JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATION- 2025

M.Sc - II Semester (MM/MB)

COURSE CODE (CREDITS): 20MS1BT213 (2) **MAX. MARKS: 15**
COURSE NAME: Bioinformatics
COURSE INSTRUCTORS: Dr. Shikha Mittal **MAX. TIME: 1 Hour**

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	You are given the following two sequences: **Sequence 1: GATTACA** **Sequence 2: GCATGCU** Perform local alignment using both the sequences with the following scoring scheme: **Match** = +2 **Mismatch** = -1 **Gap penalty** = -2	(4)
Q2	Given a list of genes from two species, describe how you would determine which are orthologs and which are paralogs.	(2)
Q3	What are 'accession numbers' in biological databases, and why they are important?	(2)
Q4	Differentiate between – a. primary and secondary biological databases b. Needleman-Wunsch and Smith-Waterman algorithms	(4)
Q5	You are given the following aligned sequences: **Sequence 1:** A T G C T A G G C T A **Sequence 2:** A T G C T G G A C T A Calculate the sequence identity and sequence similarity between these two sequences	(3)