

Course Code: BD502T
DSE Course – II: Bioinformatics

The objective of this course is to expose the students to the application of computation tools in solving Biological problems

(Credits: Theory-4, Practical-2)

THEORY
Lectures: 60

Unit 1. Introduction to Bioinformatics (5 Lectures)

Introduction, Branches of Bioinformatics, Aim, Scope and Research areas of Bioinformatics.

Unit 2. Databases in Bioinformatics (5 Lectures)

Introduction to Biological Databases, Classification format of Biological Databases, Biological Database Retrieval System.

Unit 3. Biological Sequence Databases (25 Lectures)

National Center for Biotechnology Information (NCBI): Tools and Databases of NCBI, Database Retrieval Tool, Sequence Submission to NCBI, Basic Local Alignment Search Tool (BLAST), Nucleotide Database, Protein Database, Gene Expression Database.

EMBL Nucleotide Sequence Database (ENA): Introduction, Sequence Retrieval, Sequence Submission to EMBL, Sequence analysis tools.

DNA Data Bank of Japan (DDBJ): Introduction, Resources at DDBJ, Data Submission at DDBJ.

Protein Information Resource (PIR): About PIR, Resources of PIR, Databases of PIR, Data Retrieval in PIR.

Swiss-Prot: Introduction and Salient Features.

Unit 4. Sequence Alignments (10 Lectures)

Introduction, Concept of Alignment, Pairwise sequence alignment (PSA), Multiple Sequence Alignment (MSA), MSA by CLUSTALW, Scoring Matrices, Percent Accepted Mutation (PAM), Blocks of Amino Acid Substitution Matrix (BLOSUM).Dynamic Programming Algorithms.

Unit 5. Molecular Phylogeny (8 Lectures)

Methods of Phylogeny, Software for Phylogenetic Analyses, Consistency of Molecular Phylogenetic Prediction.

Unit 6. Applications of Bioinformatics

(7 Lectures)

Structural Bioinformatics in Drug Discovery, Quantitative structure-activity relationship (QSAR) techniques in Drug Design, Microbial genome applications, Crop improvement

Course Code: BD502P
DSE Course – II - Practical: Bioinformatics

1. Nucleic acid and protein databases.
2. Sequence retrieval from databases.
3. Sequence alignment.
4. Similarity searches using BLAST/FASTA
5. Construction of phylogenetic tree.

Suggested Readings

1. Ghosh Z. and Bibekanand M. (2008) Bioinformatics: Principles and Applications. Oxford University Press.
2. Pevsner J. (2009) Bioinformatics and Functional Genomics. II Edition. Wiley-Blackwell.
3. Campbell A. M., Heyer L. J. (2006) Discovering Genomics, Proteomics and Bioinformatics. II Edition. Benjamin Cummings.