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BIOINFORMATICS
Its Role & Applications in Agriculture & other disciplines …

Bioinformatics is an interdisciplinary area of the science composed of biology, mathematics and computer science. Bioinformatics has come out as a tool to smoothing the ways for biological discoveries. With the development of Human Genome Project, the data of biology increased fabulously and marvellously. The ability to process, manage, capture, interpret and analyze data became more important than ever. Bioinformatics is the application of information technology to manage biological data that helps in decoding plant genomes.
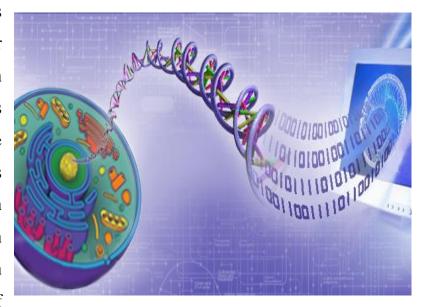
Bioinformatics is a new Discipline but it is making progress in every field of Science very rapidly. As it has its application in the medicine by providing the genome information of various organisms, similarly the field of agriculture has also taken advantage of this field because micro-organisms play an important role in agriculture and bioinformatics provides full genomic information of these organisms. The genome sequencing of the plants and animals has also provided benefits to agriculture. Application of various bioinformatics tools in biological research enables storage, retrieval, analysis,

annotation and visualization of results and promotes better understanding of biological system in fullness. This will help in plant health care based disease diagnosis to improve the quality of Plant.

Moreover, Bioinformatics is generally referred to as the application of computer technology to the processing and managing the data generated in biological experiments. The term bioinformatics was originally coined for the application of information technology to large volumes of biological, particularly, genomic data.

ROLE OF BIOINFORMATICS

Bioinformatics today has entered every major discipline in biology. In genomics, Bioinformatics has aided in genome sequencing, and has shown its success in locating the genes, in phylogenetic comparison and in the detection of transcription factor binding sites of the genes.

Bioinformatics helps in the study of protein structures and the discovery of sequence sites where protein-protein interactions take place. To help understanding biology at the system level, bioinformatics begins to show promise in unraveling genetic networks. Plant life plays important and diverse roles in our society, our economy, and our global environment. Especially crop

is the most important plants to us. Feeding the increasing world population is a challenge for modern plant biotechnology. Crop yields have increased during the last century and will continue to improve as agronomy re-assorting the enhanced breeding and develop new biotechnological-engineered strategies.

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APPLICATION

Tools of bioinformatics are playing significant role in providing the information about the genes present in the genome of these species. These tools have also made it possible to predict the function of different genes and factors affecting these genes. The information provided about the genes by the tools makes the scientists to produce enhanced species of plants which have drought, herbicide, and pesticide resistance in them. Similarly specific genes can be modified to improve the production of meat and milk. Certain changes can be made in their genome to make them disease resistant.

1. Crops

When the evolutionary changes occurred in the plants, their genome remained conserved and did not provided much information. Since the arrival of bioinformatics tools, it is possible to extract the required information from the genome of specific plants. There are two species of food plants, the genome of

which has been mapped completely for example Arabidopsis thaliana and Oryza sativa. These two species of plants have their names in English as water cress and rice respectively.

Water cress is a small plant which is found on the rocks. Researchers took interest in its genome because of its smaller genomic size and studied the plant developmental processes. Its genome consists of 5 chromosomes on which 100Mbp DNA is distributed. It reproduces in 5 weeks and makes new generation. The understanding about its genes and their expressions provides information about the other plants' proteins and their expressions. There are many uses of knowing the genome of A. thaliana but the major use is that the yield of the plants can be increased.

