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Biological Databases and Resources for Sequence Analysis

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ABSTRACT

Today is the era of bioinformatics as it uses mathematical algorithms to do DNA sequence alignment to protein structure prediction and drug designing making biological research easier? Biological research has generated lots of databases may it be in form of gene sequences, protein sequences or metabolic pathways across various species. These databases are huge and without bioinformatics one can does not make sense out of it. Bioinformatics provides wide range of tools to deal with all the queries raised in biological research and to find a solution to it. In this article we tried to compile all such freely available tools as well as biological databases, one can have ease to access them and have promising prospects in the area of biological research.

Keywords: Biological databases, Tools for sequence analysis, Protein structure, Bioinformatics, Genomics

INTRODUCTION

Data is increasing day by day in every field of research, but issues start with its arrangement, future utility, easy access for others and prospects of data in research and its applications. Experimental data collection is very important for further and increasing amount of data generated from different genomic projects has made the use of computer databases a necessity which helps in rapid assimilation. By using different computer languages and programs theses data can be further analyzed and used for research. With the remarkable increase in the results produced by different biological research, the amount of information stored in the databases doubling every 14-15 months [1] presents a huge demand for analysis and interpretation of these data [2] Bioinformatics organizes data in a way that allows researchers to access existing information and to submit new entries as they are produced, e.g., the Protein Data Bank for 3D macromolecular structures [3,4]. Its aims to develop tools and resources which helps in the analysis of data [5]. Bioinformatics deals with biological information acquisition, processing, storage, distribution, analysis along with data interpretation that uses different tools and techniques of mathematics, computer science, and biology [1]. With the help of bioinformatics, it is easier for biologists to access data from the internet and other fitting websites and easily discovers the composition of any biological molecules such as nucleic acids and proteins. Bioinformatics is having many different branches (**Figure 1**) and collections of biological sequences information's in different biological databases. The two most important biological sequences databases are protein databases and nucleic acid databases, while the structural databases are separate and having 3D structural information's. The main use of the bioinformatics tools are sequence analysis of DNA and protein with the help of different programs and databases available on the web [2].

Bioinformatics can be used for analysis of gene expression and gene analysis, detection of gene regulation networks, analysis of gene and protein structure and its function [2] Prospection of genomic and transcriptomic data [6]. Bioinformatics constitute a wide range of scientific disciplines and genomic analysis [7].

The two main classes of nucleic acids i.e., DNA and RNA functioning as the carrier of genetic information. As DNA double helical structure is well-known structure with defined function, this information is copied and passed on to the next generation [8]. One of the most important molecules in living cells is deoxyribonucleic acid (DNA). The genetic material DNA is a polymer composed of monomeric units known as nucleotides. A nucleotide is made up of a 5-carbon sugar, deoxyribose, a nitrogenous base, and one or more phosphate groups and the phosphate group is acidic, so the name nucleic acid was coined [8].

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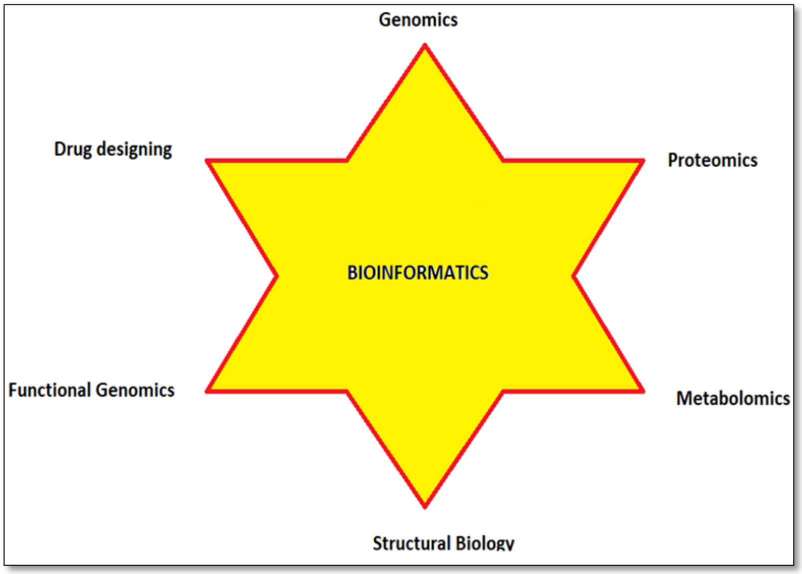

Figure 1. Showing different branches of Bioinformatics.

