JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT TEST -3 EXAMINATION- 2024

B.Tech-III Semester (BI)

COURSE CODE (CREDITS): 18B11BI313 (4)

MAX. MARKS: 35

COURSE NAME: Biological Computation

COURSE INSTRUCTORS: Dr. Raj Kumar, Dr. Tiratha Raj Singh

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		10	
	Question		CO	Marks
Q1	What are substitution matrices? How are these utilized for be sequence analysis? Discuss PAM in detail with an demonstrating how PAM100 can be fabricated?	piological example	3,4	5
Q2	Differentiate between local, global, and semi-global alignment an example of each. Align the given two sequence "TAGCTGCA" and B = "CTGCA" for the scoring system as +1, mismatch = 0, gap penalty = -1 using Dynamic Programment semi-global (ESF) approach.	es A =	3-5	6
Q3	Identify the most probable pattern by determining the HMM probabilities for the occurrence of the following sequence pattern by determining the HMM probabilities for the occurrence of the following sequence pattern as a sequence alignment. a) AVHPL b) AVQPM c) AIHPL	erns in		
	Sequence A A V H P L		3-6	9
	Sequence B A V H P L			
	Sequence C A I H P L			
	Sequence D A V Q P I			
	Sequence E A I P P M	1	ı	
Q4	There are different zones of sequence alignment identity that in the likelihood of adopting similar structures. How do zones of homology influence the process of homology modeling and ten selection?]	5	3
Q5	There are several model building steps in homology modelling. Discuss backbone generation and loop modeling steps.		5	5

