

1059  
B.E. (Biotechnology) Sixth Semester  
BIO-612: Bio-Informatics

Time allowed: 3 Hours

Max. Marks: 50

**NOTE:** Attempt five questions in all, including Question No. 1 which is compulsory and selecting two questions from each Unit.

x-x-x

I. Answer the following briefly:

- a) What is global alignment?
- b) What is expasy?
- c) What do you know about HGP?
- d) What is Ensembl?
- e) What is needed to submit a sequence through Bankit?
- f) What is the significance of E value in a BLAST result ?
- g) What is *ab intio* method of structure prediction?
- h) What is a molecular mechanics force field?
- i) If a nucleotide sequence is given, how will you distinguish ORFs?
- j) What is drag discovery process? (10x1)

UNIT - I

- II. a) What are the various objectives and applications of Bioinformatics?  
b) Write about secondary sequence databases with respect to information content and importance. (5,5)
- III. a) Discuss the major features of Protein Data Bank.  
b) What are scoring matrices? Write short note on PAM and BLOSUM scoring matrices. (5,5)
- IV. a) Explain about Maximum Parsimony and Maximum likelihood methods in phylogenetic tree construction.  
b) Differentiate between rooted and unrooted trees. (7,3)

UNIT - II

- V. a) What are the approaches of computational gene prediction?  
b) What are various features of Glimmer? (6,4)
- VI. a) Explain about fold recognition?  
b) Explain the GOR method for protein secondary structure prediction. (6,4)
- VII. Write a note on:-
  - a) Rasmol
  - b) QSAR
  - c) Docking Concepts (3,4,3)