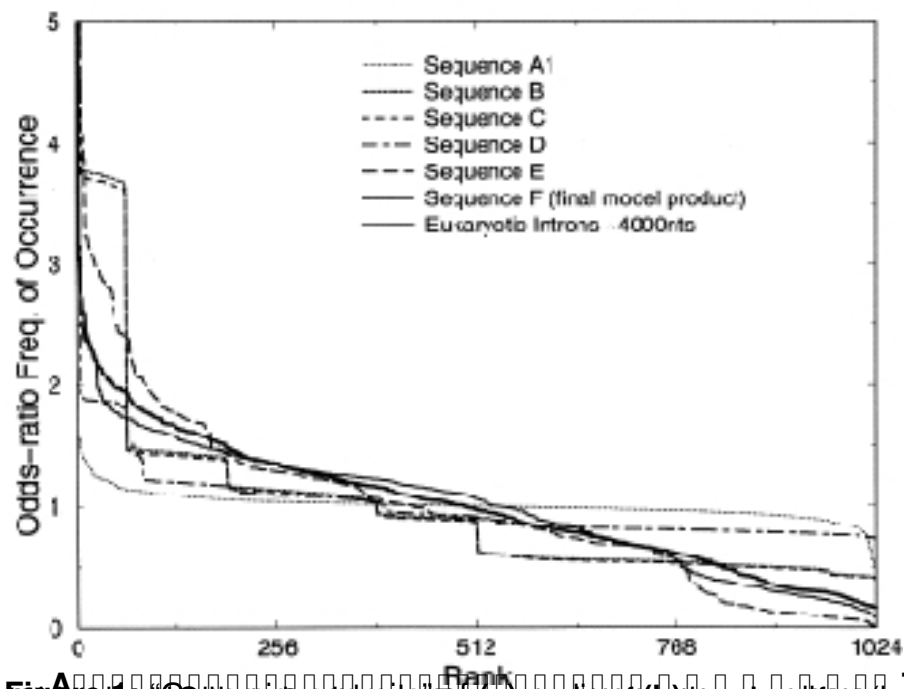
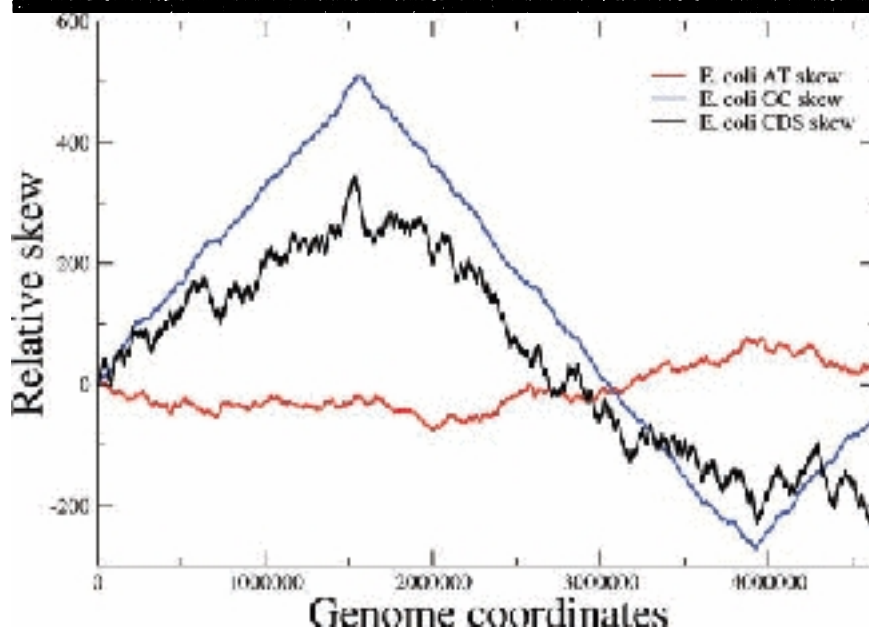


Figure 1: "Genomic coordinates" (x-axis) vs. "Relative skew" (y-axis). The x-axis ranges from 0 to 40,000,000. The y-axis ranges from -200 to 600. The legend indicates three data series: E. coli AT skew (red line), E. coli GC skew (blue line), and E. coli CDS skew (black line). The E. coli GC skew (blue line) shows a prominent peak around 15,000,000 coordinates, reaching a value of approximately 500. The E. coli CDS skew (black line) also shows a peak around 15,000,000 coordinates, reaching a value of approximately 350. The E. coli AT skew (red line) remains relatively flat, fluctuating around zero.



