Exam. Code : 103205
Subject Code : 1369

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

BIOINFORMATICS

(Computational Methods for Sequence Analysis)

Time Allowed—3 Hours] [Maximum Marks—75

Note :—Question No. **1** is compulsory.

1. Explain the following in not more than **four** lines :

   (a) Global alignment

   (b) Progressive alignment method

   (c) Gene

   (d) Fragment assembly

   (e) FASTA

   (f) Machine learning tools

   (g) Markov model

   (h) Perceptron

   (i) Molecular clock theory

   (j) Clustering. 1.5×10=15

UNIT—1

2. What are scoring matrices ? Explain different types of PAM and BLOSUM.

OR

3. What is multiple sequence alignment ? Explain any tool used for multiple sequence alignment. 15

UNIT—2

4. Explain Fourier transform and its application in gene prediction.

OR

5. What are pattern and motif ? Explain methods used for motif searching. 15

UNIT—3

6. Discuss applications of neural network in prediction of secondary structure of protein.

OR

7. Explain transition and emission probabilities in HMM. Discuss any model of HMM. 15

UNIT—4

8. Discuss differences between rooted and unrooted tree. Explain Bootstrapping.

OR

9. Discuss applications of molecular marker in evolutionary analysis. 15