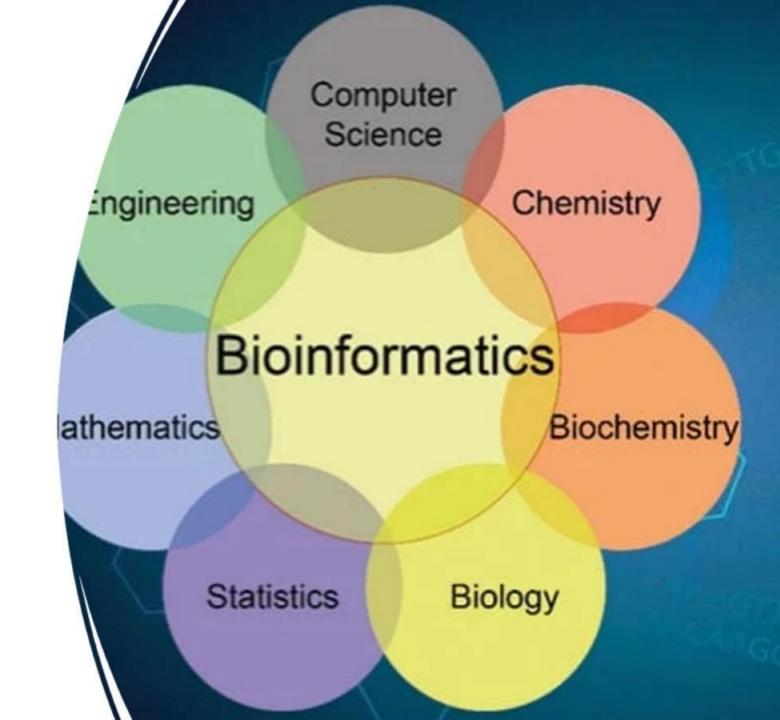
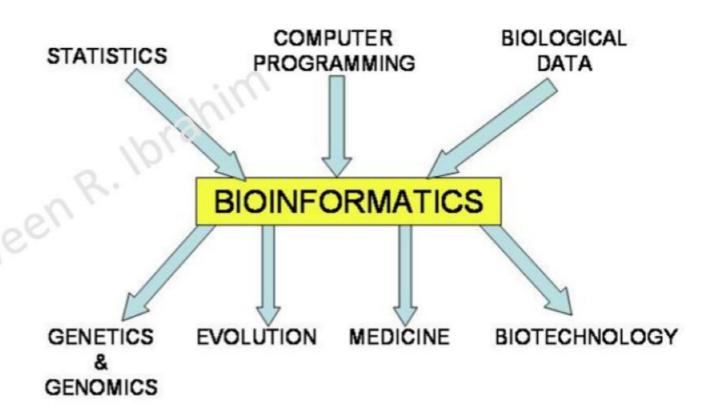
Bioinformatics Lec 1
Grade 3/ Biology Dept.

By Dr Delveen R. Ibrahim



What is Bioinformatics??

 Bioinformatics is an interdisciplinary field that develops methods and software tools for understanding biological data.



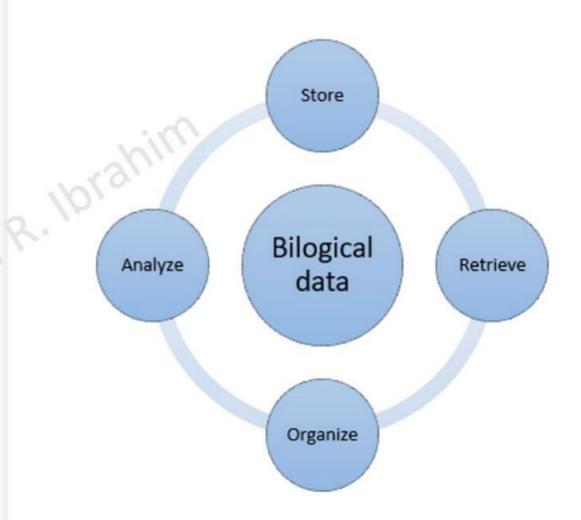
The Building Blocks of Bioinformatics

Data in Biology

 DNA, RNA, and proteins as the language of life.

