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Popular Article

## Bioinformatics: Benefits To Mankind

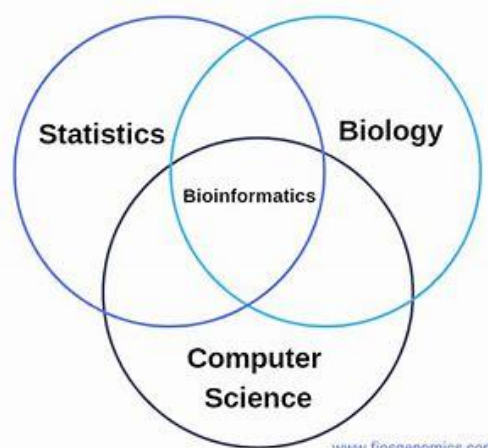
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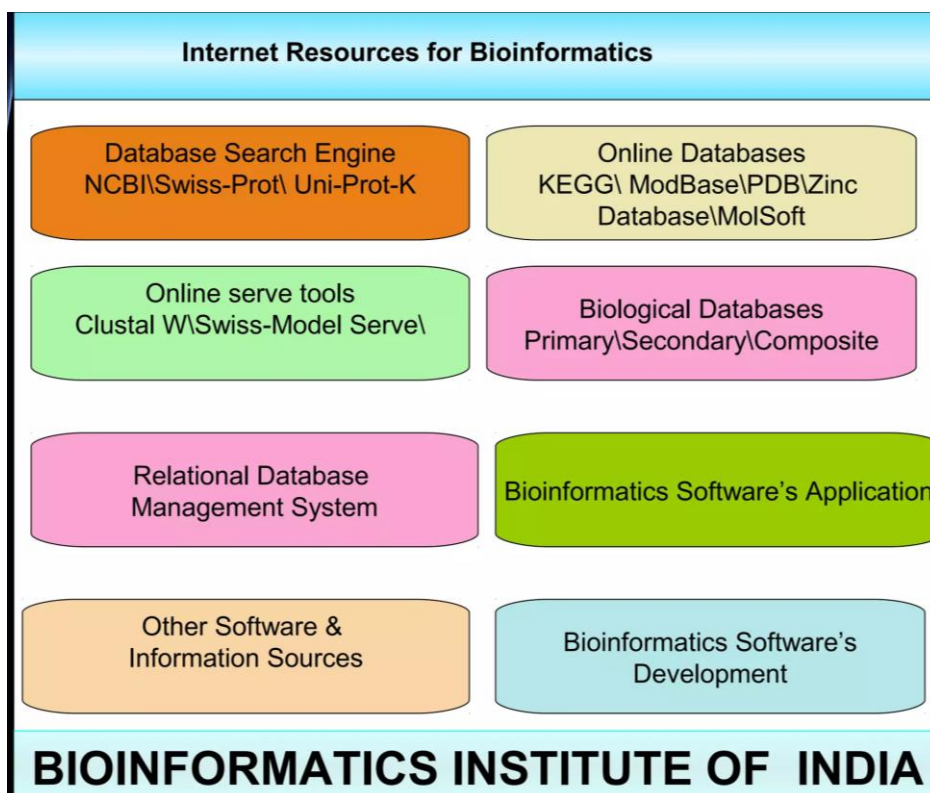
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Bioinformatics is defined as “a scientific discipline that encompasses all aspects of biological information acquisition, processing, storage, distribution, analysis, and interpretation that combines the tools and techniques of mathematics, computer science, and biology with the aim of understanding the biological significance of a variety of data”. Bioinformatics-tools include any products that store, organize, evaluate, integrate, analyse, and/or distribute biological data. Bioinformatics developed after automated protein and DNA sequencing technologies were introduced around the mid-1970s, and after researchers started to use computers as central sequence repositories that were accessible remotely, a development that occurred in the mid- to late 1980s.

Bioinformatics covers a multiple of scientific disciplines and encompasses various areas of genomic analysis, including: (i) computational genomics (the storage and analysis of DNA sequence using various software), (ii) proteomics (laboratory methods used to determine what proteins are actually expressed and possible cellular location), (iii) transcriptional profiling (the analysis of mRNAs at different stages of cell growth and conditions), (iv) functional genomics (combined function prediction and experimental biological analysis of gene function), and (v) structure function determinations (predicted as well as determined 3-D structures and comparison to known protein structures and functions).



