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REVIEW ARTICLE: Current Topics

Title: Bioinformatics: Past, Present and Future

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ABSTRACT

Biology or life science is a descriptive science which deals with the study of life. The biological data naturally fluctuate from size and state of a life form to its genomic architecture. Biodiversity in terms of 'forms and functions', generates 'data diversity'. With the development of gene sequencing and other bio-techniques the data generated in life sciences increased fabulously and marvelously. Hence, it becomes much important to capture, manage, process, analyze as well as to interpret those data. Aiming to reconcile all these, scientists developed bioinformatics, an interdisciplinary field, creating techniques and programming devices for understanding organic information, particularly when the data sets are enormous and advanced. Therefore, bioinformatics is a combination of biology, computer science, mathematics, statistics, information science and engineering to inquire about and to decipher organic information. Bioinformatics has been utilized for in silico examinations of organic inquiries utilizing scientific methods. The present endeavor explores how the bioinformatics has been evolved as an interdisciplinary science. Moreover, resources and web tools of bioinformatics are reviewed and its applications in various fields including its relevance to other disciplines are also highlighted. We tried to summarize the global bioinformatics market and bioinformatics in Indian scenario as well. In addition, the future prospects of this science are also addressed.

INTRODUCTION

Abbreviations: NCBI - National Center for Biotechnology Information; EMBL - European Molecular Biology Laboratory; HGP - Human Genome Project; CADD - Computer Aided Drug Designing.

According to David Lipman, the Director of the National Center for Biotechnology Information (NCBI), Margaret Oakley Dayhoff, an American chemist, is the "mother and father of bioinformatics" 1. Paulien Hogeweg and Ben Hesper in 1970 put forward the term "Bioinformatics" as the process of study of information processes in biological system 2-4. NCBI defined bioinformatics as a combination of biology, computer science, mathematics, physics and informational technology 5. The scope of bioinformatics includes computational resources along with organization and interpretation of a wide range of biological evidence gathered from study of genetics, proteomics, metabolomics, cell biology, molecular biology and similar information.

Due to its large inclusive zone bioinformatics has become one of the most important scientific informative resource tool in every field of science. Due to recent developments in the fields of

genomics and proteomics, it has become one of the most informative tool in area of different branches of life science. At an increasingly integrative level, it examines and lists the biological pathways and systems which are significant parts of system biology. In basic biological science, it helps in the recreation and displaying of DNA⁶, RNA⁶⁻⁷, proteins⁸ just as bimolecular interactions⁹⁻¹⁰.

After the discovery of protein sequence of insulin by Sir Fedrik Sanger in the early 1950s, the computers became essential in the field of molecular biology. It became quite difficult to compare multiple sequences manually. We know that Margaret Oakley Dayhoff was a pioneer in this subject 11. She gathered first primary protein arrangement databases and published as books and she also discovered the pioneer methods of sequence alignment 12-13.

Bioinformatics, since multidisciplinary in approach, is considered as computational biology at present. Biological computation combines bioengineering, biology and info-tech to build biological computers, whereas bioinformatics helps understanding biology more vividly by using such computations. The important role of bioinformatics in the computational biology has enabled in generation of comprehensive output of information from several newly generated organic data inputs. Using the techniques of

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bioinformatics some important advents have been made in the fields of DNA, RNA, and protein sequencing by incorporating software programs based on principles of algorithms which are attributable to several important concepts. Recent theoretical concepts like graph theory, soft computation, data mining, artificial intelligence, image processing, and computer simulation significantly have contributed to development of the graph theory algorithms. Furthermore, the advanced theoretical concepts of discrete mathematics, control theory, system theory, information theory, and statistical developments have also significantly contributed in development of algorithm based graph theories for their application of bioinformatics.

The results of the explosive development in bioinformatics after the mid-1990s are mostly attributable to the process and needs of the phenomenal task of the Human Genome Project and thereafter by the rapid advances in the techniques of DNA sequencing in lesser time period with greater accuracy Bioinformatics is a powerful tool in battling against toxicity and last stage drug failures..

A little conviction about bioinformatics

The components of bioinformatics are fascinating in true sense. These include biology, chemistry and biochemistry, information technology and computing power, databases creation, development of algorithm and statistics, analysis of data and interpretation, data management and maintenance, data integration, data mining, profile generation, molecular biology, molecular modelling, molecular medicine, computer and system sciences, applied statistics, applied physics, applied mathematics,

theoretical CS, artificial intelligence, machine learning etc. (Figure 1).

