

Devi Ahilya University, Indore, India Institute of Engineering & Technology				IV Year B.E. (Information Technology)			
Subject Code & Name	Instructions Hours per Week			Credits			
6ITRE2 Bio-Informatics	L	T	P	L	T	P	Total
		3	1	2	3	1	1
Duration of Theory Paper: 3 Hours							

Learning Objective:

- Understand the basics of DNA and protein structure, and their roles in biological systems.
- Learn various techniques used in sequence analysis, such as alignment, scoring matrices, and databases.
- Understand the principles and methods used in protein structure determination and prediction.
- Describe the factors affecting protein stability, folding, and interactions, and the methods used in their study.
- Learn about the principles and techniques used in computer-aided drug design, including docking, screening, and machine learning.

UNIT-I: Introduction, DNA sequence analysis, DNA Databases, Protein structure and function, protein sequence databases, sequence alignment, PAM matrix, Global and local alignment, BLAST: features and scores.

Unit-II: Multiple sequence alignment, Conservation score, phylogenetic trees, Protein sequence analysis, hydrophobicity profiles, non-redundant datasets, Protein secondary structures, Ramachandran plot, propensity, secondary structure Prediction

UNIT-III: Protein tertiary structure, Protein Data Bank, visualization tools, structural classification, contact maps , Protein structural analysis, protein structure prediction.

UNIT-IV: Protein stability, energetic contributions, database, stabilizing residues, stability upon mutations, Protein folding rates, proteins interactions, binding site residues.

UNIT-V: Computer aided drug design, docking, screening, QSAR, Development of algorithms, awk programming, machine learning techniques, applications using WEKA.

Books and references

- [1]. M. Michael Gromiha, Protein Bioinformatics: From Sequence to Function, Academic Press, 2010

- [2]. D.E. Krane and M.L. Raymer, Fundamental concepts of bioinformatics, Pearson Education Inc. 2006

List of practical:

1. DNA sequence analysis: Students could analyze DNA sequences using bioinformatics tools such as BLAST and examine their features and scores.
2. Protein structure and function: Students could explore protein structure and function using databases such as the Protein Data Bank and visualization tools.
3. Sequence alignment: Students could learn to perform sequence alignment using PAM matrices and global and local alignment techniques.
4. Multiple sequence alignment: Students could perform multiple sequence alignment and calculate conservation scores and construct phylogenetic trees.
5. Protein secondary structures: Students could analyze protein secondary structures using tools such as the Ramachandran plot and propensity calculations.
6. Protein tertiary structure: Students could examine protein tertiary structures using contact maps and structural classification.