B.Sc. III Year **Semester – V**

BBO-E502
DSE-1 Bioinformatics

MM : 100
Time : 3 hrs

Sessional : 30
ESE : 70
Pass Marks : 40

Learning objective:

- To understand the basic knowledge of Bioinformatics, scope and research areas of bioinformatics.
- To acquire information on classification format of biological databases and biological database retrieval system.
- To become familiar with National Center for Biotechnology Information (NCBI) and Basic Local Alignment Search Tool (BLAST), EMBL-Bank, DDBJ, Protein Information Resource (PIR) and Swiss-Prot.
- To acquire an overall knowledge on sequence alignments, molecular phylogeny and applications.

Learning outcomes:

At the end of course student will be able

- The student will be able to familiar with various tools and techniques used in Bioinformatics, and understand the utilization management of biological databases and their retrieval system.
- The student will be able to understand the tools and databases of NCBI and Basic Local Alignment Search Tool (BLAST), nucleotide database, protein database, gene expression database.
- The student will be to understand the about the Concept of Alignment, Multiple Sequence Alignment (MSA) and scoring matrices, PAM; BLOSUM, various techniques of phylogeny, software for phylogenetic analyses, consistency of molecular Phylogenetic prediction.
- The student will be able take the decisions for carrier point of views in research, industries and academia entrepreneurships etc.

Unit 1: Introduction: **(5 Lectures)**

Introduction, branches of bioinformatics, aim, scope and research areas of bioinformatics.

Unit 2: Databases: **(5 Lectures)**

Introduction, 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 (EMBL-Bank): 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, Multiple Sequence Alignment (MSA), MSA by CLUSTALW, scoring matrices, Percent Accepted Mutation (PAM);Blocks of Amino Acid Substitution Matrix (BLOSUM).

Unit 5: Molecular Phylogeny and Applications: **(8 Lectures)**

Methods of phylogeny, software for phylogenetic analyses, consistency of molecular phylogenetic prediction. Structural bioinformatics in drug discovery, quantitative structure-activity relationship (QSAR) techniques in drug design, microbial genome applications, crop improvement.

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Practical

1. Nucleic acid and protein databases.
2. Sequence retrieval from databases.
3. Sequence alignment.
4. Sequence homology and Gene annotation.
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.

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