Role of Computers

Storing and analyzing biological data.



Aims of bioinformatics



The field of bioinformatics has three main objectives:



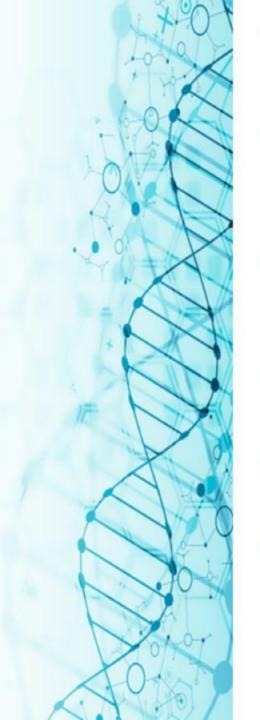
1. **Data Organization**: Store, manage, and maintain biological data systematically in databases



Data Analysis: Process and analyze biological data to extract meaningful insights.



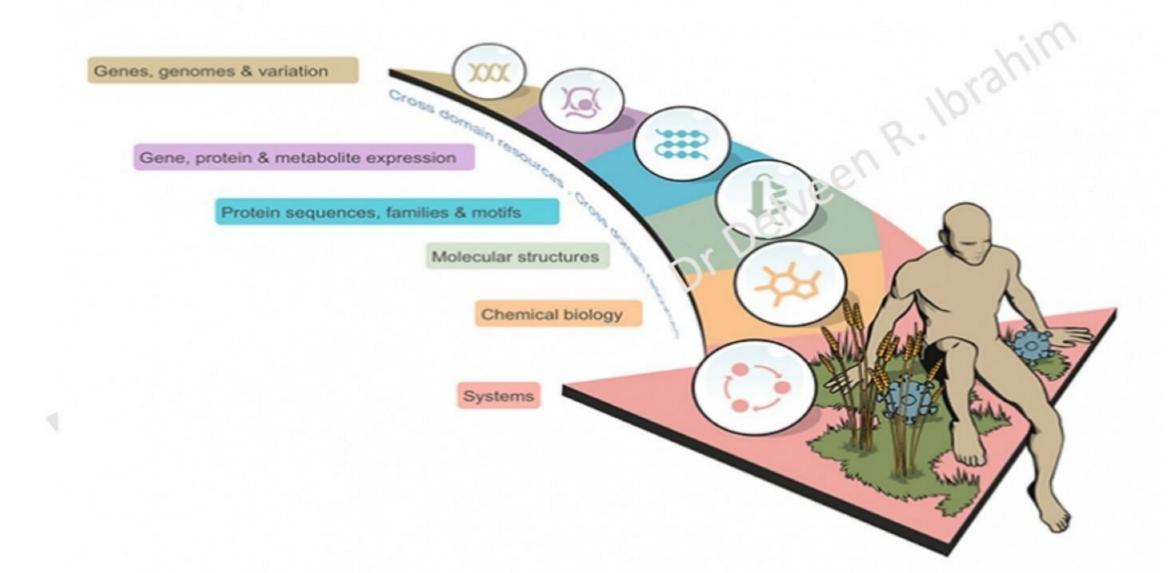
3. **Data Interpretation:** Understand the underlying biological significance of data



Types of biological data based on data type:

- Genomic Data: Involves the study of an organism's complete set of DNA, including genes and non-coding regions.
- Transcriptomic Data: Focuses on the study of RNA molecules, examining gene expression levels.
- Proteomic Data: Analyzes the structure and function of proteins within a biological system.
- Metabolomic Data: Explores the small molecules involved in metabolic pathways.
- Biological literature data: Organizing journals and articles

