

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATIONS-2022

B.Tech-IV Semester (BT)

COURSE CODE (CREDITS): 10B11BT511(4)

MAX. MARKS: 35

COURSE NAME: Introduction to Bioinformatics

COURSE INSTRUCTORS: Dr. Raj Kumar

MAX. TIME: 2 Hours

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

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Q1. We can use molecular data to study evolution of a gene. What strategy will you apply to study phylogeny of a species? [2] (CO-3)

Q2. Substitution models can be used to treat mutations in a realistic manner. What are advantages of Kimura substitution model over Jukes-Cantor model? [2] (CO-4)

Q3. In neighbor joining, how will you define the distance of each taxon from a composite taxon? [2] (CO-5)

Q4. To use molecular data to reconstruct evolutionary history requires making a number of reasonable assumptions. Discuss some of these assumptions and significance of molecular data in phylogenetics. [2](CO-5)

Q5. What is the significance of outgroup in a phylogenetic tree? [2] (CO-4)

Q6. In construction of a NJ tree, informative sites can be used and non informative sites can be discarded. How will you define informative sites? Calculate the number of informative sites in the given alignment. [3] (CO-3)

Seq 1 GNYNYKYRYLRHGKLRPFERDISNVPFSPDGKP  
Seq 2 GNYNYKYRYLRHGKLRPFERDISNVPFSPDGKP  
Seq 3 GNFNYYRIWRSEKLRPFERDIAHYDYQVGTQF  
Seq 4 GNYNYLYRWVRRSKLNPYERDLSNDIYSPGGQS  
Seq 5 GNYNYLYRWVRRSKLNPYERDLSNDIYSPGGQS  
Seq 6 GNYNYKYRSLRHGKLRPFERDISNVPFSPDGKP  
Seq 7 GNYNYLYRFRKSNLKPFERDISTEIQAGSTP



Q7. Calculate  $T_m$  for the given PCR primer. [3] (CO-3)

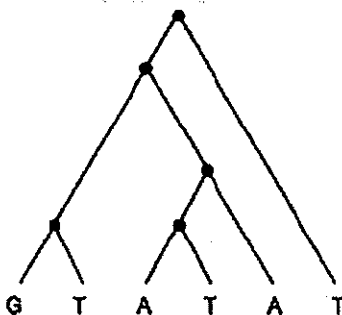
CTGATCAAGTCGATGGCTTG

Q8. What are factors responsible for non-specific pairing or banding patterns in PCR output? [3] (CO-5)

Q9. Calculate the R-transformed values for all taxa in the given pairwise distance matrix. [4] (CO-4)

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

Q10. Demonstrate, which character will be at the root according to parsimony for the given tree topology? [5] (CO-5)



Q11. Construct a UPGMA tree for the following distance matrix [7] (CO-4)

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