Bioinformatics accommodates a better global perspective in experimental design. It provides significant data based support for testing various hypotheses regarding the structure or function of a gene or protein. Due to its immense data repertoire, bioinformatics is becoming a powerful means for delineating the facts related to drug toxicity and last stage drug failures. Bioinformatics has also shown significant potentiality in the analysis and interpretation of variations and hidden information in the field of genetics and proteomics. Bioinformatics facilitates revealing of hidden patterns or fascinating relationships between genes and molecular mechanisms through data mining. Bioinformatics also help in disease state analysis and understand genome of any creature in any case (like cancer or any other disease).

Bioinformatics provides a better experimental design in global context. Bioinformatics is a powerful tool in battling against toxicity and last stage drug failures. Bioinformatics has the potentiality to assess genetic variations along with its immense capability of revealing the protein structures from the concerned data bank. Bioinformatics facilitates revealing hidden patterns or fascinating relationships between genes and molecular mechanisms through data mining. Bioinformatics also help in disease state analysis and understand genome of any creature in any case (like cancer or any other disease)

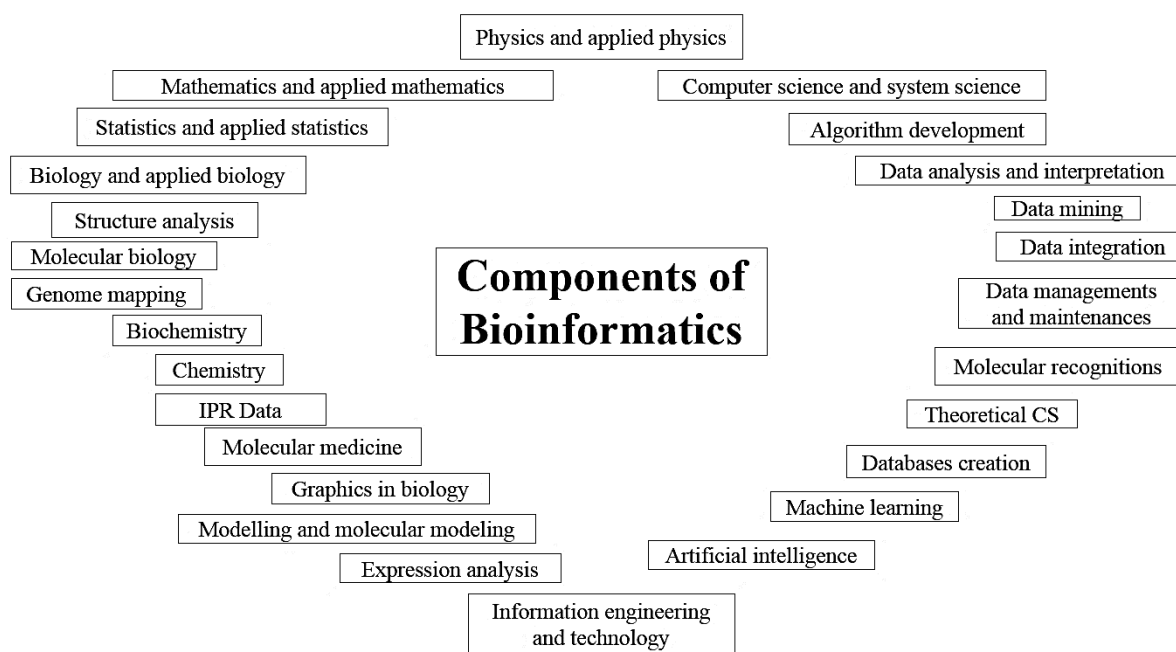


Fig 1. Components of bioinformatics

Mainly three things are to be accomplished by bioinformatics. First of all a new and novel set of algorithmic cascade and statistical system has to be developed. Second, development and implementation of tools are needed and third, analysis and interpretation are to be accomplished.

Generally, we use bioinformatics this way which including Creation and storage of biological databases, DNA/RNA/Protein sequence comparison, Unknown gene/proteins prediction, Literature searching, Compare the data with others, Compile and distribute data for others, etc.

Bioinformatics: A Historical Retrospect

In this section, we tried to focus the chronological development of bioinformatics. The story began in 1665 with the discovery of the Micrographia by Robert Hooke 14. Later it continued as follows-

1663: Antoni van Leeuwenhoek discovered bacteria 15.

