

**Exam.Code:0910**  
**Sub. Code: 6715**

**1019**  
**B.E. (Bio-Technology)**  
**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:-
- What are paralogous sequences?
  - What are signal sensors?
  - What is the difference between motif and domain?
  - What is ensemble?
  - What is ligand based drug design?
  - What is coding sequence?
  - What is nucleic acid sequence analysis?
  - What is a molecular clock?
  - What are force fields?
  - What is phylogram? (10x1)

**UNIT - I**

- II. a) Write on databases given below:
- SCOP
  - PDB sum
- b) Compare and contrast BLAST and FASTA algorithms. (5,5)
- III. a) Write in detail about human genome project.
- b) Draw a comparison between Neighbour-joining, Maximum Parsimony and Maximum likelihood methods? (5,5)
- IV. a) Write briefly on uniprot database and its important components.
- b) What are the important rules followed in Needleman Wunsch and Smith Waterman algorithms? (5,5)

**P.T.O!**

(2)

UNIT - II

- V. a) Write a note on:-  
i) Chou-Fasman  
ii) Spdbviewer  
b) Discuss briefly the various applications of bioinformatics. (5,5)
- VI. What are the various steps used in modeller for predicting protein tertiary structure by basic and advanced homology modeling methods? (10)
- VII. a) What is QSAR? Explain it in terms of Hammett equation.  
b) What are the molecular mechanics and dynamics, simulations? (5,5)

x-x-x