

## JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

## TEST -2 EXAMINATION- 2026

## BTech-VI Semester [BI]

COURSE CODE(CREDITS): 18B1WBI631(3)

MAX. MARKS: 25

COURSE NAME: Advanced Algorithms for Bioinformatics

COURSE INSTRUCTOR: Dr. Tiratha Raj Singh

MAX. TIME: 1 Hour 30 Minutes

*Note: (a) All questions are compulsory.**(b) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems.*

| Q.No | Question                                                                                                                                                                                                                                                                                                                                | CO | Marks |
|------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|-------|
| Q1   | A bacterial genome has a size of 4.5 million base pairs (bp). The sequencing platform produces reads of length 100 bp. If a sequencing depth (coverage) of $12\times$ is required, calculate the total number of reads needed.                                                                                                          | 3  | 3     |
| Q2   | Describe the concepts of reconstruction, multi-contig models and overlap multigraph concepts. Prove with an example how the greedy algorithm can fail sometimes, even after starting with a positive selection with reference to fragment assembly.                                                                                     | 3  | 4     |
| Q3   | Explain how experiments by Seymour Benzer demonstrated the fine structure of genes. Using a simple set of overlapping DNA fragments, construct an interval graph and briefly describe its role in genome assembly.                                                                                                                      | 2  | 4     |
| Q4   | You are given the following reads: ATGC, TGCA, GCAT, CATG; Determine a Hamiltonian path and reconstruct the original DNA sequence.                                                                                                                                                                                                      | 3  | 4     |
| Q5   | Compare Hamiltonian path and Eulerian path approaches in solving the fragment assembly problem. Illustrate each method with a suitable example and explain how the sequence is reconstructed in both cases.                                                                                                                             | 3  | 5     |
| Q6   | A target genome sequence is given as: ATGCGTACGAT. Using $l$ -mer size $l=3$ , generate all possible 3-mers ( $l$ -mers) from the sequence. Construct the SSP overlap graph using these $l$ -mers. Clearly indicate nodes and weighted edges (based on overlap length). Determine the optimal path and reconstruct the genome sequence. | 3  | 5     |