1058

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. I which is compulsory and selecting two questions from each Unit.*

x-x-x

I. Answer the following briefly:-

   a) What are orthologus sequences?

   b) What is Ramachandran plot analysis?

   c) What is abinitio method of structure prediction?

   d) What is gene prediction?

   e) What is QSAR?

   f) What are the important characteristics of loops secondary structure elements?

   g) What is Entrez?

   h) What is aminoacid sequence analysis?

   i) What do you mean by amber force fields?

   j) What do you understand by hydropathy plots?   (10x1)

UNIT – I

II. a) Write briefly on SCOP and PDB databases.

   b) Write in detail about human genome project.   (2x5)

III. a) What do you understand by sequence alignment? Compare and contrast BLAST and FASTA algorithms.

   b) Explain about prosite database w.r.t information and importance.   (2x5)

IV. a) What are the main features of maximum likelihood method and also give advantages and disadvantages of this method?

   b) What is the importance of Clustal omega and Phylogeny.fr tools?   (6,4)

P.T.O.

UNIT – II

V. a) Write a note on:-

   i) GOR

   ii) Molecular mechanics   (2x2½)

   b) Discuss briefly the use of molecular graphics packages.   (5)

VI. What are the various steps involved in basic and advanced modeling methods?   (10)

VII. a) Explain about computer aided drug design.

   b) What is threading? How does phyre2 work?   (2x5)

x-x-x