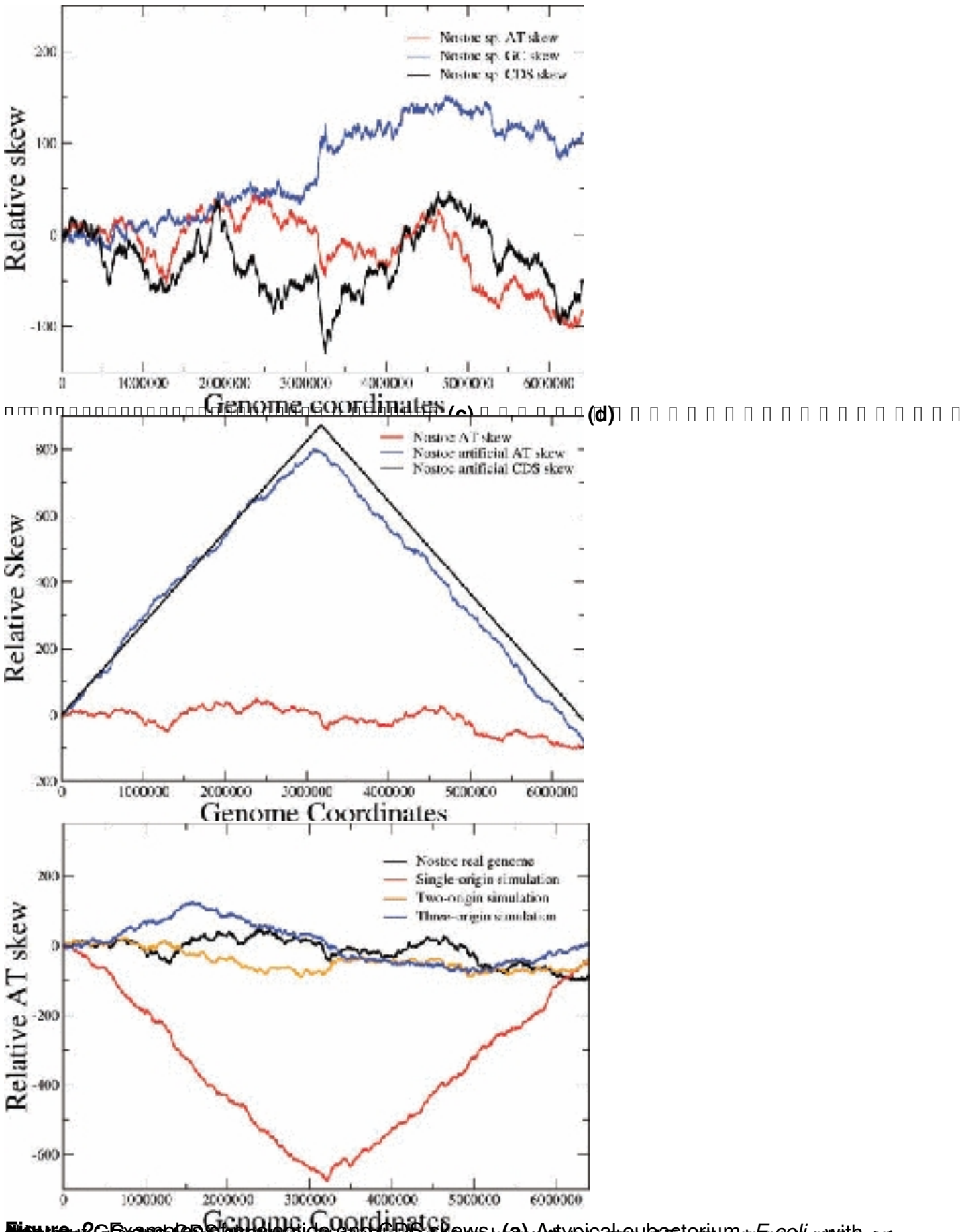
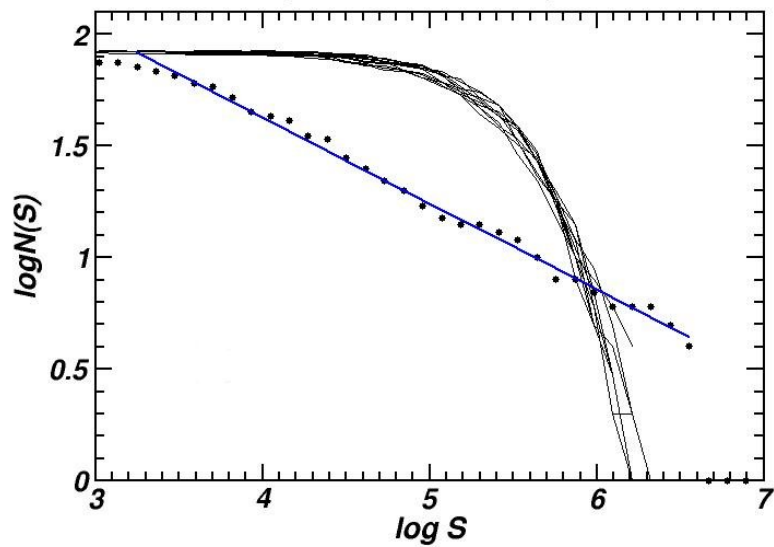
