

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

**CLASS: BTECH  
BRANCH: BIOTECHNOLOGY**

**SEMESTER: III  
SESSION: MO/2022**

**SUBJECT: BE205R1 BASICS OF BIOINFORMATICS**

**TIME: 2 HOURS**

**FULL MARKS: 25**

**INSTRUCTIONS:**

1. The total marks of the questions are 25.
2. Candidates 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.
5. Tables/Data handbook/Graph paper etc. to be supplied to the candidates in the examination hall.

- Q1 (a) Differentiate primary and secondary databases with example in bioinformatics. [2]  
 Q1 (b) Demonstrate the pattern of the following file formats with example \*.fasta, \*.pdb, \*.gb (genbank) [3]

- Q2 (a) For the following two sequences, Calculate to total score with linear and affine gap penalty: [2.5]  
 [mismatch :-4, match: +8; Gap opening penalty -2 and gap extension penalty -1]

A	T	C	A	G	A	C	G	A	G	T	G
A	T	C	—	G	A	G	C	T	—	—	—

- Q2 (b) Differentiate the substitution matrices PAM and BLOSUM. [2.5]

- Q3 (a) 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) [3]

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

- Q3 (b) Illustrate DOT matrix plot with example. [2]

- Q4 (a) Compare Needleman-Wunch algorithm with Smith-Waterman algorithm for Dynamic Programming. [2.5]

- Q4 (b) Synthesize the stepwise methodology for performing FASTA database searching method [2.5]

- Q5 (a) Compose the sequence searching algorithm BLAST stepwise. [3]

- Q5 (b) What are different types of BLAST program? What is E-value? [2]