

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

CLASS: MSc
BRANCH: BIOTECHNOLOGY

SEMESTER : II
SESSION : SP/2025

SUBJECT: BT417 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) Describe the sequence file format with example and how different from molecular file format with example. [5]
- Q.1(b) Describe the levels of SCOP database with example. [5]
- Q.2(a) Write note on PAM and BLAST [5]
- Q.2(b) Do the local alignment for the following sequences, seq1:GTACC seq2: ATAGC with match=1, gap=0 and mismatch= -2 [5]
- Q.3(a) Define molecular clock, clade, rooted tree, homologous, node [5]
- Q.3(b) Construct the tree using UPGMA method with proper methodology and steps using the following distance matrix. [5]

	Macaw	Cockatails	Parrot	Amazons
Macaw	0			
Cockatails	8	0		
Parrot	7	9	0	
Amazons	12	14	11	0

- Q.4(a) If a reference protein structure is available in PDB then how you can model a new structure. Write the steps and discuss. [5]
- Q.4(b) How secondary structure can be predicted using Chou-Fasman method? [5]
- Q.5(a) How cheminformatics can be utilized for new drug development? [5]
- Q.5(b) What is microarray and state its application [5]

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