

Exam.Code:0910  
Sub. Code: 6219

1058

B.E. (Bio-Technology) Sixth Semester  
BIO-603: Introduction to Bio-Informatics  
(2012-16)

Time allowed: 3 Hours

Max. Marks: 50

**NOTE:** Attempt five questions in all, selecting atleast two questions from each Unit.

x-x-x

**UNIT – I**

- I. a) Differentiate between:-
- i) Cladogram and Phylogram
  - ii) PAM and BLOSSUM matrices (2x2½)
- b) What are the various similarities and differences in BLAST and PASTA algorithms? (5)
- II. a) Give an account on genome projects?
- b) What are various tools used in database deposition systems. Explain any one. (2x5)
- III. a) What is gene prediction? What are the important structural characteristics of eukaryotic genomes?
- b) Write briefly about any one protein database. (2x5)
- IV. Align the following sequences using Smith and Waterman Algorithm Taking match bonus as +1, Gap penalty as -1 and mismatch as 0.  
Sequence 1 -AACCTATAGCT  
Sequence2 -GCGATATA (10)

**UNIT – II**

- V. a) How does GOR algorithm work?
- b) What is abinitio method of structure prediction? (2x5)
- VI. a) Write a note on:-
- i) Rasmol
  - ii) QSAR (2x2½)
- b) What can energy minimization do in protein modeling? (5)

P.T.O.

(2)

- VII. Explain various steps for predicting protein tertiary structure by homology modeling? (10)
- VIII. Define bioinformatics. Explain bio-informatic applications related to the following areas:
- a) Phylogenetic Analysis
  - b) Proteomics
  - c) Genome Annotation
  - d) Drug Discovery (10)

x-x-x