(i) Printed Pages : 2 Roll No. .....

(ii) Questions : 9 Sub. Code : 1 7 9 8 3

Exam. Code : 0 0 3 7

B.Sc. (Hons.) Biotechnology 5th Semester

(2125)

BIOINFORMATICS (Common with Tools in Bioinformatic)

Paper : BIOT-503-T

Time Allowed : Three Hours] **[Maximum Marks : 67**

Note :— Attempt **FIVE** questions in all. Q. No. **1** is compulsory and attempt any **ONE** question from each unit.

1. Answer briefly:

   (a) TrEMBL

   (b) BLASTp

   (c) Motifs

   (d) Global alignment

   (e) GenBank

   (f) Secondary Databases

   (g) Clade

   (h) Profile

   (i) Bit Score

   (j) Gap penalty 1.5×10=15

UNIT–I

2. (a) Write a note on the role of Bioinformatics in Biotechnology. 6

   (b) Discuss the structure and construction of Pfam. 7

3. (a) Explain any primary sequence database in detail. 6

   (b) Elaborate on the organization and applications of SCOP database. 7

UNIT–II

4. (a) Explain the Needleman and Wunsch algorithm for pairwise sequence alignment. 7

   (b) Discuss the construction of PAM matrix. 6

5. (a) Elaborate on the algorithm of BLAST and its applications. 7

   (b) What is the significance of the concept of log odd ratio? 6

UNIT–III

6. (a) Discuss the different tree topologies. 6

   (b) Elaborate on the applications of phylogenetic analysis. 7

7. Explain any one method for phylogenetic tree construction. 13

UNIT–IV

8. (a) Discuss any one method for protein secondary structure prediction. 6

   (b) Explain the strategies used for protein prediction. 7

9. (a) Elaborate on any method of gene identification. 7

   (b) Write a note on Rasmol. 6