

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

CLASS: MSc / PRE-PHD  
BRANCH: BIOTECHNOLOGY

SEMESTER: II / NA  
SESSION: SP/2023

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) State the different levels of protein structure in SCOP database with example. What is the difference between sequence and structure database? [5] CO1 BL
- Q.1(b) Define database based on data source. What are the main functions of database? What is DDL and DML? [5] CO2
- Q.2(a) Write note on PAM matrix and BLAST algorithm. [5] CO2
- Q.2(b) Do global alignment of the following two sequences ABDEF and AADDF with match=1, mismatch=0 and gap=-1. Show all the alignments option. [5] CO4
- Q.3(a) Compare cladistic and distance method for phylogenetic analysis. What is Boot strap method [5] CO3
- Q.3(b) Construct tree using UPGMA method (write the steps) [5] CO4

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

- Q.4(a) How propensity value can be used for second structure prediction? What is Chau-Fashman method? [5] CO3
- Q.4(b) If an unknown protein structure is provided to you then how structural modelling can be used to help? [5] CO3
- Q.5(a) What is MEME? Describe about first generation of sequencing. [5] CO2
- Q.5(b) Write the principle and steps of drug designing with flowchart. [5] CO3

::::::26/04/2023::::::E