

2022

B.Sc. (Hons.) Biotechnology  
Fifth Semester  
BIOT-503-T: Bioinformatics  
(Common with Tools in Bioinformatics)

Time allowed: 3 Hours

Max. Marks: 67

*NOTE: Attempt five questions in all, including Question No. 1 which is compulsory and selecting one question from each Unit.*

x-x-x

1: Explain the following briefly-

1½ x 10 = 15

- i. How you can find significance of sequence alignment?
- ii. List the programs used to submit sequence data to databases?
- iii. Explain Hamming and Levenshtein distance.
- iv. Differentiate between global and local alignment?
- v. What are unigenes?
- vi. How bootstrapping is applied in phylogenetic analysis?
- vii. Explain Gap opening, Gap extension and Gap penalty?
- viii. Discuss PHI-BLAST?
- ix. What are hydropathy plots?
- x. How MZEF works?

#### Unit-I

2: (a) Explain SCOP and CATH databases in detail?

(b) Explain primary protein sequence and structure databases with examples.

3: (a) Explain various DNA databases, information stored in these databases and how can we access them?

(b) Explain Pfam and Profiles databases of proteins?

6.5 x 2 = 13

#### Unit II

4: (a) Explain dot plot. Explain with suitable example how we can use it for sequence analysis.

(b) Explain the matrices used for scoring the sequence alignment. Discuss, whether PAM is better or BLOSUM and Why.

5: (a) Discuss BLAST? How can we use BLAST to search protein and DNA databases.

(b) What is multiple sequence alignment? What kind of information we can get from it?

6.5 x 2 = 13

#### Unit III

6: (a) What are the difference between phylogenetic trees represented as Cladogram, dendrogram and ultrametric trees?

(b) Explain MEGA and UPGMA program for tree construction.

7: (a) Explain maximum likelihood and maximum parsimony methods of phylogenetic analysis?.

(b) Explain the following terminologies with respect to phylogenetics trees: Taxon, clade, rooted and unrooted trees, edge length, start tree.

6.5 x 2 = 13

#### Unit IV

8: (a) On what principle the PSI-PRED and PHD algorithm is based on? Explain the steps in detail?

(b) Explain any two neural networks based method of Gene annotation?

9: (a) What is gene annotation? Explain GRAIL and GLIMMER?.

(b) What is the principle difference between homology modeling, fold-recognition and *ab initio* structure prediction?

6.5 x 2 = 13

x-x-x