(i) Printed Pages : 2

(ii) Questions : 9

Roll No. ....

Sub. Code : | 0 | 9 | 8 | 4 |

Exam. Code : | 0 | 0 | 3 | 7 |

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