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

CLASS: MSc   SEMESTER : II
BRANCH: BIOTECHNOLOGY   SESSION : SP/19

SUBJECT: BT417 BIOINFORMTICS

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.

Q.1(a)   Summarize different types of biological databases. Describe followings information resources and   [5]
         databases: NCBI, EMBL, RCSB, KEGG and Expasy.
Q.1(b)   Illustrate four different file formats used in bioinformatics with example.   [5]

Q.2(a)   For the following two sequences, find out three possible alignments and Calculate optimal alignment, [5]
         [mismatch :-2, match: +4 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	G	A	G	C	T	G		

         Compose the sequence searching algorithm BLAST stepwise (theory and types).
Q.2(b)   Differentiate dynamic programming Needleman-Wunsch and Smith-Waterman algorithm including   [5]
         application. For the following individual pairwise distances, construct the phylogenetic tree using
         UPGMA method, (ab:5; ac:30; ad:45; bc28; bd:42; cd:10).

Q.3(a)   Hypothesize with example: dendrogram, molecular clock and different substitution of model DNA.   [5]
Q.3(b)   Synthesize the stepwise methodology for building phylogenetic tree, Fitch-Margolish method and   [5]
         maximum likelihood method.

Q.4(a)   What are secondary structures of protein? Compose the Chou-Fasman method for prediction of   [5]
         secondary structures. Briefly Illustrate Homology modelling for structure prediction from protein
         sequence.
Q.4(b)   Originate and illustrate RMSD value and Ramachandran plot. Develop and state the algorithms for   [5]
         distance alignment (DALI) search tools.

Q.5(a)   What is pattern and profile for motif? Build the PSSM or PWM for following motif, ctataaac   [5]
         atagcgat; cagcccag; cggtatac; tgcattca. Also calculate the motif similarity index for motif tatcctt.
         Compose Gibbs sampling method for motif findings.
Q.5(b)   Summarize the different methods used in Next generation sequencing of DNA and microarray data   [5]
         analysis.

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