

**BIRLA INSTITUTE OF TECHNOLOGY, MESRA, RANCHI
(END SEMESTER EXAMINATION)**

**CLASS: B.TECH.
BRANCH: BIOTECHNOLOGY**

**SEMESTER : III
SESSION : MO/2023**

SUBJECT: BE205 BASICS OF BIOINFORMATICS

TIME: 3 HOURS

FULL MARKS: 50

INSTRUCTIONS:

1. The question paper contains 5 questions each of 10 marks and total 50 marks.
2. Attempt all questions.
3. The missing data, if any, may be assumed suitably.
4. Before attempting the question paper, be sure that you have got the correct question paper.
5. Tables/Data hand book/Graph paper etc. to be supplied to the candidates in the examination hall.

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|---|-----|-----|-----|----|----|---|---|---|---|---|----|----|----|----|----|---|----|----|----|----|----|---|----|----|----|----|----|---|----|----|----|----|----|---|----|----|----|----|----|
| Q.1(a) List five important bioinformatics databases along with brief descriptions for each. | [5] | 1 | 1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q.1(b) What are tuples and attributes in a relational database? Explain with an example. | [3] | 1 | 2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q.1(c) What is the flat file format? List its main advantages and limitations. | [2] | 1 | 1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q.2(a) Perform the alignment of the following sequences using the Smith-Waterman algorithm, considering the specified criteria. Also, write the final alignment(s).
Sequence1: AGCGTAG ; Sequence2: CTCGTC
[Criteria: Match +10, Mismatch -5, Indel -7] | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q.2(b) Write down the appropriate interpretations of the dot matrix plots given below. | [3] | 2 | 4,5 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q.2(c) Imagine we have a sample of 100 cases, 50 healthy and the others patient. If the test has been able to identify 25 of the 50 healthy cases and has reported the others as patients . Calculate sensitivity, and specificity. | [2] | 2 | 4 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q.3(a) Construct the phylogenetic trees for the given distance matrix using the UPGMA method, and report the final tree with all the distances. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <table border="1" style="border-collapse: collapse; width: 100%; text-align: center;"> <tr> <td></td> <td>A</td> <td>B</td> <td>C</td> <td>D</td> <td>E</td> </tr> <tr> <td>A</td> <td>--</td> <td>22</td> <td>39</td> <td>39</td> <td>41</td> </tr> <tr> <td>B</td> <td>--</td> <td>--</td> <td>41</td> <td>41</td> <td>43</td> </tr> <tr> <td>C</td> <td>--</td> <td>--</td> <td>--</td> <td>18</td> <td>20</td> </tr> <tr> <td>D</td> <td>--</td> <td>--</td> <td>--</td> <td>--</td> <td>10</td> </tr> <tr> <td>E</td> <td>--</td> <td>--</td> <td>--</td> <td>--</td> <td>--</td> </tr> </table> | | | | | A | B | C | D | E | A | -- | 22 | 39 | 39 | 41 | B | -- | -- | 41 | 41 | 43 | C | -- | -- | -- | 18 | 20 | D | -- | -- | -- | -- | 10 | E | -- | -- | -- | -- | -- |
| | A | B | C | D | E | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| A | -- | 22 | 39 | 39 | 41 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| B | -- | -- | 41 | 41 | 43 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| C | -- | -- | -- | 18 | 20 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| D | -- | -- | -- | -- | 10 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| E | -- | -- | -- | -- | -- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q.3(b) List the applications of phylogenetic trees and explain the following terms in the context of a phylogenetic tree: i. Branches, ii. Taxa, iii. Node, iv. Root Node. | [5] | 2 | 2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q.4(a) List all the steps of homology modeling in sequential order and explain all the factors that should be considered for template selection. | [5] | 1,2 | 1,2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q.4(b) What is Ramachandran plot? Discuss its importance and explain why glycine and proline have distinct Ramachandran plots compared to other amino acids. | [5] | 2 | 2,4 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q.5(a) How would you approach the design of a drug or vaccine against COVID-19 using computational techniques, detailing the specific steps you would take based on your knowledge of various computational methods and databases discussed in the course? | [5] | 3 | 3,5 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q.5(b) What is cheminformatics? Discuss its importance and list the differences between cheminformatics and bioinformatics. | [5] | 1 | 1,2 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |