

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 based method of evolutionary studies.

**OR**

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