1686: John Ray made the systemic catalogue of 18,600 classes of plants and also provided their description in his book "Historia Plantarum" which provided the definition of species in the context of common descent16.

1843: Richard Owen provided a detailed distinction between the principles and examples of homology and analogy17.

1864: The modern and essential zoological classification was outlined by Ernst Haeckel 18.

1865: Gregor Johann Mendel (father of genetics) discovers the molecular basis of inheritance 19-20.

1902: Sutton and Boveri suggested the chromosome theory of heredity for the first time 21-22.

1905: The terminology "genetics" was proposed by William Bateson23.

1913: First linkage map created by Alfred Sturtevant (working with T. H. Morgan) 24-25.

1930 - Electrophoresis first introduced 26.

1953 - The helix model for DNA was elaborated and explained by Watson & Crick using the data obtained from x-ray crystallography in which Franklin and Wilkins also contributed significantly 27-29.

1954 - The heavy atom method was developed by Perutz's group which played a significantly important role in delineating the crystallographic structure of proteins 30.

1955 - Sir F. Sanger analyzed primary protein sequence of bovine insulin and announced 31-33.

1969 - The ARPANET is made by linking computers at Stanford and UCLA 34-35.

1970 - Needleman-Wunsch algorithm was published in a small print which played significant role in sequence comparison 36.

XML (eXtensible Markup Language), a descendant of SGML (Standard Generalized Markup Language) was invented by Charles F. Goldfarb, Ed Mosher, and Ray Lorie at IBM [37].

1972 - The primary recombinant deoxyribonucleic acid molecule is made by Paul Berg and his group 38-39.

1973 - Protein Data Bank (PDB) is introduced by Brookhaven. The concept of Ethernet described and established by Robert Metcalfe 40-41.

1974 - The concept of upgrading the network connections in computer of distant places for creating an internet connection was developed by Vint Cerf and Robert Khan. This concept later was further developed in the Transmission Control Protocol (TCP) 41.

European Molecular Biology Laboratory (EMBL) was established 42.

1975 - Gates and Paul Allen initiated the Microsoft Corporation. P.H. O'Farrell announced the 2D-electrophoresis, for separation of proteins on SDS polyacrylamide gel based isoelectric points 43-44.

1981 - Patrick O. Brown invented DNA Microarray Technology 45.

1984 - Lipman and Pearson announced the FASTA algorithm for sequencing and primer designing techniques 46.

1985 - PCR (Polymerase Chain Reaction) technique was discovered by Kary Mullis, while working as a chemist for Cetus Corporation in Emeryville, California [47].

1988 - National Centre for Biotechnology Information (NCBI) is established at the National Cancer Institute 48.

National Research Council started research with "Human Genome" 49.

The FASTA algorithm for sequence comparison is published by Pearson and Lipman 50.

A new program, an online bug designed by a student, infects 6,000 military computers within the US 40.

1989 - The genetics Computer Group (GCG) established as a private company 51.

Oxford Molecular Group (OMG), Ltd. founded, UK by W. Graham Richards, David, Anthony Marchigton, Ricketts, Anthony Rees, and James Hiddleston. OMG start to launch their primary products like Anaconda/Anaconda, Asp, Cameleon etc. for molecular modeling, drug designing and protein designing 52.

1990 - Hypertext Markup Language (HTML) introduced by Tim Berners-Lee 53.

1990 - The BLAST program is implemented by Altschul, et al. 54.

Molecular applications group in California was established by Michael Levitt and Chris Lee. Their first products are Look and Seg Mod are used for protein designing and molecular modeling 55.

1991 - European Organization for Nuclear Research (CERN) announces the creation named "World Wide Web".

Myriad Genetics is established in Utah. The company came out with the establishment of sequencing of the major genes like: BRCA1, CHD1, BRCA1, MMSC1, MMSC2, CtIP, MMAC1, p16, p19 and MTS2 38.

1992 - European Bioinformatics Institute (EMBL-EBI) established 56.

1993 - Sun Microsystems introduced the first graphical web browser named "Mosaic for X" and the first molecular biology Web server named "ExPASy" 57.

1994 - Netscape Communications Corporation founded and releases the commercial version of NCSA's (National Center for Supercomputing Applications) Mozilla 58.

1995 - JAVA developed by James Gosling at Sun Microsystems 59.

The Haemophilus influenzae genome is sequenced 60.

