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## **Research Interests - general description**

#### Probabilistic and statistical aspects in genome organization - Nonrandomness at several length scales.

- Deviations from randomness at the level of nucleotide n-tuplets. Patterns related to the functionality of genomic regions and to global genome structure.
- Deviations from randomness at the "middle" length scale, expressed mainly through clustering of similar nucleotides. Distinction between protein-coding and non-coding functionalities.
- Long range correlations and Zipf laws in the genome structure. Powerlaws 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.
- DNA sequences seen as genomic text Linguistic features in the genome: redundancy, multiple coding, polarity and asymmetry etc.
- "Conservation laws" at the genome structure. The case of "Chargaff's 2<sup>nd</sup> parity rule". The use of deviations from this law in the study of genomic dynamics and evolution.
- 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.

- Early development Left-right asymmetries Mechanisms of activation of Hox genes during limb development.
- Reaction-diffusion systems Spontaneous symmetry breaking and pattern-formation in systems with feedbacks and non-linear dynamics
- Prebiotic and early evolution as a complex self-organization procedure.

### About recent findings, see the <u>web page of the research group</u>

#### **Educational Activities during the last ten years**

- Teaching (16H yearly) of the course "An Introduction to Computational Genomics" in the framework of the Post Graduate Specialisation Diploma *in Bioinformatics*, Biology Department, U.O.A.

- Teaching (12H yearly) of the course "An Introduction to Computational Genomics" in the framework of the Post Graduate Specialisation Diploma *in Clinical Biochemistry and Molecular Diagnostics*, Biology Department, U.O.A.

- The research work for four Master theses and three PhD dissertations have been completed or are running in the framework of the research projects of our group. For further details see in the annual reports of the Institute of Biosciences & Applications of NCSR "Demokritos" (formerly, Institute of Biology).

#### **Other Recent Activities**

Participation in the organizing committee of the satellite meeting "Genomic Complexity", <u>http://geco2012.chem.demokritos.gr</u>, held in the framework of ECCS' 12 Brussels, 3-7 Sept. 2012.

Guest editor of a special volume of *Computational Biology and Chemistry* (CBC) dedicated to "Complexity in Genomes", to appear in 2014.

Reviewer of scientific papers for: Entropy, Journal of Theoretical Biology, Computational Biology Journal, BMC Evolutionary Biology, Molecular Biology and Evolution, BMC Genomics, European Physical Journal B, Bioinformatics, Gene, Journal of Evolutionary Biology Research (JEBR), Computational Biology Journal.

#### **Participation to International Research Projects**

Project entitled: BioASQ: A challenge on large-scale biomedical semantic indexing and question answering, funded by EE with Coordinator Dr G. Paliouras (II&T, NCSR "Demokritos"). Duration: 2012-2014. Total program funding: 1.270.000 €

#### **Participation to National Research Projects**

"Genome Sequencing and Characterization of *Streptococcus macedonicus*, *Streptococcus thermophilus*, *Lactobacillus delbrueckii subsp. lactis* and *Lactobacillus acidipiscis*. Physiological, Evolutionary and Technological Implications", funded by the Greek Ministry of Education, Lifelong Learning and Religious Affairs, Coordinator Prof. Effie Tsakalidou, Agricultural University of Athens.

# LIST OF PUBLICATIONS IN REVIEWED JOURNALS

36. Y.Almirantis, A.Provata & S.Papageorgiou. Evolutionary constraints favor a biophysical model explaining hox gene collinearity. *Current Genomics* (2013) **14**, 279-288.

35. Y.Almirantis. Homeopathy – between tradition and modern science: remedies as carriers of significance. *Homeopathy* (2013) **102**, 114-122.

34. A.Klimopoulos, D.Sellis & Y.Almirantis. Widespread occurrence of power-law distributions in inter-repeat distances shaped by genome dynamics. *Gene* (2012) **499**, 88-98.

33. L.Athanasopoulou, S.Athanasopoulos, K.Karamanos, & Y.Almirantis. Scaling properties and fractality in the distribution of coding segments in eukaryotic genomes revealed through a block entropy approach. *Physical Review E* (2010) **82**, 051917.

 D.Sellis & Y.Almirantis. Power-laws in the genomic distribution of coding segments in several organisms: an evolutionary trace of segmental duplications, possible paleopolyploidy and gene loss. *Gene* (2009) 447, 18-28.

31. D.Sellis, A.Provata & Y.Almirantis. Alu and LINE1 distributions in the human chromosomes. Evidence of a global genomic organization expressed in the form of power laws. *Molecular Biology and Evolution* (2007) **24**, 2385-2399.

