

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 : 1.5×10=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

12×5=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.