

Exam. Code : 103205

Subject Code : 1419

B.A./B.Sc. 5th Semester

BIOINFORMATICS

(Computational Methods for Sequence Analysis)

Time Allowed—3 Hours] [Maximum Marks—75

Note :— Attempt ALL questions.

1. Explain the following terms :
 - (a) BLOSUM
 - (b) Progressive alignment
 - (c) E-value
 - (d) FASTA
 - (e) Promoter
 - (f) Motif
 - (g) Phylogeny
 - (h) Cladogram
 - (i) Emission Probability
 - (j) Perceptron. 10×1½=15
2. Align following sequences using Needleman Wunsch algorithm. Use identity matrix for scoring :
Sequence 1 : TTGCCGGCATTA
Sequence 2 : TGCCGCATTA.

OR

Mention tools used for searching homologous sequences in database. Discuss different types of BLAST and their application. 15

3. Explain methods used for genome sequence assembly.

OR

Discuss methods used for prediction of gene. 15

4. What is a neural network ? Explain its application in bioinformatics.

OR

What is Hidden Markov Model ? Explain one application of HMM. 15

5. What are molecular markers ? Explain molecular clock theory.

OR

What is clustering ? Explain different types of evolutionary tree. 15