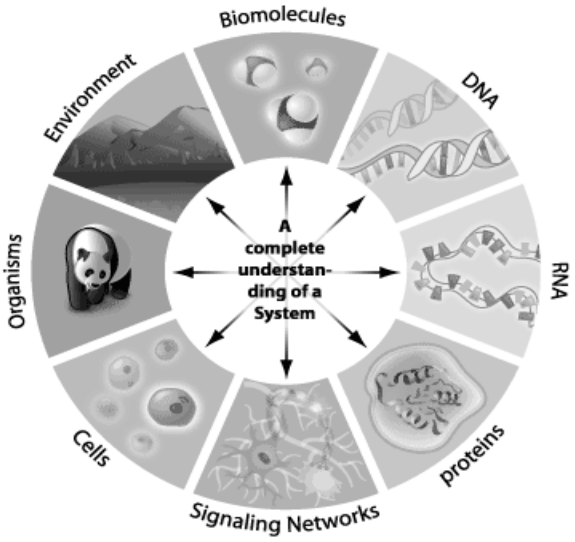
Bioinformatics

Bioinformatics is the combination of biology and information technology. The discipline encompasses any computational tools and methods used to manage, analyze and manipulate large sets of biological data. Essentially, bioinformatics has three components:

- The creation of databases allowing the storage and management of large biological data sets.
- The development of algorithms and statistics to determine relationships among members of large data sets.
- The use of these tools for the analysis and interpretation of various types of biological data, including DNA, RNA and protein sequences, protein structures, gene expression profiles, and biochemical pathways.

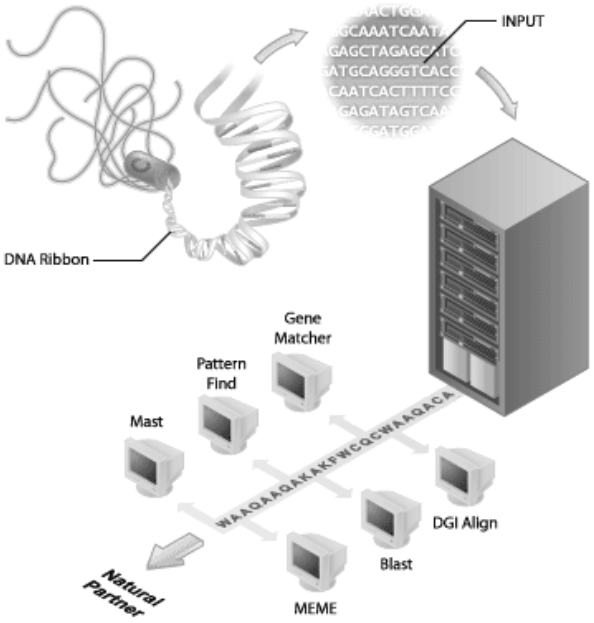


The term *bioinformatics* first came into use in the 1990s and was originally synonymous with the management and analysis of DNA, RNA and protein sequence data. Computational tools for sequence analysis had been available since the 1960s, but this was a minority interest until advances in sequencing technology led to a rapid expansion in the number of stored sequences in databases such as GenBank. Now, the term has expanded to incorporate many other types of biological data, for example protein structures, gene expression profiles and protein interactions. Each of these areas requires its own set of databases, algorithms and statistical methods.

Bioinformatics is largely, although not exclusively, a computer-based discipline. Computers are important in bioinformatics for two reasons:

First, many bioinformatics problems require the same task to be repeated millions of times. For example, comparing a new sequence to every other sequence stored in a database or comparing a group of sequences systematically to determine evolutionary relationships. In such cases, the ability of computers to process information and test alternative solutions rapidly is indispensable.

Second, computers are required for their problem-solving power. Typical problems that might be addressed using bioinformatics could include solving the folding pathways of protein given its amino acid sequence, or deducing a biochemical pathway given a collection of RNA expression profiles. Computers can help with such problems, but it is important to note that expert input and robust original data are also required.[1]



The future of bioinformatics is integration. For example, integration of a wide variety of data sources such as clinical and genomic data will allow us to use disease symptoms to predict genetic mutations and vice versa. The integration of GIS data, such as maps, weather systems, with crop health and genotype data, will allow us to predict successful outcomes of agriculture experiments. Another future area of research in bioinformatics is large-scale comparative genomics. For example, the development of tools that can do 10-way comparisons of genomes will push forward the discovery rate in this field of bioinformatics. Along these lines, the modeling and visualization of full networks of complex systems could be used in the future to predict how the system (or cell) reacts to a drug for example. A technical set of challenges faces bioinformatics and is being addressed by faster computers, technological advances in disk storage space, and increased bandwidth. Finally, a key research question for the future of bioinformatics will be how to computationally compare complex biological observations, such as gene expression patterns and protein networks. Bioinformatics is about converting biological observations to a model that a computer will understand. This is a very challenging task since biology can be very complex. This problem of how to digitize phenotypic data such as behavior, electrocardiograms, and crop health into a computer readable form offers exciting challenges for future bioinformaticians.[2]

[1] David R. Westhead, J. Howard Parish, and Richard M. Twyman, **Bioinformatics** (Oxford: BIOS, 2002).

[2] Joanne Fox, "What is Bioinformatics", **University of British Columbia. UBC Bioinformatics Centre**, http://bioinformatics.ubc.ca/node/368/print

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