

22BT306 BIOINFORMATICS

Hours Per Week :

L	T	P	C
3	0	2	4

PREREQUISITE KNOWLEDGE: Biochemistry and Enzymology, Cell and Molecular Biology.

COURSE DESCRIPTION AND OBJECTIVES:

The main objective of this course is to equip students with computational skills and to help them use computational methods to study, organize, analyze and interpret biological information at molecular and genomics levels.

MODULE-1

UNIT-1

9L+0T+6P=15 Hours

OVERVIEW OF BIOINFORMATICS

Scope & emerging are as of bioinformatics, Applications of bioinformatics in life sciences, Internet protocols - HTTP, HTML, FTP and TELNET.

UNIT-2

15L+0T+10P=25 Hours

BIOLOGICAL DATABASES

Primary databases - NCBI, EMBL and DDBJ, Secondary data bases – Swissprot, PIR, Structural database - PDB, Biochemical databases – KEGG and BRENDA, Literature database – Pub Med, Protein classification databases - CATH, SCOP.

PRACTICES:

- Analyzing nucleotide sequence from biological database like NCBI.
- Analyzing protein sequence from biological databases like Swissprot.
- Mining of protein structured at a from PDB database.
- Retrieving pathways from KEGG & BRENDA.
- Retrieve open reading frame of given query nucleotide sequence by gene prediction methods.

MODULE-2

UNIT-1

9L+0T+6P=15 Hours

SEQUENCE ALIGNMENT METHODS

Pair wise sequence alignment, Global vs local alignment, Dot plots, Heuristic alignment algorithms, Amino acid substitution matrices.

UNIT-2

15L+0T+10P=25 Hours

PHYLOGENETIC TREE AND CDNA LIBRARIES

Multiple sequence alignment - algorithms and tools, Phylogenetic tree construction methods - distance based - character based, DNA Sequencing methods, Large scale sequencing, Genomic - DNA library construction, Gene identification methods, whole genome sequence analysis, Ramachandran Plot, Drug design.



source: <https://academic.oup.com/bioinformatics>

PRACTICES:

- Sequence similarity searching of nucleotide & protein sequences (BLASTN & BLASTP).
- Homology modeling studies using SWISS modeler & I-TASSER.
- Multiple sequence alignment of sequences using ClustalW.
- Protein Secondary structure prediction by SOPMA.
- Docking studies using Auto Dock Vina.
- Phylogenetic tree construction using MEGA.

COURSE OUTCOMES:

Upon successful completion of this course, students will have the ability to:

CO No.	Course Outcomes	Blooms Level	Module No.	Mapping with POs
1	Apply different bioinformatics softwares for prediction of protein structures.	Apply	1	1,2,5,9,10
2	Analyze secondary and tertiary structure of proteins using bioinformatics tools.	Analyze	1	2,3,4,9,10
3	Use of algorithms for pair wise alignments, multiple sequence.	Apply	2	2,3,4,5,9,10
4	Evaluate the stability of drug molecules using docking tools.	Evaluate	2	3,4,5,9,10

TEXT BOOKS:

1. David W. Mount, "Bioinformatics: Sequence and Genome Analysis", 2nd edition, CSHL Press, 2004.
2. A.D. Baxevanis and B.F.F. Ouellette, "Bioinformatics: A Practical Guide to the analysis of Genes and Proteins", 3rd edition, Wiley-Inter Science, 2004.

REFERENCE BOOKS:

1. Arthur Lesk, "Introduction to Bioinformatics", 5th edition, Oxford University Press, 2019.
2. Richard Durbin, Sean R. Eddy, Anders Krogh and Graeme Mitchison, "Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids", 1st edition, Cambridge University Press, 2008.
3. H. P. Bal, "Bioinformatics- Principles and Applications", 1st edition, Tata McGraw-Hill, 2006.
4. T. K. Attwood and D. J. Smith, "Introduction to Bioinformatics", 1st edition, Pearson Education, 2005.

SKILLS:

- ✓ Screening and design of molecule using *In silico* tools.
- ✓ Statistical analysis of biological data pertaining to genomics and proteomics.
- ✓ Determination of relationships among biological species using molecular phylogeny.
- ✓ Analysis of different structures of protein.