

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

**CLASS: BTECH. AND IMSC
BRANCH: BIOTECHNOLOGY AND CHEMISTRY**

**SEMESTER : III
SESSION : MO/2024**

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.

		CO	BL
Q.1(a)	Write the most suitable name (only one) of the biological database for each type of biological content mentioned below: i. Biological Literature ii. Biomolecular Structures iii. Protein Structure Class iv. human genes and genetic phenotypes v. Protein sequence	[5] 1	1
Q.1(b)	Explain the flat file format and relational databases with their importance and limitations.	[5] 1	1,2
Q.2(a)	Perform the alignment of following sequences using the Needleman-Wunsch algorithm taking the following criteria. Also write the final alignment(s). Sequence1: AGC ; Sequence2: AAAC [Criteria: Match +1, Mismatch -1, Indel -2]	[5] 2	3
Q.2(b)	Draw the dot matrix plot patterns for the cases mentioned below: i. Perfect match but not a palindrome ii. Indel iii. Potential homologs iv. Full palindrome v. Internal repeats	[5] 1,2	4,5
Q.3(a)	List the applications of phylogenetic trees and explain the following terms in the context of a phylogenetic tree by illustrating them on phylogenetic tree. i. Branches, ii. Taxa, iii. Node, iv. Root Node	[5] 2,3	1,2
Q.3(b)	Construct all the phylogenetic trees for the following sequences using the Maximum Parsimony method and report the best tree with proper justification. <div style="margin-left: 40px;"> 1 A A G A G T G C A 2 A G C T G T G C G 3 A G A T A T C C A 4 A G A A A T C C G </div>	[5] 2	3
Q.4(a)	Explain and illustrate Ramachandran plots, highlighting their significance and the positions of various secondary structure elements. Identify the amino acids with the smallest and largest allowed regions in Ramachandran plots, and justify your choices based on the structural characteristics of each amino acid.	[5] 1,2	2,5
Q.4(b)	Protein primary structure is governed by _____ bonding; Secondary structure is governed by _____ bonding; Tertiary structure is mainly governed by the thermodynamic property _____. Several _____ combine to form motifs, and several _____ combine to form domains [Select the most appropriate options: Domain, Peptide, Entropy, Secondary structures, Enthalpy, Hydrophobic, Motifs, Hydrogen]	[5] 2	2,3
Q.5	A genome of a newly identified deadly virus has been recently sequenced, posing a significant threat to humanity. As a computational biologist, you are tasked with identifying potential drugs or vaccines against this virus. Using the techniques discussed in bioinformatics, cheminformatics, immunoinformatics, and metagenomics explain how you would approach this challenge. <ol style="list-style-type: none"> 1. Design a flowchart illustrating the step-by-step process of drug or vaccine development starting from the genome sequence of the virus. 2. Provide a detailed explanation of each step outlined in the flowchart. 	[10] 1-3	4-6