

Genome evolution: a stochastic approach

#GenomeEvolution

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Abstract

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Even though an important part of our understanding of evolution still relies on Darwin's contribution, many improvements have been done. In particular, biologist as well as mathematicians have been focusing on the main defect of Darwin's theory: it lacks a quantitative characterization of evolutionary aspects.

The recent technological changes in the sequencing has marked the transition from genetic to genomic era. This lead to a much bigger amount of data, including, for instance, whole-genome-sequencing data, proteome, transcriptome, for different taxa, from bacteria to complex eukarya. Thanks to these data, it has been possible to recognize some correlations, involving genetic quantities: the distribution of evolutionary rates between orthologous genes; the power-law distribution of membership in gene families and functional categories; the scale-free topology of many biological networks; a negative correlation between gene expression levels and gene sequence evolutionary rates.

In my work, I try to develop computational model(s) to explain indeed how genome evolution could lead to such a distribution of categories and genome sizes.

Gianrocco started his academic experience in 2007, at University of Catania, in physics program (B.Sc.). At the same time he was admitted as a student of Scuola Superiore di Catania (SSC). During those four years at the SSC, thanks to everyday life in the college community, he learn to interact with students from different areas, this contributing to his cultural grow. At the same time, the daily discussions with students from physics and math, led him to pursue the M.Sc. in theoretical physics, at Utrecht University. During the last year of his study, he became interested in mathematical modeling of biological systems.

Gianrocco is now a PhD student at University of Basel. In his current project, he tries to understand, from a quantitative point of view, how genome evolution could give rise to the particular correlations and distributions of genetic quantities that have been observed widely, across different taxa.

Host: Simone Seminara

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