

The Applications of Bioinformatics in Different Fields

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INTRODUCTION

Bioinformatics is the use of software applications and other related tools for the interpretation of biological information. This uses different disciplines like biological information, statistics and computer programming. It has become an essential tool in the study of genomics and proteomics. Bioinformatics has helped a lot to fetch data regarding Molecular Biology, Genetics, Systems Biology and Structural Biology. The pathways and the regular cellular activities in the biological systems were easily understood using these tools. Hence the changes happening in the body during the disease conditions were also known. It uses different techniques like visualization, data mining and machine learning algorithms. The field of bioinformatics has got a kick-start since the initiation of the Human Genome project. It is an international project where the genes that has built up the human has been mapped and studied, it is the exploration of the genetics of the homosapiens.

Applications of Bioinformatics:

- The disturbances or changes happening in the body during the disease conditions can be understood using bioinformatics.
- The Personalized drug therapy based on one's genetic patterns can be made available which shows good pharmacological action.
- Using the Gene therapy and Genetic Engineering the genes can be rectified and a perfect gene can be incorporated.
- Using the bioinformatics, as the mechanism of the disease or disorder can be known, based on it drugs can be designed so as to exactly target the cause.
- As the three dimensional structures of the receptors can be visualized, the drug that bind the receptors can be synthesized.

- It is also very useful in the plant science as using these techniques; drought resistant, disease resistant, superior varieties can be produced to produce higher yields and required results.

Apart from genome sequence analysis, bioinformatics is now being used for a wide range of other important tasks, including gene variation and expression analysis, gene and protein structure and function analysis and prediction, prediction and detection of transcriptional regulation, simulation environments for whole cell modelling, complex simulation of gene regulatory dynamics and networks, and presentation and analysis of biochemical mechanisms in order to underpin drug development. The genomes of cancer cells are altered in complicated and sometimes unanticipated ways. Massive sequencing efforts in cancer are being utilised to find previously unknown point mutations in a range of genes. Bioinformaticians continue to develop new methods and tools to compare sequencing results to the growing library of human genome sequences and germline polymorphisms. The extension of experimental data by predictions is another goal of bioinformatics.

The prediction of protein structure from an amino acid sequence is a core goal of computational biology. This should be conceivable, as evidenced by the spontaneous folding of proteins. The Critical Assessment of Structure Prediction (CASP) projects, which comprise blind evaluations of structure prediction algorithms, are used to track progress in the development of methods to predict protein folding. Many bioinformatics studies began with a narrow emphasis, focussing on developing algorithms for evaluating specific types of data, such as gene sequences or protein structures.

Bioinformatics' goals are becoming more integrative, with the purpose of determining how diverse types of data may be used to better understand natural phenomena such as organisms and

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disease.

CONFLICT OF INTEREST

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