

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATIONS- 2026

B. Tech-VIII Semester [All except Bio]

COURSE CODE (CREDITS): 21B1WBT833 (3)

MAX. MARKS: 25

COURSE NAME: Computational Biology for Engineers

COURSE INSTRUCTOR: Dr. Raj Kumar

MAX. TIME: 1 Hour 30 Min

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	Explain Chargaff's rule. In a double-stranded DNA molecule, adenine (A) constitutes 30% of the total bases. Calculate the percentage of thymine (T), guanine (G), and cytosine (C).	1	3
Q2	Describe noise in dot plot method in sequence alignment. Which strategies you can use to reduce noise for clear alignments.	2	3
Q3	Describe the Protein Data Bank (PDB) file format used to store structural information of biological molecules.	2	3
Q4	Calculate the sequence identity for the given sequence alignment: ATTACTTACGGATCAGGTAC ATT----ACGGATC--GTAC	3	3
Q5	Implement dynamic programming for global alignment for the following sequences: Sequence-1: CTATAGT Sequence 2: CATCGT Use scoring system as Match = 1, Mismatch = -1, Gap Penalty = -2.	3	7
Q6	Short notes: a) Homologous sequences b) Significance of gaps in sequence alignments c) HSP	1	2 × 3 = 6