2014
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 Section.*

x-x-x

Q.1 Answer the following briefly:

a. What are primary biological databases?
b. What are objectives of bioinformatics?
c. What is importance of Pubmed?
d. What is SCOP database?
e. State the role of Clustal omega.
f. Distinguish Gene bank and Genbank.
g. What is *ab intio* method of structure prediction?
h. What is a molecular mechanics force field?
i. What is gene annotation?
j. What are clades?   **(10 X 1 = 10)**

SECTION-A

Q.2 (a) Give a detail account on history of Bioinformatics.   **(5)**
     (b) Write about technical aspects, benefits and ethical issues of Human Genome Project.   **(5)**
Q.3 (a) What are various methods of pairwise alignment. Write down about various applications and types of blast programs.   **(5)**
     (b) What are scoring matrices? How is Blossum matrix generated?   **(5)**
Q.4 (a) What are different kinds of trees used to depict different aspects of evolutionary history?   **(4)**
     (b) What are various distance and character based phylogenetic tree construction methods? Explain any one in detail.   **(6)**

SECTION-B

Q.5 (a) What are the various features for gene prediction in prokaryotes?   **(5)**
     (b) Explain intrinsic method of gene prediction?   **(5)**
Q.6   Enlist various tools used in homology modeling, fold recognition and abintio structure prediction. Explain steps of structure prediction used in homology modelling.   **(10)**

Q.7 Write a note on:
     (a) SwissPDB viewer
     (b) QSAR
     (c) Drug Discovery   **(3 + 4 + 3)**

x-x-x