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

CLASS: BE **SEMESTER : III**
BRANCH: BT **SESSION : MO/19**

SUBJECT: BE205 BASICS OF BIOINFORMATICS

TIME: 3.00Hrs. **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, Composite, and Secondary databases of Nucleic acids and Protein? [5]
Briefly describe following databases: CATH, NCBI; TIGR, RCSB.

Q.1(b) Illustrate four different file formats used in bioinformatics to restore information regarding sequences and structures with example. [5]

Q.2(a) Compose the sequence searching algorithm FASTA stepwise (theory and types). [5]
For the following two sequences, Calculate to total score with linear and affine gap penalty: [mismatch :-4, match: +8; Gap opening penalty -2 and gap extension penalty -1]

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

Q.2(b) 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 :-4, match: +8; Gap penalty:2

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

Q.3(a) Evaluate the followings: molecular clock, Phylogenetic tree, DNA substitution model. [5]

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

Q.4(a) What is protein secondary and quaternary structures formation? Develop and state the algorithms for Protein secondary structure prediction methods: PSI-Pred using neural networks (ANN). [5]

Q.4(b) Evaluate RMSD value, Propensity and Ramachandran plot. Write algorithms for the Homology modelling for protein sequence analysis. [5]

Q.5(a) Briefly discuss Chemoinformatics and System Biology with different softwares. [5]

Q.5(b) What are different super secondary structures of protein? Build the position weight matrix using log odd values (PWM) for following motif, ataaac agcgat; gcccag; gtatac; cattca. Also calculate the motif similarity index for motif tcctca. [5]

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