

Role of Bioinformatics in the Field of Biological Research - An Overview

Muhammad Sulaman Saeed^{1*}, Ayesha Saeed², Mohsin Iqbal³ and Muhammad Adnan⁴

¹Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan

²Department of Botany, University of Education, Dera Ghazi Khan Campus,
Sub Campus of University of Education, Lahore, Pakistan

³Institute of Horticultural Sciences, University of Agriculture, Faisalabad, Pakistan

⁴Department of Agronomy, College of Agriculture, University of Sargodha, 40100, Pakistan

*Corresponding Author E-mail: muhammadsulamansaeed2598@gmail.com

Received: 18.06.2020 | Revised: 23.07.2020 | Accepted: 4.08.2020

ABSTRACT

After completing the project of human genome in the year 2003, the concept of the computer mouse arose after the laboratory rat. Bioinformatics can be termed as the applications of different computational protocols to learn the complications in biological systems is called as Bioinformatics. There are many available genomic databases that have made possible to diagnose and cure many human disorders. These techniques include DNA microarrays technology and proteomics experimentations. Although to use these techniques, there are many problems and hindrances like which method comes fit, proper and concise. It also needs the sophisticated protocols to be done for the testing of enormous heterogeneity databases. This review mainly describes the Bioinformatics and the role of it in medical sector.

Keywords: DNA Microarray Technology, Proteomics Experiments, Bioinformatics, Genome.

INTRODUCTION

By the development of the Bioinformatics in 1980, the channel of it has been expanding day by day by processing a lot of genome sequenced database. It is a branch of conceptualized biology in which computerized control of the macro or micro molecules is taken up and these molecules are analyzed well and are used for the benefits of human beings (Altschul et al., 1997). In other words, we can say that this is computational biological branch in which different

computerized protocols are utilized to access molecules to make wonderful utilizations for human beings (Attwood et al., 1999). This is totally intended for the biological purposes only. We can simply justify the life as the combinations of different genes in the form of storehouse databases of genes (Attwood et al., 2013). Conventionally, the bioinformatics had structural orientations like Structure-based drug design (SBDD) and Rational Drug Design (RDD).

Cite this article: Saeed, M. S., Saeed, A., Iqbal, M., & Adnan, M. (2020). Role of Bioinformatics in the Field of Biological Research - An Overview, *Int. J. Rec. Biotech.* 8(4), 13-15. doi: <http://dx.doi.org/10.18782/2322-0392.1297>

Both these methods are used for discovering new compound with greater selectivity and effectiveness. Now we take the example of laboratory rat that is giving way to the computerized mouse as after the completion of human genome project it has revolutionized the whole world. In many countries of the world, wet labs experiments and bioinformatics together work very clearly and concise in different clinical and biological complications. The previous work is totally filled with huge databases of the genomic libraries which enabled the researchers to cure human diseases using different techniques like DNA microarrays and the proteomics experimentations. But there is always a crucial problem that method should be used which is safe, effective and well. The basic aim of this paper is to show the use of bioinformatics in the field of medical research (Baker et al., 2000).

Fundamentals of Bioinformatics Tools

The bioinformatics has many applications like some are given below:

1. The production of database in such a way that a researcher may find out informative knowledge from that and newly information could be added to that genome database. DNA Data Bank of Japan (National Institute of Genetics).
2. To produce the new data tools and analysis techniques for data like FASTA.
3. To utilize the tools to interpret results in biological systems.
4. By bioinformatics, any researcher can interpret the results from given database and can recover the human genomic diseases by using microarray technologies (Batemen et al., 2000).

