## 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. $10 \times 1.5=15$

## 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.

