BTC DSC 353T

BIOINFORMATICS

Contact Hours: 45

Full Marks = 100 [ESE (70) CCA (30)]

Course Objective: *The Bioinformatics course aims to teach students how to use biological databases like GENBANK, EMBL, DDBJ, PDB, and SWISSPROT effectively, along with search tools like BLAST. They will learn to interpret search results, analyze sequences for homology and polymorphisms, perform sequence alignments, and conduct phylogenetic analyses. Additionally, students will gain insights into computer-aided drug design and basic PERL programming for bioinformatics applications.*

UNIT 1 *(7 Lectures)*

Biological database: definition; types and applications. **Nucleotide databases** GENBANK; EMBL; DDBJ. **Protein database**: PDB, SWISSPROT. **Other database:** organism specific database; structural database.

UNIT 2 *(8 Lectures)*

Searching databases: BLAST; types of BLAST; steps involved in BLAST; E-value; BLAST result interpretation; **Sequence analysis:** sequence homology; detecting open reading frames; single nucleotide polymorphisms.

UNIT 3 *(8 Lectures)*

Sequence alignment: global and local alignment; pairwise alignment (BLAST and FASTA) and multiple sequence alignment (Clustal W); Needleman-Wunsch and Smith-Waterman algorithms.

UNIT 4 *(10 Lectures)*

Phylogenetic Analysis: Phylogenetic tree and terminology; different methods of phylogenetic tree prediction - maximum parsimony, distance matrix methods (UPGMA, neighbor joining), maximum likelihood methods.

UNIT 5 *(12 Lectures)*

Computer aided drug designing: drug discovery process; target identification and validation; lead optimization and validation; virtual screening, Lipinski's rule of five; ADMETox screening. **Perl programming:** basic concepts in PERL programming; finding the length, reverse, reverse compliment of a DNA sequence; concatenating DNA fragments; transcription- DNA to RNA; reading DNA/protein from files in FASTA format.

Course Outcome: *After completing this course, students will proficiently utilize biological databases for research and applications. They will conduct precise searches and interpret the results. Students will also perform sequence analysis tasks, including identifying homology and polymorphisms, and master sequence alignment techniques. Furthermore, they will understand phylogenetic analysis methods and grasp the principles of computer-aided drug design. Basic PERL programming skills will enable them to excel in bioinformatics-related tasks.*

SUGGESTED READING

1. Ghosh Z. and Bibekanand M. (2008) Bioinformatics: Principles and Applications. Oxford University Press.
2. Pevsner J. (2009) Bioinformatics and Functional Genomics. II Edition. Wiley-Blackwell.
3. Campbell A. M., Heyer L. J. (2006) Discovering Genomics, Proteomics and Bioinformatics. II Edition. Benjamin Cummings.
4. Felsenstein, J. (2004). Inferring Phylogenies. Sinauer Associates.
5. Schwartz, R. L., & Phoenix, T. (2011). Learning Perl. O'Reilly Media.