Review Article

Bioinformatics in Cancer Research: An Overview

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Abstract

Bioinformatics is a new science that's glowing call at the recent years. It is a multidisciplinary science that's made out of various sorts of other scientific fields like biology, computing, chemistry, statistics, mathematics etc. It was an enormous challenge for researchers to explain this new field during a systematic scientific way and convey out the eye of its applications and services; one among these important services that Bioinformatics are often applied in, is that the cancer studies, research and therapies for several beneficial reasons. This paper will provide a clear glance overview of bioinformatics, its definition, aims, applications, technologies, the massive amount of knowledge produced within the biological field and the way bioinformatics can organize, analyze and store them, discuss some algorithms which will be implemented over bioinformatics data, and the way to use bioinformatics to get and diagnose diseases like cancer.

Keywords

Bioinformatics; Cancer; Computational biology

Introduction

Bioinformatics is a new multidisciplinary field that comes out from the mixture of other sciences and fields like biology, computing, statistics, chemistry, mathematics and even more. In recent years new sciences have risen up thanks to the demand in understanding more the planet around us like Bioinformatics, Biotechnology, Computational Biology, Biochemistry etc. It was an enormous challenge for researchers and scientists to offer an adequate definition for every of those newly emerged sciences. One of these sciences that have an enormous influence within the medical field is Bioinformatics but can also play a key role in other fields like agriculture, livestock and even space explorations [1,2]. There were many contributions, to define and explain Bioinformatics in scientific ways, but all researchers agree that it's a mixture of Biology, computing, Statistics and arithmetic. Each one of those disciplines are playing a crucial role for collecting, organizing, analyzing and digitizing the biological data. This paper will target three categories of readership who are interested in the field [3]. Students who are interested in this field [1]. Researchers who would really like to know more about Bioinformatics and therefore the relationship with cancer [2]. Experts in the medical field who are interested in implementing the understanding of this field in the medical life.

The model was designed by studying bacteria we're not going to talk about viruses that have been downloaded and used. But there are many ways of infecting bacteria, all the time. It's an easy way to get around immunity systems and reduce stress. That way of doing it is called infection-sensory system-related immune system interactions [4].

One of the biggest differences is that when you see a very small virus at the very end of a electronic chain of activities, you just don't know which of it will become infected. In most cases where a virus has been infected, once it goes through your cell and infects your body there are no other viruses remaining for you to infect. But when you have a bacterium and a gene, it's like what you have when you have bacteria that are able to survive. These changes in the electronic environment are all incredibly subtle

Methodologies

As well as there are sufficient number of papers, articles, websites, and books are talking about Bioinformatics. it had been clear to us that each one hasn't any unified definition for Bioinformatics as a science or a replacement born field emerging within the lifetime of biology and technology, increase that there have been rare papers systematically constructing and directing the road for all Bioinformatics basic knowledge. From now an attempt was implemented to conduct a deep search to gather as many papers and articles discussing the historical and fundamentals of Bioinformatics so as to determine a unified basis form understanding the fundamentals of Bioinformatics and links that with importance of applying the sector within the cancer study, research and therapy. quite seventy papers, articles, websites and books that are talking about introduction in bioinformatics were collected. The storage and analysis of biological data using certain algorithms and computer software is named Bioinformatics, so it had been defined because the design, construction and use of software tools to get, store, annotate, access and analyze data and knowledge associated with biology [5-7].

Bioinformatics Definition

Bioinformatics, a field of computational science that has got to do with the analysis of sequences of biological molecules. It usually refers to genes, DNA, RNA, or protein, and is especially useful in comparing genes and other sequences in proteins and other sequences. It also shows evolutionary relationships between various organisms, and using the patterns that exist across DNA and protein sequences to work out what their function is. In short, bioinformatics may be a management data system for biology and has many practical applications. So, Bioinformatics are often defined as a replacement hybrid emerging field of science during which biology, computing mathematics, statistics and knowledge Technology merge and interact together to make a whole new discipline field. It is a science want to manage, analyze, organize, and classify the large amount of biological data by using well developed algorithms, computational and statistical techniques, designing and construction of software tools and theories to unravel different problems arising from biological data and help in generating, storing, accessing and analyzing data and knowledge that are associated with biology. So, Biology + Computer Science = Bioinformatics [4,8-10].

