

Bioinformatics Today

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This presentation was originally in Chinese. The following is only a brief description of it.

Bioinformatics is the application of statistics and computer science to the field of molecular biology. Initially it was applied in the creation and maintenance of a database to store biological information at the beginning of the "genomic revolution", 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. Under the topic of 'bioinformatics today' which covers wide and complex ranges of literature, it is quite difficult to comprehensively overview this area in the limited time of only 30 minutes. Therefore my presentation today aims only to describe the framework of this area.

The rapid development of molecular biology and the information technology which started from later 80's of last century greatly promoted the genomic and genetic research, resulting in a great quantity of molecular biology data and the information! Although generating data is the basic task of all scientific research, without accurate and high effective analysis these data only can be the wastes. In front of the voluminous amount of data, people are dazzled and even unable to know where to go. In order to understand, analyse and unscramble useful information from these data, bioinformatics is generated. In this presentation, I discussed the following sub-topics:

1. The history of bioinformatics.
2. The developmental speed of bioinformatics: examples of NCBI and Ensembl databases.
3. The hot areas of bioinformatics:
 - Development of even powerful software tools and web techniques in order to promote exchange, digging and integration of different databases.
 - Innovation of new statistical data processing theory and algorithm.
 - Data analysis and annotation, such as DNA and protein sequence analysis, multiple sequences comparison, function localization, structure forecast, new gene discovery, gene expression-microarray, discovery and design of new drugs ...