

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

CLASS: BTECH  
BRANCH: BIOTECHNOLOGY

SEMESTER : III  
SESSION : MO/2022

SUBJECT: BE205R1 BASICS OF BIOINFORMATICS

TIME: 3:00 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) Differentiate primary and secondary databases with example in bioinformatics. [2]  
Q.1(b) Designate in terms of data content and application of followings information resources and databases: NCBI, RCSB and CATH [3]  
Q.1(c) Write following file formats with example \*.fasta, \*.pdb, \*.genbank, and \*.dnd. [5]

- Q.2(a) Differentiate the substitution matrix PAM and BLOSUM with proper application. [2]  
Q.2(b) Compose the sequence searching algorithm BLAST stepwise. What is tBLAST? [3]  
Q.2(c) What is Sum of pairs method in multidimensional dynamic programming? [5]  
Using N-W algorithm for Global Alignment used in Dynamic Programming, complete the following alignment matrix (array) and predicts the possible alignment, (mismatch :-2, match: +2; Gap penalty: -2)

0	T (-2)	C (-4)	G (-6)	A(-10)
T (-2)				
C (-4)				
C(-6)				
A(-8)				

- Q.3(a) Theorize with example: Dendogram and Kimura 2P model of DNA substitution with transversion and transition. [2]  
Q.3(b) For the following individual pairwise distances, construct the phylogenetic tree using UPGMA method, (ab:16; ac:32; ad:48; bc28; bd:42; cd:12). [3]  
Q.3(c) What is molecular clock? Synthesize the stepwise methodology for building phylogenetic tree, Fitch-Margolish method OR maximum parsimony method. [5]
- Q.4(a) Originate and illustrate RMSD value and Ramachandran plot. [2]  
Q.4(b) Develop and state the algorithms for Protein secondary structure prediction methods: Chou-Fasman method. [3]  
Q.4(c) Write algorithms/flow-chart for Homology modelling for protein structure prediction. What is SCOP? [5]
- Q.5(a) Briefly discuss Chemoinformatics with different applicable softwares. [2]  
Q.5(b) Briefly introduce Systems Biology. [3]  
Q.5(c) Build the position specific scoring matrix (PSSM) for following motif, ctata atagg; cagcc; cgggt; tgcac. [5]