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THE IMPORTANCE OF USING BIOINFORMATICS IN THE FIELD OF MEDICINE

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Resume: In this article, the analysis of biological databases, the opinion of health analysts, Metabolic diseases, urea cycle disorders, various bioinformatic calculation tools of congenital malformations, medical data, physiological data of organs, electronic components, computer chips, DNA, RNA, 3D protein structures, and reconstruction of bio-molecular interactions in biology.

Keywords: biological data, health, metabolic diseases, urea cycle, birth defect disease, bioinformatics, medical data, DNA, RNA, 3D protein structures.

Data overload is one of the many problems in biology, and represents a computational challenge. Bioinformatics, the application of computational techniques to the large-scale analysis of data related to biomolecules, is now firmly established as a discipline in molecular biology and covers a wide range of topics from structural biology to genomics to the study of gene expression. includes Bioinformatics is the combination of information, data and knowledge about health. It uses computational techniques and tools to analyze huge biological databases. Metabolic diseases, urea cycle disorders, birth defects can be detected early using various bioinformatic computing tools. These tools are used to process genetics and proteomics data and compare them with medical data. Medical data consists of, for example, physiological data of various muscles or organs; agreed to use several electronic components, cost reports, billing claims, and patient satisfaction surveys. Healthcare analysts help provide the best healthcare at a lower cost that fits the family's economic system. This article briefly explains the historical application of bioinformatics. A brief overview of the various computing tools and databases involved in the application is also provided.

The interest in health is unusual for many, as the desire for consumer goods and administration stems from the direct use of health care. The craving does not come directly from the use of the drugs themselves. Instead, it comes from an immediate appreciation of the improved health that health care provides. People ask for their health in advance and with pleasure considering their work. Health can be characterized by two dimensions: life expectancy and personal satisfaction (EOPCEA, 2008). A man derives the incentive from personal satisfaction in a separate and circular way: because a direct measure of a man's health affects the enjoyment and recreation of the product he consumes, and thus however, a measure of health increases efficiency. Likewise, any innovation tailored to improve the health care system is a way to value an excellent open methodology (Oyelade et al., 2015). Bioinformatics is an interdisciplinary field that develops methods and software tools to understand biological data, especially when data sets are large and complex. As a

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multidisciplinary field of science, bioinformatics combines biology, chemistry, physics, computer science, information engineering, mathematics, and statistics to analyze and interpret biological data. Bioinformatics uses mathematical and statistical methods to investigate biological questions using In-Silico techniques (in biology and other experimental sciences, an in silico experiment is performed on a computer or computer simulation program. : in silicio), refers to silicon in computer chips. It was coined in 1987 as a reference to the Latin terms in vivo, in vitro, and in situ, which are, in turn, in living organisms, outside of living organisms, and refers to experiments conducted in places found in nature.) used in the analysis. Bioinformatics is an integrated field that creates procedures and software tools to represent biological data and code, usually characterized by a large amount of data. Bioinformatics integrates various fields such as software engineering, computer science, statistics, informatics and engineering to evaluate and describe biological and genomic data. The field of bioinformatics involves the analysis of molecular data to identify clinical, imaging and diagnostic data for personalized medicine and healthcare. Bioinformatics is used to identify candidate genes to better understand the genetic basis of disease, unique adaptations, and differences between populations. It also includes learning about qualitative articulation, understanding the fundamentals of biology and the evolutionary history of life. Helps reconstruct and display DNA, RNA, 3D protein structures and bio-molecular interactions in basic biology. Gene therapy, genetic engineering, gene editing and drug discovery are helping to make rapid progress.

