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

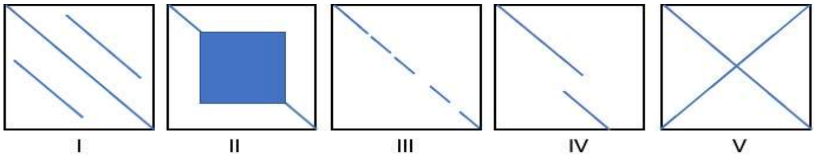
CLASS:	**MSC/PRE-PHD**	**SEMESTER : II/I**
BRANCH:	**BIOTECH**	**SESSION : SP/2024**

SUBJECT: BT417 BIOINFORMATICS

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.

			CO	BL
Q.1(a)	Briefly describe the following databases with respect to biological content. i. PubMed ii. PDB iii. Swiss-Prot iv. Expasy v. SCOP	[5]	1	1
Q.1(b)	What is the necessity of multiple sequence alignments (MSA)? Briefly explain the three main classifications of MSA methods.	[5]	1,2	2,3
Q.2(a)	Interpret the dot matrix plots shown below, and provide examples of hypothetical sequences that could generate these dot matrix plots.	[5]	2,3	4,5



Q.2(b)	Perform the alignment of following sequences using the Needleman-Wunsch algorithm taking the following criteria. Also write the final alignment(s). Sequence1: AGT ; Sequence2: AAGC ; [Match: +1, Mismatch: -1, Gap: -2]	[5]	1,2	3
Q.3(a)	List the applications of phylogenetic trees and explain the following terms in the context of a phylogenetic tree by illustrating them on phylogenetic tree. i. Branches, ii. Taxa, iii. Node, iv. Root Node.	[5]	2,3	1,2
Q.3(b)	Construct the phylogenetic trees for the given distance matrix using the UPGMA algorithm, and report the final tree with all the distances.	[5]	2	3

	A	B	C	D	E
A	-	22	39	39	41
B	-	-	41	41	43
C	-	-	-	18	20
D	-	-	-	-	10
E	-	-	-	-	-

Q.4(a)	What is Ramachandran plot? Discuss its importance and explain why glycine and proline have distinct Ramachandran plots compared to other amino acids.	[5]	3,4	2,4
Q.4(b)	List all the steps of homology modeling in sequential order and explain all the factors that should be considered for template selection.	[5]	3,4	1,2
Q.5(a)	Explain one of the topics mentioned below, along with its applications and limitations. i) Docking ii) Pharmacophore iii) QSAR iv) Microarray v) NGS vi) Motif Analysis	[5]	3	2
Q.5(b)	Imagine a situation like COVID-19 where we were dire need of drug/vaccine, in such scenario how you will utilize the bioinformatics techniques mentioned in question number 5a and design a personalized drug/vaccine. Provide a detailed technical explanation of the computational methodologies, databases involved, accompanied by a concise flowchart detailing each step.	[5]	1,3,4	3,5

::::::25/04/2024:::::E