

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST - 3 EXAMINATION- MAY-2023

COURSE CODE(CREDITS): 18B1WBI631(3)

MAX. MARKS: 35

COURSE NAME: Advanced Algorithms for Bioinformatics

COURSE INSTRUCTORS: Dr. Tiratha Raj Singh

MAX. TIME: 2 Hours

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

- Q.1. Elucidate the analytical version of sequence alignments. Justify that MSA can perform exponentially better than pairwise alignment while analyzing biological sequences. Discuss the respective role of both these alignments in bioinformatics analyses. (CO-4,5) [4]
- Q.2. Generate MSA for the following three sequences: ATGAC, TGAC and ATGA. If score for Match = 1, Mismatch = -1 and Gap = -2, then calculate the final score using SoP method. (CO-4) [6]
- Q.3. What are various recent developments in MSA algorithms? Discuss progressive and iterative refinement algorithms with an example of each. (CO-4,5) [4]
- Q.4. Write Brute Force PDP algorithm. How its performance can be improved? Experimental results of PDP were as follows: 2,3,7,8,9,10,11,12,17,18,19,21,26,29. Solve this PDP by assuming that  $X = L$ . (CO-3-5) [2+4]
- Q.5. What are the various characteristics of algorithms? Discuss the journey of algorithm developments to its applications in computational biology and biomedical sciences with a brief discussion at application part. (CO-1-5) [1+3]
- Q.6. For a given candidate genomic fragment of size 12, codon wise defragmentation can be used to solve this problem through Hamiltonian approach. Solve this problem through the same approach and draw its node based diagram. (CO-2-4) [5]
- Q.7. Discuss in brief with a comparative analysis of multiple algorithms developed for the identification and analysis of motifs in biological sequences. Explain Greedy Profile Motif Search (GPMS) algorithm with a suitable example. Assume that standard parameters were used for these motifs in GPMS algorithm. (CO-3-4) [3+3]