Bioinformatics includes biological research that uses computer programming as part of its methodology, and specific analysis that is used repeatedly, especially in genomics, "Cross Sections". Typical uses of bioinformatics include the identification of candidate genes and single nucleotide polymorphisms (SNPs). Such identification is often done to better understand the genetic basis of a disease, specific adaptations, desirable traits (especially in agricultural species), or differences between populations. Less formally, bioinformatics attempts to understand the organizing principles in nucleic acid and protein sequences, called proteomics (Lesk, 2013). Bioinformatics has become an important part of many fields of biology. In experimental molecular biology, bioinformatics methods such as image and signal processing allow obtaining useful results from large amounts of incomplete data. In genetics, it helps in sequencing and interpreting genomes and the mutations observed in them. Plays a role in extracting the text of the biological literature and developing biological and gene ontologies for organizing and querying biological data. It also plays a role in the analysis of gene and protein expression and regulation. Bioinformatics tools help in comparing, analyzing and interpreting genetic and genomic data, and in general, in understanding the evolutionary aspects of molecular biology. It helps to analyze and catalog the biological pathways and networks that are an important part of systems biology at a more integrated level. In structural biology, DNA (Sim, 2012), RNA (Sim et al., 2012; Dawson et al., 2016), proteins (Kmiecik et al., 2016), as well as bio-modeling, modeling, molecular interactions helps to identify secrets. (Joyce et al., 2015). Next-Generation Sequencing (NGS) technology, which is often considered the basis of precision medicine, is successfully used in oncology diagnostics and immunotherapy. Advances in gene diagnostics and immunotherapy may have the potential to control cancer progression and ease the suffering of patients undergoing chemotherapy. Next-Generation Sequencing (NGS) and the development of new analysis methods for genetic data are needed to promote the translation of precision medicine from genetic testing to personalized medicine. For example, Next-Generation Sequencing (NGS) panels are quite different from Whole Genome

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Sequencing (WGS), which focus on fewer genes or regions but require higher accuracy and efficiency. Dynamic genes usually consist of genes in the regulatory network of complex diseases such as cancer. Graph theories such as shortest path analysis and random walk algorithms can help disentangle genome-wide interactions into key modules or pathways whose dysfunction is associated with disease progression. Bioinformatics conceptualizes biology in terms of molecules (in the sense of physical chemistry) and uses "informatics" (borrowed from disciplines such as multiscale applied mathematics, computer science, and statistics) to understand and organize information about these molecules.

Bioinformatics is a management information system for molecular biology with many practical applications (Oxford English Dictionary). As a result of the increase in data, many problems in biology have become computationally difficult. This approach is ideal because computers can process large amounts of data and investigate complex dynamics observed in nature. Bioinformatics, the subject of this review, is often defined as the application of computational techniques to understand and organize information about biological macromolecules. It is related to the fact that biology itself is information technology; the physiology and behavior of a living organism is largely determined by its genes, which can be viewed as a digital data store at a basic level. At the same time, significant progress has been made in technologies that provide incomplete information; According to Celera's Anthony Kerlavagi, an experimental lab can easily produce more than 100 gigabytes of data per day (Bernstein et al.). Developments have matched this incredible processing power in computer technology, with the most significant areas of improvement being in the processor, disk storage, and the Internet, enabling faster computing, better data storage, and revolutionizing the way information is accessed and shared.

Only twenty years ago, people saw biology and computer science as completely unrelated fields of knowledge. From our school days, we remember that biology is the science of living nature and computer science is about computers and data processing. Even today, few people know how two distant sciences can be connected.

Bioinformatics is the use of computer, mathematical and statistical methods in solving biological problems.

In recent decades, a large amount of biological data has been collected that needs to be analyzed. It has increased significantly since the human genome was deciphered. Before that, humanity used information stored directly in our blood to allow scientists to determine a person's origins, predict the body's "response" to certain drugs, and even imagine before birth. they didn't get it. child, it is possible to learn about the presence of hereditary diseases.

Bioinformatics methods and bioinformatics experts are worth their weight in gold today helping scientists advance these studies.

Yevgeny Denisov, Head of the Laboratory of Tumor Development Biology, Research Institute of Oncology, Tomsk National Scientific Medical Center:

- In our laboratory, we study the way of life of tumor cells, but not all of them, only the cells that form metastases and relapses. Why do metastases and relapses occur? There are many theories, but at the moment we cannot say for sure that only a few out of a million or even

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several hundred million cells have the ability to metastasize and recur, and how they differ from others.

A completely new profession - the guys of bioinformatics helps to understand the reasons that lead to metastasis and recurrence of tumors. Only they can process a large amount of data collected during many years of research. There are only two specialists in our laboratory, and all of them are absolute fans of their field;

Rostislav Vorobyov, bioinformatician, junior researcher at the Laboratory of Tumor Development Biology, Tomsk Research Institute of Oncology, talks about the nuances of his specialty.

- Rostislav, tell me, what do bioinformaticians do?

- Bioinformatics is a science at the intersection of biology, mathematics, physics and cybernetics. This combination gives bioinformatics its own broad directions, which flow seamlessly into other disciplines. Several main areas of research in bioinformatics can be roughly distinguished: assembly and analysis of genomes, search and classification of mutations, analysis of DNA and RNA sequences and prediction of protein functions, and functional analysis of biological systems in general.

