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JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -2 EXAMINATIONS- 2026
B.Tech-IV Semester (BT)

COURSE CODE (CREDITS): 25B11BT414 (4)
MAX. MARKS: 25
COURSE NAME: Introduction to Bioinformatics
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	Calculate the sequence identity for the given sequence alignment:
	`CGTCTGATAC`
	`C-T-TGA--C`
		2	3

Q2	In a dot plot comparing two genomic sequences, random noise may obscure biologically meaningful alignments. What is noise and propose and justify strategies to distinguish true homology by reducing noise.	3	3
Q3	Analyze role of chemical databases. Discuss the role of ZINC compound library in drug discovery applications.	2	3
Q4	Explain the working of a word method for sequence alignment. List advantages of word method compared to dynamic programming.	2	4
Q5	Implement dynamic programming for local alignment for the following sequences: Sequence1 : A T A C C G G A T A T T Sequence2 : A A C G G A C C C T Use scoring system as Match = 1, Mismatch = 0, Gap Penalty = -2.	3	7
Q6	Short notes: 1) Sensitivity vs. selectivity 2) three zones of protein sequence alignments 3) Missense vs. non-sense mutations 4) Sequence identity vs. sequence homology 5) Orthologous vs. paralogous sequences	1	1 × 5 = 5