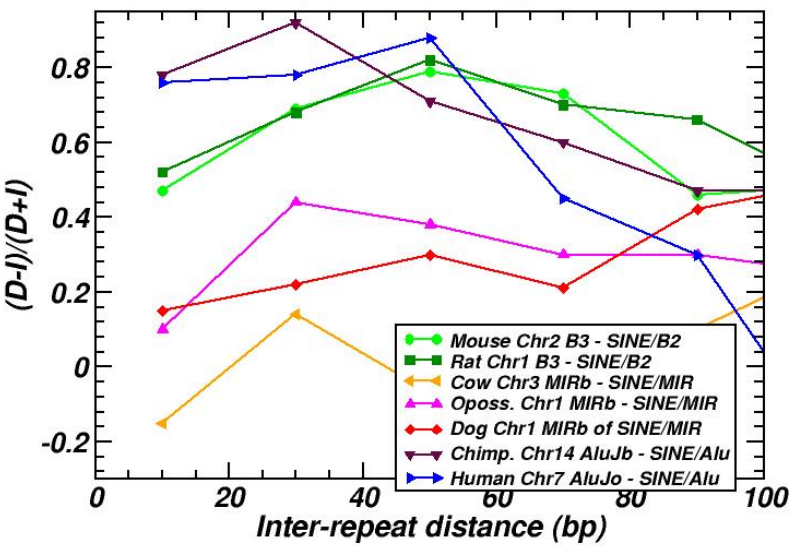


