

[Time: 2½ Hours]

[Marks:60]

Please check whether you have got the right question paper.

- N.B:**
1. All questions are **compulsory**.
 2. **Figures** to the **right** indicate **full marks**.

- Q.1 Attempt any THREE questions from the following. 15
- a) What is Sequence alignment? Which pairwise sequence alignment method is followed by FASTA? Explain.
 - b) Elaborate on the steps and input criterias involved when you perform BLAST for a protein sequence.
 - c) Explain Mummer and state its significance.
 - d) Enlist differences between BLAST and FASTA.
 - e) What is PHI BLAST? Explain its working.
- Q.2 Attempt any THREE questions from the following. 15
- a) What is dendogram? Explain its role in MSA.
 - b) Explain the steps in MSA Algorithm.
 - c) Elaborate on multiple sequence alignment methods.
 - d) Give the significance of patterns and profiles.
 - e) Enlist various applications of MSA.
- Q.3 Attempt any THREE questions from the following. 15
- a) Explain the concept of taxonomy and systematics.
 - b) What is a phylogenetic tree? What are the various methods used to build the same?
 - c) Elaborate on UPGMA.
 - d) Write a note on Phylip.
 - e) Give an account of the steps involved in phylogenetic analysis study.
- Q.4 Write short note on any THREE questions from the following. 15
- a) Parsimony
 - b) PSI BLAST
 - c) Clustal Omega
 - d) Pipmaker
 - e) PSSM