

Network and Systems Biology in Bioinformatics

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DESCRIPTION

Bioinformatics is defined as the application of tools of computation and analysis to the capture and interpretation of biological data. It is an interdisciplinary field, which harnesses computer science, mathematics, physics, and biology. Biological systems are often represented as networks which are complex sets of binary interactions or relations between different entities. Network analysis seeks to understand the relationships within biological networks such as metabolic or protein-protein interaction networks [1,2]. Although biological networks can be constructed from a single type of molecule or entity (such as genes), network biology often attempts to integrate many different data types, such as proteins, small molecules, gene expression data, and others, which are all connected physically, functionally, or both. Image and signal processing allow extraction of useful results from large amounts of raw data. In the field of genetics, it aids in sequencing and annotating genomes and their observed mutations [3-6]. It plays a role in the text mining of biological literature and the development of biological and gene ontologies to organize and query biological data. It also plays a role in the analysis of gene and protein expression and regulation. Bioinformatics tools aid in comparing, analyzing and interpreting genetic and genomic data and more generally in the understanding of evolutionary aspects of molecular biology. At a more integrative level, it helps analyze and catalogue the biological pathways and networks that are an important part of systems biology. In structural biology, it aids in the simulation and modeling of DNA, RNA, proteins as well as bio molecular interactions.

Molecular Interactions

Molecular Interactions are between molecules, or between atoms that are not linked by bonds. Molecular interactions include cohesive (attraction between like), adhesive (attraction between unlike) and repulsive forces between molecules [7-9]. They can help us to predict the biological processes that a protein of unknown function is involved in: We may assume "Guilty by association" if a protein of unknown function associates with one of known function. Tens of thousands of three-dimensional protein structures have been determined by X-ray crystallography

and protein Nuclear Magnetic Resonance Spectroscopy (protein NMR) and a central question in structural bioinformatics is whether it is practical to predict possible protein-protein interactions only based on these 3D shapes, without performing protein-protein interaction experiments.

Single cell data analysis: Computational techniques are used to analyze high-throughput, low-measurement single cell data, such as that obtained from flow cytometry.

Biodiversity informatics: Biodiversity informatics deals with the collection and analysis of biodiversity data, such as taxonomic databases, or micro biome data. Examples of such analyses include phylogenetic, niche modeling, species richness mapping, DNA barcoding, or species identification tools.

Ontologies and data integration: Biological ontologies are directed acyclic graphs of controlled vocabularies. They are designed to capture biological concepts and descriptions in a way that can be easily categorized and analyzed with computers.

High-throughput image analysis: Computational technologies are used to accelerate or fully automate the processing, quantification and analysis of large amounts of high-information-content biomedical imagery. Modern image analysis systems augment an observer's ability to make measurements from a large or complex set of images, by improving accuracy, objectivity, or speed.

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