Dr. Sudha Kumari

Assistant Professor

Department of Veterinary Microbiology

Bihar Animal Sciences University, Patna

What is Bioinformatics?

Bioinformatics is the application of computer technology to get the information that's stored in certain types of biological data.

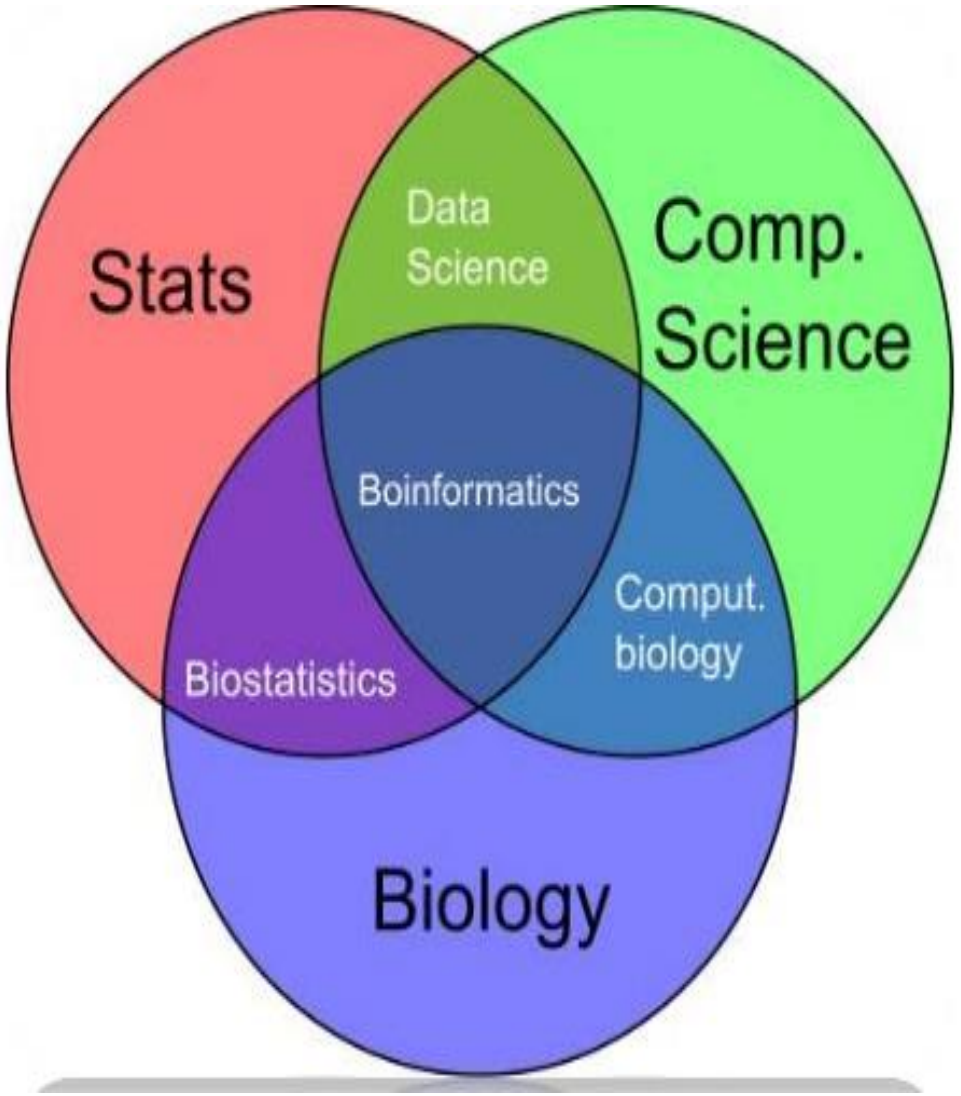
Bioinformatics provides central, globally accessible databases that enable scientists to submit, search and analyze information.

What is Bioinformatics?

- It is an interdisciplinary field that develops methods and software tools for
- Under standing biological data. As an interdisciplinary field of science, bioinformatics
- Combines computer science, statistics, mathematics and engineering to analyze and

Interpret biological data.

Bioinformatics is the field of science in which biology, computer science and informatic technology merge to form a single discipline



History of bioinformatics

- Paulien Hogeweg and Ben Hesper coined it in 1970 to refer to the study of information processes in biotic systems.

- The term **bioinformatics** was first introduced in 1990s.

Originally, it dealt with the management and analysis of the data pertaining to DNA, RNA and protein sequences.

- As the biological data is being produced at an unprecedented rate, its management and interpretation invariably requires **bioinformatics**.

Why Bioinformatics is necessary

- The need for bioinformatics has arisen from the resent explosion of publically available genomic informatics, such as resulting from the human genome project.

- Gain a better under standing of gene analysis, taxonomy and evolution.

- To work efficiently on the rational drug designs and reduce the time taken for the development of drug manually.

Goal of bioinformatics

- Extension of experimental data by predictions.

- To uncover the wealth of Biological information hidden in the mass of sequence, structure, literature and biological data

- It is being used now and in the foreseeable future in the areas of molecular medicine.

It has environmental benefits in identifying waste and clean up bacteria.

- In agriculture, it can be used to produce high yield, low maintenance crops.

Where bioinformatics helps

In experimental molecular biology

In genetics and genomics

In generating biological data

Understanding biological pathway and network s in system biology

Evolutionary aspect of evolution

In simulation and modeling of DNA, RNA and protein.