2.   Insect Resistance

Many plants have been made insect resistant by incorporating the desired genes. Bacillus thuringiensis is bacterial specie which increases the soil fertility and protects the plants against pests. When the researchers mapped its genome, they used its genes to incorporate into the plant to make it resistant against insects. For example, corn, cotton and potatoes have been made insect resistant so far. By having the genes of bacteria in the plants genome, when insects eat the plants, the bacteria enter in their bloodstream and make them starved, ultimately they die. Bt corn is one species of food plants which have been modified by inserting bacterial genes in it. It is effective against insects by developing resistance against them. The use of Bt genes in the plants genome has made the agriculturists to use the insecticides in very little amount. As a result the productivity and nutritional value of plants will also increase and will be beneficent for human health.

3.   Improve nutritional Quality

When the changes are made in the genome of the plants, the nutritional value of plants also increases. For example some genes are inserted in the rice genome to increase the Vitamin A level in the crop. Vitamin A is an important component for the eyes and if the Vitamin A deficiency occurs in the body, it may result in blindness. This work has allowed the scientists to reduce the rate of blindness from the world by giving genetically modified rice to the people.

4.   Poorer soils and Drought Resistant

Some varieties of cereals are developed which have the ability to grow in poor soils and are drought resistant. Due to this method, those areas can also be used which have less soil fertility.

GOALS

The field of bioinformatics has evolved such that the most pressing task now involves the analysis and interpretation of various types of data. This includes nucleotide and amino acid sequences, protein domains, and protein structures. The actual process of analyzing and interpreting data is referred to as computational biology. Important sub-disciplines within bioinformatics and computational biology include:

- Development and implementation of computer programs that enable efficient access to, use and management of, various types of information.
- Development of new algorithms (mathematical formulas) and statistical measures that assess relationships among members of large data sets. For example, there are methods to locate a gene within a sequence, to predict protein structure and/or function, and to cluster protein sequences into families of related sequences.

- To increase the understanding of biological processes. What sets it apart from other approaches, however, is its focus on developing and applying computationally intensive techniques.

Over the past few decades, rapid developments in genomic and other molecular research technologies and developments in information technologies have combined to produce a tremendous amount of information related to molecular biology. Bioinformatics is the name given to these mathematical and computing approaches used to glean understanding of biological processes.

STRUCTURE OF BIOINFORMATICS

Protein structure prediction is another important application of bioinformatics. The amino acid sequence of a protein, the so-called primary structure, can be easily determined from the sequence on the gene that codes for it. In the vast majority of cases, this primary structure uniquely determines a structure in its native environment. Knowledge of this structure is vital in understanding the function of the protein. Structural information is usually classified as:

- Secondary Structure
- Tertiary Structure
- Quaternary Structure

One of the key ideas in bioinformatics is the notion of homology. In the genomic branch of bioinformatics, homology is used to predict the function of a gene: if the sequence of gene *A*, whose function is known, is homologous to the sequence of gene *B,* whose function is unknown, one could infer that B may share A's function. In the structural branch of bioinformatics, homology is used to determine which parts of a protein are important in structure formation and interaction with other proteins. In a technique called homology modeling, this information is used to predict the structure of a protein once the structure of a homologous protein is known. This currently remains the only way to predict protein structures reliably.

RELATION WITH OTHER FIELDS

Bioinformatics is a science field that is similar to but distinct from biological computation, while it is often considered synonymous to computational biology.

- Biological computation uses bioengineering

- biology to build biological computers

- Bioinformatics uses computation to better understand biology.

Bioinformatics and computational biology involve the analysis of biological data, particularly DNA, RNA, and protein sequences. The field of bioinformatics experienced explosive growth starting in the mid-1990s, driven largely by the Human Genome Project and by rapid advances in DNA sequencing technology.

Analyzing biological data to produce meaningful information involves writing and running software programs that use algorithms from graph theory, artificial intelligence, soft computing, data mining, image processing, and computer simulation. The algorithms in turn depend on theoretical foundations such as:

- Discrete mathematics

- Control theory

- System theory

- Information theory

- Statistics