

B. E. BIOTECHNOLOGY			
Outcome Based Education (OBE) and Choice Based Credit System (CBCS)			
SEMESTER - VI			
BIOINFORMATICS			
Course Code	18BT63	CIE Marks	40
Teaching Hours/Week (L:T:P)	(4:0:0)	SEE Marks	60
Credits	04	Exam Hours	03
Course Learning Objectives:			
<ul style="list-style-type: none"> • To use online resources, databases related to biological data. • To learn the underlying concepts of Bioinformatics • To learn the various tools in bioinformatics to manipulate and analyse biological data 			
Module-1			
DATABASES & SEQUENCE ALIGNMENT TOOLS:			
Introduction to Bioinformatics, Need for informatics tools and exercises, Bioinformatics resources: NCBI, EBI, ExPASy, RCSB. Significance of databases towards informatics projects. Databases and classifications. GenBank, DDBJ, EMBL, PIR, Uniprot-KB, SWISS-PROT, TrEMBL. Gene bank flat file. Protein Data Bank (PDB) flat file; FASTA Format, PIR Format; Structure file formats. the Modular Nature of proteins, Optional Alignment Methods, Substitution scores, substitution matrices, PAM, BLOSUM, Gap penalties, Statistical significance of Alignments, BLAST and its different types and function, Practical Aspect of Multiple Sequence Alignment, Progressive Alignment Methods, MUSCLE, Motifs and Patterns, PROSITE, Hidden Markov Models (HMMs), and Threading methods. Conceptual numericals.			
Module-2			
PHYLOGENETIC ANALYSIS AND GENOME BIOINFORMATICS			
Introduction to Phylogenetic analysis, rooted and unrooted trees, Elements of phylogenetic Models, Phylogenetic Data Analysis: Alignment, Substitution Model Building, Tree Building, and Tree Evaluation, Tree - Building Methods-Distance based and character based methods, Evaluating Trees and Data- Boot strapping (parametric and non-parametric), Phylogenetic softwares (CLUSTAL -omega, PHYLIP etc), Conceptual numericals.			
Bioinformatics tools and automation in Genome Sequencing, analysis of raw genome sequence data, Utility of EST database in sequencing, Bioinformatics in detection of Polymorphisms, SNPs and their relevance, Bioinformatics tools in microarray data analysis. Tools for comparative genomics: BLAST2, Vista, MUMmer, COG, VOG.			
Module-3			
PREDICTIVE METHODS:			
Predictive Methods using Nucleotide sequences: Framework, Masking repetitive DNA, Databasesearches, Codon Bias Detection, Detecting Functional Sites in the DNA (promoters, transcription factor binding sites, translation initiation sites), Integrated Gene Parsing, finding RNA Genes, Web based tools (GENSCAN, GRAIL, GENEFINDER).			
Predictive Methods using Protein sequences: Protein Identity based on composition, Physicalproperties Based on sequence, secondary structure and folding classes, specialized structures or features, tertiary structure. Related web based software (JPRED, NNPREPDICT, SOPMA, DSSP, STRIDE).			
Module-4			
MOLECULAR MODELING & VIZUALIZATION:			
Concepts in Molecular Modeling: Coordinate Systems, concept of energy minimization, different types of interactions and formulation of force fields. Basic MD algorithm, its limitations, treatment of long range forces. Comparative modeling, Constructing an initial model, refining the model, manipulating the model; molecular superposition and structural alignment,. Structure Visualization: small molecules (low molecular weight – peptides, nucleotides, disaccharides, simple drugs molecules) and macromolecules (high molecular weight molecules - proteins, DNA, RNA, membranes). Usages of visualization software available in public domain like VMD, Rasmol, Pymol, SpdbViewer, and Cn3D.			

Module-5				
PLASMID MAPPING, PRIMER DESIGN AND INSILICO DRUG DESIGN:				
Restriction mapping, Utilities, DNA strider, MacVector and OMIGA, gene construction KIT, Vector NTI, Web based tools (MAP, REBASE); Primer design – need for tools, Primer design programs and software (PRIME3). Molecular modeling in drug discovery, molecular docking, quantitative structure-activity relationship (QSAR), deriving the Pharmacophoric Pattern, Receptor Mapping, Estimating Biological Activities, Ligand - Receptor Interactions: Docking softwares (AUTODOCK, HEX), Energy Calculations (no derivation). Conceptual numericals.				
Course Outcomes:				
<ul style="list-style-type: none"> • Know the relevant online resources, databases and software tools • Understand the underlying concepts of Bioinformatics • Apply alignment and modelling tools • Analyse biological data using phylogenetic, predictive and comparative methods • Design in silico various biomolecules 				
Question paper pattern:				
<ul style="list-style-type: none"> • The question paper will have ten full questions carrying equal marks. • Each full question will be for 20 marks. • There will be two full questions (with a maximum of four sub- questions) from each module. • Each full question will have sub- question covering all the topics under a module. • The students will have to answer five full questions, selecting one full question from each module. 				
Sl No	Title of the Book	Name of the Author/s	Name of the Publisher	Edition and Year
Textbooks				
1	Computational methods for macromolecular sequence analysis:	R F Doolittle.	Acad. Press.	1996
2	Bioinformatics: Methods And Applications	P aragRastogi and S.C. Rastogi	PHI	Fourth Edition 2004
Reference Books				
1	Computational methods in Molecular Biology.	S.L.Salzberg, D B Searls, S Kasif,	Elsevier Science	1998
Web links and Video Lectures: -				