## JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT TEST-3 EXAMINATION- 2025

## M.Sc.-II Semester (MB/MM)

COURSE CODE (CREDITS): 20MS1BT213 (2)

MAX. MARKS: 35

COURSE NAME. Riginformatics

COURSE INSTRUCTORS: Dr. Shikha Mittal

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

Q.No	Question	Marks
Q1	Discuss how MSA results can be used to infer evolutionary relationships.  Explain substitution matrices used in phylogenetic tree generation	(4)
Q2	Outline the steps involved in homology or comparative modelling for construction of protein structure.	(4)
Q3	How many unrooted and rooted trees can be constructed for 5 taxa.	(4)
Q4	You are given the following distance matrix representing the evolutionary distances between 4 species:    A B C D   A 0 0   B 4 0 0   C 6 6 0   D 8 8 4 0   Create a UPGMA tree for the above distance matrix	(4)
Q5	Describe in detail the four levels of protein structure. For each level, mention the types of bonds or interactions and give examples.	(4)
Q6	Explain the principle, working, and applications of BLAST. Describe different types of BLAST programs and interpret a typical BLAST output.	(4)
Q7	You are given the following aligned sequences:  Sequence 1: M A R T H A Sequence 2: M K R T Q A Consider R-K and H-Q as similar (based on biochemical properties)  a) Calculate the percent identity. b) Calculate the percent similarity.	(3)
Q8	a) Homologs & Orthologs b) FASTA c) Phylogram vs Cladogram d) Ramachandran plot	(8)