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

CLASS: M.Sc. SEMESTER : II
BRANCH: BIO-ENGINEERING AND BIOTECHNOLOGY SESSION : SP/2025

SUBJECT: BI201-BIOLOGICAL SEQUENCE ANALYSIS AND ALGORITHMS

TIME: 3 Hours FULL MARKS: 50

INSTRUCTIONS:
1. The question paper contains 5 questions each of 10 marks and a 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.

			CO	BL
Q.1(a)	What do you mean by Sequence Similarity Searching? Describe the algorithm of BLAST.	[5]	1	1
Q.1(b)	Give a brief account on Position Specific Scoring Matrix and its application in database searching.	[5]	1	1
Q.2(a)	What is Pairwise and Multiple Sequence Alignment? Describe the algorithm of ClustalW/X.	[5]	2	2
Q.2(b)	Describe HMM in Bioinformatics.	[5]	2	3
Q.3(a)	What is Genome and Genomics? Explain any one method of gene prediction.	[5]	2	2
Q.3(b)	What are synonymous codons? Explain how ORF are used for gene discovery.	[5]	2	2
Q.4(a)	What is the Dot Plot method? Explain how stringency and window-size affect the dotplot results. Mention a few of its applications in Bioinformatics.	[5]	2	1
Q.4(b)	What is a PROSITE database? Explain how MSA is used to build prosite databases.	[5]	2	1
Q.5(a)	What is molecular Phylogenetics ? Explain with example the UPGMA method of phylogenetic tree reconstruction.	[5]	3	2
Q.5(b)	What is bootstrapping? How is it useful in phylogenetics?	[5]	3	2

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