

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATIONS- 2026

B.Tech-IV Semester (BT)

COURSE CODE (CREDITS): 25B11BT414 (4)

MAX. MARKS: 35

COURSE NAME: Introduction to Bioinformatics

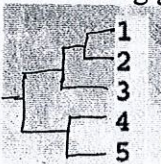
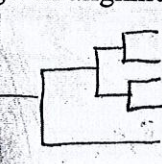
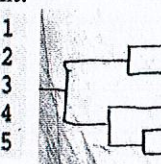
COURSE INSTRUCTOR: Dr. Raj Kumar

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

(c) Use of calculator is allowed.

Q. No	Question	CO	Marks																																																																														
Q1	Calculate the phylogenetic tree and respective branch lengths for the given matrix using an unweighted pair group method with arithmetic mean method. <table border="1"> <thead> <tr> <th></th><th>A</th><th>B</th><th>C</th><th>D</th><th>E</th></tr> </thead> <tbody> <tr> <th>A</th><td>0</td><td></td><td></td><td></td><td></td></tr> <tr> <th>B</th><td>20</td><td>0</td><td></td><td></td><td></td></tr> <tr> <th>C</th><td>60</td><td>50</td><td>0</td><td></td><td></td></tr> <tr> <th>D</th><td>100</td><td>90</td><td>40</td><td>0</td><td></td></tr> <tr> <th>E</th><td>90</td><td>80</td><td>50</td><td>30</td><td>0</td></tr> </tbody> </table>		A	B	C	D	E	A	0					B	20	0				C	60	50	0			D	100	90	40	0		E	90	80	50	30	0	3	7																																										
	A	B	C	D	E																																																																												
A	0																																																																																
B	20	0																																																																															
C	60	50	0																																																																														
D	100	90	40	0																																																																													
E	90	80	50	30	0																																																																												
Q2	Find out the most parsimonious tree using given alignment: <table border="1"> <thead> <tr> <th></th><th>1</th><th>2</th><th>3</th><th>4</th><th>5</th><th>6</th><th>7</th><th>8</th><th>9</th><th>10</th><th>11</th><th>12</th></tr> </thead> <tbody> <tr> <th>1</th><td>G</td><td>C</td><td>A</td><td>A</td><td>A</td><td>A</td><td>A</td><td>A</td><td>A</td><td>C</td><td>T</td><td>T</td></tr> <tr> <th>2</th><td>G</td><td>C</td><td>A</td><td>A</td><td>A</td><td>A</td><td>A</td><td>A</td><td>A</td><td>C</td><td>C</td><td>T</td></tr> <tr> <th>3</th><td>G</td><td>C</td><td>A</td><td>A</td><td>A</td><td>A</td><td>A</td><td>A</td><td>A</td><td>A</td><td>A</td><td>C</td></tr> <tr> <th>4</th><td>A</td><td>C</td><td>A</td><td>G</td><td>G</td><td>A</td><td>G</td><td>A</td><td>A</td><td>A</td><td>A</td><td>A</td></tr> <tr> <th>5</th><td>A</td><td>A</td><td>C</td><td>A</td><td>A</td><td>G</td><td>A</td><td>A</td><td>C</td><td>A</td><td>A</td><td>A</td></tr> </tbody> </table>  Tree -I  Tree -II  Tree -III		1	2	3	4	5	6	7	8	9	10	11	12	1	G	C	A	A	A	A	A	A	A	C	T	T	2	G	C	A	A	A	A	A	A	A	C	C	T	3	G	C	A	A	A	A	A	A	A	A	A	C	4	A	C	A	G	G	A	G	A	A	A	A	A	5	A	A	C	A	A	G	A	A	C	A	A	A	3	7
	1	2	3	4	5	6	7	8	9	10	11	12																																																																					
1	G	C	A	A	A	A	A	A	A	C	T	T																																																																					
2	G	C	A	A	A	A	A	A	A	C	C	T																																																																					
3	G	C	A	A	A	A	A	A	A	A	A	C																																																																					
4	A	C	A	G	G	A	G	A	A	A	A	A																																																																					
5	A	A	C	A	A	G	A	A	C	A	A	A																																																																					
Q3	Calculate the sum of pairs (SP) score for the given alignment. Use the following scoring scheme: Match: 1, Mismatch: 0, Gap penalty: -1 Seq1: TVKA Seq2: TVKA Seq3: VVKV Seq4: TVKV	4	5																																																																														
Q4	Calculate the statistical propensity of Arginine (R) in beta-strand conformation in the given dataset:	4	5																																																																														

	Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC AA: MASGATCVQRLDGSROSAIHTKYRISLRSSMQEPRSPLP 10 20 30 40 Pred: EEEEECCCCCCCCCCCCCCCCCCCCCCCCCHHH AA: RVILYNVSKRNPKEHRLRCMPCLRSELNENSLTHSAPGF 50 60 70 80 Pred: HHHHHHHHHCCCCCCCCCCCCC AA: VLLAQRRTHESTSEPEVGGGG 90 100		
Q5	PCR primers are short, single-stranded DNA fragments that define the specific target sequence to be amplified by binding to the beginning and end of the region. Discuss important characteristics of a good primer?	2	4
Q6	Explain the progressive alignment method for multiple sequence alignment.	4	3
Q7	Discuss the role of molecular fossils in phylogenetic analysis?	3	2
Q8	Define expect value (E-value) used in BLAST alignments.	1	2