In general, the aims of bioinformatics are three-fold. First, at its simplest bioinformatics organize data in a way that allows researchers to access existing information and to submit new entries as they are produced. The second aim is to develop tools and resources that aid in the analysis of data. Development of such resources dictates expertise in computational theory, as well as a thorough understanding of biology. The third aim is to use these tools to analyse the data and interpret the results in a biologically meaningful manner. Some of the well-known databases include GenBank (Genetic Data Bank), SWISS-PROT, PDB (Protein Data Bank), PIR (Protein Information Resource), SCOP (Familial and Structural Protein Relationships), CATH (Hierarchical Classification of Protein Domain Structures), etc. These databases are available as public domain information and hosted on various Internet servers across the world. Basic research and modelling is done using these databases with the help sequence analysis tools like BLAST (Basic Local Alignment Search Tool), FASTA(Fast-All), CLUSTALW, etc., and the modelled structures are visualized using visualization tools such as WebLab, MOLMOL, Rasmol, etc.



Bioinformatics is faced with a strong demand for immediate solutions; because the genomic data that are being uncovered encode many biological insights whose deciphering can be the basis for dramatic scientific and economical success. With the pre-genomic era that was characterized by the effort to sequence the human genome just being completed, the post-genomic era that concentrates on harvesting the fruits hidden in the genomic text. Today



the researcher investigating humans or any interesting organism, whether microbe, plant or animal, for which the data on the genome sequence are already or will be available in the near future, is offered all the necessary information concerning the complete DNA sequence. It is predicted that bioinformatics research will have a dramatic impact on improving our understanding of diverse areas. Bioinformatics is expected to be an important contributor to the global economy. Research in this field has already made a major impact on the pharmaceutical industry and drug discovery, agriculture, and health care and environment. Bioinformatics tools will increase the potential of curing inherited human diseases and producing new human medicines. Benefits of bioinformatics to mankind are vast; some of these are discussed below.

### **Health Care**

Bioinformatics is a rapidly emerging field of biomedical research. As genomic and biomedical data is accumulating, bioinformatics tools are helping in managing and analyzing this data for health care. Bioinformatics can be considered a sub-discipline of Biomedical Informatics which addresses the biomedical challenges at molecular level. It has a direct impact not only on the development of new diagnostics, therapeutics, and vaccines but also on understanding of infectious disease mechanisms, pathogen-host interactions and transmission cycles. Availability of bioinformatics tools is helping in realizing the potential benefits of human genome project by identification of disease susceptibility genes and the development of many new treatments, the ability to predict those patients at risk for experiencing adverse reactions or patients with a high probability of experiencing improved efficacy. Application of bioinformatics approach for understanding of proteomic data can lead to accurately correlate clinical parameters of patient responsiveness to a particular therapy.

Uncovering of the differences in people's genetic makeup will not only yield increased understanding of the genes that cause or contribute to diseases, but ultimately will help health care providers to prescribe the right medicine in the right amount for each person. In addition, this knowledge might prevent the negative side effects of the "one-size-fits-all" method of prescribing drugs that is most often used today. Bioinformatics is also likely to lead to new classifications of diseases. Diseases traditionally characterized through symptoms (phenotype) may be reclassified according to their genetic characteristics (genotype).



## **Drug Discovery**

The drug discovery process is complex, time consuming and very expensive. Typically, about 5 years' time is required to develop a candidate drug, while the clinical phases leading, possibly, to the commercial availability of the drug are even longer for a total cost of more than 700 million dollars [13]. The focus of the pharmaceutical industry has shifted from the trial-and-error process of drug discovery to a rational, structure-based drug design. A successful and reliable drug design process could reduce the time and cost of developing useful pharmacological agents.

Computational methods are used for the prediction of 'drug-likeness' which is nothing but the identification and elimination of candidate molecules that are unlikely to survive the later stages of discovery and development. Drug-likeness could be predicted by genetic algorithms. Genomics has become a major source of drug targets, and bioinformatics is crucial for finding and validating novel targets so as to minimize investment in laboratory resources. With regularly updated public databases, bioinformatics can contribute to these processes by providing functional information of target candidates and correlating this information to the biological pathways. Bioinformatics tools can be used to understand the mode of action and the efficacy of a given compound and to help elucidating the pathophysiology of a diseases.

Many tools have been developed for drug discovery. A comprehensive bioinformatics software package 'Bio Suite' was developed that integrates the functions of macromolecular sequence and structural analysis, chemo informatics and algorithms for aiding drug discovery. DOVIS: a utility software was developed for high-throughput virtual screening using Auto Dock as molecular-docking-based virtual screening is an important tool in drug discovery that is used to significantly reduce the number of possible chemical compounds to be investigated.

## **Forensic Analysis**

Bioinformatics and forensic DNA are inherently interdisciplinary and draw their techniques from statistics and computer science bringing them to bear on problems in biology and law. Personal identification and relatedness to other individuals are the two major subjects of forensic DNA analysis. Mass disaster cases require managing, analyzing, and comparing large numbers of biological samples and DNA profiles, making necessary the use of electronic laboratory information management systems for large-scale sample logging and tracking, coupled with bioinformatics tools for DNA database searching [20].