In the tumor development biology laboratory, we use sequencing ("reading" DNA) and subsequent bioinformatics analysis to search for mutations and determine the activity of genes responsible for the development of cancer metastases and relapses.

- In which direction is bioinformatics developing now?

- Sequencing and analysis technologies themselves are improving every year, allowing for more targeted research to test scientific hypotheses. In particular, single-cell sequencing technology is developing rapidly. This allows you to "read" the sequence of each cell in the sample, rather than just some abstract collection of cells in the body tissue sample. This makes it possible to identify interesting mutations that, for example, with the old sequencing approach, against the background of other cells, appear as statistically insignificant noise and go unnoticed by the clinician.

- How can bioinformatics help in the fight against various diseases?

- Bioinformatics, first of all, allows a better understanding of certain processes in the body, which will reveal more effective ways to fight diseases in the future or develop vaccines for prevention or treatment. For example, systematic bioinformatics allows to identify changes in the protein composition of new strains of coronavirus to find ways to treat or prevent the disease.

Saraton kasalligida bioinformatika nafaqat ma'lum bir bemor uchun eng mos terapiyani tanlashga, balki butunlay sog‘lom odamda saratonning ayrim turlariga genetik moyilligini baholashga imkon beradi. Bioinformatika saraton kasalligi uchun mavjud terapiya kursini sozlash uchun ham ishlatilishi mumkin.

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Are advances in bioinformatics used only in medicine?

- Bioinformatics is also used in evolutionary and systematic biology. In addition to medicine, bioinformatics is also used in genetics and bioengineering: for example, from the creation of a new variety of tomato that keeps its marketability longer to the development of biomaterials for prostheses that do not cause rejection in the patient's body.

Alexey Zarubin, a junior researcher at the Laboratory of Genomics of Orphan Diseases of the Research Institute of Medical Genetics of the Tomsk National Scientific Medical Center:

- Bioinformatics is the ability to analyze a very large amount of data, and in many cases, draw conclusions from things that cannot be perceived by a person due to the size and complex structure of the data. These are billions of lines of text, and only a computer can do such complex work. I am attracted by this perspective. The research I am participating in focuses on the interaction of epigenetic mechanisms and their role in the formation of atherosclerotic plaques.

- There are various epigenetic mechanisms for regulating gene activity (such as methylation and microRNA expression). My work focuses on integrating these epigenetic mechanisms with the genetic context and how they relate to the development of atherosclerosis. In practice, this is an attempt to find biomarkers of various complex courses of the atherosclerotic process and search for new targets to which therapeutic drugs can be directed.

Bioinformatics methods are becoming increasingly popular, in demand in scientific laboratories, and becoming an integral part of research in various fields. How to get this specialty?

- People come to bioinformatics from almost any related field. These can be biologists, mathematicians, physicists, cybernetics and others, says Rostislav Vorobyov. - These could also be statisticians, machine learning specialists, programmers or database design specialists who had to immerse themselves in the field of biological science .

If you choose bioinformatics as a future specialty, it is worth considering two main directions of entry into the specialty: by genetics, genomics, molecular biology, immunology and other biological sciences - this is the development of technical sciences and tools; in data processing and analysis by applied technical sciences - immersion in biology.

Harvard, Princeton, and most importantly, practical training in the biochemical part and in direct cooperation with representatives of large companies that manufacture equipment and reagents for bioinformatics data analysis.

Tashkent Medical Academy, Department of "Biomedical Engineering, Informatics and Biophysics" has full educational programs based on international standards. There are also various refresher and retraining courses.

Bioinformatics is developing rapidly, and therefore the need for qualified specialists in various fields is increasing: from agriculture to immunology and bioengineering.

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Joy L. Rodak is a highly accomplished and respected individual in the healthcare industry, known for her outstanding leadership and strategic vision. Bioinformatics and beyond: unlocking the potential of data-driven health

In the information age, data has become a transformative force in healthcare. Bioinformatics—the combination of biology, informatics, and data analytics—has emerged as a powerful tool that unlocks insights, accelerates medical research, and informs clinical decisions. This article explores the field of bioinformatics and its potential to revolutionize healthcare through data-driven approaches.

I. Flood of information.

Healthcare is generating massive amounts of data, from genomics to electronic health records. Bioinformatics processes and analyzes this data to extract meaningful patterns, uncover genetic signatures, and inform personalized treatment plans.

