BI0202- BIOINFORMATICS ALGORITHMS

LESSON PLAN

Semester: IV   **Course: Bioinformatics Algorithms**
Sub Code: BI0202   **Staff Handling: Ms. S. Lavanya**
                                                                        Total Hours: 45

Day	Topic	Learning outcome
1	**Algorithms and Complexity**	• Introduction to algorithm in general
2	Biological algorithms versus computer algorithms	
3	The change problem –Correct versus Incorrect Algorithms	• Knowledge on time complexities
4	Recursive Algorithms, Iterative versus Recursive Algorithms	• Introduction to various algorithmic design techniques
5	Big-O Notations	
6	Algorithm Design Techniques	
7	Molecular Biology Primer	
8	Exhaustive Search Mapping Algorithms	• Application of various algorithms in solving specific biological problem
9	Motif-Search Trees	
10	Finding a Median String	
11	Branch and Bound motif search	• Study on the advantages and disadvantages of various methods
12	Branch and Bound median search	
13	Greedy Algorithm – Genome Rearrangements	
14	Sorting by Reversals – Approximation Algorithms	
15	A Greedy Approach to Motif Finding.	
16	DNA Sequence comparison	
17	Manhattan Tourist Problem	• Knowledge on the importance of sequence alignment
18	Edit Distance and Alignments – Longest Commons Subsequences	
19	Global, Local & Multiple Sequence Alignment	• Application of dynamic programming methods in sequence alignment
20	Scoring Alignment	
21	Alignment with Gap Penalties	

22	Gene Predictions – Approaches to Gene Prediction	
23	Spiced Alignment	
24	Divide and Conquer Algorithms	
25	Block alignment and four Russian speedups	
26	Graphs and Genetics	• Methods To Solve The Biological Problem With Graph Concept
27	DNA Sequencing, Shortest Superstring Problem	
28	DNA arrays as an alternative sequencing techniques, Sequencing by Hybridization	• Knowledge on theoretical method of protein identification
29	Eularian path problem Hamiltonian path problem	
30	Fragment assembly in DNA Sequencing	
31	The Peptide Sequencing Problem – Spectrum Graphs	
32	Protein Identification- Spectral Convolution and Alignment	
33	Combinatorial Pattern matching	
35	Heuristic pattern search tools	
36	Gene expression analysis	• Application of clustering methodology
37	Hierarchical clustering-k-means clustering	
38	Clustering and corrupted Cliques	• Application of machine learning approach –HMM
39	Distance-based tree reconstruction-Additivity	
40	UPGMA & NJ Method	• Knowledge on randomized algorithm
41	Character-based tree reconstruction-Small and large Parsimony Problem	
42	Hidden Markov Models	
43	Profile HMM	
44	Randomized Algorithms-Gibbs Sampler	
45	Random Projections	

TEXTBOOKS
1. Neil C. Jones and Pavel A. Pevzner, *An Introduction to Bioinformatics Algorithms*, MIT Press, First Indian Reprint 2005.
2. Gary Benson Roderic page (Eds), *Algorithms in Bioinformatics*, Springer International Edition, First Indian Reprint 2004.

REFERENCE BOOKS

1. Gusfields G, Algorithms *on strings, trees and sequences- Computer Science and Computational Biology*, Cambridge University Press 1997.

Steffen Schulze-Kremer, *Molecular Bioinformatics: Algorithms and Applications*, Walter de Gruyter, 1996

E Mail ID: lavanyas@ktr.srmuniv.ac.in

Contact No: 9790811758