## JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT TEST -2 EXAMINATION- 2025

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

COURSE CODE (CREDITS): 20MS7BT372 (2)

MAX. MARKS: 25

**COURSE NAME: Bioinformatics** 

COURSE INSTRUCTORS: 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

Q.N		
-	Question	Mark
Q1	What is BLAST, and how does it help in sequence analysis? Provide an example of how BLAST is used to search for homologous sequences.	(04)
Q2	Two protein sequences are aligned, and out of 120 positions, 90 are identical.  Calculate the sequence identity percentage.	(02)
	Percontage.	(02)
Q3	Explain what multiple sequence alignment (A.S.A.)	
	Explain what multiple sequence alignment (MSA) is and why it is important in bioinformatics.	(04)
Q4	Given two sequences:	
	Sequence A: AGGCT	(04)
	Sequence B: AGCA	` /
	Using the Needleman-Wunsch alassid	
	Using the Needleman-Wunsch algorithm, perform global sequence alignment.  Assume the following scoring system:	
	Match: +1	
	Mismatch: -1	
	Gap penalty: -2	
)5	Perform BLOSUM	
	Perform BLOSUM matrix calculation for the following sequences -	
	Seq1	05)
<b>5</b>	a. Difference between PAM and DY Ogym	
	a. Difference between PAM and BLOSUM with an example b. Primary and secondary databases (00)	5
	c. Variants of BLAST	7