JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATION- 2025

PhD-I & II Semester (BTBI)

COURSE CODE (CREDITS): 25P1WBT233 (3) MAX. MARKS: 35
COURSE NAME: Advances in Bioinformatics
COURSE INSTRUCTORS: 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*

<table>
<tr><th>Q.No</th><th>Question</th><th>Marks</th></tr>
<tr><td>Q1</td><td>Consider you are working on a drug discovery project which involves large chemical library screenings to identify potential drug molecules. Which chemical libraries will you consult to construct an in-house drug-like virtual screening library</td><td>3</td></tr>
<tr><td>Q2</td><td>Enlist some important characteristics of a good PCR primer.</td><td>3</td></tr>
<tr><td>Q3</td><td>Give an overview of a typical NGS experiment data analysis pipeline.</td><td>3</td></tr>
<tr><td>Q4</td><td>Discuss the criteria for choosing among various methods of tertiary structure prediction? What is the homology modeling approach and outline the steps involved in model building.</td><td>5</td></tr>
<tr><td>Q5</td><td>Calculate the sequence identity score for the given alignment:<pre>
CAT-TCA-C
| |  || |
C-TCGCAGC
</pre></td><td>3</td></tr>
<tr><td>Q6</td><td>Claculate sum of pairs (SP) score for following multiple sequence alignment:<pre>
Seq1 : G T A C G      Scoring scheme:
Seq2 : T G C C G      Match = +1
Seq3 : C G G C C      Mismatch = -1
</pre></td><td>4</td></tr>
<tr><td>Q7</td><td>Find the most parsimonious tree for the given alignment. Describe the steps involved.</td><td>4</td></tr>
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<table>
<tr><th></th><th colspan="12">Characters</th></tr>
<tr><th>Taxon</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>
<tr><td>A</td><td>G</td><td>G</td><td>G</td><td>G</td><td>T</td><td>T</td><td>C</td><td>G</td><td>C</td><td>T</td><td>C</td><td>A</td></tr>
<tr><td>B</td><td>A</td><td>G</td><td>A</td><td>G</td><td>G</td><td>T</td><td>T</td><td>G</td><td>C</td><td>T</td><td>C</td><td>T</td></tr>
<tr><td>C</td><td>C</td><td>G</td><td>A</td><td>G</td><td>G</td><td>C</td><td>T</td><td>G</td><td>C</td><td>T</td><td>C</td><td>A</td></tr>
<tr><td>D</td><td>T</td><td>G</td><td>A</td><td>G</td><td>G</td><td>C</td><td>T</td><td>C</td><td>G</td><td>T</td><td>C</td><td>A</td></tr>
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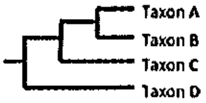
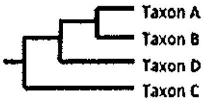
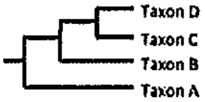
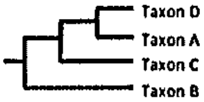
A)


B)


C)


D)


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<tr>
<td>Q8</td>
<td>Given two sequences Seq1: GTGCCT, Seq2: TGCT, and a scoring scheme Match: +1, Mismatch: -1, Gap: -2. Find out the suitable alignment using Needleman-Wunsch algorithm.</td>
<td>5</td>
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<tr>
<td>Q9</td>
<td>Calculate the first corrected distance matrix in construction of a NJ-phylogenetic tree:
<table>
<tr><th></th><th>A</th><th>B</th><th>C</th><th>D</th></tr>
<tr><td>A</td><td></td><td></td><td></td><td></td></tr>
<tr><td>B</td><td>2</td><td></td><td></td><td></td></tr>
<tr><td>C</td><td>4</td><td>4</td><td></td><td></td></tr>
<tr><td>D</td><td>4</td><td>4</td><td>2</td><td></td></tr>
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<td>5</td>
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