Similarly, RNA is chemically identical to DNA as it is a chain of similar monomers. RNA is further of three types: mRNA, tRNA and rRNA. RNA molecules are required at all stages of protein synthesis. Messenger RNA transmits the code that specifies the amino acid sequence of the protein; transfer RNA molecules translate the code word for word into protein; and ribosomal RNAs in the ribosome provide part of the machinery to perform the synthesis. Protein structure is known to have a higher degree of conservation compared to sequences due to large variations in sequence within the protein family which can still result in very similar three-dimensional structures [9]. The structure of any protein molecule helps in determining its function [10]. There are many important such findings and, we can analyze it by using different tools used in bioinformatics. Here we are discussing about some most common biological databases and tools used in sequence analysis of protein and nucleic acids.

Databases for Protein (Table 1)

Table 1. Databases for Protein.

Databases	**Use**	**Links**
PROSITE	It is first secondary database having information ofdomains, functional and all documentation entries.	http://prosite.expasy.org/
Pfam	Database of protein with multiplesequence alignments by using hidden Markov models.	http://pfam.xfam.org/
PIR	Contain comprehensive, annotated and non-redundant protein sequence information.	https://proteininformationresource.org/
TrEMBL	Curated protein sequence database with high level of annotation, computer annotated supplement of Swiss-Prot.	https://www.uniprot.org/news/1999/06/01/full#:~:text=Introduction%20TrEMBL%20is%20a%20computer,yet%20integrated%20in%20SWISS%2DPROT
PDB	It contains 3-D structures protein, DNA, RNA obtained by NMR and X-Ray crystallography methods.	https://www.rcsb.org/
PRINTS	It contains a protein fingerprint that is used to assign family and functional attributes.	http://130.88.97.239/PRINTS/ind ex.php
Swiss-Prot	It contains protein descriptions, domain structure, function, subcellular location and post-translational modifications.	https://www.expasy.org/resources/uniprotkb-swiss-prot

Database for Nucleic Acid (Table 2)

Table 2. Database for Nucleic Acid.

Databases	Use	Links
DDBJ	DNA Data bank of Japan is a DNA sequences database and member of INSDC.	https://www.ddbj.nig.ac.jp/index-e.html
EMBL	It is European Molecular Biology Laboratory nucleotide sequence database.	https://www.ebi.ac.uk/
GenBank	Annotated collection of all publicly available DNAsequences also part of INSDC.	https://www.ncbi.nlm.ni h.gov/

Tool for Protein (Table 3)

Table 3. Tool for Protein.

