

(i) Printed Pages : 2

Roll No.

(ii) Questions : 9

Sub. Code :

0	9	8	4
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Exam. Code :

0	0	3	7
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B.Sc. (Hons.) Biotechnology 5th Semester
(2122)

BIOINFORMATICS (Common with Tools in Bioinformatic)

Paper : BIOT-503-T

Time Allowed : Three Hours]

[Maximum Marks : 67

Note :— Attempt FIVE questions in all, including Question No. 1 which is compulsory and select ONE question each from Units I-IV. All parts of a question should be done in continuation.

1. (a) PAM matrix
- (b) PAM
- (c) PSI-BLAST
- (d) Homology
- (e) Local alignment
- (f) EMBL
- (g) Bit Score
- (h) Consensus sequences
- (i) Dot Plot
- (j) Motifs.

10×1.5

UNIT—I

2. (a) Write an overview of Sequence Analysis. 6
(b) Discuss the salient features of SwissProt and explain how it is different than TrEMBL. 7
3. (a) Write in detail about any primary nucleotide database. 6
(b) Describe the need for and construction of PDB. 7

UNIT—II

4. (a) Discuss the principle and applications of BLASTN. 7
(b) Write a note on concept of log odd ratio. 6
5. Explain the methods used for Multiple Sequence Alignment. 13

UNIT—III

6. (a) Discuss any one method used for phylogenetic tree construction. 6
(b) Differentiate between Cladogram and Phylogram. 7
7. (a) Explain the applications of phylogenetic analysis. 6
(b) Discuss the different phylogenetic tree topologies. 7

UNIT—IV

8. Explain the significance of gene identification and explain the construction and applications of GenScan. 13
9. (a) Elaborate on the significance of Genome annotation. 4
(b) Discuss any one method for protein secondary structure prediction. 9