It offers analysis software for data studies and comparisons and provides tools for modelling, visualising, exploring and interpreting data.Main goal is to convert multitude of complex data into useful information and knowledge.

Bioinformatics has been used for in silico analyses of biological queries using mathematical and statistical techniques.

bioinformatics also tries to understand the organisational principles within nucleic acid and protein sequences, called proteomics.

Relation to other fields

Bioinformatics is a science field that is similar to but distinct from biological computation, while it is often considered synonymous to computational biology.

Biological computation uses bioengineering and biology to build biological computers, whereas bioinformatics uses computation to better understand biology.

Bioinformatics and computational biology involve the analysis of biological data, particularly DNA, RNA, and protein sequences.

The field of bioinformatics experienced explosive growth starting in the mid-1990s, driven largely by the Human Genome Project and by rapid advances in DNA sequencing technology.

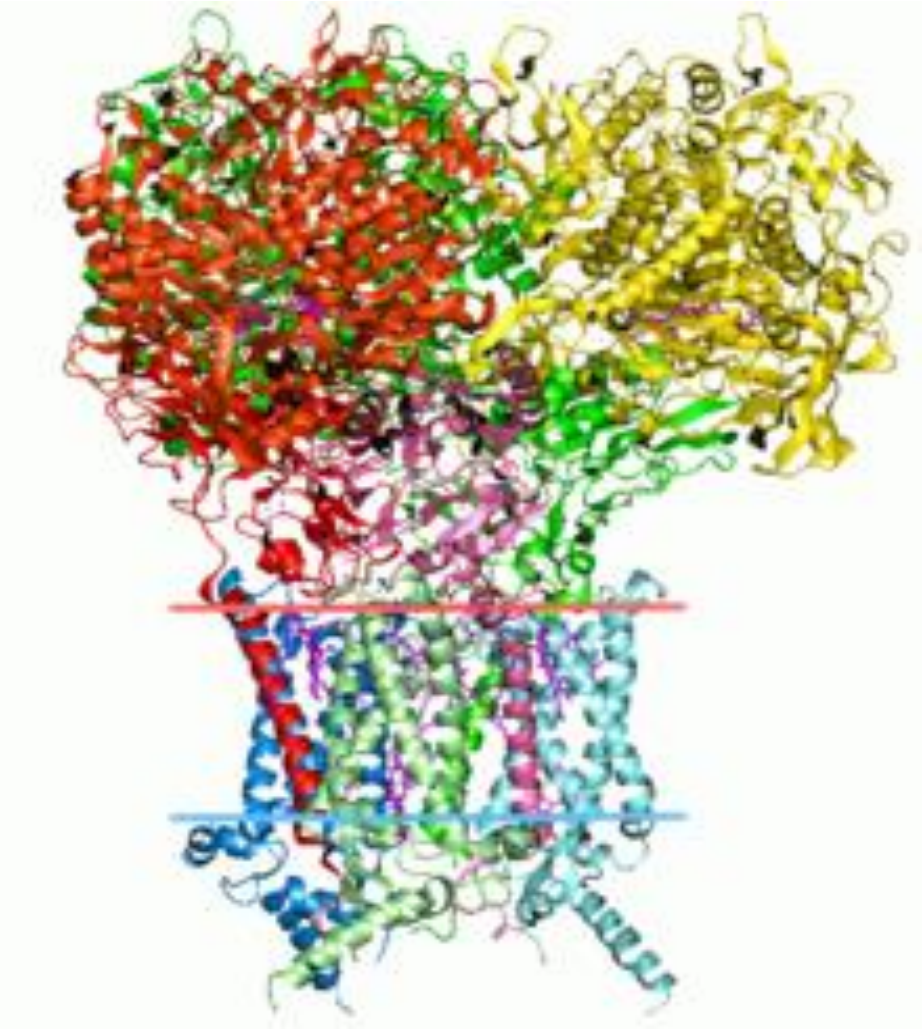
Analyzing biological data to produce meaningful information involves writing and running software programs that use algorithms from graph theory, artificial intelligence, soft computing, data mining, image processing, and computer simulation.

The algorithms in turn depend on theoretical foundations such as discrete mathematics, control theory, system theory, information theory, and statistics.

Structural bioinformatics

Structural bioinformatics and Protein structure prediction

See also: Structural motif and Structural domain



Protein structure prediction is another important application of bioinformatics.

The amino acid sequence of a protein, the so-called primary structure, can be easily determined from the sequence on the gene that codes for it.

In the vast majority of cases, this primary structure uniquely determines a structure in its native environment. (Of course, there are exceptions, such as the bovine spongiform encephalopathy (mad cow disease) prion.)

Knowledge of this structure is vital in understanding the function of the protein. Structural information is usually

classified as one of *secondary*, *tertiary* and *quaternary* structure.

A viable general solution to such predictions remains an open problem.

Most efforts have so far been directed towards heuristics that work most of the time.

Bioinformatics workflow management systems

A bioinformatics workflow management system is a specialized form of a workflow management system designed specifically to compose and execute a series of computational or data manipulation steps, or a workflow, in a Bioinformatics application

Such systems are designed to

- provide an easy-to-use environment for individual application scientists themselves to create their own workflows,
- provide interactive tools for the scientists enabling them to execute their workflows and view their results in real-time,
- simplify the process of sharing and reusing workflows between the scientists, and
- enable scientists to track the provenance of the workflow execution results and the workflow creation steps.

Some of the platforms giving this service: Galaxy, Kepler, Taverna, UGENE, Anduril,

THANK YOU