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Bioinformatics Aim

There are five main aims of bioinformatics:

1. To rearrange the biological data during a simple manner that helps biologists and researchers to store and access exiting information [1]. To develop and elegance software tools that help within the analysis and management of data [2]. To use these biological data within the analysis and interpretation of the results in a biological meaningful manne [11]. To assist researchers within the pharmaceutical industry to understand the protein structures that lead and help within the drugs industry development [4] to help and assist physicians within the medical fields to understand gene structures which can help in detecting and diagnosing disease like cancer.

Biological Databases

Biological Data is usually characterized by huge size. There are four important data generated and picked up at biological points: DNA, RNA, Protein Sequences, and Micro Array images [3]. The primary three of them are text data and therefore the last one may be a digital image. Because the different biological data generated, it is often noticed that these data is represented with differing types. There are four sorts of the info structures, String to represent DNA, RNA, and protein sequences [12,13]. Trees to represent protein structures; Graphs to represent metabolic and signaling pathways; and Strings (like words and phrases) also are wont to express comments that reflect meanings to researchers. Moreover, researchers and biologists also are curious about substrings, subtrees and subgraphs.

The sequence databases represent sequence information. Gene Bank, EMBL (European biology Laboratory) DNA database, DNA Data Bank Japan (DDNJ), and Protein databases at SWISS-PORT (Protein sequence database) all of them are the most important databanks. Micro array databases include micro array organic phenomenon under different biological conditions. Example databases of this category are Array Express. Genome databases collect organisms' gene (DNA) sequences. Example of this category databases are Xenbase, Corn, SEED, and RGD11. there's another example of Bioinformatics database that comes from the mixing with cheminformatics which is that the Drug Bank database.

The large, huge and sophisticated amount of biological data needed to be stored, accessed and manipulated in an efficient and powerful manner. So, it had been the necessity to create Bioinformatics databases which are classified into sequence databases, microarray databases, genome databases, protein structures databases and lots of more.

The following are some important algorithmic trends:

1. Finding similarities among proteins of different organisms.

2. Detecting certain patterns within genes.

3. Finding similarities among motifs.

4. Constructing phylogenetic trees expressing the evolution of organisms whose DNA or proteins are currently known.

5. Classifying new data consistent with previously clustered sets of annotated data.

6. Reasoning about microarray data and therefore the corresponding behavior of pathways.

Bioinformatics & Cancer Research

Cancer is classified as a genetic disease in which the cells cannot follow the sequential phases of the cell cycle and divide in a normal manner [1]. That is cells will lose the control within the cell cycle and starts to divide uncontrollably and therefore the chromosomes of the cancer cells are going to be arranged incorrectly, or have large pieces missing.

Due to large and fast steps within the medical field research, tons of efforts are extended so as to seek out how to detect, diagnose and treat such hazardous disease. Also, the raise of the Human Genome project discovery in 2003 had put more pressure on Bioinformatics to be applied within the cancer therapy. Bioinformatics is now being applied in the cancer research and therapy, and it is clear that experts and researchers have implemented rapid and expanded amount of research on the tools of bioinformatics that are considered necessary during the therapies [14].

It was noticed that experts and physicians try to use the multiple databases available and the different search engines like Google in order to look for biological data and apply bioinformatics in cancer research and treatment, that due to some organizations and experts limit their work and information and do not allow other experts to benefit from the same work and information. In other words, integration of bioinformatics databases data types, and structures are a crucial factor to make a decision the longer term of Bioinformatics application the medical field science and particularly in the cancer treatment and therapies [15-18].

The Human Genome Project has enriched the human research community with massive amount of huge biological data and information by the year 2003. In this case Bioinformatics has found its applications in many areas, and below may be a list of a number of the important problems where applications in Bioinformatics are often applied in.

Analyzing DNA sequence data to locate genes

1. Analyzing RNA sequence data to predict their structures.

2. Analyzing protein sequence data to predict their location inside the cell.

3. Analyzing gene expression images.

4. Understanding genetic diseases like cancer, cystic fibrosis, and sickle cell anemia.

5. For gene therapy in general.

6. In designing drugs for better treatment, and avoid drugs side effects and develop better drug delivery system.

Conclusion

It is concluded that a summary of this multidisciplinary field, by forming a singular clear definition that's introduced by the reaction of Biology and computing additionally to some assessment factors like statistics and mathematics to result into the newly born field "Bioinformatics" after this strong reaction. At the top the paper highlighted the importance of applying bioinformatics in cancer research which can open the horizons for experts and researchers to continue during this specialized field. The future of Bioinformatics is going to be bright in many biological and life areas, but one among the important issues that has got to be worked certain this; is that the integration of the wide and huge amount of data sources and

databases to unify them for better life and for a huge revolution in the biological life.

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