

II Year B.Tech. Bioinformatics I - Semester	L	T	P	To	C
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BI 205 BIOINFORMATICS NETWORKS & APPLICATION

Course Description and Objective s:

This course provides the necessary basic protocols for utilization of various biological databases available on the internet. It consists of the tools utilized for biological sequential data analysis and methods of analyzing genetic and protein information.

Course outcomes:

1. Students will learn basic knowledge of modern molecular biology and genomics.
2. They will be able to perform sequence alignment and dynamic programming.
3. They will be able to perform various operations in Biological databses
4. They will understand the advantages and disadvantages of different machine learning techniques in bioinformatics.
5. They will be able to evaluate ways by which theoretical approaches can be used to model and analyze complex biological systems.

UNIT - I : Introduction To Bioinformatics and Networks :

Scope of Bioinformatics - Elementary commands and Protocols, ftp, telnet, http. Databanks - nucleotide databanks - Genbank, NCB I, EMBL, DDBJ - protein databanks - sequence databanks - PIR, SWISSPROT, TrEMBL _ structural databases - PDB, SCOP, CATH, SSEP, CADB, Pfam and GDB.

UNIT - II : Sequence Alignment and Dynamic Programming :

Introduction - Strings - Edit distance two strings - string similarity local alignment -gaps - parametric sequence alignments - suboptimal alignments - multiple alignment - common multiple alignment methods.

UNIT - III : Sequence Databases And Their Uses :

Introduction to databases - database search - Algorithms issues in database search - sequence database search - FASTA - BLAST - Amino acid substitution matrices PAM250 and BLOSUM62. GCG Sequence Analysis (Basic concepts only).

UNIT - IV : Evolutionary Trees and Phylogeny :

Basic concepts in systematics, taxonomy and phylogeny; molecular evolution; nature of data used in Taxonomy and Phylogeny, Definition and description of phylogenetic trees and various types of trees-connection between multiple alignment and tree construction.

UNIT - V : Metabolic Networks and Interaction Maps :

Metabolic pathways metabolic regulation, genome proteome connection microarrays and analysis of metabolic control. Lethality and centrality in protein networks, the protein-protein interaction map of Helicobacter pylori, Global protein function prediction from protein-protein interaction networks. Oncomine maps.

TEXT BOOKS:

1. T.K.Attwood & D.Parry-Smith, Introduction to Bioinformatics, Pearson Education, 2001.
2. R.Durbin, R.Eddy, K.Anders and M.Graeme, Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids, Cambridge University Press, 1997.

REFERENCE BOOKS:

1. Dan Gusfield, Algorithms on Strings Trees and Sequences, Cambridge University Press, 1997.
2. Lesk, Introduction to Bioinformatics, Oxford University Press, 2002.