

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATIONS- 2026

B. Tech-VIII Semester [All except Bio]

COURSE CODE (CREDITS): 21B1WBT833 (3)

MAX MARKS: 35

COURSE NAME: Computational Biology for Engineers

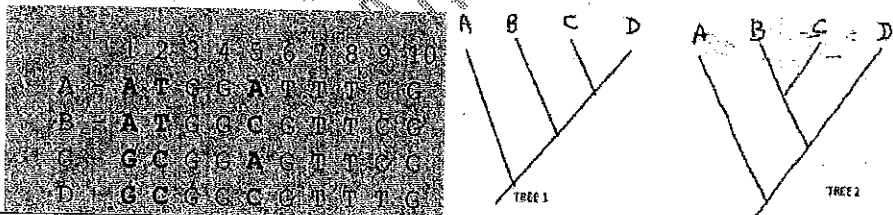
COURSE INSTRUCTOR: Dr. Raj Kumar

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	Describe various steps used in global sequence alignment using dynamic programming. Align the given sequences using Needleman-Wunsch algorithm. Use the following scoring scheme: Match: 1, Mismatch: 0, Gap penalty: -1 Seq1: TGGACG Seq2: GGAG	4	7
Q2	Find out the most parsimonious tree using given alignment: 	4	7
Q3	Describe the principle behind homology modeling method. Explain model building steps involved in protein tertiary structure prediction using homology modeling.	5	5
Q4	Calculate the sequence identity score for the given alignment: CTGTTACCTA CTACTA-CTA	2	3
Q5	Discuss the major database resources for nucleotide sequence information and explain the role of the INSDC in the nucleotide sequence data.	2	5

Q6	Discuss the role of central dogma in transfer of information from DNA to proteins.	1	5
Q7	Discuss various terminologies used in a phylogenetic tree?	5	3

JUNIT TEST-3 EXAMINATIONS- MAY-2026