

Exam. Code : 103205

Subject Code : 1412

B.A./B.Sc. Semester—V

BIOINFORMATICS

(Computational Methods for Sequence Analysis)

Time Allowed—3 Hours]

[Maximum Marks—75

SECTION—A

1. Explain the following terms :

- (a) PAM
- (b) Dynamic programming
- (c) Motif
- (d) Contigs
- (e) Gap penalty
- (f) PSI-PRED
- (g) Alpha helix
- (h) Rooted tree
- (i) Clustering
- (j) Molecular markers.

10×1.5=15

SECTION—B

2. Compare local and global alignments using an example. Discuss their significance.

OR

What is multiple sequence alignment ? Discuss a tool based on progressive alignment for multiple sequence alignment.

3. Explain application of Fourier transform in gene prediction and other bioinformatics application.

OR

What do you understand by regulatory region ? Discuss tools used for its analysis and prediction.

4. Discuss any two tools based on neural network for protein secondary structure prediction.

OR

What are probabilistic models ? Discuss their application.

5. Explain difference between phyllogram and dendogram. How molecular markers can be used to study evolution ?

OR

What is boot strapping ? Explain its application.

15×4=60