Chapter 94

Emerging Web Tools and Their Applications in Bioinformatics

Shailendra Singh
PEC University of Technology, India

Amardeep Singh
Punjabi University, India

ABSTRACT

Bioinformatics is an emerging area of interest for many researchers and scientists. It has unlimited applications in many areas. The most important application of this is to know about genes, et cetera. But nowadays, research has also started in the emerging areas of network security and threats using bioinformatics. In the present scenario, we are highly dependent on Internet. The Web has invited different people from different backgrounds to work together sitting at far places. And to fulfill the needs of the interested and involved people, lots of Web based tools have been developed, and many others are being developed. In this chapter, the area of bioinformatics has been introduced along with its applications, Web, developed Web based tools, and a case study of one such tool.

INTRODUCTION TO BIOINFORMATICS

Bioinformatics is the study and analysis of biological information using computers and statistical techniques. It is the science of developing and utilizing computer databases and algorithms to accelerate and enhance biological research. Bioinformatics is taken as more of a tool than a discipline for the analysis of biological data. From information technology point of view, bioinformatics is the use of IT in biotechnology for the data storage, data warehousing and analyzing the biomolecular sequences. The knowledge is required from other branches of science and engineering like biology, mathematics, laws of physics & chemistry, computer science & engineering and IT to analyze biological data. Bioinformatics is not only limited to the analysis of biological data, but in reality it is being used to solve many biological

DOI: 10.4018/978-1-4666-3604-0.ch094

problems like various disorders in human beings and to find out how living things work.

Bioinformatics has emerged out of the need to understand the code of life, DNA (Mount, 2001). Enormous DNA sequencing projects have been evolved and added in the growth of the science of Bioinformatics. The fundamental molecule of life (DNA) directly controls the fundamental biology of life. It codes for genes which in turn code for proteins that decide the biological makeup of humans or any living organism. The variations and errors in the genomic DNA define the possibility of developing diseases or resistance to disorders. The ultimate goal of bioinformatics is to reveal the assets of biological information hidden in the crowd of sequence, structure, literature and other biological data and to use this information to enhance the standard of life for mankind.

APPLICATIONS OF BIOINFORMATICS

Bioinformatics is being used in various areas and the applications are limitless (Bosu, 2009). This is possible not only by having collaborative efforts of different people from different background but also widely using web based tools and Internet. There are constantly new research projects and studies being mdone on this amazing new line of DNA analysis. Scientists are now using bioinformatics to detect genetic abnormalities in different species. This is also creating breakthroughs in the medical community. Applications of Bioinformatics have allowed doctors to conduct genetic testing in unborn babies to predict and find any signs of certain genetic disorders and conditions.

Some of its applications are listed below:

- **DNA Identification:** The identification of DNA profile of a person can help the investigators in identifying criminals, ascertaining family associations, protecting rare species, matching organ donors, and for security.
- **Analysis of Gene Expression:** The analysis of gene expression is very important for the understanding of disorders in humans and other species. A chemical and physical change in a living being is not caused by a single gene but the mutual effect of many genes. Understanding the function of many genes on a particular condition will, in due course of time, present a genetic basis for many diseases.
- **Analysis of Gene Regulation:** The regulation is the sequence of events that begins with an extracellular event and leads to a change in the activity of proteins. The analysis of gene that promotes and regulates the activity of genes and proteins helps us to understand the behavior of species.
- **Risk Assessment:** The deep and intense research on human genome can help us to assess individual risk exposure to toxic elements as resistance to external agents that varies from person to person. It can also help to reduce the likelihood of heritable mutations.
- **Human Migration:** The understanding of human and other genomes will help us to understand the human evolution, inheritance, traits, and disease carriers. The study of genome comparison across organisms can help to understand similar genes with associated disease.
- **Adapted Medicine:** The development in the field of pharmacogenomics will change the prospect of clinical medicine. It shows how an individual's genetic inheritance affects the body's response to drugs. At present, some drugs disappear from the market because a small percentage of the clinical patient population shows unfavorable affects to a drug due to sequence variant in their DNA. As a result, many potentially life-saving drugs never make it to the mar-

13 more pages are available in the full version of this document, which may be purchased using the "Add to Cart" button on the publisher's webpage:
www.igi-global.com/chapter/emerging-web-tools-their-applications/76147

Related Content

Analyzing the Text of Clinical Literature for Question Answering
Yun Niuand Graeme Hirst (2009). *Information Retrieval in Biomedicine: Natural Language Processing for Knowledge Integration (pp. 190-220).*
www.irma-international.org/chapter/analyzing-text-clinical-literature-question/23062

Computational Modeling and Simulations in Life Sciences
Athina Lazakidou, Maria Petridouand Dimitra Iliopoulou (2013). *International Journal of Systems Biology and Biomedical Technologies (pp. 1-7).*
www.irma-international.org/article/computational-modeling-and-simulations-in-life-sciences/89397

Clustering Genes Using Heterogeneous Data Sources
Erliang Zeng, Chengyong Yang, Tao Liand Giri Narasimhan (2010). *International Journal of Knowledge Discovery in Bioinformatics (pp. 12-28).*
www.irma-international.org/article/clustering-genes-using-heterogeneous-data/45163

Genetic Diagnosis of Cancer by Evolutionary Fuzzy-Rough based Neural-Network Ensemble
Sujata Dashand Bichitrananda Patra (2016). *International Journal of Knowledge Discovery in Bioinformatics (pp. 1-16).*
www.irma-international.org/article/genetic-diagnosis-of-cancer-by-evolutionary-fuzzy-rough-based-neural-network-ensemble/171415

Interaction of Nucleic Acids: Hidden Order of Interaction
Gennadiy Vladimirovich Zhizhin (2021). *International Journal of Applied Research in Bioinformatics (pp. 1-8).*
www.irma-international.org/article/interaction-of-nucleic-acids/278747