30. C.Nikolaou & Y.Almirantis. Deviations from Chargaff's second parity rule in organellar DNA - Insights into the evolution of organellar genomes. *Gene* (2006) **381**, 34-41.

29. P.Katsaloulis, T.Theoharis, W.M.Zheng, B.L.Hao, A.Bountis, Y.Almirantis, A.Provata. Long-range coorelations of RNA polymerase II promoter sequence across organisms. *Physica A Physica A* (2006) **366**, 308-322.

28. Y.Almirantis. The Paradox of the Planetary Metals. *Journal of Scientific Exploration* (2005) **19**, no.1, 31-42.

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26. C.Nikolaou & Y.Almirantis. "Word" preference in the genomic text and genome evolution. Different modes of n-tuplet usage in coding and noncoding sequences" *Journal of Molecular Evolution* (2005) **61**, 23-35.

25. Y.Almirantis & C.Nikolaou. Multi-criterial coding sequence prediction. Combination of GeneMark with two novel, coding-character specific quantities. *Computers in Biology and Medicine.* (2005) **35**, 627-643.

24. C.Nikolaou & Y.Almirantis. Measuring the Coding Potential of Genomic Sequences through a Combination of Triplet Occurrence Patterns and RNY Preference. *Journal of Molecular evolution*. (2004) **59**, 309-316.

23. C.Nikolaou & Y.Almirantis. Mutually symmetric and complementary triplets: Differences in their use distinguish systematically between coding and non-coding genomic sequences. *Journal of Theoretical Biology* (2003), **223**, 477-487.

22. C.Nikolaou & Y.Almirantis. A Study of the Middle-scale Nucleotide Clustering in DNA Sequences of Various Origin and Functionality, by means of a Method based on a Modified Standard Deviation. *Journal of Theoretical Biology* (2002), **217**, 479-492.

21. A.Provata & Y.Almirantis. Statistical dynamics of clustering in the genome structure. *Journal of Statistical Physics* (2002), **106**, 23-56.

20. Y.Almirantis & A.Provata. An evolutionary model for the origin of nonrandomness, long-range order and fractality in the genome. *BioEssays*, (2001) **23**, 647-656.

19. A.Provata & Y.Almirantis. Fractal Cantor patterns in the sequence structure of DNA. *Fractals (2000)* **8**, 15-27.

18. Y.Almirantis. Pattern formation in a Turings' type model with minimal reactional complexity. *Computers and Chemistry (2000)* **24**, 159-170.

17. Y.Almirantis & A.Provata. Long- and short-range correlations in genome organisation. *Journal of Statistical Physics (1999)* **97**, 233-262.

16. Y.Almirantis & S.Papageorgiou. Modes of morphogen cooperation for limb formation in vertebrates and insects. *Journal of Theoretical Biology* (1999) **199**, 235-242.

15. Y.Almirantis. A standard deviation based quantification differentiates coding from non-coding DNA sequences and gives insight to their evolutionary history. *Journal of Theoretical Biology* (1999) **196,** 297-308.

14. A.Provata & Y.Almirantis. Scaling properties of coding and non-coding DNA sequences. *Physica A.* (1997) **247**, 482-496.

13. Y.Almirantis & A.Provata. The "clustered structure" of the purines/pyrimidines distribution in DNA distinguishes systematically between coding and non-coding sequences. *Bulletin of Mathematical Biology* (1997) **59**, 975-992.

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11. D.Venieratos, Y.Almirantis & S.Papageorgiou. Small angle dislocations of the newt limb axes can test the validity of several models. *Growth, Development and Aging* (1995) **59**, 45-54.

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9. Y.Almirantis & M.Kaufman. Chiral selection of rotating waves in a reactiondiffusion system: Ôhe effect of a circularly polarized electromagnetic field. *International Journal of Bifurcation and Chaos* (1995) **5**, 507-518.

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7. S.Papageorgiou & Y.Almirantis. Diffusion or autocatalysis of retinoic acid cannot explain pattern formation in the chick wing bud. *Developmental Dynamics*, (1992) **194**, 282-288.

6. Y.Almirantis. Pattern formation in far-from-equilibrium systems due to crossdiffusion. *Journal of the Mechanical Behavior of Materials*, (1992) **4**, 1-11.

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3. Y.Almirantis & S.Papageorgiou. Cross-Diffusion effects on chemical and biological pattern formation. *Journal of Theoretical Biology* (1991) **151**, 289-311.

2. Y.Almirantis & G.Nicolis. Morphogenesis in an asymmetric medium. *Bulletin of Mathematical Biology* (1987) **49**, 519-30.

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