

1128

B.Sc. (Hons.) Biotechnology
Fifth Semester
BIOT-Sem-V-IV-T: Bioinformatics
(Common with Tools in Bioinformatics)

Time allowed: 3 Hours

Max. Marks: 67

NOTE: Attempt five questions in all, including Question No. I which is compulsory and selecting one question from each Unit.

x-x-x

I. Explain the following briefly:

- a) TrEMBL
- b) BLASTn vs BLASTx
- c) PSI-BLAST
- d) Log Odd Ratio
- e) Affine Gap Penalty
- f) Protein Motifs
- g) Dicotomy trees
- h) Rooted vs Unrooted Trees
- i) mmCIF
- j) Glimmer

(10x1½)

UNIT - I

- II. a) Explain the role of Bioinformatics in post genomics era.
- b) Differentiate between 1° and 2° databases? Write note on GenBank nucleotide sequence database. (6,7)
- III. a) How SCOP and CATH classifies the proteins?
- b) Explain how macromolecular structure information is submitted into PDB? (6,7)

UNIT - II

- IV. a) Explain with examples, how Dot Plot can be used to perform sequence alignments. Give merit and demerits of this method.
- b) Give various types of basic BLAST. Explain briefly algorithm of BLAST. (6,7)

P.T.O.

(2)

- V. a) What do you mean by Local Alignment? Explain how Smith Walter-man method.
b) Explain Hierarchical method of multiple sequence alignment. (6,7)

UNIT - III

- VI. a) Give different tree topologies *and* terminologies used in molecular phylogeny.
b) Enlist different approaches of phylogenetic tree construction. Explain with example UPGMA method. (6,7)
- VII. a) Write short note on:-
i) Maximum Parsimony Method
ii) GenScan
b) Write note on gene prediction in prokaryotic genome. (6,7)

UNIT - IV

- VIII. a) Explain Fold Recognition method of protein tertiary structure prediction.
b) What are protein 2° structures? Explain Chou-Fasman method to predict 2° structures of globular proteins. (6,7)
- IX. a) Explain the concept of Homology Modeling to predict the protein 3D structures.
b) Give features and applications of Rasmol? (7,6)

x-x-x

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