The Mycoplasma genitalium genome is sequenced 61.

algorithms for new bioinformatic software whereas existing software are getting continually updated 79.

1996 - The genome of baker's yeast i.e. *Saccharomyces cerevisiae* (12.1 Mb) is sequenced 62.

Bairoch, et.al reported Prosite database 63.

Affymetrix creates the first commercial DNA chips 64.

1997 - The genome for *Escherichia coli* (4.7 Mb) is published 65.

1998 - The genome for *Caenorhabditis elegans* are published 66.

Establishment of the Swiss Institute of Bioinformatics was announced 67.

2000 - Development in bioinformatics tool led to the delineation and publication of the genome for *Pseudomonas aeruginosa* (6.3 Mb) 68.

The *Arabidopsis thaliana* genome (100 Mb) is sequenced 69.

The *Drosophila melanogaster* genome (180 Mb) is sequenced 70.

2001 - The human (*Homo sapiens sapiens*) genome (3,000 Mb) is published 71.

The chronological history gives us a clear idea about how bioinformatics evolves.

Applications of bioinformatics □ current scenario worldwide

Bioinformatics have a lot of application in various fields. Nowadays bioinformatics is used for evolutionary studies and phylogenetics. The knowledge of the sequence alignment based on the principles of various algorithms in bioinformatics helped in construction of Phylogenetic trees 72. These phylogenetic trees help to identify the close ancestors of a species.

Bioinformatics help in climate change studies. Due to global climatic change ice is lost, both in north & south poles, causing the rise of sea level and ultimately leading to the fluctuation of temperature across the world. To address the issue, bioinformatics may help by sequencing microbial genomes which are able to reduce levels of CO₂ and other greenhouse gases (which are also responsible for this temperature raising) from the atmosphere 73.

Bioinformatics and genomics combinedly shape personalized medicine 74. Molecular medicine is a combination of traditional knowledge worldwide, modern science and technology. The needful sequencing of Human genome can immensely develop biomedical research and clinical medicine. Diseases having a genetic component are adjusted to individual response to the outer environmental factors which may further influence the genome by causing mutation or polymorphic variations. The multigenetic diseases like cancers, heart disease, and diabetes are classical examples of this. Advances in the bioinformatics has enabled the completion of the human genome sequencing and thereby has enabled the researchers to look after the genes responsible for different disorders and variations within the human species at their molecular levels. Moreover, with the development of pharmacogenomics, clinical medicine became more personalized. The logic of bioinformatics are simple. Sequence of genome of a particular person is transformed into digital parameters that are converted into digital data. These digital data may be further stored, analysed, processed and retrieved as needed. The physicians can use these information to develop and tailor the most suitable drugs and other therapeutic molecules for treating a particular patient. 75. Furthermore, bioinformatics also enable us in bringing out therapy and management by altering the preventable lifestyle measures at the earlier stages before development of the disease itself. This may be advantageous in controlling various common as well as infectious diseases 40. Besides, in the field of biomedical applications, bioinformatics also helps to analyse infectomes (microbial pathogens and hosts interactions related studies) and studying pathology 76. Currently bioinformatics is known as transitional bioinformatics in the world of medicine and health. Transitional bioinformatics is another developmental tool that helps in generating novel techniques for bringing together the biological and clinical data. In this way it enables to integrate the evolution of clinical informatics methodology and the biological observations 77-78.

Bioinformatics have huge contribution in Human Genome Project (HGP). The functions of almost half of the genes detected in human body are unknown till date. Using bioinformatics as a tool, scientists are trying to identify the activities of many such genes to establish proper correlations with the functional genes, and, developing molecular mechanisms for prevention (with diagnosis and treatment) of diseases. Moreover, scientists are also trying to develop new

Bioinformatics can help in gene therapy. Gene therapy is an approach to treat, cure or even to prevent disease by changing the gene expression of a person. The progress in this field is yet to reach satisfactory level. Therefore, in future bioinformatics may help to understand gene therapy better.

The computational algorithm of bioinformatics have provided important tools for documentation of vaccine targets from sequenced data from the genome or proteome of organisms. Therefore, both contribute to advance the course of research as well as to design veterinary vaccines 80.

