JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- 2025

B.Tech-III Semester (BI)

COURSE CODE (CREDITS): 25B11BI311 (3) **MAX. MARKS:** 25
COURSE NAME: Biological Computation
COURSE INSTRUCTORS: Dr. Shikha Mittal **MAX. TIME:** 1 Hour 30 Min

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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>Given the distance matrix for four taxa (A, B, C, D):
<table>
<tr><th></th><th>A</th><th>B</th><th>C</th><th>D</th></tr>
<tr><td>A</td><td>0</td><td>5</td><td>9</td><td>9</td></tr>
<tr><td>B</td><td>5</td><td>0</td><td>10</td><td>10</td></tr>
<tr><td>C</td><td>9</td><td>10</td><td>0</td><td>8</td></tr>
<tr><td>D</td><td>9</td><td>10</td><td>8</td><td>0</td></tr>
</table>
Draw the Neighbor Joining tree and label all branch lengths.</td><td>[V]</td><td>(5)</td></tr>
<tr><td>Q2</td><td>What are PAM and BLOSUM matrices? How are they constructed and what are their differences?</td><td>[III]</td><td>(3)</td></tr>
<tr><td>Q3</td><td>A BLAST output snippet:
<table>
<tr><th>Query</th><th>Subject</th><th>Align Length</th><th>Identical</th><th>Positive</th><th>Gaps</th></tr>
<tr><td>Seq1</td><td>Seq2</td><td>120</td><td>90</td><td>105</td><td>5</td></tr>
</table>
a. Calculate sequence identity (%)
b. Calculate sequence similarity (%)
c. Discuss the effect of gaps on identity and similarity.</td><td>[II]</td><td>(3)</td></tr>
<tr><td>Q4</td><td>Explain the general strategy of progressive alignment methods with an example.</td><td>[IV]</td><td>(3)</td></tr>
<tr><td>Q5</td><td>Define the following -
a. Applications of MSA
b. Maximum parsimony
c. Sequence homology and orthology</td><td></td><td>(6)</td></tr>
<tr><td>Q6</td><td>Explain the heuristic approach of BLAST and how it improves speed compared to exhaustive dynamic programming methods like Smith–Waterman.</td><td>[I, II]</td><td>(3)</td></tr>
<tr><td>Q7</td><td>Calculate the number of unrooted binary trees and rooted binary trees possible for-
a. 4 taxa
b. 6 taxa</td><td>[II]</td><td>(2)</td></tr>
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