JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATIONS- 2025

B.Tech-III Semester (BI)

COURSE CODE (CREDITS): 25B11BI311 **MAX. MARKS: 35**

COURSE NAME: Biological Computation

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**	**CO**	**Marks**
Q1	You are given a sequence with 40% identity to a template. Predict whether homology modeling will be reliable. Explain.	[IV, V]	(5)
Q2	Describe the principle of minimum free energy (MFE) models in RNA secondary structure prediction. How do algorithms like the Nussinov and Zuker algorithms work?	[VI]	(5)
Q3	Explain in brief – **A**. Define torsion angles (phi, psi, omega) in proteins **B.** What is a Ramachandran plot, and how is it used? **C.** BLAST Variants **D.** HMM **E.** Genome specific databases	[II, III V, VI]	(10)
Q4	Compare **UPGMA** and **Neighbor-Joining**, including the concept of ultrametric assumption.	[III, VI]	(4)
Q5	Explain how to calculate the alignment score using affine gap penalty with the help of an example.	[I, II]	(3)
Q6	List the applications of MSA in Bioinformatics.	[II, III]	(4)
Q7	**a.** Given an mRNA of 300 nucleotides: How many amino acids will the protein have? (Stop codon not included) **b.** Match = +1 Mismatch = –1 Gap = –2 **Align:** Seq1: A G C Seq2: A – C Calculate total alignment score	[III, IV]	(4)