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Editorial

A Brief Note Traditional Bioinformatics

Dr. Xiaoyi XU

Research Scientist, School of Medicine
Stanford University, USA.

As an interdisciplinary field of science, bioinformatics combines biology, computer science, information engineering, mathematics and statistics to analyze and interpret the biological data. Bioinformatics has been used for in silico analyses of biological queries using mathematical and statistical techniques. As an interdisciplinary field of science, bioinformatics combines biology, computer science, information engineering, mathematics and statistics to analyze and interpret the biological data. Bioinformatics has been used for in silico analyses of biological queries using mathematical and statistical techniques. Bioinformatics includes biological studies that use computer programming as part of their methodology, as well as a specific analysis "pipelines" that are repeatedly used, particularly in the field of genomics.

Common uses of bioinformatics include the identification of candidates genes and single nucleotide polymorphisms (SNPs). Often, such identification is made with the aim of better understanding the genetic basis of disease, unique adaptations, desirable properties (esp. in agricultural species), or differences between populations. Bioinformatics has become an important part of many areas of biology. In experimental molecular biology, bioinformatics techniques such as 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. 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. The foundations of bioinformatics were laid in the early 1960s with the application of computational methods to protein sequence analysis (notably, de novo sequence assembly, biological sequence databases and substitution models).

Later on, DNA analysis also emerged due to parallel advances in (i) molecular biology methods, which allowed easier manipulation of DNA, as well as its sequencing, and (ii) computer science, which saw the rise of increasingly miniaturized and more powerful computers, as well as novel software better suited to handle bioinformatics tasks. In the 1990s through the 2000s, major improvements in sequencing technology, along with reduced costs, gave rise to an exponential increase of data. Bioinformatics is an interdisciplinary scientific field of life sciences.

Bioinformatics research and application include the analysis of molecular sequence and genomics data; genome annotation, gene/protein prediction, and expression profiling; molecular folding, modeling, and design; building biological networks; development of databases and data management systems; development of software and analysis tools; bioinformatics services and workflow; mining of biomedical literature and text; and bioinformatics education and training. Astronomical accumulation of genomics, proteomics, and metabolomics data as well as a need for their storage, analysis, annotation, organization, systematization, and integration into biological networks and database systems were the main driving forces for the emergence and development of bioinformatics.

Current critical needs for bioinformatics among others highlighted in this chapter, however, are to understand basics and specifics of bioinformatics as well as to prepare new generation scientists and specialists with integrated, interdisciplinary, and multilingual knowledge who can use modern bioinformatics resources powered with sophisticated operating systems, software, and database/networking technologies.

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