II. Genomic medicine.

Genomic medicine is an approach to medicine that uses genomics, the study of the genome (all genetic material), to diagnose, treat, and prevent disease. This field aims to create individualized medical approaches tailored to the genetic characteristics of patients through the study and analysis of the genome. Below we consider the main aspects of genomic medicine:

1. Genetic Diagnostics

• Genetic Causes of Diseases: Determining the causes of hereditary diseases through genetic tests. For example, identifying diseases based on genetic mutations or anomalies.

• Genetic Testing: Used to detect mutations or genetic changes, which can ensure early detection and treatment of diseases.

2. Personalization and Individualization

• Genomic Profiling: Tailoring treatment strategies based on each patient's genetic profile. For example, in the field of oncology, more accurate and effective treatment plans can be made through genetic profiling.

• Pharmacogenomics: Individualized drug selection by predicting drug response. It can increase the effectiveness of drugs and reduce their side effects.

3. Obtaining Genetic Information from Parents.

• Prenatal Genetic Testing: Tests to identify genetic disorders in a child before birth. Through this, parents can detect diseases in advance, treat them or take other measures.

4. Medical Research.

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• Genomic Research: Using genetic information to study new diseases and their genetic basis, develop new treatments and drugs.

• Clinical Trials: Using genomic data to test new treatments and evaluate their effectiveness.

5. Genomic Data Management.

• Data Storage and Analysis: State-of-the-art technologies and systems for storing, analyzing and securing large volumes of genomic data.

6. Social and Ethical Issues

• Privacy and Confidentiality: Maintaining the confidentiality of genetic information and preventing its misuse.

• Genetic Discrimination: Discrimination and injustice against certain individuals or groups based on genetic information.

Genomic medicine is one of the important fields that will define the future of medicine, as it creates opportunities for individualizing patients and more effective treatment. This approach is opening up new opportunities in the diagnosis and treatment of many genetic diseases and conditions.

III. Bioinformatics drug discovery.

Bioinformatics accelerates drug discovery and development. By analyzing molecular interactions and simulating drug interactions with biological systems, researchers can identify potential drug candidates and predict their effects.

IV. Predictive analytics and disease prevention

Data-driven approaches enable predictive analytics for disease prevention. By analyzing risk factors and patient data, healthcare providers can identify individuals at risk and take preventive measures.

V. Individualized treatment plans.

Bioinformatics supports the creation of personalized treatment plans. By considering genetic, environmental and lifestyle factors, health professionals can tailor interventions to the unique needs of each patient.

V. Data Privacy and Ethical Considerations.

The potential of bioinformatics raises ethical concerns, especially issues related to data privacy and security. Striking a balance between the use of data and the protection of patient privacy is critical to progress in healthcare.

VI. Artificial intelligence and machine learning

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Bioinformatics uses artificial intelligence (AI) and machine learning (ML) algorithms to analyze complex data sets. These technologies enable faster and more accurate identification of trends and correlations.

In conclusion, the benefits of data-based health care can be applied to everyone by creating and launching a database to reveal the possibilities of bioinformatics by implementing this project in practice using the MS Access program. Bioinformatics has ushered in an era of data-driven healthcare that transcends traditional boundaries. Harnessing the power of data analytics, genomics, artificial intelligence, and personalized approaches, bioinformatics has the potential to transform medical research, clinical practice, and patient outcomes.

Reference

1. Pranav Deepak Pathak, Roshani Raut, Sebastian Jaramillo-Isaza, Pradnya Borkar, Computational Approaches in Biotechnology and Bioinformatics.-London: CRCPress, pp. 200-219.
2. Marcus F.B. Bioinformatics and systems biology: Collaborative Research and Resources / F.B. Marcus. - Berlin : Springer, 2011. - 287 p.
3. Multiscale Approaches to Protein Modeling / Ed. by A. Kolinski. - New York : Springer, 2011. - 355 p.
4. Pharmacogenetics / Ed by I.P. Hall. - New York : Taylor & Francis, 2014. 324 p.
5. Procter J.B. Visualization of multiple alignments, phylogenies and gene family evolution / J.B. Procter, J. Thompson, I. Letunic, [et al.] // Nature Methods. - 2010. - V. 7, № 3s. - P. 16-25.
6. Protein Data Bank. - Интернет-ресурс. - http://wvvw.pdb.org/.
7. Stephenson F.H. Calculations for molecular biology and biotechnology / H. Stephenson. - Amsterdam : Elsevier, 2003. - 302 p.
8. The 1000 Genomes project consortium. A map of human genome variation from population-scale sequencing // Nature. - 2012. - V. 467, № 7319. - P. 1061-1073.