2015

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 Section.

x-x-x

QI.   Answer the following:-

   i.)   What is the application of PAM program?
   ii.)   What is significance of a molecular clock in a phylogeny tree.
   iii.)   Briefly describe the difference in rooted and unrooted trees.
   iv.)   Can we have concept of similarity in DNA sequences.
   v.)   What information is provided by Maize GDB database.
   vi.)   What is the significance of poly A sites in genome prediction program?
   vii.)   Name a protein secondary structure prediction program.
   viii.)   Briefly write applications of Sequin system in bioinformatics databases.
   ix.)   What information can be retrieved from SCOP database.
   x.)   What is the application of spdb viewer program?   **(1x10)**

Section-A

Q.2a) What are primary database for nucleotide sequence, give suitable examples from such databases.
    b) Write a note on PUBMED and MEDLINE database.   **(6+4)**

Q.3 a) Discuss the algorithm for database searches for homologous sequences to a query sequence.
    b) Write a short note on EMBL database.   **(6+4)**

Q.4a) Briefly describe the amino acid sequence scoring matrices and add notes on significance
      of the same.
    b) Discuss the key mile stones of Human Genome Project.   **(6+4)**

Section-B

Q.5a) Briefly discuss the prediction methods for coding regions in eukaryotic genome?
    b) Briefly discuss the prediction of secondary structure from the amino acid sequence.   **(6+4)**

Q.6a) Discuss the basics of drug discovery process.
    b) Write a short note on structural features of regulatory regions in prokaryotic genome?   **(6+4)**

Q.7a) Briefly describe the gene prediction approaches in prokaryotic genome.
    b) Write a short note on homology-based   method for three-dimensional structure prediction in
      amino acid sequences.   **(6+4)**

x-x-x