Exam. Code : 103205
Subject Code : 1370

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

BIOINFORMATICS

(Computational Methods for Sequence Analysis)

Time Allowed—3 Hours] [Maximum Marks—75

SECTION—A

1. Explain the following terms :— 10×1.5=15

   (a) Local alignment.

   (b) CLUSTALw.

   (c) Regulatory regions.

   (d) Fourier transform.

   (e) BLASTX.

   (f) Markov model.

   (g) Molecular markers.

   (h) Dendrogram.

   (i) Unrooted tree.

   (j) Perceptron.

SECTION—B

2. What are scoring matrices ? Discuss differences between PAM and BLOSUM. 15

OR

Align following sequences using Smith Waterman algorithm. Use + 3 for match, –0.3 for mismatch and –1.5 for gap.

Sequence 1 : TGCCTTGGCAT

Sequence 2 : TGCCTTGCCATTA

3. What is motif ? Discuss tools used for searching pattern and motif. Also explain its significance. 15

OR

What do you understand by fragment assembly ? Discuss tools used for genome sequence assembly.

4. What do you understand by machine learning tool ? Explain application of neural network in protein structure prediction. 15

OR

What are transition and emission probabilities in HMM ? Explain application of HMM.

5. What are evolutionary trees ? Discuss distances b ased method of evolutionary studies.

OR

What is molecular clock hypothesis ? Explain methods used to judge the quality of evolutionary tree. 15