Name of Tool	Use	Website Link	References
CPHModels	Web server used for predicting 3D structure of protein by using single template homology modeling.	http://www.cbs.dtu.dk/services/CPHmodels/	[11]
ESyPred3D	It is automated homology modeling program alignment performances increased of any new alignment strategy with the help of neutral networks. MODELLER is used finally for 3D structure prediction.	https://www.unamur.be/sciences/biologie/urbm/bioinfo/esypred/	[12]
PHYRE 2	Contains collection of tools prediction and analysis of protein structure.	http://www.sbg.bio.ic.ac.uk/phyre2/html/page.cgi?id=index	[13]
SWISS MODEL	Homology server for protein 3D structure prediction.	https://swissmodel. expasy.org/	[14]
I-TASSER	Hierarchical approach based protein structure prediction and structure based function annotation.	https://zhanggroup.org/I-TASSER/	[15]
Robetta	Comparative modeling based protein structure prediction server.	http://robetta.bakerlab.org/	[16]
PEP-FOLD 3	Follows de novo approach for predicts peptide structures prediction.	https://bioserv.rpbs.univ-paris-diderot.fr/services/PEP-FOLD3/	[17]
(PS)2	Automatic server for protein structure prediction by using MODELLER.	http://ps2.life.nctu.edu.tw/	[18]
AS2TS system	It is used for protein structure comparison and 3D modeling.	http://proteinmodel.org/AS2TS/AS2TS_MB/index.html	[19]
RaptorX	Used for the calculation of protein secondary, tertiary structure, contact and distance map solvent accessibility, disorder regions, functional annotation and buildingsite analysis.	http://raptorx.uchicago.edu/	[20]
MODELLER	Used for homology or comparativemodeling of protein 3-dimensional structures.	https://salilab.org/modeller/	[21]
ProtSkin	Used to converts protein sequence alignment in BLAST, CLUSTAL, or MSF based on identity or similarity ontoa protein structure to visualize also help to analyses conserved/ non-conserved regions within proteins.	https://sbgrid.org/software/titles/protskin	[22]
GeNMR	Generating 3D structure of protein by using amino acid sequence data.	http://www.genmr.ca/index.php	[23]
FATCAT	Used to compare two PDB-format protein structures.	https://fatcat.godzi klab.org/fatcat/fatcat_pair.html	[24]
SuperPose	Calculates protein superpositionusing a modified quaternion approach.	http://superpose.wishartlab.com/	[25]
PSIPRED	PSIPRED used to identify protein structure.	http://bioinf.cs.ucl.ac.uk/psipred/#	[26]
Protein Peeling	Used to predict protein structure descriptions between protein domain and secondary structure.	https://www.dsimb.inserm.fr/dsimb_tools/peeling/	[27]
InterProSurf	Predicts interactive amino acid residues within a protein that are interactive with other proteins also give 3D structures of subunits of protein complex.	http://curie.utmb.edu/pdbcomplex.html	[28]

MulPBA	Tool used for multiple structures comparison of available protein.	https://www.dsimb.inserm.fr/dsimb_tools/mulpba/	[29]
WHAT IF	Generate 3D model for a pre-aligned sequence template structure.	https://swift.cmbi.umcn.nl/whatif/	[30]
MAPSCI	Multiple alignment of proteinstructure and consensus identification.	http://www.geom-comp.umn.edu/mapsci/	[31]
iPBA	Tool used for comparison of protein structure by sequence alignment methods.	https://www.dsimb.inserm.fr/dsimb_tools/ipba/	[32]
CEP	Predict conformational epitope forprotein antigen.	https://www.hsls.pitt.edu/obrc/index.php?page=URL112 7484564	[33]
SAS	Tool for applying structural information to a given protein sequence.	https://www.ebi.ac.uk/thornton-srv/databases/sas/	[34]
ORION	Optimized protein fold recognitionis a sensitive method for protein template detection.	https://www.dsimb.inserm.fr/ORION/	[35]
Auto-mute	A server for predicting functionalamino acid mutation in protein.	http://binf.gmu.edu/automute/	[36]
MovieMaker	A web server used to generates smallmovies of protein dynamics studies.	http://wishart.biology.ualberta.ca/moviemaker/	[37]
DUET	A server that helps in analysis of mutations effects on protein.	http://biosig.unimelb.edu.au/duet/stability	[38]
Clustal Omega	It is a multiple sequence alignment program based on HMM profile-profile techniques that help to generate alignment between three or more sequences.	https://www.ebi.ac.uk/Tools/msa/clustalo/	[39]

Tools for DNA Analysis (Table 4)

Table 4. Tools for DNA Analysis.

