Roll No. ☐☐☐☐☐☐☐☐☐☐☐☐ **Total No. of Pages : 02**

Total No. of Questions : 08

M.Tech. (Bio Tech.) (Sem.–3)

ADVANCED BIOINFORMATICS

Subject Code : MTBT-203

Paper ID : [E1052]

Time : 3 Hrs. **Max. Marks : 100**

INSTRUCTION TO CANDIDATES :

1. **Attempt any FIVE questions out of EIGHT questions.**
2. **Each question carries TWENTY marks.**

1. a) Discuss the importance of biological databases in bioinformatics.

   b) Compare PAM and BLOSUM matrices.

2. a) Explain the working of BLAST based on your knowledge of sequence alignment.

   b) What is maximum parsimony? Briefly describe how phylogenetic trees are constructed using maximum parsimony method.

3. a) Briefly describe the Markov chain dealing the key assumption involved.

   b) Write a note on PSSMs.

4. a) What are molecular visualization softwares? Discuss about Rasmol.

   b) What is multiple sequence alignment? Briefly describe MUSCLE and Clustal W.

5. a) What is computer aided drug design (CADD)? Describe how bioinformatics supports CADD research.

   b) Explain microarray spotting process flow in detail. How is microarray result analysis done?

6. a) By using Needleman and Wunsch algorithm align the following sequences

   Seq 1 : ACTGATTCA seq 2 : ACGCATCA (Use +2 for match and -2 for mismatch and -3 for gap).

b) Briefly describe 13C NMR based metabolic flux analysis.

7. a) Briefly describe the steps involved in homology modeling to predicting the 3D structure of a protein.

b) By using the following distance matrix, reconstruct a phylogenetic tree with UPGMA method.

	A	**B**	**C**	**D**
B	17	-	-	-
C	21	30	-	-
D	31	34	28	-
E	23	21	39	43

8. a) How do you quantify the expression data by using Real Time PCR?

b) What is molecular docking? Briefly describe the steps involved in molecular docking.