JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

Make-up Examination-Nov-2025

COURSE CODE (CREDITS): 25B11BI311 (3) **MAX. MARKS: 25**

COURSE NAME: Biological computation

COURSE INSTRUCTORS: Dr. Shikha Mittal **MAX. TIME: 1 Hour 30 Minutes**

Note: 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	Explain the principles of sequence alignment algorithms (Needleman–Wunsch and Smith–Waterman).	[I]	(3)
Q2	Describe in detail how BLAST works and also the variants of BLAST.	[II]	(3)
Q3	Write in short – **a.** Difference between homologous and orthologous **b.** Differnce between sequence identity and sequence similarity **c.** FASTA format **d.** Applications of Bioinformatics **e.** Difference between EMBL and DDBJ	[I,II]	(10)
Q4.	Using a scoring scheme: match = +1, mismatch = −1, no gaps. Compute alignment score for seq1 = A C G T vs seq2 = A G G T (position-wise)	[I]	(3)
Q5	Two sequences of length 1000 bp have 845 identical positions. Compute sequence identity.	[I,II]	(3)
Q6	Explain the different types of biological databases and their interrelationships using suitable examples	[II]	(3)

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