

# FEATURE: BIOINFORMATICS

Bioinformatics is a field of science in which biology, computer science, and information technology merge to form a single discipline. The term bioinformatics was coined by Paulien Hogeweg in 1979 for the study of informatic processes in biotic systems. Its primary use since at least the late 1980s has been in genomics and genetics, particularly in those areas of genomics involving large-scale DNA sequencing.

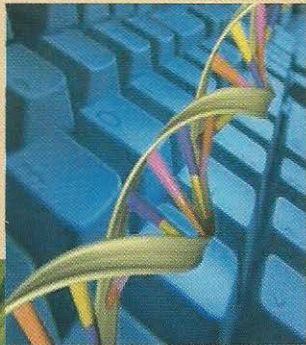
The ultimate goal of the field is to enable the discovery of new biological insights as well as to create a global perspective from which unifying principles in biology can be discerned. At the beginning of the "genomic revolution", a bioinformatics concern was the creation and maintenance of a database to store biological information, such as nucleotide and amino acid sequences.

Development of this type of database involved not only design issues but the development of complex interfaces whereby researchers could both access existing data as well as submit new or revised data. Ultimately, however, all of this information must be combined to form a comprehensive picture of normal cellular activities so that researchers may study how these activities are altered, for example, in different disease states.

The rationale for applying computational approaches to facilitate the understanding of various biological processes includes:

- ♦ a more global perspective in experimental design;
- ♦ the ability to capitalize on the emerging technology of database-mining - the

process by which testable hypotheses are generated regarding the function or structure of a gene or protein of interest by identifying similar sequences in better characterized organisms.



(Condensed from NCBI,  
A Science Primer)