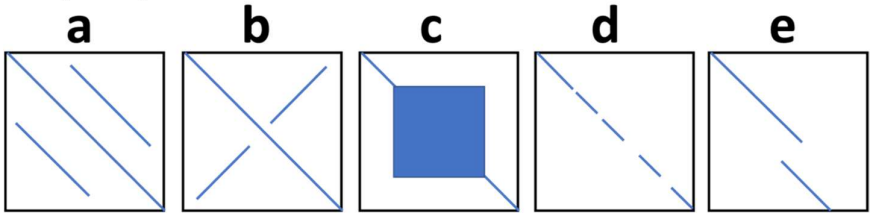
BIRLA INSTITUTE OF TECHNOLOGY, MESRA, RANCHI
(MID SEMESTER EXAMINATION)

CLASS: B. TECH./BSC **SEMESTER : III/ADD**
BRANCH: BIOTECHNOLOGY/CHEMISTRY **SESSION : MO/2025**

SUBJECT: BE24244/BE205 BASICS OF BIOINFORMATICS

TIME: 02 HOURS **FULL MARKS: 25**

INSTRUCTIONS:
1. The question paper contains 5 questions each of 5 marks and total 25 marks.
2. Attempt all questions.
3. The missing data, if any, may be assumed suitably.
***4*. Tables/Data handbook/Graph paper etc., if applicable, will be supplied to the candidates**

			CO	BL
Q.1	For each of the following categories, enlist **one appropriate database**. Be careful, some categories may have multiple databases, but only the one most relevant to the specific type should be chosen: **1.** Biomolecular 3D structure **2.** Gene Expression **3.** functional annotation of metabolic pathways **4.** conserved motif **5.** Nucleotide sequences	[5]	1	1
Q.2(a)	Enlist the limitations of the flat file format.	[2]	1	1
Q.2(b)	What are the three major classifications of the biological databases in terms of data source?	[3]	1	1
Q.3(a)	Enlist and explain all four hierarchical levels used in the CATH database.	[2]	1	1
Q.3(b)	Why do we need an amino acid substitution matrix in sequence alignment? Explain with a clear example. Now, if you are aligning two protein sequences that are extremely similar, which matrix BLOSUM80 or PAM250 would be more appropriate? Justify your answer with reasoning.	[3]	2	1,2
Q.4	Consider the following dot plots. Select the most appropriate choice for each plot from the options given below:  **1.** Low complexity region **2.** Tandem repeat **3.** Enzyme restriction site **4.** Potential homologous sequences **5.** Indel	[5]	2	4
Q.5	Perform the pairwise global alignment using the Needleman–Wunsch algorithm. Use the following scoring scheme: **(Match +1, Mismatch -1, Gap Penalty -1).** Also, report the final optimal alignment(s). Seq-1: **GATTAC** Seq-2: **GATAC**	[5]	2	3

:::::23/09/2025 :::::E