Bioinformatics is very supportive in drug development and Computer Aided Drug Designing (CADD). In spite of availability of numerous

Nowadays, based on the bioinformatics, a new technology has been developed known as “omic” technology. This means the use of bioinformatic tools for a holistic sequencing and documentation of the genes from a particular person (genomics) or the messenger RNAs which help in transcription (transcriptomics), the proteins present at a particular time or in a particular system (proteomics) or the metabolite system of an organism (metabolomics). These omics have brought out a huge leap forward advancement in the screening and diagnosing processes of different disorders as well as their management and prognosis. The bioinformatic lead development of omics have also strengthened the techniques and applications of the microarray and mass spectrometry techniques. One of the most important applications of the omic technology has been found in development of screening tests for gynaecological cancers and obstetric complications 84. Moreover, bioinformatics plays a significant role in genomics and proteomics. This includes gene identification and functional annotation, finding repetitive and regulatory sequences, characterization of SNP’s, haplotype analysis, finding protein interactions, restriction analysis/primer design, protein structure modelling/prediction, identification of protein active/binding sites etc. Nowadays, computational proteomics has emerged as a new and promising branch 85.

Cancer bioinformatics, a combination bioinformatics and omic technologies, deals with the organization and data analysis so that important trends and patterns of a particular cancer can be identified including its epigenetics. The ultimate aim of cancer bioinformatics to discover and develop new therapeutic and/or diagnostic protocols for cancer 86.

Bioinformatics is a crucial tool for microbial genome applications. We

drugs in market, a good number of diseases are still incurable. Bioinformatics and other modern computational tools are used to identify the mechanisms of infections with many other aspects of those diseases and Computer Aided Drug Designing (CADD) helps to design new drugs for their control 81.

We know that, Bioinformatics is a major part of biotechnology and its application to biotechnology includes animal breeding agriculture, environmental and energy management, fermentation technology, healthcare/pharmaceuticals, recombinant DNA technology (RDT), dairy production (white bio-tech), aquaculture (blue bio-tech), genetically modified organisms (GMO) production, vaccine designing etc 82-83.

know that, Microbes are used for many years for addressing numerous issues. It is known that microbes are ubiquitous and can be found everywhere even under extreme conditions like high temperature etc. Bioinformatics may be fruitful for understanding the genomes of those microbes which have broad and far reaching implications on environment, health, energy and industries. To aid this the Department of Energy (DOE) of the United states initiated the Microbial Genome Project in 1969 which targets to carry out the sequencing of genomes of bacteria that may play useful roles in energy production, environmental cleaning up, industrial processing and toxic waste reduction40. Moreover, Bioinformatics focusses on those microbes which are useful as an alternative energy source and waste cleaningbio. Scientists identified Chlorobium tepidum, a bacterium which is capable for generating energy from light 87-88. Bioinformatics also helps to examine the genome antibiotic resistance bacteria like Enterococcus faecalis-a 89.

These days forensics science is very important. Bioinformatics based tools play a major role in Forensic Sciences and Research. Many things like extracting the tiniest DNA from the tiniest field sample or microbial sample, DNA profiling and analysis, identifying parentage, criminal investigation etc. can be done in more advanced ways. Automatic Fingerprint Recognition System (AFRS), computational tools are aiding to the Forensics in every possible way 90.

Bioinformatics is very important for agriculture/crop improvement. The combination of bioinformatics & agri-genomics help to analyze and integrate plant genomes. As a result, crop productivity gets increased, nutritional quality and quantity of crop also become much better, crop may become more pest resistant and water tolerant and so on 91.