Name of Tool	Use	Website Link	References
DNAproDB	It is a tool that is used for structural analysis of DNA-protein complexes.	https://dnaprodb.usc.edu/search.html	[40]
RNA fold webserver	Used for the prediction of secondary structures of single stranded RNA or DNA sequences.	http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi	[41]
DSSR	It stands for Dissecting the Spatial Structure of RNA. It is an integrated software tool for the analysis/annotation, model building, and schematic visualization of 3D nucleic acid structures.	http://forum.x3dna.org/rna-structures/	[42]
R-chie	A web server for visualizing cis and trans RNA-RNA, RNA-DNA, DNA-DNA interactions.	https://www.e-rna.org/r-chie/	[43]
WebFR3D	It is a suite of programs that is designed to search RNA 3D structures.	http://rna.bgsu.edu/webfr3d/fr3d.php	[44]
FRASS	A web-server used for comparison of 3D structures of two RNA molecules.	https://sourceforge.net/projects/frass/	[45]
SARA	SARA stands for Structure Alignment of Ribonucleic Acids. It is an automated server used for aligning two RNA structures.	https://structure.bi ofold.org/sara/	[46]
w3DNA	A tool used for analysis, reconstruction and visualization of nucleic acid structures.	http://w3dna.rutgers.edu/	[47]
MOLProbity	Validation of macromolecular 3D structures for nucleic acid and their complexes.	http://molprobity.biochem.duke.edu/index.php?MolProbSID=eli71k2nfofd1u261asaho69i 5&eventID=2	[48]
SETTER webserver	a web server used to caparison of RNA structure.	http://setter.projekty.ms.mff.cuni.cz/	[49]

Ribo Vision	ribosome information viewer open source website	http://apollo.chemistry.gatech.edu/RiboVision/	[50]
R3D Align	An application used for detailed nucleotide to nucleotide pairwise alignment of 3D RNA structure based on a method.	http://rna.bgsu.edu/r3dalign/	[51]
RNA viewer	A programme for visualizing the two-dimensional structure of RNA, as well as base pairs and RNA patterns.	http://ndbserver.rutgers.edu/ndbmodule/services/rna_viewer/rnaViewerIndex.html	[52]
SAVoR	An application used for visualizing RNA seq-data and other genomic annotations on RNA secondary structure.	https://savor.lisanwanglab.org/	
SARA	Structure Alignment of Ribonucleic Acids is a fully automated approach for aligning two different RNA structures.	https://structure.biofold.org/sara/	[46]
Forna	It is RNA secondary structure visualization, feature rich and easy to use web-based tool which enables the users to easily change sequences or RNA secondary structures for clean, concise and personalized visualization without the need of installing any software.	http://rna.tbi.univie.ac.at/forna/	[53]
Clustal Omega	It is a multiple sequence alignment program which uses HMM profile-profile techniques for generating alignment between more than three sequences.	https://www.ebi.ac.uk/Tools/msa/clustalo/	[39]

DISCUSSION

Bioinformatics is a discipline of biology that grows extensively in last few years. Sequences analysis and identification of new gene, proteins and structure are few important applications of bioinformatics [54]. The most important application is designing of 3D structure of proteins whose structures were not predicted by Nuclear magnetic resonance (NMR) and crystallographic method, due to protein bulky size and other limitations [55]. Genome analysis and sequencing of genome of new varieties is possible only because of extensive computational applications of bioinformatics. In this article we tried to compile most of the resources related to protein and nucleic acids that gives new insight to biological research [56-58].

CONCLUSION

Bioinformatics is a young discipline, which is widely used for analysis of genome, prediction of protein and gene structures, cell modeling, analysis of molecular pathways etc. As per the requirement of these tasks, various tools like the ones mentioned in this paper have been successfully curated and has made something as complex as genome sequencing much easier to work with. These tools can be used for various tasks like retrieval of structures, prediction and formation of new structures, comparison of different structures etc. that could be helpful for research of a new macromolecule. All these tools are easy to use and free to access.

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