Polymerase chain reaction (PCR) amplification of short tandem repeat (STR) loci is followed by use of bioinformatics tools such as GeneScan™ and GenoTyper™ for determination of the presence or absence of STR alleles associated with a sample.

Whenever crime scene investigation needs identification of bacteria, insects, and plants, genomic sequences can be sequenced using microarray and analyzed using bioinformatics standard techniques.

Bioinformatics tools such as CODIS (Combined DNA Index System), DNA-View, MDKAP (Mass Disaster Kinship Analysis Program), MFISys (Mass Fatality Identification System) were used for forensic analysis of World Trade Centre disaster, New York, USA, September 11, 2001. DNA database searching bioinformatics tools have also been used for the victims of the South Asian Tsunami disaster.

### **Biodiversity Management**

Scientific information about biodiversity is either scattered in many databases or resides on paper or available through museums, herbaria and repositories. The information about organisms is usually not available and thus not used for making policies and decisions regarding them. Biodiversity management and conservation requires that information about it be available easily. Research activities are being conducted around the world to improve our ability to manage biodiversity information, and the emerging field of biodiversity informatics is attempting to meet the challenges posed by this domain. This new suite of methodologies and tools extends contemporary computer science and informatics principles within the context of biodiversity data. Biological complexity of the organisms, presence of large number of species and ecosystems, interactions of species with multiple abiotic factors makes biodiversity information very complex. Good database designs are required for management and long-term stewardship of information related to biological diversity. Biodiversity informatics requires frameworks and approaches that can accommodate the full range of biological information - from molecules to morphological features, to populations, to habitats. Mechanisms are required that enable us to make correlations among new datasets and traditional data and data from even more disparate sources, such as ecosystem-scale global change and carbon cycle data, compile those data in new ways, analyse and synthesize them, and present the results in an understandable and usable manner. Many nations are now Parties to the Convention on Biological Diversity, and many have joined other treaties related to biodiversity conservation. These treaties will have direct consequences to the way in which biodiversity information is gathered, organised, maintained and disseminated within



countries.

Technologies such as ‘scratchpads’ and ‘DNA bar code methods’ have been developed for managing and sharing biodiversity information. Software packages such as Plant Info, Garden Info, Seed Pack, Biolit and databases such as Fungal Database Melirolales, Sacred Groves of Kerala and Wild Ornamental Plants of the Western Ghats have also been developed for organizing, managing and monitoring biodiversity information. Tools can be developed for invasive species risk assessment by creating predictive ecological models for all species not native to a particular region and then using these models to develop strategies for avoiding species invasions. The fledgling field of biodiversity informatics looks set to deliver major advances that could turn the Internet into a giant global biodiversity information system.

### **Other Benefits**

Genomics, proteomics and bioinformatics offer the potential to identify genes or loci regulating traits of economic importance in animals. Production traits that are proposed as eligible for transgenic modification include increased growth rate and improved carcass composition, improved feed utilization, modified milk composition, improved mohair production improved reproductive performance and increased disease resistance. In veterinary research, bioinformatics tools were used in the detection of new castle diseases and to generate novel solutions for the continued improvement and development of molecular diagnostics.

Bioinformatics is being used in the building of global databases in microbiology to build an accumulative knowledge repository that captures the reams of experimental data and meta-data about micro- organisms and to develop general data mining tools for knowledge discovery within this data-rich environment, in order to establish dynamically updated and flexible portals upon the observed bacterial diversity and related biotechnological innovations with the ultimate goal of valorising newly discovered insights as new applications or end-products.

Bioinformatics is also helping in climate change studies. There are many organisms which use carbon dioxide as their sole carbon source and increasing levels of carbon dioxide emission is one of the major causes of the global climate change. The study of genomes of these microbial organisms, which is possible through bioinformatics, helps in proposing ways to decrease the carbon dioxide content.



## Ethical Issues

Bioinformatics research creates number of ethical, legal and social, security concerns like fairness in the use of genetic information, privacy and confidentiality of genetic information, psychological impact and stigmatization due to an individual's genetic differences. If personal data become accessible to unauthorized persons, if information on genetic dispositions are passed on to employers and insurers, they can use the genetic information to the unfair disadvantage of some people. It can also promote racism as particular diseases appear in particular groups only. The more exact investigation of the human genome will show specific differences between the DNA sequences of ethnical groups, which are connected with their environment and the physiological particularities of the group. Development of drugs that target specific individuals might lead to stratification.

The Ethical, Legal and Social issues research programme (ELSI) is considered the world's largest bioethics program. The programme is jointly funded by the US Department of Energy (DOE) and the National Institutes of Health (NIH). The programme is concerned about safeguarding the privacy of individuals and groups who contribute DNA samples for large-scale sequence variation studies.