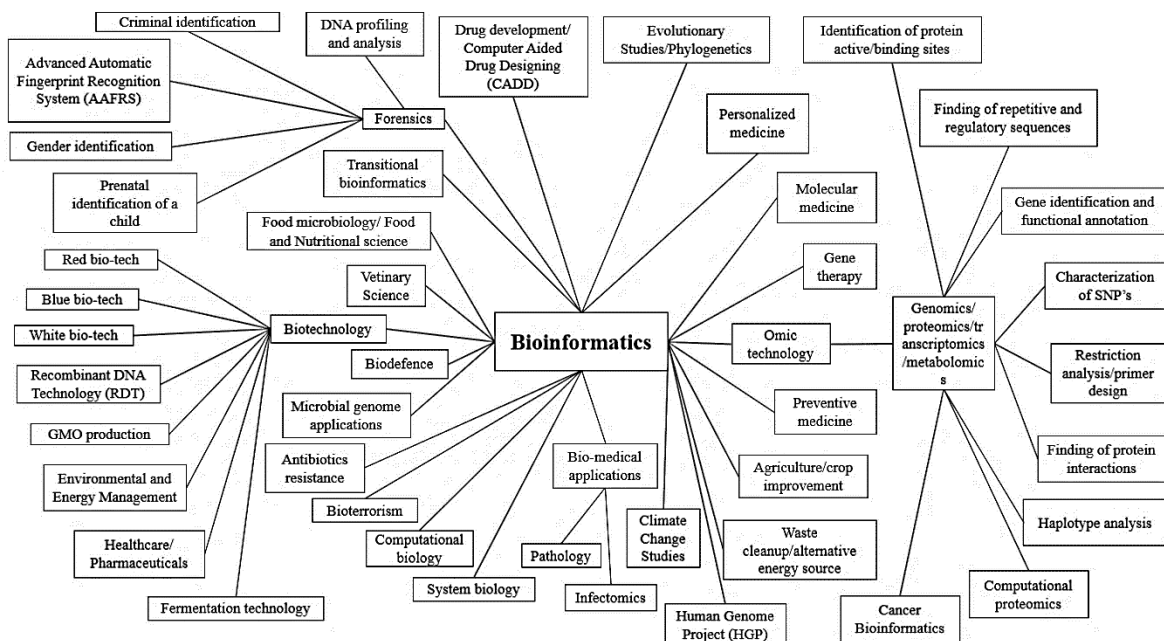


Fig 2. Relation with the other field of applications of bioinformatics

Bioinformatics is related with biodefense, bioterrorism, and bioweapon creation. Biodefense protects against a group of organisms which are potentially threats (or infectious diseases) for human beings. The contribution of bioinformatics to biodefense is not substantial. More algorithms need to be created for the same purpose 92. Bioterrorism is using microbes to harm people. A bioterrorist may design many such harmful agents using biological data bank, and, on the contrary, a scientist may develop preventive drugs against such micro elements applying bioinformatics. Bioinformatics may also be helpful to identify those bioterrorists 93-94.

Nowadays biotechnology, genetic engineering, bioinformatics advanced sufficiently. It is not impossible for human to create a “superbug” which may be highly lethal for mankind and resistant to environmental fluctuations 95. Synthetic Biology, a newly emerging field, has the

Bioinformatics help to develop various new tools and techniques for computational biology. Bioinformatics is also helpful for System Biology. Bioinformatics and computational biology help to model biological processes at levels of system biology, genome, transcriptome, or organism. Moreover, bioinformatics and computational biology attempt to provide answers by whole cell modelling and linear optimizations in system biology.

Little view of global bioinformatics market from at present as well as future

A forecast of 25 % annual growth rate has been made for the global Bioinformatics for the period of 2016 – 2027. The profit availed from the market of global bioinformatics is expected to increase from \$12465 million in 2016 to \$95365 million by 2025. Most responsible fact for this huge growth is the crucial role of bioinformatics in the field of drug discovery¹⁰⁰⁻¹⁰³.

Bioinformatics in Indian scenario

Nowadays it is estimated that there are approximately 450 million internet users across India. In our country, Bioinformatics developed enough due to its advancement in different fields like basic research, new software creation, development of databases and web-servers with its application. India is currently a treasure trove with talented young minds in computation and IT¹⁰⁴. In 1960s, bioinformatics started its journey in India after the discovery of Ramachandran plot by Prof. G. N. Ramachandran and his colleagues¹⁰⁵. Presently, India has already been able in developing an extensive network in the field of education and training needed to develop the bioinformatic application in different fields that include different Centers of excellence, Bioinformatics centers and facilities out of which more than 170 are supported by the Department of Biotechnology, Government of India. Moreover, Dept. of Health, Dept. of Agriculture, Dept. of Electronics and Telecommunication etc are also developing strong infrastructure for the bioinformatics related educational programs and their research outputs¹⁰⁴.

Addressing manifold and versatile challenges, today India has substantial and global contribution to bioinformatics through her powerful computation skill, well developed IT industries, wonderful software and fascinating manpower. Few acclaimed national institutes significantly contributed to Indian bioinformatics since last few decades. The list includes CDFD (Centre for DNA Fingerprinting & Diagnostics), IOB (Institute of Bioinformatics), C-DAC (Centre for Development of Advanced Computing), IITD (Indian Institute of Technology, Delhi), CCMB (Centre for Cellular and Molecular Biology) etc. Between 2014-2017, nearly 10% of web servers including 3% of tools and software for bioinformatics in the global market were developed in India¹⁰⁴.

