



## Role of Bioinformatics in Agriculture

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**B**ioinformatics is a branch of science that integrates computer sciences, mathematics and statistics, chemistry and engineering for analysis, exploration, integration, and exploitation of biological sciences data in research and development. Bioinformatics deals with storage, retrieval, analysis and interpretation of biological data using computer-based and software-based software and tools. Bioinformatics is used to analyze and predict the structure and function of genomic content, biological sequence data, and macromolecules.

### Objective of Bioinformatics

1. Development of new algorithms and statistics for assessing the relationships among large sets of biological data.
2. Application of these tools for the analysis and interpretation of the various biological data.
3. Development of database for an efficient storage, access and management of the large body of various biological information.

### Role of Bioinformatics in Agriculture

Plant life plays important and diverse roles in our society, our economy, and our global environment. Especially crop is the most important plants tous. 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. The onset of genomics is providing massive information to improve crop phenotypes. The accumulation of sequence data allows detailed genome analysis by using friendly database access and information retrieval. Genetic and molecular genome co linearity allows efficient transfer of data revealing extensive conservation of genome organization between species. The goals of genome are the identification of the sequenced genes and the deduction of their functions by metabolic analysis and reverses genetic screens of gene knockouts.

Over 20% of the predicted genes occur as cluster of related genes generating a considerable proportion of gene families. Multiple alignment provides a method to estimate the number of genes in gene families allowing the identification of previously undescribed genes. This information enables new strategies to study gene expression patterns in plants. Available information from news technologies, as the database stored DNA microarray expression data, will help plant biology functional genomics. Expressed sequence tags (ESTs) also give the opportunity to perform “digital northern” comparison of gene expression levels providing initial clues toward unknown regulatory phenomena. Crop plant networks collections of database and bioinformatics resources for crop plant genomics have been built to harness the extensive work in genome mapping. Within the field of agricultural genomics, or agri-genomics, bioinformatics is playing an increasingly important role in the collection,

storage, and analysis of genomic data. There are importance of bioinformatics in agriculture such as Improving plant resistance, enhancing the quality of soil.

### **Available Tools Used for Bioinformatic Agriculture**

Plant genome analysis is of great economic importance for not only the agricultural industry but also for the overall maintenance of animal and human health. Many different bioinformatics tools have been developed to assist in the gathering, consolidation, and analysis of the vast amount of information that is available on these living systems. Some of the most widely used plant/crop bioinformatics online databases include BGI Rice Information System, Gateway of Brassica Genome, ChloroplastDB, The Crop Expressed Sequence Tag (CR-EST\_ database, CyanBase, the European Molecular Biology Laboratory (EMBL) nucleotide sequence database, and many more. Conclusion Aside from assisting technologists to improve the nutritional quality of crops for human consumption, bioinformatics can also provide information on the presence of certain contaminants within soil. Most soils consist of highly complex microbial communities that, in turn, are made up of a diverse set gene sequences.

### **References**

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