

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATION- 2024

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: (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. Explain how to account for factors such as substitution rates, indels, and sequence divergence in multiple sequence alignments? (CO-3) [2]

Q2. Enlist some important characteristics of a good PCR primer. (CO-3,4) [3]

Q3. Describe the iterative refinement approach for multiple sequence alignments? (CO-3) [3]

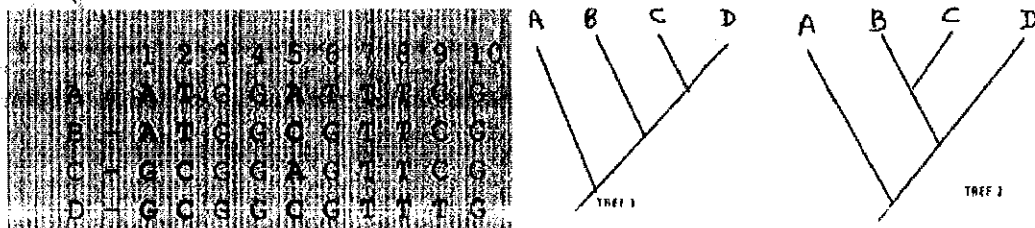
Q4. Tree topology summarizes the patterns of evolutionary relatedness among a group of species independent of the branch lengths of a phylogenetic tree. Can you explain the difference between rooted and unrooted phylogenetic trees in terms of their topology? (CO-5) [3]

Q5. Interpret the given multiple sequence alignment and write your inferences briefly. (CO-3) [3]

```

S.scrofa  NTELPAPLSYFQNAQMSEDNHVSNVSSQND SRE RHENSIERRRRRGNSELSNGGAQQMS 60
B.taurus NTELPAPLSYFQNAQMS EDNHL SNTVRSQND SRE RHENHGNERRRONTESVSNGRAPSSS 60
H.sapiens NTELPAPLSYFQNAQMS EDNHL SNTVRSQND NRERQEH -NDRRSLGNPELNGRPQMS 59
M.musculus NTEIPAPLSYFQNAQMS EDSSHSSAIRSQND SQERQQQ -HDRQRLDNP EISNGRPQMS 59
***;*****.* * . ; ****;***: :* : . : * . : * * . . . *
    
```

Q6. Find the most parsimonious tree for the given alignment. Describe the steps involved. (CO-4,5) [5]



Q7. For the given BLOSUM-62 matrix:

(CO-4,5) [2 × 4 = 8]

BLOSUM-62 Matrix

	C	S	T	P	A	G	N	D	E	Q	R	K	M	I	L	V	F	Y	W
C	4																		
S	-1	4																	
T	-1	1	4																
P	-3	-1	-1	4															
A	0	1	0	-1	4														
G	-3	0	-2	-2	0	4													
N							4												
D								4											
E									4										
Q										4									
R											4								
K												4							
M													4						
I														4					
L															4				
V																4			
F																	4		
Y																		4	
W																			4

a) Calculate the max score for the given alignment:

DFNVILM
DFEVIIM

b) Calculate the sum of pairs for the given alignment:

Seq1: PKTV
Seq2: PKTV
Seq3: PKVV

Q8. Calculate the phylogenetic tree for the given matrix, based on a distance based method that uses molecular clock hypothesis. (CO-5) [5]

	A	B	C	D
A	0			
B	3	0		
C	5	4	0	
D	7	1	2	0

Q9. Using NJ method, calculate the corrected distance matrix for the matrix given in Q8. (CO-5) [3]