

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

**CLASS: MSC.(BT) / PRE-PHD  
BRANCH: BIOTECH**

**SEMESTER : II / NA  
SESSION : SP/2022**

**SUBJECT: BT417 BIOINFORMATICS**

**TIME: 2 HOURS**

**FULL MARKS: 50**

**INSTRUCTIONS:**

- 1. The question paper contains 14 questions each of 5 marks and total 70 marks.**
  - 2. Candidate may attempt any 10 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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1. What is primary and secondary database? State the characteristics of biological database.
2. Classify biological database depending on data types. State the different levels of protein structure in CATH database.
3. How relational database is beneficial than another database? How protein sequence information is stored in GenBank file format.
4. With proper flowchart write the stages of motif finding in MEME suite.
5. What is propensity value regarding CHAU-FASHMAN method? Describe the methodology.
6. Classify protein structure on the basis of SCOP database with example and diagram.
7. Write the steps Sanger's method of sequencing. What is the significance of microarray analysis in biotechnology?
8. Compare local and global sequence alignment, PAM and BLOSUM, NJ and UPGMA method.
9. Do the steps of performing local alignment (Smith Waterman) for following two sequences (ABCD and AACD) with match=2, mismatch=-1 and gap=0.
10. Write short notes: Dotplot with palindromic sequence, Phylogenetic tree.
11. Construct the tree using UPGMA method with proper methodology and steps using the following distance matrix

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

12. If you are having a protein sequence of catalase but not structure available in database then how you can predict the 3D structure? State the steps with diagram. What is the importance of the said principle?
13. Write note on computer aided drug designing approach. How cheminformatics is applicable to healthcare sector?
14. What is heuristic method of sequence alignment? With diagram describe BLAST algorithm for sequence alignment

11/05/2022 E