

Exam. Code : 206602
Subject Code : 4710

18-622
MRE

M.Sc. Bioinformatics 2nd Semester (Batch 2021-23)
**COMPUTATIONAL METHODS FOR SEQUENCE
ANALYSIS**

Paper-BI-524

Time Allowed—3 Hours] [Maximum Marks—75

Note :- Attempt **FIVE** questions in all, selecting at least **ONE** question from each Section. The **fifth** question may be attempted from any Section. All questions carry equal marks.

SECTION—A

- Describe the following with proper explanations :
 - PAM and BLOSUM matrix 7.5
 - Local and Global alignment concepts. 7.5
- Describe the following with proper explanations :
 - Needleman-Wunsch algorithm 7.5
 - Smith-Waterman algorithm. 7.5

SECTION—B

- Describe the following with proper explanations :
 - Concept of evolutionary trees 7.5
 - Maximum Likelihood methods for phylogenetic trees. 7.5

4. Write notes on the following points :
- (a) Complications from phylogenetic analysis 7.5
 - (b) Neighbor joining method for the phylogenetic trees. 7.5

SECTION—C

- 5. Write a note on promoter prediction in E.Coli. 15
- 6. Describe any two software packages for gene prediction in eukaryotes. 15

SECTION—D

7. Write notes on the following :
- (a) Alpha helix in protein structure 7.5
 - (b) Motifs in the protein structure. 7.5
8. Write a detailed note on the B cell epitope prediction. 15