

ST. ANN'S COLLEGE FOR WOMEN
DEPARTMENT OF BIOTECHNOLOGY

INTERSHIP REPORT
BIOINFORMATICS - COMPUTATIONAL
BIOLOGY

An internship program on bioinformatics – a computational biology was conducted in online session by Verzeo – IBM from 1-11-2022 to 31-12-2022. This internship was conducted for two months by online training and hands on training.

INTRODUCTION

Bioinformatics is a multidisciplinary field that combines biology, computer science, mathematics and statistics to analyse and interpret the biological data, especially from proteomics, genomics, DNA sequencing and many other omics disciplines. Computational, statistical, and computer programming techniques have been used for computer simulation analyses of biological queries. They include reused specific analysis "pipelines", particularly in the field of genomics, such as by the identification of genes and Single Nucleotide Polymorphisms (SNPs).

IT INCLUDES

- Gap penalties and substitution score and matrices
 - Phylogenetics and Evolutionary biology
 - Phylogenetic tree construction
 - Molecular evolution
 - Comparative genomics
 - Protein-ligand docking
 - Metagenomics sequencing and Microbiome community Analysis
 - Sequence analysis – DNA sequence analysis and RNA sequence analysis
 - Biological databases – GenBank, Uniport, Protein database, BLAST & FASTA
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- Introduction to bioinformatics – computational biology
 - Classification of different database and tools
 - Introduction to alignment – pairwise sequence alignment and multiple sequence alignment
 - It majorly includes NCBI (National centre for biotechnology information) and PubMed and PubMed Central.
 - Retrieving FASTA (Format for nucleotide sequences)

CONCLUSION

ABOUT IT

Bioinformatics begins with the analysis of vast amounts of biological data, including DNA sequences, RNA sequences, protein sequences, and structural information. Techniques such as sequence alignment, motif discovery, and statistical analysis are employed to extract meaningful insights from these data sets. Genome assembly involves reconstructing the complete DNA sequence of an organism from fragmented data obtained through sequencing technologies. Genome annotation is the process of identifying genes, regulatory elements, and functional regions within a genome. Both processes are essential for understanding genetic information and its role in biological processes. Structural bioinformatics focuses on predicting and analysing the three-dimensional structures of biological macromolecules, such as proteins and nucleic acids. Methods such as homology modelling, protein folding simulations, and molecular docking are used to study protein structure-function relationships and drug design.

Phylogenetics is the study of evolutionary relationships among organisms based on molecular sequence data. Bioinformatics methods are used to construct phylogenetic trees and infer the evolutionary history of species. Comparative genomics further explores genome evolution and genetic variation across different organisms. Functional genomics aims to understand the functions of genes and other genomic elements. This includes gene expression analysis, regulatory network inference, and functional annotation of genes. Techniques such as microarrays, RNA sequencing, and CRISPR/Cas9 gene editing are commonly used in functional genomics studies. Metagenomics involves studying genetic material directly extracted from environmental samples, such as soil, water, or the human microbiome. It provides insights into microbial diversity, community structure, and functional potential. Bioinformatics tools are essential for analysing metagenomic data and uncovering microbial interactions.

Hands-on workshop on gene sequencing of two genes of different organisms through NCBI website. By integrating

computational and experimental approaches, bioinformatics continues to drive discoveries in diverse areas of biology, medicine, agriculture, and environmental science, paving the way for innovative solutions to complex biological problems.

Bioinformatics has emerged as a cornerstone of modern biological research, providing powerful tools and methodologies for analysing, interpreting, and leveraging biological data. By integrating computational and experimental approaches, bioinformatics continues to drive discoveries in diverse areas of biology, medicine, agriculture, and environmental science, paving the way for innovative solutions to complex biological problems.

CERTIFICATE



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