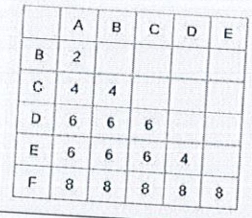
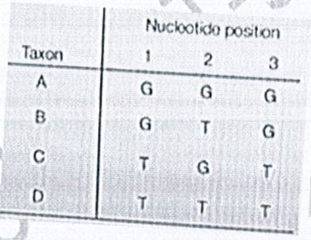
JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -3 EXAMINATION- 2025
B.Tech-IV Semester (BT)

COURSE CODE (CREDITS): 18B11BT413 (4)
COURSE NAME: Introduction to Bioinformatics
COURSE INSTRUCTORS: Dr. Raj Kumar, Prof. Tiratha Raj Singh

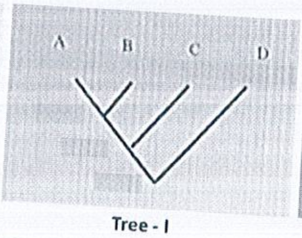
MAX. MARKS: 35
MAX. TIME: 2 Hours

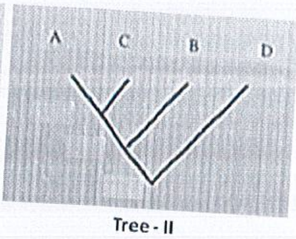
Note: *(a) All questions are compulsory.*
(b) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems

<table>
<tr><th>Q.No</th><th>Question</th><th>CO</th><th>Marks</th></tr>
<tr><td>Q1.</td><td>Calculate the phylogenetic tree for the given matrix using a UPGMA method.


	A	B	C	D	E
B	2				
C	4	4			
D	6	6	6		
E	6	6	6	4	
F	8	8	8	8	8
</td><td>5</td><td>5</td></tr>
<tr><td>Q2.</td><td>UPGMA and Neighbor-Joining are both distance-based methods used in phylogenetic tree construction. Explain the difference between both methods in terms of how branch lengths are calculated.</td><td>4,5</td><td>5</td></tr>
<tr><td>Q3.</td><td>Find the most parsimonious tree for the given alignment. Describe the steps involved.


Taxon	Nucleotide position 1	2	3
A	G	G	G
B	G	T	G
C	T	G	T
D	T	T	T



Tree - I


Tree - II</td><td>3-5</td><td>5</td></tr>
<tr><td>Q4.</td><td>Write short notes:
a) Molecular clock hypothesis
b) Back mutation
c) Kimura model
d) Substitution matrices
e) Dot plots</td><td>1-5</td><td>5 × 1 =5</td></tr>
</table>

Q5.	Construct the local alignment matrix for the sequences given below using the Smith-Waterman approach: A = ‘ATGCTGCA’, B = ‘GCTG’. Follow the scoring: Match = +1, Mismatch = -1, Gap = -2.	3	4
Q6.	How does the Central Dogma in Molecular Biology differ from that in Computational Biology in terms of flow of information? Differentiate between orthology and paralogy with an example. Explain how homology is associated with structural and functional aspects of biological data?	1,2	2
Q7.	What is MSA? What are its various applications? Discuss various methods available for MSA along with their implementations in tools or server forms. Calculate MSA through sum of pairs method for a given set of 5 amino acid sequences of your choice with minimum length 5 and maximum length 7 amino acid residues. Explain How this method is different from star method of MSA?	5	6
Q8.	What are phylogenetic trees? Discuss basic properties of these trees along with their respective implementations through various approaches. Generate the phylogenetic tree for the example of MSA taken in previous question for sum of pairs method.	5	3