FAMILIARIZATION WITH INFORMATION ABOUT MODERN BIOINFORMATIC DATABASES

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Abstract

The article reveals the role of bioinformatics in the development of biological sciences, in particular genetics, genomics and transcriptomics. The role of bioinformatics as a science is described, which includes the creation and application of computational tools, algorithms, databases for storing, extracting, managing and analyzing biological information

Keywords: bioinformatics, genomics, genetics, transcriptomics, alogorhythm, program, statistics, DNA, RNA.

Introduction

Bioinformatics is an interdisciplinary science that analyzes and interprets biological data, combining biology, computer science, mathematics and statistics. It includes the creation and application of computational tools, algorithms, databases for storing, extracting, managing and analyzing biological information. Bioinformatics is necessary to organize, analyze, and gain meaningful understanding of large amounts of biological data generated using techniques such as genomics, proteomics, and transcriptomics.

In bioinformatics, computational methods are used to study biological processes, as well as to understand the structre and functions of biological molecules (RNA and DNA). The structure of proteins, prediction of functions, analysis of gene expression and the relationship between species are studied. Using bioinformatics tools and techniques, researchers can identify genes, annotate genomes, compare sequences, draw conclusions about protein structures, perform various analyses, and gain insight into complex biological systems.

METHODOLOGY

A biological database is a set of biological data that is usually stored electronically, which allows you to store extract and efficiently analyze biological data. These databases serve as a repository for several categories of biological information, such as genomic sequences, protein sequences, gene expression data, protein structures, and genetic variants. Biological databases are a key component of bioinformatics and provide researchers with valuable resources.

Biological databases are designed to store data in a standardized and organized format, making it easier for researchers to access and extract data for specific research purposes. They often use special data models and formats to accommodate different categories of biological

information. These databases can be global resources open to the scientific community, or they can be local databases specific-to-specific research groups or initiatives.

Organizations, research institutes and consortia such as the National Center for Biotechnological Information (NCBI), the European Institute of Bioinformatics (EBI) and the Protein Data Bank (PDB) create and maintain biological databases. The comprehensive and up-to-date information in these databases is information from experimental studies, calculations, forecasts and literature.

RESULTS

The use of biological databases is necessary for many bioinformatics analyses and scientific issues. Using specialized search tools, researchers can extract information about specific genes, proteins, genomes and other biological objects from these databases. For the most part, databases provide tools and interfaces for data visualization, sequence matching, structural predictions, and other computational analysis, allowing researchers to obtain meaningful information and hypotheses.

By centralizing and systematizing biological information, these databases help to share data, collaborate and discover new knowledge in the scientific community. They play an important role in advancing research in disciplines such as genomics, proteomics, transcriptomics, and systems biology, providing a foundation for data-driven research and discovery.

Organizations and research institutions specializing in biological data management are responsible for the preparation and maintenance of these databases. Their main goal is to ensure the accuracy, relevance, timeliness of data delivery, and database compliance with the general community of researchers and scientists. The aforementioned databases serve as an important basis for various bioinformatics analyses. For example, in areas such as sequence matching, homology search, structural modeling, and data analysis.

The classification of databases in bioinformatics depends on the nature of the biological information contained in them. Below we will talk about some of them:

-nucleotide databases: nucleotide databases are, in fact, repositories in which DNA nucleotide sequences are stored. Examples of such repositories are GenBank, the European Nucleotide Archive (ENA) and the Japanese DNA Databank (ddbj). These objects serve as a repository for genomic sequences, transcriptome data, and other types of nucleotide-based data;

- protein databases: These databases are repositories containing information about proteins and their sequences. These resources are effective in protein identification, characterization, and functional analysis. Examples of protein databases are UniProt, Protein Data Bank (PDB), Protein Information Resource (PIR);

-genomic databases: These are databases that store complete or partial genome sequences of various organisms. Genome annotations, gene predictions, and additional genome-related information will be included. Examples: Ensembl, National Center for Biotechnology Information (NCBI), Saccharomyces Genome Database (SGD);

- Structural databases: structural databases are databases containing proteins, nucleic acids and complexes, three–dimensional structures of biomolecules. The structures under consideration are determined experimentally using various methods such as X-ray crystallography, NMR spectroscopy and cryo-electron microscopy. Examples are The Protein Data Bank (PDB), the Protein Structure Initiative (PSI-sbkb) Structural Biology Knowledge Base, and the Structural Bioinformatics Research Laboratory (RCSB);

- Databases of paths and interactions: These databases provide information about biological pathways, signaling networks, and molecular interactions. The Kyoto Encyclopedia of Genes and Genomes (kegg), Reactome and Biogrides are examples;

-literary databases: These databases are databases that collect and regulate scientific literature on biological sciences.This allows researchers to search for relevant articles, abstracts, and links. For example, Pubmed, Medline and Scopus.

DISCUSSION

Over the past decade, huge efforts have been made to improve the methods of analyzing molecular biological data. This has led to a variety of new algorithms specialized for processing data related to biological phenomena such as gene expression and protein interactions. In contrast, environmental data analysis continues to focus to some extent on off-the-shelf statistical methods, although this is starting to change with the introduction of modern methods, when few assumptions can be made about the data and a more exploratory approach is required.

In recent years, significant advances in molecular biology and genomic technologies have led to an exponential increase in the volume of biological information. With the flow of genomic information, the need for tools for data storage and management, as well as software development for analyzing, visualizing, modeling and forecasting large amounts of data, is growing in parallel.

The volume of information, especially in plant biotechnology, has increased exponentially due to the large number of databases available for many individual plant species. Effective bioinformatics tools and methodologies have also been developed to quickly sequence the genome and study the plant genome within the framework of the "omics" approach. This review focuses on the various applications of bioinformatics in plant biotechnology and their benefits in improving agricultural outcomes.

The problems or limitations faced by plant biotechnology in the aspect of the bioinformatic approach, which explain the low progress in plant genomics compared to animal genomics, are also considered and evaluated. There is an urgent need for effective bioinformatics tools that are capable of providing longer-term data reading with objective coverage in order to overcome the complexity of the plant genome. Progress in bioinformatics is not only useful for the field of plant biotechnology and agriculture, but will also make a huge contribution to the future of mankind. The introduction of bioinformatics and computational biology into the field of plant biology dramatically accelerates scientific discoveries in the life sciences. Using sequencing technology, scientists in the field of plant biology have uncovered the genetic architecture of various plant species and microorganisms, such as the proteome, transcriptome, metabolome, and even their metabolic pathway. Sequence analysis is the most fundamental approach to obtaining a complete genome sequence, such as DNA, RNA, and protein sequence, from an organism's genome in modern science. Whole genome sequencing allows you to determine the organization of different species and provides a starting point for understanding their functionality. Complete sequence data consists of coding and non-coding regions that can act as a necessary precursor for any functional gene that defines the unique traits possessed by organisms. The resulting sequence includes all regions such as exons, introns, regulators, and promoters, which often results in an extremely large amount of genomic information.

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