Figure 2. Example of nucleotide and CDS skews. (a) Atypical eubacterium, *E. coli*, with artificial AT skew and artificial GC skew. (b) Atypical eubacterium, *E. coli*, with artificial AT skew and artificial CDS skew. (c) Atypical eubacterium, *E. coli*, with artificial AT skew and artificial GC skew. (d) Atypical eubacterium, *E. coli*, with artificial AT skew and artificial CDS skew. (e) Atypical eubacterium, *E. coli*, with artificial AT skew and artificial GC skew.

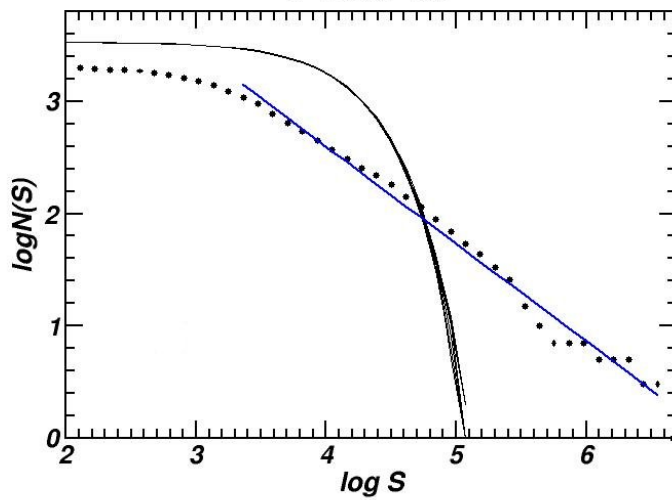
D. melanogaster chr. 3R, DNAREP1_DM - Helitron
Length min. = 200, E=3.31, $\mu=0.38$



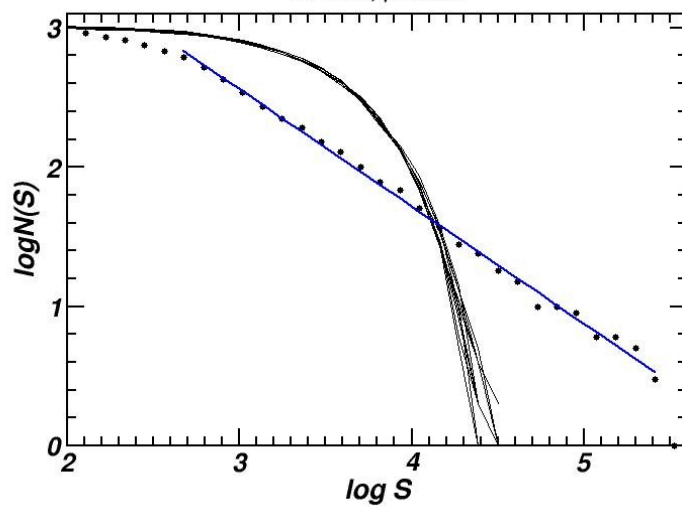
Inverted vs. Direct SINE pairs
Comparison between organisms



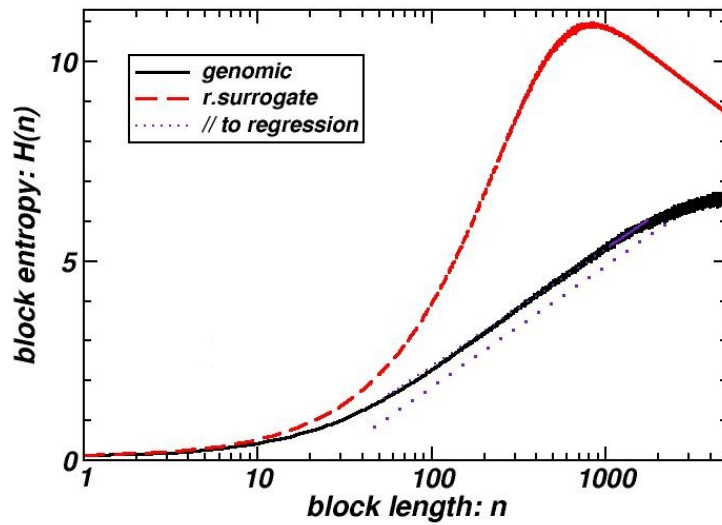
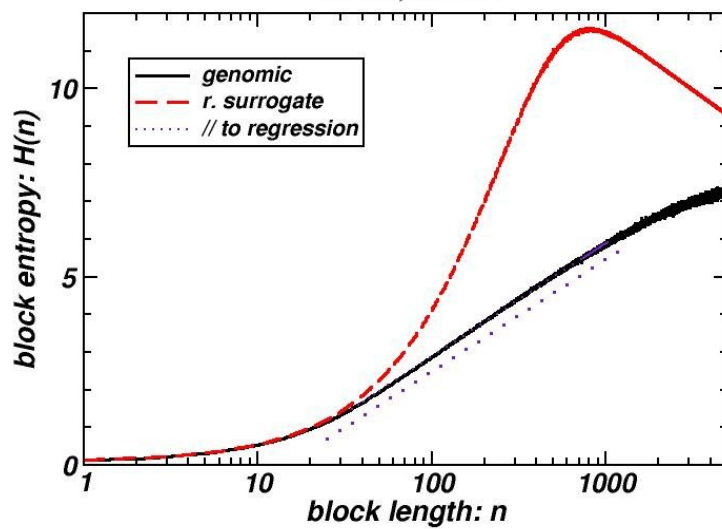
H. sapiens chr. 21, Protein Coding Segments
 $E = 3.17, \mu = 0.87$



