

**Exam. Code : 206602**  
**Subject Code : 8479**

**M.Sc. (Bioinformatics) Semester-II**  
**COMPUTATIONAL METHODS FOR SEQUENCE**  
**ANALYSIS**

**Paper—BI-524**

Time Allowed—3 Hours] [Maximum Marks—75

**SECTION—A**

Explain the following in not more than ***four*** lines each :  $1.5 \times 10 = 15$

1. Scoring matrix
2. Local alignment
3. PSI-Blast
4. Clustalx
5. Phylogenetic tree
6. Cladogram
7. Interpolated Markov model
8. Promoter
9. Domain
10. Epitopes.

**SECTION—B**  $12 \times 5 = 60$

1. Explain BLOSUM scoring matrices and discuss its derivation. Explain Dot matrix of sequence comparison.

**OR**

2. Align GTCCATGCGCTA with ATTCCATGCGCT using Needleman Wunsch algorithm. Use score +2 for match, -1 for mismatch.
3. What is BLAST ? Mention any four different types of BLAST and its application. Discuss algorithm of BLAST.

**OR**

4. Discuss algorithm of FASTA. Compare it with BLAST.
5. Explain in brief how to validate phylogenetic predictions. Discuss different types of phylogenetic tree.

**OR**

6. Discuss maximum parsimony approach of phylogenetic analysis.
7. What is Glimmer ? Discuss methods used for gene prediction in eukaryotic organism.

**OR**

8. Describe gene structure of a prokaryotic organism. Explain any two methods used for gene prediction.
9. What is secondary structure of protein ? Explain one method used for protein secondary structure prediction.

**OR**

10. Discuss any tool used to predict B cell epitopes using protein sequence.