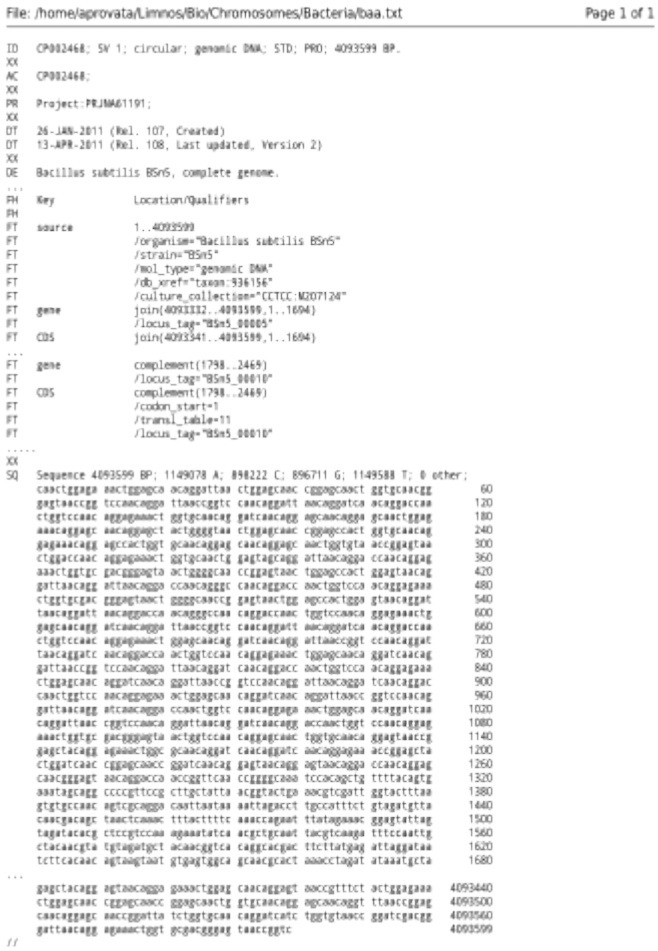
# Master's Thesis Proposal

**Thesis Title:** Complexity analyses in Bioinformatics: Comparison of DNA sequence complexity across organisms.
[Collaboration between the University of Athens & the National Center for Scientific Research "Demokritos" ]

**Aim:** The recent expansion in the field of Molecular Biology has produced complete **DNA sequences** of many organisms, ranging from higher Eukaryotes (humans, animals) to Bacteria and Viruses. These sequences carry most of the information about the organism's main characteristics. **Bioinformatics** has already designed specific computational tools to study and compare these sequences. Inspired from recent advances in the Theory of **Complex Systems** our aim is to use quantitative indices (**Correlation dimensions, Information dimensions, Fractal dimensions, Entropy production)** in order to quantify and compare the relative genomic complexity of test organisms belonging to different Kingdom: Animalia, Plantae, Fungi, Protista, Bacteria.

Typical image of a DNA sequence consisting of the 4 nucleotides (A,C,G,T) is depicted in the figure. This data originates from the bacterium ***Baccilus Subtilis*** which is commonly found in the human body and is widely used as a test organism for bacteria.


File: /home/aprovata/Limnos/Bio/Chromosomes/Bacteria/baa.txt Page 1 of 1

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DT   13-APR-2011 (Rel. 108, Last updated, Version 2)
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//
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**Typical DNA sequence (for analysis)**

**Methodology:**

For each test organism the following steps will be followed:

- The most recent genomic sequences of the organism will be downloaded from the genomic databases (EMBL, GenBank)
- Statistical characteristics of the organism will be calculated (e.g. number of A,C,G,T basepairs, coding percentage, repetition percentage, etc).
- Quantitative indices, such as the information dimension, fractal dimension, correlation dimension and entropy production will be evaluated.
- Classification of the organisms will be undertaken, based on the above indices.

Comparison of the above dimensionality classifications with the classical phenomenological classifications will be undertaken.

**Literature:**


- C. K. Peng, S. V. Buldyrev, S. Havlin, M. Simons, H. E. Stanley and A. L. Goldberger, "Mosaic Organization of DNA Nucleotides", *Physical Review E* **49**, 1685-1689 (1994).
- C. K. Peng, S. Buldyrev, A. Goldberger, S. Havlin, F. Sciortino, M. Simons and H. E. Stanley, "Long-Range Correlations in Nucleotide Sequences", *Nature* **356**, 168-171 (1992).
- W Li, J Freudenberg, P Miramontes , "Diminishing return for increased mappability with longer sequencing reads: implications of the k-mer distributions in the human genome", *BMC Bioinformatics*, **15**, 2 (2014).
- A. Provata, C. Nicolis, G. Nicolis, "DNA viewed as an out-of-equilibrium structure", *Physical Review E* **89,** 052105 (2014) .
- A. Provata, C. Nicolis, G. Nicolis, "Complexity measures for the evolutionary categorization of organisms", *Computational Biology and Chemistry,* **53**, 5–14 (2014).


**Collaboration:**

This Master Thesis is performed in the framework of a collaboration between:
-the Department of Informatics of the University of Athens (Prof. T. Theoharis),
-the Institute of Nanoscience and Nanotechnology of the National Center for Scientific Research "Demokritos" (Dr. A. Provata)

**Requirements:**

We are looking for an MA student with excellent knowledge of:

a) image analysis techniques
b) programming language C/C++ (or other)
d) English

Additional Skills (not required) could be useful:
a) Knowledge of Linux operating system
b) Knowledge of Fractal and Multifractal Analysis

**Interested students, please contact:**


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