16BT402 BIOINFORMATICS

Hours Per Week:

L	Т	Р	С
3	-	2	4

Course Description and Objectives:

This course offers basic concepts in computational skills and computational methods to study, organise, analyse and interpret biological information at molecular, genetic and genomics levels. The objective of this course is to introduce the analysis of biological data using software tools.

Course Outcomes:

Upon completion of the course, the student will be able to

CO1: Understand the theoretical basis and emerging areas of bioinformatics.

CO2: Categorize the different types of biological databases.

CO3: Apply bioinformatics tools for protein structure prediction.

CO4: Evaluate the evolutionary relationship among species using MEGA.

CO5: Raise queries on biological data, interpret and model biological information and applyto solve biological problems in any area involving molecular data.

SKILLS:

- ✓ Design, conduct and interpret scientific research on bioinformatics.
- ✓ Conduct statistical analysis of biological data pertaining to genomics and proteomics.
- ✓ Apply a scientific approach to problems involving molecular phylogeny.



Source: www.bioplatforms.com/ wp-content/uploads/BPA-EBI-Bioinformatics-Trainingthumb.jpg

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ACTIVITIES:

- Retrieval of FASTA format from databases.
- Perform
 BLAST and
 FASTA software
 analysis for
 both nucleic
 acids and
 amino acid
 sequences.
- Perform pair wise and multiple sequence alignments.
- Construct phylogenetic trees using software tools such as PHYLIP and PAUP.

UNIT - 1 L-9

INTRODUCTION TO BIOINFORMATICS:Basics of bioinformatics; Elementary commands and protocols, ftp, telnet, http, html; Scope of bioinformatics.

UNIT - 2 L-9

SEQUENCING ALIGNMENT AND DYNAMIC PROGRAMMING: Heuristic alignment algorithms; Global sequence alignments -Neddleman, Wunsch algorithm, Smith-Waterman algorithm; Local sequence alignments- amino acid substitution matrices (PAM, BLOSUM).

UNIT - 3

BIOLOGICAL DATABASES AND THEIR USE: Introduction to biological databases; Organization and management of databases; Searching and retrieval of information from the world wide web; Structure databases - protein data bank (PDB), molecular modeling databases (MMDB); Primary databases NCBI, EMBL, DDBJ; Introduction to secondary databases organization and management of databases- Swissprot, PIR, KEGG; Introduction to biochemical databases- organization and management of databases; KEGG, EXPASY, BRENDA, WIT.

UNIT - 4 L-9

EVOLUTIONARY TREES AND PHYLOGENY: Ultrametric trees- parsimony, ultrametric problem; Perfect phylogeny, phylogenetic alignment, connection between multiple alignment and tree construction.

UNIT - 5

APPLICATIONS OF BIOINFORMATICS: DNA Mapping and sequence alignment, Gene predictions - molecular predictions with DNA strings; Secondary structure predictions - Ramachandran Plot.

LABORATORY EXPERIMENTS

List of Experiments:

Total hours-30

- Analyzing nucleotide and protein sequences from biological databases like NCBI, SwissProt.
- 2. Retrieving structure data for query protein from PDB.
- 3. To retrieve pathways from KEGG, BRENDA, METACYC, ECOCYC.
- 4. Retrieving biological Information from PubMed of NCBI.
- To retrieve open reading frame of given query nucleotide sequence by gene prediction methods.
- 6. Analysis of protein sequence using Expasy.
- 7. Sequence similarity searching of nucleotide sequences.
- 8. Sequence similarity searching of protein sequences.
- 9. Protein structure prediction by docking.

TEXT BOOKS:

- D. Mount, "Bioinformatics: Sequence and Genome Analysis", Indian edition, Cold Spring Harbor Lab, 2001.
- 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 Publications, 2005.

REFERENCE BOOKS:

- 1. C. S. V. Murthy, "Bioinformatics", 1st edition, Himalaya Publishing House, 2003.
- H. P. Bal, "Bioinformatics- Principles and Applications", First Reprint, Tata McGraw-Hill, 2006.
- 3. T. K. Attwood and D. J. Smith, "Introduction to Bioinformatics", Pearson Education, 1st edition, 11th reprint, 2005.

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