

Exam. Code : 206602

Subject Code : 4089

M.Sc. Bioinformatics 2nd SemesterBI-524 : COMPUTATIONAL METHODS FOR
SEQUENCE ANALYSIS

Time Allowed—3 Hours] [Maximum Marks—75

Note :— The question paper consists of **four** sections with **two** questions in each Section. Candidates are required to attempt **five** questions, selecting at least **one** question from each Section. The **fifth** question may be attempted from any Section. All questions carry equal marks.

SECTION-A

1. Explain the following :
 - (a) Dot Matrix sequence comparison 5
 - (b) Dynamic programming 5
 - (c) PAM and BLOSUM matrices. 2.5+2.5
2. Write the difference between :
 - (a) Local and Global sequence alignment. 5
 - (b) Multiple sequence alignment and pairwise alignment. 5
 - (c) PILEUP and CLUSTALW. 5

SECTION-B

3. What is phylogenetic tree ? Write a note on the reliability of phylogenetic predictions and complications from phylogenetic analysis. 15
4. Describe the complexity of Eukaryotic Genomes ? Explain the difference between Eukaryotic and Prokaryotic genome complexity. What is C-value paradox ? 15

SECTION-C

5. How is the gene prediction in prokaryotes different than eukaryotes ? Explain the methods of gene prediction with examples of software packages for each category. 15
6. What is promotor and its role (explain with figure)? What is the difference between the promotor prediction in prokaryotes and eukaryotes ? 15

SECTION-D

7. What are epitopes ? What is the difference between B Cell epitopes and T cells epitopes ? Elaborate the method of B cell epitope prediction from protein sequence. 15
8. Explain the following :
- (a) Ramachandran Plot 3
- (b) Loops, Coils, Domains and Motifs 8
- (c) α Helix and β sheet structure of proteins. 4