JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT TEST -3 EXAMINATIONS- 2023

B.Tech-III Semester (BI)

COURSE CODE (CREDITS): 18B11BI313

MAX. MARKS: 35

COURSE NAME: Biological computation

COURSE INSTRUCTORS: Dr. Shikha Mittal

MAX. TIME: 2 Hours

Note: (a) All questions are compulsory.

(b) Marks are indicated against each question in square brackets.

(c) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems

Q1. Define the UPGMA algorithm and state and justify its complexity. What is the output of the algorithm given the distance matrix of the species A, B, C, D, and E below? (5 marks) [CO-4]

	A	В	C	D	E
A	0		j.	(No. 1)	W. ""
В	20	0	The same	. 7	
C	60	50	0	grand.	
D	100	90	40	0	
E	90 🖔	80	50	30	0

- Q2. Discuss the importance of biological databases in bioinformatics. (3 marks) [CO-2]
- Q3. What are the common structural motifs in RNA? What base-pairing are used in RNA? (4 marks) [CO-3]
- Q4. Consider the DNA strings TCGCA and TCCA. Compute the best global alignment of the two strings assuming match score of 1, and mismatch/indel penalty of -1? [CO-1] (4 marks)
- Q5. Differentiate between template modeling and template-free modeling. Explain the steps of comparative modeling in detail (5 marks) [CO-4 & CO-5]
- Q6. Define root node and clade in an evolutionary tree with the help of a diagram. If we have 4 nodes in a phylogenetic tree, how many rooted and unrooted trees can be constructed from them (4 marks) (CO-4)
- Q7. Draw a dotplot of the following sequence from the Wheat dwarf virus genome: ttttcgtgagtgcgcggaggctttt against itself. In what respects is it not a perfect palindrome? (4 marks) [CO-2 & CO-3]
- **Q8.** Explain the following (6 marks) [CO-1, CO-4 & CO-6]

- (a) Sensitivity and specificity in BLAST
- (b) Different between global and local alignment
- (c) Functions of mRNA, tRNA and rRNA