

Syllabus template

Semester: 5				
Course: Major 4				
Paper Title: Bioinformatics				
Paper code: C3BT230542T/P				Credits: (Th:3+Pr:1)
Hours/week: 6 Hours				
Category: Core/MDC/SEC/VAC: Core				
Theory / Practical / Composite: Composite				
No of Modules: 2				
Course Overview:				
<p>This course provides an introduction to the principles and applications of bioinformatics with a focus on the analysis of biological data using computational tools and databases. Students will learn to navigate primary and secondary biological databases, perform sequence alignment, analyze phylogenetic relationships, and predict macromolecular structures. The course also covers genome analysis, microarray technology, pathway databases, and systems biology, enabling students to understand how complex biological information can be integrated and interpreted. Practical modules emphasize hands-on training in programming, use of bioinformatics software, structural modeling, genome annotation, and data mining. By the end of the course, students will be equipped with both the theoretical foundation and computational skills required to solve biological problems and engage in modern research in the life sciences.</p>				
Course Outcome:				
1. Remember details of major biological databases, data formats, and their applications in bioinformatics.				
2. Understand, explain and explore, sequence alignment methods, substitution matrices, and phylogenetic tree construction techniques. Perform protein and RNA structural predictions using computational tools such as homology modeling, threading, and AlphaFold.				
3. Analyze macromolecular interactions, docking simulations, and molecular dynamics data using appropriate bioinformatics software.				
4. Evaluate genome analysis methods, microarray technology, and pathway enrichment approaches for functional annotation of biological data.				
5. Apply data mining workflows using database management systems, ER diagrams, decision trees, and cloud-based platforms.				
6. Create short programs using programming skills in Python and apply them to solve machine learning and bioinformatics problems.				
Prerequisites: <i>Basic knowledge about Computing</i>				
SYLLABUS				
UNIT/Module	CONTENT	HOURS or NUMBER OF CLASSES	CO Mapping	COGNITIVE LEVEL
MODULE A	UNIT I - Introduction to Bioinformatics; Sequence Information resources: SWISSPROT, TrEMBL,	10 Classes	CO 1 to CO3	K1 to K4

	<p>PDB; GenBank, EMBL, DDBJ; Composite Databases: NRDB, UniProt, ExPASy server.</p> <ul style="list-style-type: none"> - Literature Databases: Open access and organism-specific databases; Annotation of databases; Information Retrieval; Sequence formats. - Sequence similarity searches: Global & Local alignments, BLAST; Mutation/Substitution Matrices: PAM250 & BLOSUM62. - Pairwise and Multiple Sequence Alignments: ClustalW, Multalin; Alignment score and gap penalty; Phylogenetic Analysis. 			
	<p>UNIT II</p> <ul style="list-style-type: none"> - Structural Classification of Proteins – CATH, SCOP. - Protein Tertiary Structure Prediction: Homology Modeling, Threading and Fold Recognition, Alphafold. - RNA structure prediction: Circular plot, Dot plot analysis of protein and RNA sequences. 	10 Classes	CO1 to CO3	K1 to K4
	<p>UNIT III</p> <ul style="list-style-type: none"> - Characteristics of Protein-protein, Protein-DNA and Protein-RNA interaction surfaces, related databases. - Solvent Accessible Surface Area of Protein (SASA), interactive tool PISA. - Overview of Docking & Molecular Dynamics (MD) simulation. 	12 Classes	CO 1 to CO4	K1 to K6

Module B	UNIT IV - Prokaryotic and Eukaryotic Genome Analyses – File Formats and Retrieval, genome assembly. - Microarray Technology – DNA, MMChips, Protein, Antibody and chemical compound based arrays. GEO database. - Pathway Databases and Pathway Analyses – Concept of Enrichment. - Database Management Systems. Data Mining using cloud platforms; ER diagrams, Decision Trees; ARIES algorithm. - Introductory idea on Systems Biology.	15 Classes	CO 1, CO3 to CO6	K1 to K6
	Practical: - Retrieval of protein information, sequence similarity searches, MSA, phylogenetic tree construction. - Modelling of protein structure, structure analysis, interactomics. - Microbial Genome Analyses: functional annotation using suitable tools. - Overview of operating systems. - Python programming basics and applications in machine learning. - Bioinformatics Projects.	14 Classes	CO1 to CO6	K1 to K6
Text Books				
1. Bioinformatics: Sequence and Genome Analysis, Second Edition David W Mount; CSHL Press				
2. Bioinformatics and Molecular Evolution Paul G. Higgs, Teresa K. Attwood Wiley-Blackwell				
3. Introduction to Protein Structure, Carl Ivar Branden and John Tooze; Garland Science				
4. Microarray Data Analysis: Methods and Applications; Pietro Hiram Guzzi; https://doi.org/10.1007/978-1-4939-3173-6				

5. Computational Genome Analysis; An Introduction; Richard C. Deonier, Michael S. Waterman, Simon Tavaré; https://doi.org/10.1007/0-387-28807-4
Suggested readings
1. Bioinformatics: Experiments, Tools, Databases, and Algorithms by Orpita Basu and Simminder Kaur Thukral; OXFORD HIGHER EDUCATION
2. Biological Networks and Pathway Analysis; Tatiana V. Tatarinova, Yuri Nikolsky; https://doi.org/10.1007/978-1-4939-7027-8
Web Resources
1. https://www.youtube.com/watch?v=oATUjAxNf6U
2. https://www.youtube.com/watch?v=OrXRI_8UFHU
Evaluation: Theory: CIA-10, Assignment-2, Attendance-3, Semester Exam-45 Practical: CA-30, Attendance-2, Semester Exam-8
Paper Structure for Theory Semester Exam Module: Module A (30 Marks): 1 Compulsory Objective Question (10 marks), Any 2 out of 3 questions (10 marks each). Module B (15 Marks): 1 Compulsory Objective Question (5 marks), Any 2 out of 3 questions (5 marks each).

COURSE OUTCOMES (COS) AND COGNITIVE LEVEL MAPPING

COs	CO Description	Cognitive levels
CO1	Remember the techniques of data and information retrieval from different biological databases and tools.	K1 to K3
CO2	Understand algorithms for searching the biological databases.	K1 to K3
CO3	Apply different sequence alignment methods and phylogenetic tree construction algorithms.	K 1 to K6
CO4	Analyze protein secondary and tertiary structure.	K1 to K6
CO5	Evaluate and annotate genomes and perform functional annotation along with gene expression analyses and pathway enrichment studies.	K1 to K6
CO6	Navigate across different operating systems for performing programming based operations. Create short programs for exploring different biological problems	K1 to K6