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

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(Contd.)

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SECTION-B

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.

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

OR

What are probabilistic models? Discuss their application.

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

OR

What is boot strapping? Explain its application.

 $15 \times 4 = 60$