M.Tech. (Bio Tech) (2018 Batch) (Sem.–3)
ADVANCED BIOINFORMATICS
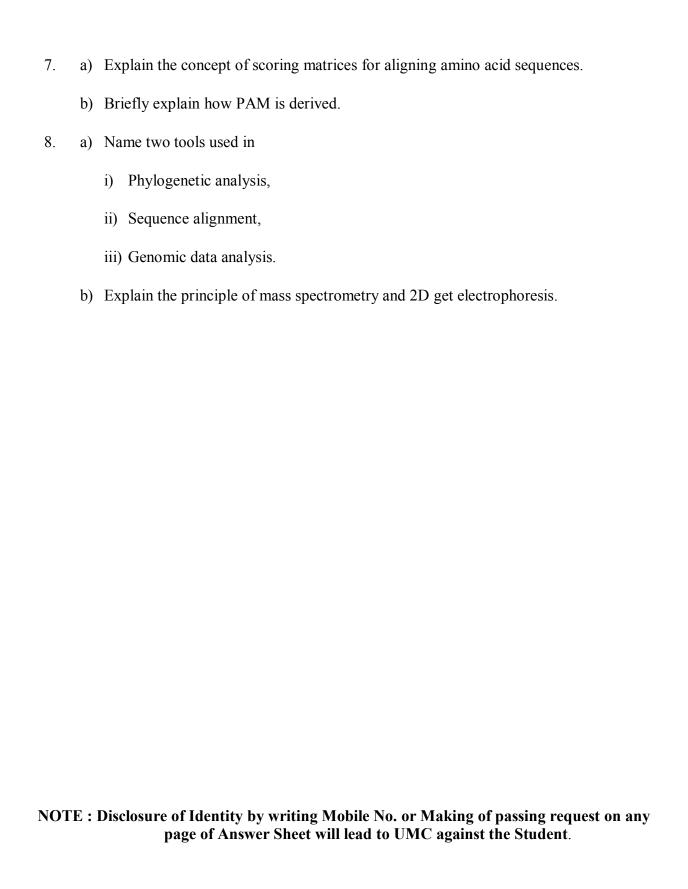**Subject Code : MTBT-303/18**
M.Code : 76763

Time : 3 Hrs.   Max. Marks : 60

INSTRUCTIONS TO CANDIDATES :
1.Attempt any FIVE questions out of EIGHT questions.
2.Each question carries TWELVE marks.

1.   Write a short note on the following :

   a) Bioinformatics and Genomics

   b) BLAST

   c) Biological Databases and comparative sequence analysis

   d) Scoring matrices

2.   What is the main role of a bioinformatician in present biological research and development area?

3.   a) Write a detail note on SMBL.

   b) Discuss E-cell and V-cell simulations and their applications.

4.   a) What is non-redundant database? What is consensus sequence?

   b) What is proteomics? Write a short note on SAGE.

5.   What do you understand by e-value, query coverage, sensitivity and specificity in BLAST?

6.   If you get a particular protein named 'Keratin'. How will you retrieve its

   a) Nucleic acid sequence

   b) Protein sequence

   c) Protein chains

   d) 'Amino acid frequency or properties etc'. Describe briefly.

7. a) Explain the concept of scoring matrices for aligning amino acid sequences.

    b) Briefly explain how PAM is derived.

8. a) Name two tools used in

        i)   Phylogenetic analysis,

        ii) Sequence alignment,

        iii) Genomic data analysis.

    b) Explain the principle of mass spectrometry and 2D get electrophoresis.

NOTE : Disclosure of Identity by writing Mobile No. or Making of passing request on any page of Answer Sheet will lead to UMC against the Student.