

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- 2025

PhD-I & II Semester (BTBI)

COURSE CODE (CREDITS): 25P1WBT233 (3)

MAX. MARKS: 25

COURSE NAME: Advances in Bioinformatics

COURSE INSTRUCTORS: Dr. Raj Kumar

MAX. TIME: 1 Hour 30 Min

Note: (a) All questions are compulsory.

(b) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems

Q. No	Question	Mar ks																									
Q1.	The dot matrix method is one of the most basic sequence alignment techniques. What does 'noise' refer to in dot plots, and how can it be reduced or eliminated?	3																									
Q2	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.	5																									
Q3	Describe the iterative refinement approach for multiple sequence alignments?	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?	3																									
Q5	Calculate the phylogenetic tree for the given matrix, based on a distance-based method that uses molecular clock hypothesis. <table border="1"><tr><td></td><td>A</td><td>B</td><td>C</td><td>D</td></tr><tr><td>A</td><td>0</td><td></td><td></td><td></td></tr><tr><td>B</td><td>3</td><td>0</td><td></td><td></td></tr><tr><td>C</td><td>5</td><td>4</td><td>0</td><td></td></tr><tr><td>D</td><td>7</td><td>1</td><td>2</td><td>0</td></tr></table>		A	B	C	D	A	0				B	3	0			C	5	4	0		D	7	1	2	0	5
	A	B	C	D																							
A	0																										
B	3	0																									
C	5	4	0																								
D	7	1	2	0																							
Q6	For the given BLOSUM-62 matrix:	2×3 = 6																									

	C	S	T	P	A	G	N	D	E	Q	H	R	K	M	I	L	V	F	Y	W
C	9																			
S	-1	4																		
T	-1	1	5																	
P	-3	-1	-1	7																
A	0	1	0	-1	4															
G	-3	0	-2	-2	0	6														
N	-2	0	-2	-2	0	0	6													
D	-2	0	-1	-1	0	1	0	6												
E	-2	0	-1	-1	0	1	0	2	6											
Q	-1	0	-1	-1	0	0	0	0	0	6										
H	-3	-1	-2	-2	-2	-2	-1	-1	0	0	5									
R	-3	-1	-1	-2	-1	-2	0	-2	0	1	0	5								
K	-3	0	-1	-1	-1	-2	0	-1	1	1	-1	2	5							
M	-1	-1	-1	-2	-1	-3	-2	-3	-2	0	-2	-1	-1	5						
I	-1	-2	-1	-3	-1	-4	-3	-3	-3	-3	-3	-3	-3	1	4					
L	-1	-2	-1	-3	-1	-4	-3	-4	-3	-2	-3	-2	-2	2	2	4				
V	-1	-2	0	-2	0	-3	-3	-3	-2	-2	-3	-3	-2	1	3	1	4			
F																				
Y																				
W																				

a) Calculate the max score for the given alignment:

D F N V I L M
D F E V I I M

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

Seq1 - AREAL
Seq2 - SREIL
Seq3 - VVNAL