

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -2 EXAMINATION- 2025

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	Write pseudocode for a fragment assembly problem where any two complications of the assembly should be considered to find the solution.	2,3	3
Q2	Discuss how the shortest superstring problem is associated with the travelling salesman problem? How these approaches could be utilized for fragment assembly genomic solutions?	3	3
Q3	Assemble the possible fragments for the target genome 'CGACTGATCGAC'. Solve the problem using SSP followed by TSP approaches for l -mer where $l=3$. Generate proper and systematic graphs for both the approaches. Consider nodes and vertices parameters for the respective approaches and adjust l -mers accordingly.	3	5
Q4	Provide a comparative analysis of Hamiltonian and Euler's graphs for solving fragment assembly problem. Give an example of both the approaches with their respective solutions through each approach.	3	4
Q5	Explain Benzer's experiment for genome structure. Define interval graph with an example. Realize the significance of interval graph in the genome assembly.	2	4
Q6	If you are having a small bacterial genome of size 3 million bp and Read length = 150 bp. If you need a coverage of 9x then determine the number of reads required to accomplish this job.	3	3
Q7	Solve the Exon chaining problem for the following exons set: (2,6,2), (10,15,8) (5,12,5) (1,5,3) (9,15,6) (7,9,6).	3	3