

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

**CLASS: BTECH
BRANCH: BIOTECHNOLOGY**

**SEMESTER: III
SESSION : MO/2019**

SUBJECT : BE205 BASICS OF BIOINFORMATICS

TIME: 2.00 HOURS

FULL MARKS: 25

INSTRUCTIONS:

1. The total marks of the questions are 25.
 2. Candidates may attempt for all 25 marks.
 3. Before attempting the question paper, be sure that you have got the correct question paper.
 4. The missing data, if any, may be assumed suitably.
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Q1 (a) Describe followings information resources and databases: NCBI, EMBL, RCSB, SGD, TIGR and SCOP. [2]

Q1 (b) Demonstrate four different formats used in bioinformatics databases with example. [3]

Q2 (a) For the following two sequences, find out three possible alignments and Calculate optimal alignment, [mismatch :-2, match: +4 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	G	A	G	C	T	G			

Q2 (b) Compose the sequence searching algorithm BLAST stepwise (theory and types). What is E-value? [3]

Q3 (a) Differentiate the matrix PAM and BLOSUM with proper application. [2]

Q3 (b) Using Needleman-Wunsch algorithm used in Dynamic Programming, complete the following alignment matrix (array) and predicts the possible alignment, [Match : +4; mismatch: -4, linear GAP penalty: -2]

0	A (2)	G (4)	C (6)
A (2)			
G (4)			
G(6)			

Q4 (a) Theorize with example: molecular clock, transversion and dendogram. [2]

Q4 (b) For the following individual pairwise distances, construct the phylogenetic tree using UPGMA method, (ab:5; ac:30; ad:45; bc28; bd:42; cd:10). [3]

Q5 (a) Hypothesize different substitution of model DNA. [2]

Q5 (b) Synthesize the stepwise methodology for building phylogenetic tree, Fitch-Margolish method. [3]