Department of Computer Science

II Semester M.Tech Computer Science and Engineering
First Internal Exam May 2022
(21-479-0204: Bioinformatics)

Time: 2 Hrs   **Max.Marks : 20**

(Answer all Questions)

1) Explain central dogma of molecular biology with an example.   [5 marks]

2) Write a short note on Gene expression profiling and microarray Technology.   [5 marks]

2) Write the algorithmic view of the smith-waterman algorithm.   [4 marks]

3) Find the optimal alignments between the sequences GTACTAT and ATGACTAT using Smith-
Waterman algorithm.   [6 marks]

Department of Computer Science

IInd Semester M.Tech Computer Science and Engineering

End semester Exam April 2023

(21-479-0204: Bioinformatics)

Time: 3 Hrs

Max.Marks : 50

(Answer all Questions)

Module I

1. Write a short note on protein sequence databases.   [10 marks]

OR

2. Explain the concepts of DNA structure, gene expression, and protein synthesis and discuss their significance in understanding the underlying mechanisms that govern biological processes?

[10 marks]

Module II

3. Describe the progressive alignment approach for multiple sequence alignment, and provide an example that illustrates the steps involved?   [10 marks]

OR

4. Explain steps of the Smith-Waterman algorithm for pairwise sequence alignment, and then apply this algorithm to find the optimal alignment for the two sequences $AGCGTACGTA$ and $AGTACGTTAC$? (Assume that match score $= 2$ and Mismatch score $= -1$)   [10 marks]

Module III

5. Write down the steps for Improved Break Point Reversal Sort in genome rearrangement. Apply Break Point Reversal Sort for the genome $\pi = [5\ 2\ 8\ 3\ 1\ 6\ 9\ 4\ 7]$.   [10 marks]

OR

6. Write a short note on Short gun genome sequencing.   [10 marks]

Module IV

7. Write algorithmic view of UPGMA (Unweighted Pair Group Method with Arithmetic Mean Algorithm). Construct a phylogenetic tree based on a distance matrix 1 using UPGMA approach.

[10 marks]

	A	B	C	D	E
A	-	5	9	9	8
B		-	10	10	9
C			-	8	7
D				-	3
E					-

Table 1: Distance Matrix 1

OR

8. Explain maximum parsimony method for phylogenetic tree construction with an example.

[10 marks]

Module V

9. Explain Adleman's solution of the Hamiltonian Path Problem (HPP) using DNA computing.

[10 marks]

OR

10. Predict the secondary structure of the RNA *AUGCUA* using Nussinov's folding algorithm.

[10 marks]