A broad overview of the different types of data that fall within the scope of bioinformatics



Applications of bioinformatics:

 There are Many applications of Bioinformatics, here are some of the most important applications:

1. Health and Medicine

Application	Description	Examples
Genomics	ldentifying genes responsible for diseases.	BRCA genes in breast cancer.
Drug Discovery and Development	Designing and simulating drug- target interactions.	COVID-19 antivirals.
Personalized Medicine	Tailoring treatments based on genetic makeup.	Pharmacogenomics studies.
Vaccine Development	Designing vaccines using pathogen genomes.	mRNA vaccines for COVID-19.

2. Agriculture

Application	Description	Examples
Crop Improvement	Identifying genes for traits like drought tolerance or pest resistance.	Bt cotton, Golden Rice.
Livestock Breeding	Enhancing breeding programs for healthier livestock.	High-yield dairy cows.
Food Safety	Detecting pathogens in food supplies.	Tracing foodborne outbreaks.

3. Environment

Application	Description	Examples
Microbial Analysis	Studying microbial composition of ecosystems.	Soil health improvement.
Bioremediation	Identifying organisms for pollutant degradation.	Cleaning oil spills.
Climate Change	Studying plant and animal adaptation to changing climates.	Drought-tolerant crops.

Others:

Evolution	Comparative Genomics	Understanding evolutionary relationships by comparing genomes.	Tracing organisms' ancestry.
Forensic Science	DNA Analysis	Identifying individuals from DNA at crime scenes.	DNA fingerprinting.
Education and Outreach	Teaching Tools	Online resources for teaching bioinformatics concepts.	NCBI tools, phylogenetic tree builders.

History of the bioinformatics

Term bioinformatics was invented by Paulien Hogeweg and Ben Hesper in 1970 as "the study of informatic processes in biotic system While the first informatician is
Margaret Dayhoff (1925–1983),
was an american physical
chemist who pioneered the
application of computational
methods to the field of
biochemistry

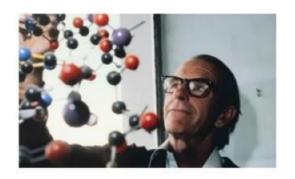


Paulien Hogeweg

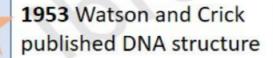


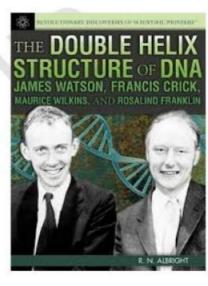
Ben Hesper

History of Bioinformatics



1952 Sanger sequenced bovine insulin





Margaret Dayhoff

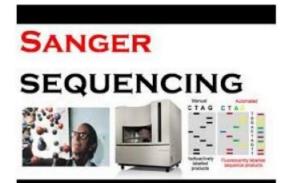


An American physical chemist and pioneer in the field of bioinformatics, she pioneered the use of mathematics and computational methods in the field of biochemistry.

1965 Margert Dayhoffs published protein sequence Atlas

1970 Paulien Hogeweg and Ben Hesper invented the term of Bioinformatics

1977 DNA sequencing (Sanger) and software to analyze it (Staden)



History of Bioinformatics

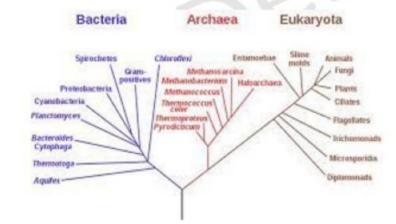




1993 Sanger center for sequencing, UK



1995 Hemophilus influnzae
genome Sequenced and
Methanococcus genome
sequenced, which confirmed the
existence of third major branch of
life on earth





In the 1990–2000s, use of the Internet, coupled with next-generation sequencing (NGS), led to an exponential entry of data and a rapid increase of bioinformatics tools.



