

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATION- 2024

BTech-VI Semester [BI]

COURSE CODE(CREDITS): 18B1WBI631(3)

MAX. MARKS: 35

COURSE NAME: Advanced Algorithms for Bioinformatics

COURSE INSTRUCTOR: Dr. Tiratha Raj Singh

MAX. TIME: 2 Hours

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

Q.1. Formulate the motif finding problem. Differentiate between BFMS and BFMS Again algorithms with an example of each. Mention the exact point of difference in the algorithm.

(CO-4) [5]

Q.2. Discuss the Lander Waterman model for fragment assembly. For a genomic segment of 5000 bp and length of each read is 450 pb, then how much reads will be required for 7X coverage?

(CO-5) [3]

Q.3. Prove the hypothesis with an example that the distance between two motifs is more than the distance between any motif and the consensus sequence.

(CO-3,4) [5]

Q.4. Write various applications of MSA. Align any 5 sequences (ATGCTAC, ATCTAC, ATGTAC, TGCTAC, ATGCTC) using SoP method and scoring systems as Match = +2, Mismatch = 0, Gap = -3.

(CO-4) [5]

Q.5. Explain following terms with an example of each:

(CO-3-5) [2*4=8]

(i) Median String Search

(ii) Similarity and Distance

(iii) Bypass Move

(iv) Berger and Munson Algorithm

Q.6. A nucleotide sequence of length 15 is given (GATGCGTAGACGTGC). A motif of length 8 is implanted in this sequence. How you can identify that which is the P-most probable motif? Prove through all the required calculations.

(CO-4,5) [6]

Q.7. Differentiate between progressive and iterative methods for MSA. Which method is better? Prove with the help of an example.

(CO-4,5) [3]