

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATION- 2023

B.Tech-IV Semester (BT)

COURSE CODE(CREDITS): 18B11BT413 (4)

MAX. MARKS: 35

COURSE NAME: Introduction to Bioinformatics

COURSE INSTRUCTORS: Dr. Raj Kumar

MAX. TIME: 2 Hours

Note: All questions are compulsory. Marks are indicated against each question in square brackets.

Q1. Answer the following questions in context to protein tertiary structure prediction: (CO-4)

- a) Protein structure information is critical for understanding its function. What are various methods and criteria for protein tertiary structure prediction? [3]
- b) Realignment of protein sequences is a crucial step in homology modeling. Justify this statement. [2]

Q2. Answer the following questions in regard to PCR primer designing: (CO-3)

- a) Calculate the melting temperature (T_m) for the given PCR primer: [2]
AAGCTGATCAACGATGGCTTGCC
- b) If the T_m of a primer is 70 and that of its product is 75. What will be the primer's annealing temperature? Based on the results, justify if it's a good primer or not? [3]

Q3. Answer the following questions in context to molecular phylogenetics:

(CO-5)

- a) How will you define evolution? [2]
- b) Homoplasy [2]
- c) Molecular fossils [1]

Q4. Answer the following questions in context to database similarity search: (CO-2)

- Sensitivity and selectivity [2]
- Low complexity regions [2]
- HSP [1]

Q5. Using the given scoring scheme, calculate the sum of pairs score for the following multiple sequence alignment: (CO-3) [5]

Match: 2; Mismatch = -1; Gap = -1

X: G T A C G

Y: T G C C G

Z: C G G C C

W: C G G A C

Q6. Generate a UPGMA tree using the following dataset:

(CO-5)[5]

	A	B	C	D	E
B	50				
C	40	70			
D	70	100	70		
E	60	90	60	50	
F	80	110	80	90	80

Q7. Demonstrate the calculation of only first reduced matrix and clustering of taxa for the given dataset using NJ method:

(CO-5)[5]

	A	B	C
B	40		
C	35	45	
D	60	70	55