

Exam. Code : 206602

Subject Code : 5212

M.Sc. Bioinformatics 2nd Semester

**COMPUTATIONAL METHODS FOR SEQUENCE
ANALYSIS**

Paper-BI-524

Time Allowed—3 Hours] [Maximum Marks—75

Note :— Question 1 from **Section-A** is compulsory. Attempt **five** questions from **Section-B** i.e. at least **one** from each unit.

SECTION—A

1. Define the following : 1.5×10=15

- (a) E value
- (b) Local vs Global alignment
- (c) Orthologous vs Paralogous
- (d) Cladogram
- (e) Nodes, braches and Sister taxa
- (f) Pribnow box
- (g) Protein Folds

- (h) PSSM
 (i) Weight matrix
 (j) Sliding window in sequence alignment.

SECTION—B

UNIT—I

12×5=60

2. Use the Needleman-Wunsch algorithm to align WGHEWEG with WHEGEG. Use a gap creation penalty of 8. Show your work. A portion of the scoring matrix is given.

	E	G	H	W
E	5	-2	0	-3
G	-2	6	-2	-2
H	0	-2	8	-2
W	-3	-2	-2	11

3. Explain Dot matrix sequence alignment methods. Describe its advantages, disadvantages and applications. Why this method is not good for finding the optimal alignment ? What measures has been taken to improve alignment ?

UNIT—II

4. Describe MSA and progressive algorithm used in MSA. What are the steps used by the algorithm used in PILEUP ?

5. Explain FASTA and its different types. Draw a comparison between BLAST tool.

UNIT—III

6. Give a detailed account on methods of phylogeny. Describe the relationship between phylogenetic analyses to sequence alignment.
7. Discuss distance based approach of phylogenetic analysis. Draw a comparison between maximum parsimony and maximum likelihood.

UNIT—IV

8. What is FGENESH ? Describe the working of FGENESH. Discuss methods used for gene prediction in eukaryotes.
9. List the features and methods used for promoter prediction in prokaryotes. List the ways prediction methods were evaluated.

UNIT—V

10. Describe the secondary structures of protein. Explain the usage of pattern for protein structure prediction.
11. Explain epitopes and why there is a need predict their structure. Describe the methods used for prediction and identification of epitopes.