1990-2003 Human genome sequenced complete (13 years)

- Modern Advances (2010s-Present)
- Advances in Sequencing Technologies: Next-generation sequencing (NGS) enabled rapid, cost-effective genome sequencing.
- Big Data and Machine Learning: Bioinformatics involved artificial intelligence for analyzing massive datasets in genomics, proteomics, and systems biology.
- AlphaFold (2020): A breakthrough in protein structure prediction, demonstrating the power of AI in solving biological problems.

Future of Bioinformatics

- Career Opportunities: Bioinformatician, genetic researcher, computational biologist.
 - How ?
 - By learning programming (Python, R) and biology together.

Practical Lec 1/ Biological Databases



Biological Databases



A brief history of biological databases

1965

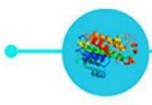
1980

1982

2002

2005

PRESENT



Margaret Dayhoff created the Atlas of Protein Sequence and Structure



The EMBL Data Library created a catalog of biological data



GenBank became a public database.



ArrayExpress released



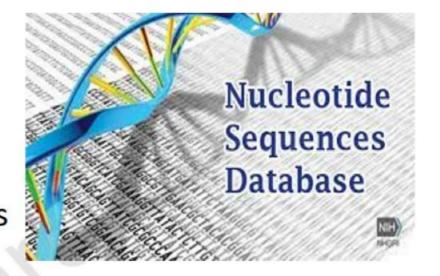
The first highthroughput sequencing systems was used to sequence a full *E. coli* genome



Many directories for multi-omic data were created. Let's explore some databases!

Biological databases

- Nucleotide and protein sequences databases can be classified based on accessibility to:
- Primary databases
- Secondary databases
- Tertiary databases



Primary databases

- It can also be called an archival database since it archives the experimental results submitted by the scientists. The primary database is populated with experimentally derived data like genome sequence, macromolecular structure, etc.
- It obtains unique data obtained from the laboratory and these data are made accessible to normal users without any change.
- The data are given accession numbers when they are entered into the database. The same data can later be retrieved using the accession number. Accession number identifies each data uniquely and it never changes.
- Examples –
- Nucleic Acid Databases: GenBank, EMBL and DDBJ
- Protein Databases are: PDB

Secondary databases

- The data stored in these types of databases are the analyzed result of the primary database.
- The data here are highly curated (processing the data before it is presented in the database). A secondary database is better and contains more valuable knowledge compared to the primary database.
- Examples –
- DNA databases: Refseq (comprehensive, integrated, well-annotated set of sequences, including genomic DNA)
- SNP- disease databases
- Protein Databases:
- InterPro (protein families, motifs, and domains)
- UniProt/KB (sequence and functional information on proteins)

Based on Accessibility	Primary Databases	Contain raw experimental data submitted by researchers.	GenBank, PDB, GEO
	Secondary Databases	Contain curated and processed data derived from primary databases.	UniProt, Pfam
	Tertiary Databases	Integrate data from multiple primary and secondary	KEGG, Ensembl

Abbreviation

- NCBI: National Center for Biotechnology information
- EMBL: European Molecular Biology Library
- DDBJ: DNA Databank of Japan
- UniProt/KB: Universal Protein Knowledgebase
- PIR: Protein Information Resources
- PDB: Protein Data Bank
- NRDB: Non-Redundant Databases
- PubMed: Public/Publisher MEDLINE
- NLM: National library of medicine
- PMC: PubMed Central
- BLAST: The Basic Local Alignment Search Tool

How Journals and Articles Are Organized in Biological Databases

 Organizing journals and articles is an integral part of many biological databases, as they help researchers stay updated and access relevant literature for their studies. This is commonly achieved through literature databases or integrated resources within bioinformatics systems

Specialized Literature Databases

- Databases like PubMed, Europe PMC, and Medline specialize in indexing biological and medical research articles.
- They organize articles by:
 - Titles, authors, and abstracts.
 - Keywords and MeSH (Medical Subject Headings) terms for easy retrieval.
 - Citations and cross-references to other articles.

