

# Bioinformatics essay

[Science](#), [Biology](#)



As the world has changed into computer based and more of technology based, so has the various fields changed. Molecular biology is concerned with how the systems of a cell interact which also includes the DNA and RNA interactions plus the protein biosynthesis. It therefore involves several techniques which include Polymerase Chain Reactions, Western Blotting, southern blotting, expression cloning, gel electrophoresis and so many other techniques.

Since it is mostly involved in the interactions of the cell systems, it requires means to be able to identify the DNA which are similar, if the DNA of some organism are evolving, if some mutation in a DNA can help in new inventions about how to deal with certain problems of the world among others. Determination of all these requires the use of information technology. There have been major advances in molecular biology and advances in technologies of genomic study too. This is the reason why there has been growth in biological information created by the scientists (Gibas and Jambeck, 2001).

Because of these advances, genomic information has to be computerized and stored in databases in an organized manner for use. The databases are organized in a manner that scientists can retrieve information about a genome and more, add more information if need be and for future references (Gibas and Jambeck, 2001). It therefore means that the databases index the data for viewing and analysis purposes. Application of information technology in the field of molecular biology is what is known as Bioinformatics.

It involves the creation of algorithms statistical techniques, databases and computational techniques in molecular biology. There are theories on how the biological data should be solved and how they should be managed. These are the theories that are the base of computation, data storage, data analysis and formation of algorithms (Letovsky, 1999). Bioinformatics This is a field of science, created due to the changing world enabling advances in molecular biology, that merge molecular biology, information technology and computer science together (Baxevanis and Ouellette, 2001).

It is therefore a single discipline meant to make possible biological insight discoveries. It also creates an international perspective of biological principles discernation (Letovsky, 1999). As has been noted, this field was created due to the advances in molecular biology. At the beginning, as the world of computer began to take over, Bioinformatics was just meant for biological information storage. It was as simple as creation of the databases and maintaining them. Information stored at that time was amino acid sequences and nucleotide sequences.

At this time though, the researchers could retrieve information and put in more either revised or new invention (Baxevanis and Ouellette, 2001). As time and more advances are being made and more information is needed about the interaction of the cell system, Bioinformatics is evolving too. It is getting more complex with more information and more activities on molecular biology. This is due to the need to comprehend the normal cellular activities so that any abnormalities can be easily detected. Bioinformatics currently provides options of analysis and interpretation of data.

Most analyzed and interpreted data include amino acid sequences, nucleotide sequences, structures of protein and protein domains. This is what is referred to as computational biology (Baxevanis and Ouellette, 2001). There are two sub disciplines in Bioinformatics and computational biology. One is algorithm and statistics development for the assessment of large data sets. This includes data sets such as gene allocation from a specific sequence, formation of protein families from related protein sequences, protein structure prediction and protein function prediction (Westhead et al. , 2002).

The other sub discipline is information management which requires development of tools that allow retrieval, use and management of information (Westhead et al. , 2002). Importance of Bioinformatics Since there is advancement in the world of technology, bioinformatics is to improve the understanding of the so many biological processes. This involves research areas of involvement such as evolutionary biology, gene expression analysis, analysis of cancer mutations, determination of biodiversity, analysis of sequences, comparative genomics, genome annotation and several others (Lesk, 2005). Gene Expression Analysis

As this information technology system enables storage of information, analysis and interpretation, gene expression can be performed. This is done by the use of appropriate techniques which measure RNA levels such as sequencing of expressed complementary DNA, Serial Analysis of Gene Expression, micro arrays and so many other techniques. This is important in the determination of genes expressed in certain disorders (Lesk, 2005). Determination of such kinds of genes is important in the development of

therapies, as developments have gone further in molecular biology so that disorders can be corrected using gene therapies.

An example is gene replacement therapy. When a gene causing a specific disorder or disease is determined, a means of replacing it with a normal one could also be determined (Lesk, 2005). Evolutionary Biology Bioinformatics enables measurement of changes in the DNA of animals therefore determination of origins of evolution of animals from their ancestors. Other ways in which Bioinformatics has enabled researchers to study the origins of organism and animal species is through comparison of their genomes, hence classifying animals that originated from the same ancestor.

Bioinformatics through computational models enable prediction of system outcome over a specified period of time (Lesk, 2005). Analysis of Sequences There are so many sequences that decode different proteins. These sequences are made available in the databases. This provides sequences for analysis, for example if a scientist has a sequence of a gene obtained from a species of organism and would like to know the sequence, he/she would check with the sequences in the data bases. In these databases, the information helps determine the genes that encode specific polypeptides and regulatory sequences.

Sequence analysis also enables comparison of genes of species hence determination of certain protein functions (Lesk, 2005). Biodiversity Measurement Bioinformatics is also important as it enables measurement of biodiversity of an ecosystem. Biodiversity is all the genomes of all the different species of organisms and animals in an ecosystem. The animals and organisms' names have therefore to be collected, including their

descriptions, genetic information and distribution in a specific ecosystem. There are so many other important information about the organisms that have to be noted alongside the genetic information.

These are such as habitat needs, species and population size (Barnes and Gray, 2003). All this information is stored in the databases and is collected for a reason. Several studies that require animal genomic constitution in an ecosystem do take place, therefore need an information source. Information technology has enabled formation of specialized programs of software which are used by the scientists and researchers to retrieve, analyze and share information about their research. This leads to more progress in the field of molecular biology.

The importance of this is that it helps in the conservation of the ecosystem. For example, in an ecosystem, there are always those species that are endangered, this can easily be determined by this information technology system of biodiversity determination. Computer simulations has enabled modeling of conservation, population dynamics and calculation of a breeding pool's genetic health (Barnes and Gray, 2003). Cancer Mutation Analysis Since bioinformatics has enabled storage of sequences of several genes and provided means through which analysis can be carried out, cancer mutations can be detected.

Sequences of normal genes are stored in the databases. Determination of a cancer mutation is therefore not difficult as the normal sequence can be compared to the abnormal one and the area of difference marked. This has been used to find out point mutations and other types of mutations. As noted earlier, this is important in cancer therapy (Higgins and Taylor, 2000; (Lesk, <https://assignbuster.com/bioinformatics-essay/>

2005). Conclusion Bioinformatics has led to enormous discoveries due to the provision of information about the genomes of different species, their characteristics and other biological information in the databases.

The main issue here is the biological information, how to retrieve it, provision of analysis methods and provision of interpretation methods thereby assisting many studies in many areas. Application of information technology in molecular biology has enabled discoveries of therapies and genetic information about disease causing organisms. This application of information technology is very important as with the changes in the world, evolution is taking place and several different organisms are coming up. Some of these organisms can cause diseases to human and can be a threat if nothing is done about them.

Since genome sequences, analysis methods and other important biological information are provided in the programs and databases, determination of the origin of such an organism can be easy and ways of treating it can also be established, therefore eliminating the threat to humans. If for example HIV mutates, like it does, and there are no effective ways of determining the mutation, it means the virus will kill so many people as the new strain has no way to be controlled. Bioinformatics is therefore very important in molecular biology. References Barnes, M. R. and Gray, I. C. (2003). Bioinformatics for Geneticists. US: Wiley.

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