Tools for Organization of Biologically Diversified Data

Biological databases are the databases that are big collections of gene libraries and are collected from various sources like different experiments, literature history, computational analysis and high experimentations technologies. But here is an important point that creating the databases it needs little raw stuff (Benson et al., 2013).

a) Source of Information for databases

Raw DNA arrangements, proteins sequences, genomes sequences, macromolecules and whole genome sequences make up the sources for databases. GenBank (R) is that place where comprehensive and detailed database is present that is nearly comprising of more than 240000 organisms along with their complete genome database. This configuration and organization of data is kept by National Center for Biotechnology Information (NCBI) which is part of International Nucleotide Sequence Database Collaboration (INSDC). GenBank works with collaboration with three organizations namely DDBJ, EMBL and NCBI (Benson et al., 2000).

b) Classification of Databases

The biological database is classified into 3 classes. 1. Primary 2. Secondary 3. Composite. First of all, we discuss the primary databases. This is the database which contains the information of the sequence alone. For example, GenBank. Secondary databases are those databases which are derived from the primary database. And composite database is which that is obtained from primary source but needs to find out its multiple sources. The NCBI is the example of composite database (Benson et al., 2013).

Data Integration

It is very important step in the bioinformatics field. As individualized data has no value but it is needed to be integrated well. In other words, we can say that these individual information must be put into systematic way. But it has no access to file formats and nomenclature. But this problem can be resolved by cross referencing in a well manner. So, after the process of integration the process of integrated data is used in different areas (Bermen et al., 1992).

CONCLUSION

It is concluded from the above discussion that bioinformatics is very advanced field and is touched with computational study of the databases of macromolecules of the organisms. It has wide range of techniques like microarrays technology and proteome

experimentations. These are very helpful to cure human genomic diseases. So, it is obvious that bioinformatics may revolutionize in the field of research and technology.

REFERENCES

- Altschul, S. F., Madden, T. L., Schaffer, A. A., Zhan, J., Zhang, Z., Miller, W., & (1997). Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res.* 25(17), 3389-3402. DOI: 10.1093/nar/25.17.3389.
- Attwood, T. K., Flower, D. R., Lewis, A. P., Mabey, J. E., Morgan, S. R., Scordis, P., & (1999). PRINTS prepares for the new millennium. *Nucleic Acids Res.* 27(1), 220-225. DOI: 10.1093/nar/27.1.220.
- Attwood, T. K., Gisel, A., Eriksson, N. E., & Bongcam-Rudloff, E. (2011). Concepts, Historical Milestones and the Central Place of Bioinformatics in Modern Biology: A European Perspective". *Bioinformatics - Trends and Methodologies. InTech.* Retrieved 8 Jan 2012. DOI: 10.5772/23535.
- Baker, W., Van den Broek, A., Camon, E., Hingamp, P., Sterk, P., Stoesser, G., & (2000). The EMBL nucleotide sequence database. *Nucleic Acids Res* 28(1), 19-23. DOI: 10.1093/nar/28.1.19.
- Bateman, A., Birney, E., Durbin, R., Eddy, S. R., Howe, K. L., & Sonnhammer, E. L. (2000). The Pfam protein families database. *Nucleic Acids Res.* 28(1), 263-266. DOI: 10.1093/nar/28.1.263.
- Benson, D. A., Karsch-Mizrachi, I., Lipman, D. J., Ostell, J., Rapp, B. A., & Wheeler, D. L. (2000). GenBank. *Nucleic Acids Res.* 28(1), 15-18. DOI: 10.1093/nar/28.1.15.
- Benson, D. A., Cavanaugh, M., Clark, K., Karsch-Mizrachi, I., Lipman, D. J., Ostell, J., & Sayers, E. W. (2013). GenBank. *Nucleic Acids Res.* 41, (Database issue): D36-42. DOI: 10.1093/nar/gks1195. DOI: 10.1093/nar/gks1195.
- Berman, H. M., Westbrook, J., Feng, Z., Gilliland, G., Bhat, T. N., Weissig, H., & (2000). The Protein Data Bank. *Nucleic Acids Res.* 28(1), 235-242. DOI: 10.1093/nar/28.1.235.
- Berman, H. M., Olson, W. K., Beveridge, D. L., Westbrook, J., Gelbin, A., Demeny, T., & (1992). The Nucleic Acid Database. A comprehensive relational database of three dimensional structures of nucleic acids. *Biophysics Journal* 63(3), 751-759. DOI: 10.1016/S0006-3495(92)81649-1.