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Ranking of Prokaryotic Genomes to Reveal Evolutionary Factors

Alexander Bolshoy

Univesity of Haifa, Israel

Abstract

Whether variations of gene lengths (some genes become longer than their predecessors, while other genes become shorter and the sizes of these factions are randomly different from organism to organism) are neutral or depend on organismal evolution and adaptation is still an open question. We believe that the ranking of genomes according to lengths of their genes, followed by the calculation of coefficients of association between genome rank and genome property, is a very reasonable approach in revealing evolutionary driving factors. The main purpose of this study is to test effectiveness and robustness of several ranking methods that are based on maximization of overall sortedness and are suitable for revealing factors affecting gene lengths. The selected method of comparison is combinatorial optimization. We have demonstrated that all considered methods give consistent results and that Bubble Sort and Simulated Annealing approaches perform the best. Also, Bubble Sort is considerably faster than the Simulated Annealing method.

Biography

Dr. Bolshoy is an Associated Professor in the Department of Evolutionary and Environmental Biology, and a member of the Institute of Evolution at the University of Haifa, Israel. He completed his PhD from the Weizmann Institute of Science in Computational Structural Biology in 1993. Dr. Bolshoy has been a major player in the field of DNA Linguistics and in the field of DNA curvature and bendability since the 1990-ies. He is the author of the book and many scientific articles, and has been serving as an editorial board member of several bioinformatics journals.