G. gallus chr. 22, Protein Coding Segments
 $E = 2.74, \mu = 0.84$

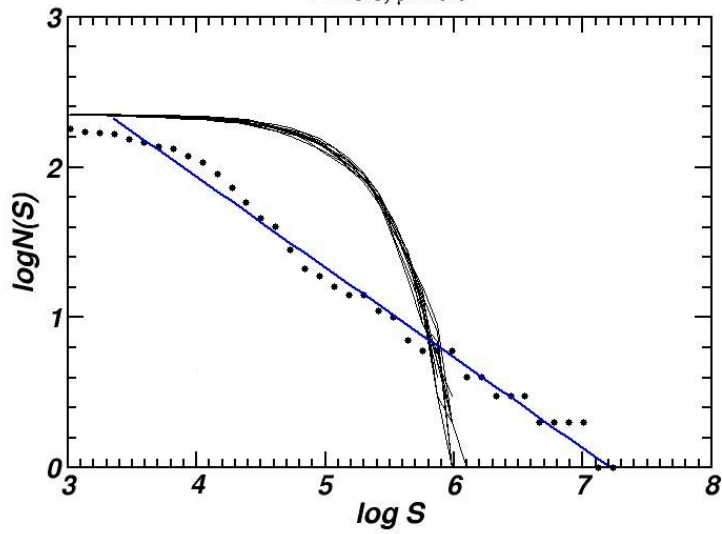


(a) (b)

H. sapiens chr. 20, Protein Coding Segments $E = 2.03, R = 2.38$ ***G. gallus chr. 4, Protein Coding Segments*** $E = 1.94, R = 2.12$ 

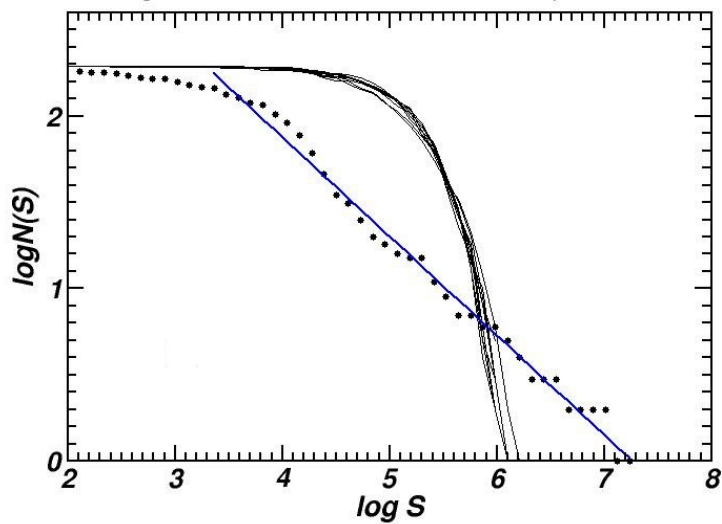
H. sapiens chr.19, CNEs (type: Amniotic)

