

Lecture: 3 periods/week

Internal assessment: 30 marks

Tutorial: 1 period /week

Semester end examination: 70 marks

Course Objectives:

- Bioinformatics as means for computational learning.
- Basic biological databases and algorithms for proteomics and genomics analysis.
- Bioinformatics packages to solve the biological problems.

Learning Outcomes:

By the end of this course, the students will be able to

- Know the differences between genomics and proteomics.
- Understand and analyse how to solve the biological problems using computational approach
- Understand and analyse internet packages of bioinformatics.

UNIT I :

HISTORY, SCOPE AND IMPORTANCE : Important contributions - sequencing development - aims and tasks of Bioinformatics - applications of Bioinformatics - challenges and opportunities - Computers and programs – internet - world wide web – browsers - EMB net – NCBI.

UNIT II :

DATABASES - TOOLS AND THEIR USES : Importance of databases - nucleic acid sequence databases - protein sequence data bases - structure databases - bibliographic databases and virtual library - specialized analysis packages.\

UNIT III :

SEQUENCE ALIGNMENT METHODS

Algorithm, Goals and Types of alignment, Study of similarities, scoring Mutations, Deletions and Substitutions, Sequence Alignment Methods, Pairwise alignment, Multiple sequence Alignment, Algorithms for Identifying Domains within a protein Structure, Algorithms for Structural comparison, Carrying out a Sequence search.

UNIT IV :

PREDICTIVE METHODS USING DNA AND PROTEIN SEQUENCES: Gene predictions strategies - protein prediction strategies - molecular visualization - Homology - phylogeny and evolutionary trees - Homology and similarity - phylogeny and relationships.

UNIT V :

DRUG DISCOVERY AND PHARMAINFORMATICS

Discovering a drug - target identification and validation - identifying the lead compound - optimization of lead compound - chemical libraries.

UNIT VI :

ALGORITHMS: Algorithms and Complexity- Biological algorithms versus computer algorithms – The change problem –Correct versus Incorrect Algorithms – Recursive Algorithms – Iterative versus Recursive Algorithms – Big-O Notations – Algorithm Design Techniques.

UNIT VII :

GREEDY ALGORITHMS: Molecular Biology Primer – Exhaustive Search – Mapping Algorithms – Motif-Search Trees – Finding Motifs – Finding a Median String – Greedy Algorithm – Genome Rearrangements – Sorting by Reversals – Approximation Algorithms – A Greedy Approach to Motif Finding.

UNIT VIII :

CLUSTERING AND TREES: Clustering and trees – Gene expression analysis – Hierarchical clustering-k-means clustering – Clustering and corrupted Cliques – Evolutionary Trees – Distance-based tree reconstruction – Reconstruction trees from additive matrices – Evolutionary trees and hierarchical clustering – Character-based tree reconstruction – Small and large Parsimony Problem – Hidden Markov Models- Randomized Algorithms.

TEXTBOOKS

1. S. Ignacimuthu, S.J., Basic Bioinformatics, Narosa Publishing House, 1995
2. Neil C. Jones and Pavel A. Pevzner, An Introduction to Bioinformatics Algorithms, MIT Press, First Indian Reprint 2005.

REFERENCES BOOKS

1. T K Attwood, D J parry-Smith, Introduction to Bioinformatics, Pearson Education, 1st Edition, 11 th Reprint 2005.
2. C S V Murthy, Bioinformatics, Himalaya Publishing House, 1st Edition 2003.
3. Gusfields G, Algorithms on strings, trees and sequences- Computer Science and Computational Biology, Cambridge University Press 1997.
4. Steffen Schulze-Kremer, Molecular Bioinformatics: Algorithms and Applications, Walter de Gruyter