Course Code	Course Title	L	T	P	C
BABIT202	FUNDAMENTALS OF BIOINFORMATICS	2	1	2	4
Pre-requisite	BABIT101 - Biochemistry	Syllabus Version			
		1			

Course Objectives

1. Understanding the fundamentals of biological databases, sequence comparison and molecular phylogenetics
2. Exploring protein structure visualization, classification and computational prediction of secondary and tertiary structures
3. Developing skills to use machine learning and computational techniques for drug design

Course Outcomes

1. Gain proficiency in using biological databases and sequence comparison for data analysis
2. Perform sequence alignments and similarity search for any biological data
3. Construct phylogenetic trees and analyze evolutionary relationships among organisms using sequence data
4. Predict protein secondary and tertiary structures and analyze using visualization tools
5. Utilize ML algorithms and computational tools for drug design and drug repurposing

Module:1	Biological databases	4 hours

Bioinformatics-Goal, Scope, Applications and limitations; Biological Databases-Types of Databases, Pitfalls of Biological Databases, File formats (GenBank, uniport, PDB).

Module:2	Sequence Alignment and Database Similarity Search	6 hours

Biological Sequence comparison - Dot plot; Pairwise Sequence Alignment - Smith and Waterman; Needleman and Wunsch algorithms; Statistical Significance of Sequence Alignment; Scoring Matrices Heuristic Database Searching BLAST and its types, PSI-BLAST, PHI-BLAST, FASTA and its applications, Comparison of BLAST & FASTA.

Module:3	Molecular Phylogenetics	6 hours

Multiple Sequence Alignment Algorithms; Phylogenetics basics; Phylogenetic tree construction methods - Distance-based methods, Character-based methods, Phylogenetic tree evaluation.

Module:4	Structural Bioinformatics	6 hours

Protein Structure Basics; Protein Structure Visualization, Comparison,

and Classification; Protein Secondary Structure Prediction; Protein Tertiary Structure Prediction.		
Module:5	**Drug discovery and Machine learning**	**6 hours**
Structure-Based Rational Drug Design and discovery – Drug repurposing; Chemoinformatics; Overview of Machine Learning Algorithms in drug discovery process.		
Module:6	**Contemporary Topics**	**2 hours**
	Total Lecture Hours:	**30 hours**
	Tutorial Hours:	**15 hours**

Text Book(s)

S.C. Rastogi, Namita Mendiratta, and Parag Rastogi, "**Bioinformatics: Methods and Applications – Genomics, Proteomics, and Drug Discovery**", PHI Learning, 5th Edition, **2022**

Jin Xiong, "**Essential Bioinformatics**", Cambridge University Press NY, 1st Edition, **2015**

Reference Books

Vinay Sharma, Ashok Munjal, Ashish Shanker,, "**A Textbook of Bioinformatics**", Rastogi Publications, 2nd Edition, **2018**

J Howard Parish, Richard M Twyman, Charlie Hodgman, Andrew French and David Westhead, "**Instant Notes in Bioinformatics**", Taylor and Francis London, 2nd Edition, **2015**

Indicative Experiments

1. Biological Databases and Data Retrieval	3 hours
2. Pairwise Sequence Alignment	3 hours
3. Multiple Sequence Alignment and Phylogenetic Tree Construction	3 hours
4. BLAST - Basic Local Alignment Search Tool	3 hours
5. Database search using FASTA	3 hours
6. Homology Modeling of Protein Structures	3 hours
7. Protein Structure Visualization	3 hours
8. Pharmacokinetic and dynamic analysis	3 hours
9. Protein-Ligand and Protein-Protein interaction analysis	3 hours
10. Gene prediction analysis	3 hours
Total Laboratory Hours:	**30 hours**

Mode of Evaluation : Continuous Assessment Test, Digital Assignment, Quiz, Final Assessment Test, Lab Continuous Assessment, Lab Final Assessment, Seminar	
Recommended by Board of Studies :	26-05-2025
Approved by Academic Council : No. 78	12-06-2025