

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -3 EXAMINATIONS, May 2019

B.Tech VIth Semester (Bioinformatics)

Course Code: 10B11BI614

MAX. MARKS: 35

Course Name: Advanced Algorithms for Bioinformatics

Course Credits: 04

MAX. TIME: 2 Hrs.

Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means. Marks are indicated in square brackets against each question.

Q.1. Discuss Mathematical properties of similarity and distance. (CO 1-3) [3]

Q.2. Provide a Bioinformatic analysis for Cystic Fibrosis disease. (CO 2-3) [2]

Q.3. Formulate the shortest superstring problem. Map SSP to TSP for the following set of fragments: (CO 1-3) [5]

$S = \{ATG, GAC, CGT, TAC, TGA, ACG, GTA\}$

Q.4. What is sequencing by hybridization? Realize how graph theory could help us in this process? Provide available algorithms for the same. (CO 2-3) [4]

Q.5. What are repeats in genomes? How repeats can mislead to the assembly of genomes? Provide a case study for the same. (CO 1-4) [4]

Q.6. What is STAR alignment method? Why it is called STAR? (CO 4-5) [2]

Q.7. What is popular about MSA? What is the location and role of MSA in Bioinformatics analyses? Describe SoP method with the final calculations for the following alignment:

ATGCTA (CO 4-5) [5]

A - GC-A

AT - CT -

ATGCT

(Scoring system: Match = +1, Mismatch = 0, Gap = -1)

Q.8. Define following with a suitable example: (CO 1-5) [2*5=10]

(a) Interval Graph

(b) Spectrum

(c) Gene prediction methods

(d) Benzer's experiment for genomes

(e) Greedy Profile Motif Search