

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- 2024

BTech-VI Semester [BI]

COURSE CODE(CREDITS): 18BIWBI631(3)

MAX. MARKS: 25

COURSE NAME: Advanced Algorithms for Bioinformatics

COURSE INSTRUCTOR: Dr. Tiratha Raj Singh

MAX. TIME: 1 Hour 30 Minutes

Note: All questions are compulsory. Marks are indicated against each question in square brackets.

- Q.1. Correlate shortest superstring and travelling salesman problems for fragment assembly. Assemble following fragments to generate SSP followed by TSP: CGAC, AGTA, ATCG, ACTG, TATC, GTAT, TCGA, GACT. Generate proper and systematic graphs. (CO-3) [4]
- Q.2. Discuss the significance of interval graphs in fragment assembly. How the linearity of the genomes were proved by Benzer's experiment? (CO-2) [4]
- Q.3. Compare Hamiltonian and Euler's graphs for solving fragment assembly problem. Give an example of both the approaches. (CO-4) [4]
- Q.4. Formulate a sequencing by hybridization (SBH) problem using computational approach. include the significance of spectrum. A candidate genome 'ATGGCGTGCA' is given to you. Solve this problem through Hamiltonian approach. (CO-4) [4]
- Q.5. What are three models of fragment assembly? Discuss Reconstruction model for the following fragments: $F = \{TCAG, GTAG, TGAC, AGTC\}$ with error tolerance 0.1. Find out the best layout for F. (CO-3) [4]
- Q.6. What are various kind of errors/complications in sequencing? How these errors/complications can be managed while doing fragment assembly? Explain each complication with an example. (CO-3,4) [5]