

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATION- 2026

BTech-VI Semester [BI]

COURSE CODE(CREDITS): 18BIWBI631(3)

MAX. MARKS: 35

COURSE NAME: Advanced Algorithms for Bioinformatics

COURSE INSTRUCTOR: Dr. Tiratha Raj Singh

MAX. TIME: 2 Hours

*Note: (a) All questions are compulsory.**(b) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems**(c) Use of calculator is not allowed*

Q.No	Question	CO	Marks
Q1	A DNA sequence of length 16 is given below: ATGCGTACGTTAGCTA. An implanted motif of length 6 is suspected to occur within the sequence. Explain the process of identifying the most probable motif using a Position Weight Matrix (PWM) or profile-based approach. Show all intermediate calculations required to determine the most probable motif occurrence.	4	5
Q2	Discuss the biological and computational applications of Multiple Sequence Alignment (MSA). Compare various algorithms for MSA along with their applications.	4	5
Q3	Explain the significance of the Lander–Waterman model in genome sequencing and fragment assembly. A bacterial genome contains 12,000 bp and the average read length is 600 bp. Calculate the number of reads required to achieve 8X genome coverage.	5	3
Q4	Describe the concept of consensus sequence and Hamming distance in motif analysis. Demonstrate with an example that the total distance between two motifs is always greater than or equal to the distance between each motif and the consensus sequence.	3	4
Q5	Define the motif discovery problem in computational biology. Compare the Brute Force Motif Search (BFMS) and Branch and Bound Motif Search	4	4

	(BBMS) algorithms with suitable examples. Clearly explain the major optimization step that makes BBMS faster than BFMS.		
Q6	Explain the following terms with one suitable example each: (i) Profile Matrix (PSSM) (ii) Needleman–Wunsch Algorithm (iii) Median String Motif Search (iv) Edit Distance	3-5	2x4=8
Q7	Differentiate between global and local alignment methods in bioinformatics. Which alignment strategy is more appropriate for identifying conserved regions in distantly related sequences? Justify your answer with an example.	5	3
Q8	Write the Brute Force PDP algorithm. How can its performance be improved? The experimental results of a Partial Digest Problem are: $L=\{2,4,5,7,9,11,12,14,16,18,20,21,23,25,27\}$ Solve this PDP by assuming that: $X=1$	5	3