JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATION- 2026

B.Tech-VI Semester (BI)

COURSE CODE (CREDITS): 18B1WBI631(3) MAX. MARKS: 15

COURSE NAME: Advanced Algorithms for Bioinformatics

COURSE INSTRUCTORS: Dr. Tiratha Raj Singh MAX. TIME: 1 Hour

Note: *(a) All questions are compulsory.*

(b) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems.

(c) Use of calculator is not allowed.

Q.No	Question	CO	Marks
Q1	What is biological sequence alignment problem? Solve it for any two RNA sequences using ESF alignment approach, Seq 1: AUCGGUAC ; Seq 2: GUAC. Use scoring systems as Match = 1, Mismatch = 0, Gap penalty = -1. Provide final score of the alignment. Solve it without filling the dynamic programming matrix.	2	3
Q2	Provide a comparative analysis of Hamming and Edit distances using any suitable example of biological sequences of any type.	1	2
Q3	Recognize fundamental algorithm design principles and evaluate the specific parameters that make biological problems and their associated algorithms distinct from conventional computational problems.	1	3
Q4	Solve the following fragment assembly using shortest superstring concept: ATGA, ATGC, GCAT, CATG, TGCA. Apply TSP_{max} to compare it for the solution.	2	4
Q5	Explain the concepts of distance and similarity in biological sequence analysis. How can these be represented mathematically? Mention any two mathematical properties of distance measures with an example.	2	3

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