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JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATIONS- 2026

MSc -I Semester (BT/MB)

COURSE CODE (CREDITS): 20MS1BT213 **MAX MARKS: 25**

COURSE NAME: Bioinformatics

COURSE INSTRUCTOR: Dr. Shikha Mittal **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	Marks
Q1.	**a.** Two alignments have E-values: 1e-20 and 0.01. Which is more significant and why? **b.** Calculate number of rooted and unrooted topologies if number of taxa is 5. **c.** Seq1: ATGCTAGCTA Seq2: ATGATGGCTA Count matches, mismatches and identity (%)	(6)
Q2.	Design a workflow to identify homologous sequences using BLAST.	(4)
Q3.	Calculate BLOSUM substitution matrix for given block of sequences	(4)
Q4.	Differentiate between – **a.** Cladogram and phylogram **b.** Tandem and segmental duplication **c.** Local and global alignment **d.** BLAST variants	(4)

Sequences				
H	P	P	C	H
H	P	P	C	H
H	H	P	C	W
H	H	P	C	W
W	P	P	P	H

Q5.	Explain how MSA helps in identifying conserved regions in sequences.	(3)
Q6.	Discuss in detail the concept of random and non-random substitutions and explain how PAM matrices are constructed based on non-random evolutionary changes.	(4)