Examples of Biological Databases Integrating Literature

*PubMed: Focuses on biomedical and life sciences literature.

Europe PMC: Provides access to full-text articles and links to datasets.

❖NCBI Gene: Links genes to PubMed articles and related research.

UniProt: Links protein entries to peer-reviewed publications explaining their properties.

Benefits of Organizing Articles in Biological Databases:

- · Facilitates literature review for researchers.
- Enhances the reliability of biological data by linking it to peerreviewed evidence.
- Saves time by combining experimental data and relevant studies in one place.



Search

Advanced

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How to use PubMed and PMC

What is the difference between PMC and PubMed?





Dr Delveen Ramdan Ibrahim

Search

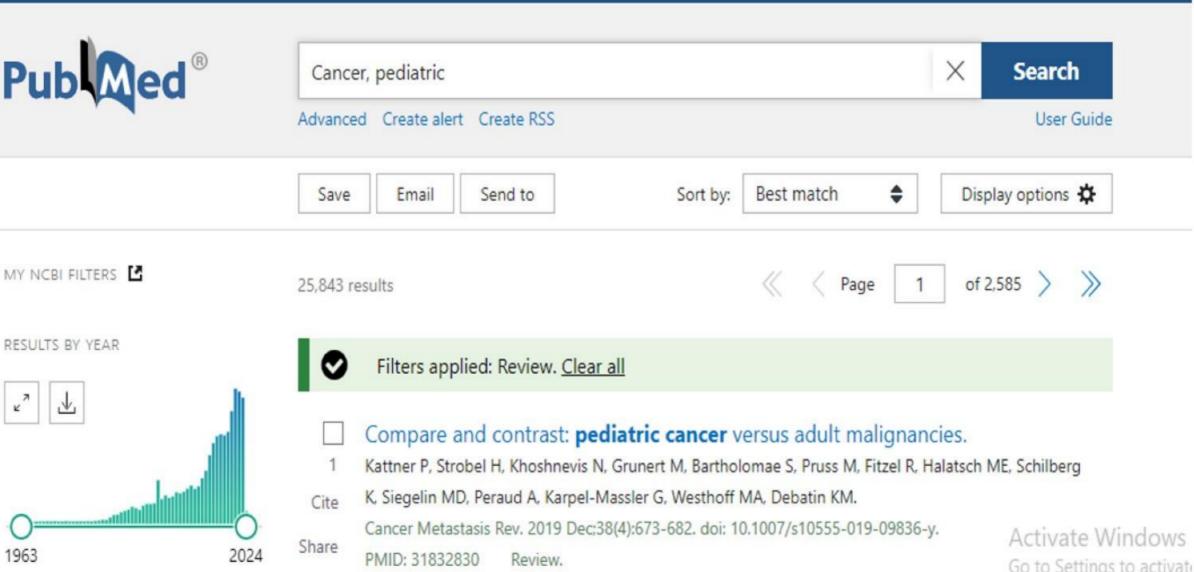
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Cancer AND Pediatric AND sepsis