India is planning to combine its strength in IT and biotech to create a new Bio-IT park¹⁰⁶. Till date, scientists of various fields in our country are in research to develop bioinformatics. It is expected that Indian bioinformatics may play a significant role in global bioinformatics.

The future of bioinformatics

It is almost impossible to determine the future of any scientific

potential to design new types of bioweapons. Horsepox virus, an erstwhile extinct virus, has been brought again to forefront by a research team lead by virologist David H. Evans at the University of Alberta 96. The \$100,000 project was started by Tonix pharmaceutical company. This has been ethically challenged as being a close relative of smallpox, the horsepox virus may rage havoc once again if mutated accordingly by any means. Only the Russia and U.S. retain copies of that horsepox virus 97.

Bioinformatics related to microbial world brings out the advantageous and disadvantageous effects of different microbes on foods. Research and data analysis by bioinformatic tools significantly help in understanding the genomics and proteomics of these organisms and analyse their requirements in food production, food processing, improving the quality and nutritive value of food sources 98-99.

disciplines, especially for one as young as bioinformatics. As Janet M. Thornton has predicted rightly that the future of biology will increasingly be controlled by the mutual interaction of bioinformatics and ‘classical’ biology¹⁰⁷.

If we look at the data centric view of bioinformatics, then, nowadays, a huge data come out from any biological research. The huge large, complex and sophisticated data generally come out of various types of biological researches including genomic sequences, molecular pathways, protein structures and many more. Bioinformatics machinery and tools are needed to be improved further for better analysis of data related to metagenomics, proteomics, and metabolomics. It is also important to develop more sensitive powerful devices for high throughput data collection and new software to rapidly analyze those big data in better ways. It is very crucial to make various new ways to represent biological data. Moreover, to better understand between the biological things and integration of biological data is very important and for this data integration technology (DIT) need to be more developed in future.

In future biotechnology become more developed based on bioinformatics¹⁰³. In near future, we will able to fight against various types of infectious diseases with the help of bioinformatics. Genetic disorders may be identified more vividly by bioinformatics. The microbiome analyses may develop manifold. Immunotherapies may also gain impetus from bioinformatics. Today the 2nd generation sequencers (or next generation sequencers) with higher data combining ability are introduced to the world of biotechnology. But, in future it is very possible that the 3rd or 4th generation sequencers may come and it will be equipped with sequencing 1000 to 100000 human genomes at a time. In future, it is also possible that newer branches like immunoinformatics, neuroinformatics, ecology and environmental informatics and many more will emerge from bioinformatics.

There are some new future challenges for bioinformatics related research. Firstly, development of new sequencing technologies which will be able to determine different variations in human, to link population and molecular studies, to link genetics with biodiversity, to generate barcode for life (genome bar-coding system) and to improve plant and animal breeding. Secondly, Implementation of Bio-banks is essential for storing molecular and phenotypic information and multi-omic data sets. Thirdly, opening of semantic web (web 3.0) for text mining. Fourthly, implementation of new highly advanced modeling and molecular modeling techniques. Fifthly, development of more advanced cloud computing and grid technologies which include new methods for handling data, new image technologies and new data analysis techniques. Sixthly, improvements regarding molecular diagnoses, pharmacogenomics, and many more could be done by the help of bioinformatics¹⁰³. More funding, more manpower and more intelligence are needed to make bioinformatics more advanced.

Scientists nowadays are trying to include all the genetic information to an electronic device. In future, the genomic information will integrate with electronic health records and it may be possible that we will get all necessary information related to our genome & health together in one

chip/device/app. With the development of bioinformatics personal genetic services will become more developed and accessible to everyone in near future. Moreover, a genetic database of people of any particular region may be developed in future¹⁰³.

Conclusion

Bioinformatics being the end product of amalgamation of many sciences is a highly sophisticated tool to address biological problems in a holistic manner. It may also significantly contribute to make the life process of human beings much better in many ways. Mining, processing & interpreting data with absolute precision; expanding areas of intervention with perfect correlation to all other related branches of interest; ever increasing demand for products in global market and many such aspects have made bioinformatics one of the most promising fields in modern science & technology. India is also marching towards excellence in this field. Further extension in research may lead bioinformatics playing a pivotal role in our entire life process, both individual & collective manners.

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