

## **Bioinformatics for Genomics**

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Mass sequencing of complete prokaryote, eukaryote and organelle (mitochondria and chloroplasts) genomes has produced an enormous amount of data which need to be analyzed, interpreted and then stored in suitably structured databases in order to make them available to the scientific community.

In this scenario, Bioinformatics plays a primary role and is at the core of all disciplines having as an object “Genomics” and its applications.

Indeed, the “genomic” perspective is providing a new vision to modern Biology and Molecular Evolution which is no longer limited to the analysis of single genes and proteins, but covers the structure, function and evolution of genomes intended as unities.

Presently, the number of completely sequenced genomes for prokaryotes, eukaryotes and organelles is still limited. Nevertheless, some unforeseen properties of genetic material have already been discovered, which would have been impossible through the analysis of single genes and/or gene products. This has been made possible thanks to the development of bioinformatics tools.

Some of the unexpected properties of genome structure and evolution will be dealt in this contribution together with the critical discussion of the methods used for their study.