$E = 3.8, \mu = 0.6$



H. sapiens chr.19, CNEs (type: Amniotic)

genes and flanks are masked; $E = 3.9, \mu = 0.57$



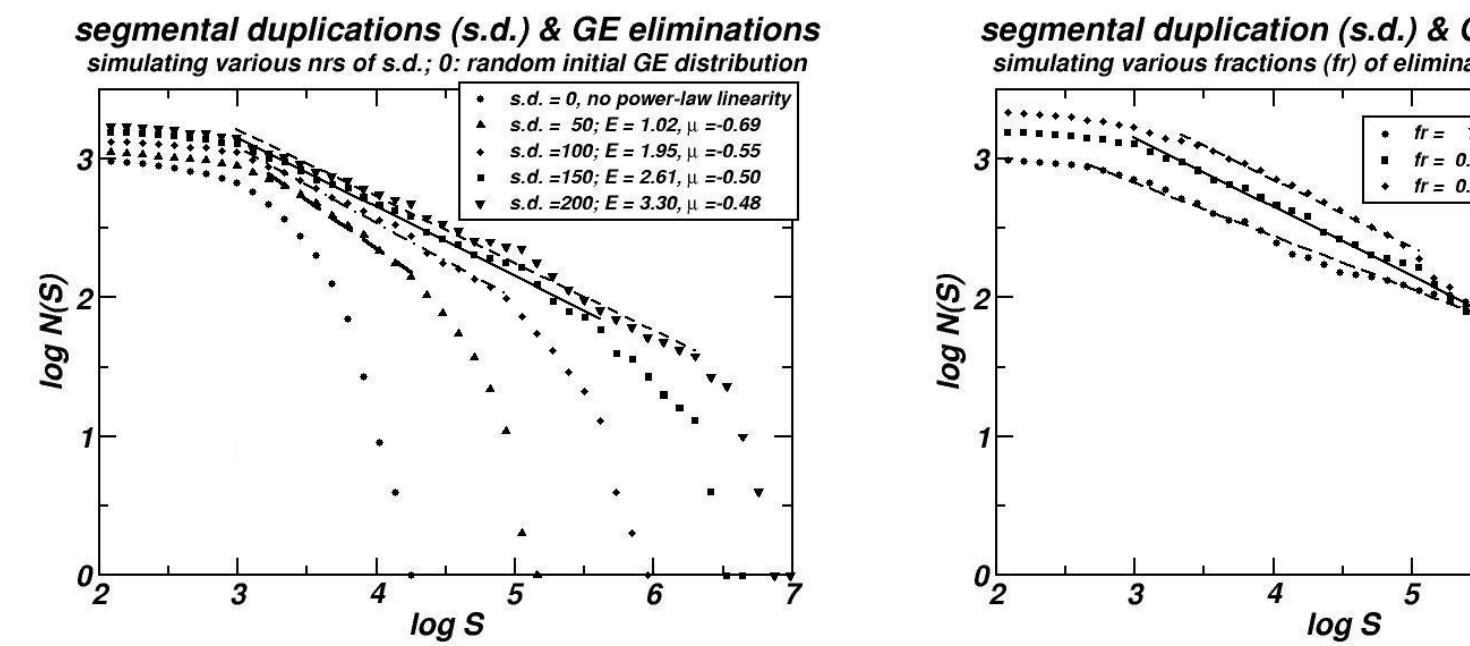


Figure 6: (a) Log-log plot of $N(S)$ vs S for segmental duplications and GE eliminations with varying numbers of s.d. (0, 50, 100, 150, 200). The plot shows a power-law distribution for s.d. > 0, with steeper slopes for higher s.d. values. The y-axis is $\log N(S)$ from 0 to 3, and the x-axis is $\log S$ from 2 to 7. (b) Log-log plot of $N(S)$ vs S for segmental duplications and GE eliminations with varying fractions of eliminations (0.0, 0.2, 0.4, 0.6, 0.8). The plot shows a power-law distribution for fr > 0, with steeper slopes for higher fr values. The y-axis is $\log N(S)$ from 0 to 3, and the x-axis is $\log S$ from 2 to 5.