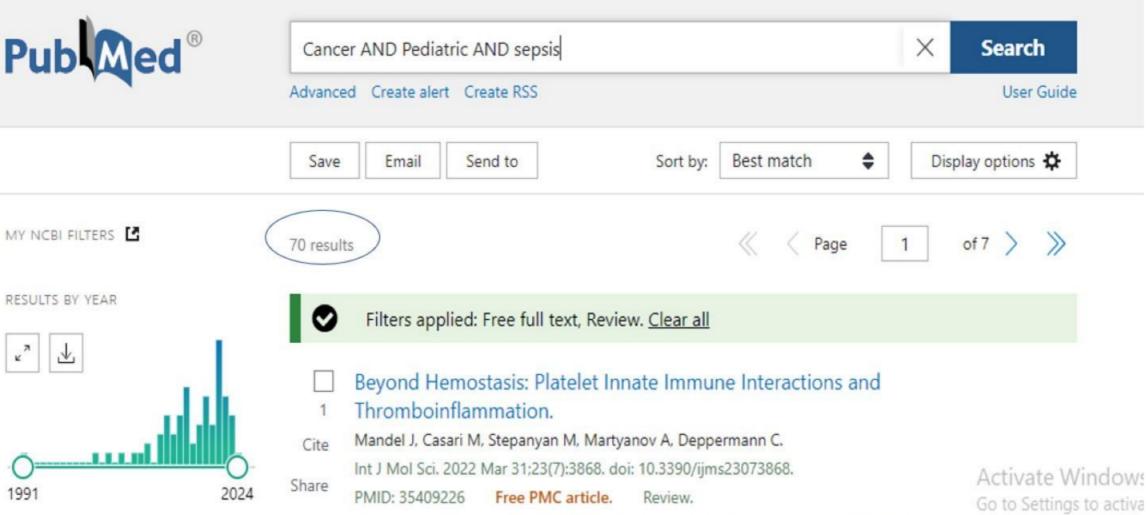
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There is accumulating evidence that platelets play roles beyond their traditional functions in thrombosis

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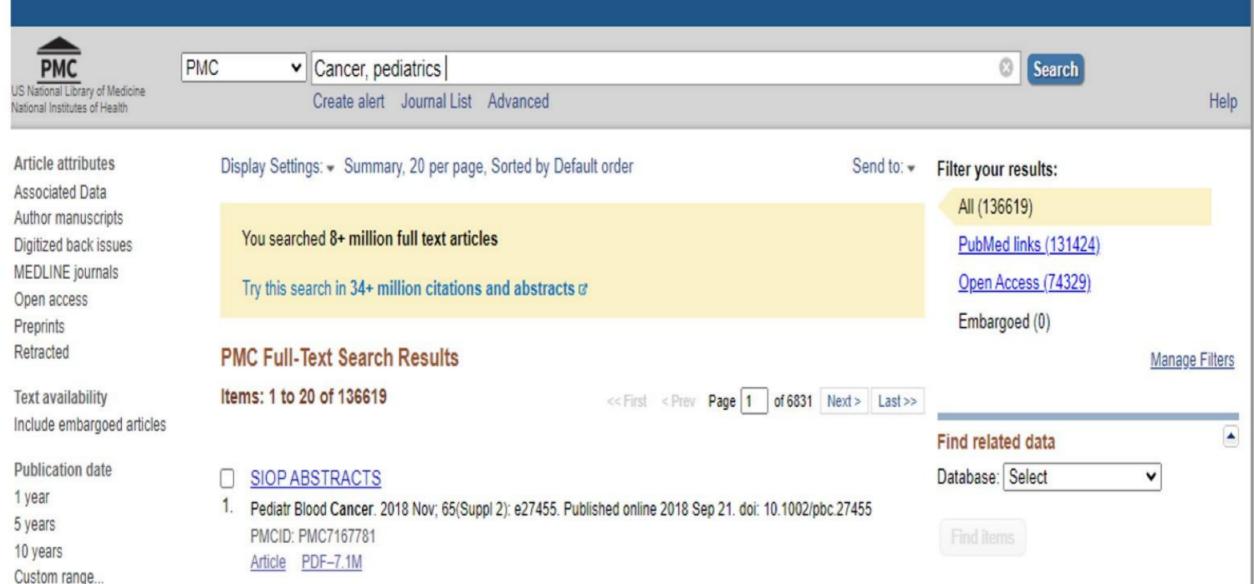




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Literature Search and anim Retrieval

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• Example:

- Search for papers on "CRISPR-Cas9 applications in gene therapy."
- Refine results using filters like publication date, author, journal, or study type.