

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATIONS- 2024

M.Sc - II Semester (BT/MM/PhD)

COURSE CODE (CREDITS): 20MS1BT213 (2)

MAX. MARKS: 35

COURSE NAME: Bioinformatics

COURSE INSTRUCTORS: Dr. Shikha Mittal

MAX. TIME: 2 Hours

Note: (a) All questions are compulsory.

(b) Marks are indicated against each question in square brackets.

(c) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems

Q1. It is noted that major sequence alignments differ in approach computational complexity and accuracy. Do you agree with this? Explain with suitable examples. (3 marks)

Q2. Write down the significance of multiple sequence alignment in biological data analysis. (3 marks)

Q3. Explain the concept of molecular clocks and their use in estimating divergence times between species. Discuss the assumptions and challenges associated with molecular clock methods. (3 marks)

Q4. Calculate possible number of topologies if taxa is 4 for rooted and unrooted trees. (3 marks)

Q5. Briefly explain- (8 marks)

- i. Difference between phylogram and cladogram
- ii. Ramachandran plot
- iii. Alpha-helix and beta pleated sheets
- iv. E-value and Bit-Score in BLAST results

Q6. Consider a simple distance matrix for four taxa (A, B, C, D): (5 marks)

	A	B	C	D
A	-	5	9	9
B	-	-	6	8
C	-	-	-	10
D	-	-	-	-

Apply the UPGMA algorithm to construct a phylogenetic tree.

Q7. Explain the concept of homology modeling in bioinformatics. Discuss the steps involved in building a homology model of a protein and its applications in structural biology. (4 marks)

Q8. Define the following – (6 marks)

- i. Affine gap penalty
- ii. Write short note on PAM and BLOSUM scoring matrices.
- iii. Discuss the importance of biological databases in bioinformatics.

UNIVERSITY OF SHEFFIELD EXAMINATION - JUNE 2024