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

CLASS: IMSC & PRE-PHD **SEMESTER : VII**
BRANCH: MATHS & COMP. **SESSION : MO/2022**

SUBJECT: BT417 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.

Q.1(a) What are Primary and Secondary databases of Nucleic acids and Protein? [2]
Q.1(b) Briefly describe following databases: CATH, NCBI and RCSB. [3]
Q.1(c) Illustrate the following bio-file formats with details: .fasta, .pdb, .genbank and .dnd. [5]

Q.2(a) For the following two sequences, Calculate to total score with linear and affine gap penalty: [mismatch :-2, match: +2; Gap opening penalty -2 and gap extension penalty -1] [2]

s	T	C	A	G	A	C	G	A	G	T	G
t	T	C	—	G	A	G	C	T	G	—	—

Q.2(b) Compose the sequence searching algorithm FASTA stepwise (theory and types). [3]
Q.2(c) Differentiate the substitution matrix PAM and BLOSUM with proper application. Build the phylogenetic tree using UPGMA method for the following individual pairwise distances, (pq:8; pr:28; ps:44; qr:28; qs:36; rs:12). [5]

Q.3(a) What are the differ methods for multiple sequence alignment and phylogenetic tree plotting? [2]
Q.3(b) Using Needleman-Wunsch algorithm used in Dynamic Programming, complete the following alignment matrix (array) and predicts the possible alignment, [Match: +2; mismatch: -2, linear GAP penalty: -1] [3]

0	T (-1)	C (-2)	G (-3)	C (-4)
T (-1)				
C (-2)				
C(-3)				

Q.3(c) Synthesize the stepwise methodology for building phylogenetic tree: Neighbor Joining method and maximum parsimony method with proper example. [5]

Q.4(a) What are RMSD value and Ramachandran plot related to protein structure? [2]
Q.4(b) Compose the stepwise methodology for Chou-Fasman method for prediction of secondary structures. [3]
Q.4(c) What is Homology Modelling? Briefly discuss different components of Cheminformatics. [5]

Q.5(a) What is sequence logo? [2]
Q.5(b) Construct the schematic of Next generation sequencing (NGS) of DNA using Pyro-sequencing. [3]
Q.5(c) Build the PSSM for following motif, ctataa; atagcg; cagccc; cggtat; tgcatt. Also calculate the motif similarity index for motif 'tatcc'. [5]

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