DI-1703

M. Sc. (Int. Biotechnology) (Sem. IX) Examination
March / April - 2016
BT-3001 : Advances in Bioinformatics
(New Course)

Time : 3 Hours] [Total Marks : 70

Instructions :
(1) Figures to the right indicate full marks.
(2) Draw neat and labelled diagrams wherever necessary.

1 Answer the following : (Any Two) 18
   a) Differentiate pairwise and multiple sequence alignment. Explain any one method of multiple sequence alignment.
   b) What is Clustal W? How multiple sequence alignment is useful in genome study?
   c) What is BLAST & FASTA? Give detail account on BLAST tool.

2 Attempt the following: (Any Two) 18
   a) List distance based method for phylogenetic analysis. Describe any one in detail.
   b) Explain role of statistics in phylogenetic tree making.
   c) Describe Mechanism of molecular Phylogeny.

3. Answer the following: (Any Two) 18
   a) Explain Ab initio approach for gene prediction.
   b) Compare and contrast between Markov & HMM models.
   c) Give brief account on homology based approach on gene prediction method.
.4 Write short notes on the following: (Any Two)

a) Chou-Fasman method for secondary protein structure prediction.
b) Explain the technique of molecular docking.
c) Swiss model.