

B.E/B.Tech. Degree Examination, December 2020
Seventh Semester

BT16701 – Bioinformatics and Computational Biology
(Regulation 2016)

Time: Three hours

Maximum : 80 Marks

Answer **ALL** questions

PART A - (8 X 2 = 16 marks)

1. Which one of the following BLAST search programs is used to identify homologs of a genomic DNA query in a protein sequence database?
A) Blastp B) blastn C) blastx D) tblastn
2. α -helix has
 - a) 3.4 aminoacid residues / turn.
 - b) 3.6 aminoacid residues / turn.
 - c) 3.8 aminoacid residues / turn.
 - d) 3.0 aminoacid residues / turn.
3. A perceptron is:
 - a. A single layer feed-forward neural network with preprocessing
 - b. An auto-associative neural network
 - c. A double layer auto-associative neural network
 - d. A neural network that contains feedback.
4. What is the default scope of PERL variables?
 - a) Global b) private c) protected d) friend
5. Mention the types of data present in NCBI Genome.
6. Write about Dot matrix plot.
7. How many rooted trees can be constructed from 5 sequences?
8. What are the applications of peptide mass fingerprinting?

PART B - (4 X 16 = 64 marks)

9. (a) Explain how data is managed in a pharmacogenomic laboratory, with (16) necessary sketches and definitions.

(OR)

- (b) (i) Compare PAM/BLOSUM matrices and discuss when one is preferred (8) over the other.
- (ii) Describe the steps involved in FASTA algorithm. (8)

10. (a) Trace the optimal alignment for the given sequences using Smith-Waterman algorithm. Sequence-1: AGGTTTC, Sequence-2: ACGTTT, (Match Score: 2, Mismatch score: 1, Gap score: -1). (16)

(OR)

- (b) (i) Draw a UPGMA tree for the following data. (16)

Operational Taxonomic Unit				
OTU	A	B	C	D
B	5			
C	10	9		
D	9	8	5	
E	11	12	15	14

11. (a) (i) Write a short note on Biomolecular computing. (8)
(ii) Describe the bioinformatics tools employed in drug discovery. (8)

(OR)

- (b) What is the microarray technique? How is used to distinguish between healthy and diseased samples? Discuss the analytical methods used in microarray data analysis. (16)

12. (a) Write a program in PERL to accept a protein sequence and find its length and the count of each of the three aromatic aminoacids Y, F and W. (16)

(OR)

- (b) (i) Discuss in detail about the different operators used in PERL. (8)
(ii) Explain the Hashes and Lists with suitable example. (8)