CUET PG 2026 Bioinformatics Question Paper(Memory Based)

Time Allowed :1 Hour 30 Mins	**Maximum Marks :**300	**Total Questions :**75

General Instructions

Read the following instructions very carefully and strictly follow them:

- The exam lasts 90 minutes (1 hour 30 minutes).
- There are 75 Multiple Choice Questions (MCQs) to be answered.
- +4 marks for every correct answer. -1 mark (negative marking) for every incorrect answer. 0 marks for unanswered or un-attempted questions.
- For any discrepancy in questions, the English version is considered final (except for language-specific papers).
- Click one of the four options to choose an answer.
- You must click "Save & Next" to confirm your response. Only saved answers are considered for evaluation.
- Use "Mark for Review & Next" to flag a question for later. You can unselect or change your answer using the "Clear Response" button.
- All calculations must be done on the Rough Sheets provided at the centre. These must be returned to the invigilator after the exam.

1. Which algorithm is used for performing Global Sequence Alignment?
(A) Smith–Waterman Algorithm
(B) Needleman–Wunsch Algorithm
(C) BLAST Algorithm
(D) FASTA Algorithm

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2. What is the primary difference between PAM and BLOSUM scoring matrices?
(A) PAM matrices are based on global alignments, while BLOSUM matrices are based on local alignments
(B) PAM matrices are used only for DNA sequences, while BLOSUM matrices are used for proteins
(C) PAM matrices are derived from highly divergent sequences, while BLOSUM matrices use closely related sequences
(D) PAM matrices are heuristic methods, while BLOSUM matrices use dynamic programming

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3. Which biological database is considered a curated, secondary database for protein sequences?

(A) GenBank
(B) UniProtKB/Swiss-Prot
(C) EMBL
(D) DDBJ

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4. In the Michaelis-Menten equation, what does the constant K_m represent?
(A) Maximum reaction velocity
(B) Substrate concentration at half of V_{max}
(C) Enzyme concentration
(D) Rate of enzyme degradation

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5. Which amino acid is responsible for forming disulfide bridges in a protein structure?
(A) Glycine
(B) Cysteine
(C) Lysine
(D) Alanine

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6. What is the specific function of the BLASTn program?
(A) Compare protein sequences
(B) Compare nucleotide sequences
(C) Predict protein structure
(D) Align protein structures

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7. Which tool is most commonly used for Multiple Sequence Alignment (MSA)?
(A) BLAST
(B) ClustalW
(C) FASTA
(D) Needleman–Wunsch

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8. The p53 protein is primarily known for which cellular role?
(A) DNA replication
(B) Tumor suppression
(C) Protein synthesis
(D) Cell membrane transport

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9. Which molecular technique is used to detect specific mRNA molecules in a sample?

(A) Southern Blot
(B) Northern Blot
(C) Western Blot
(D) PCR

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10. In computer science, what does the Markov Property assume about future states?
(A) Future states depend on all previous states
(B) Future states depend only on the current state
(C) Future states depend only on the initial state
(D) Future states are completely random

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11. Which database serves as the main archive for 3D macromolecular structures?
(A) GenBank
(B) Protein Data Bank (PDB)
(C) UniProt
(D) EMBL

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12. What is the purpose of Emulsion PCR (ePCR) in Next-Generation Sequencing?
(A) To sequence DNA directly without amplification
(B) To amplify individual DNA fragments in isolated microreactors
(C) To detect proteins in sequencing samples
(D) To separate RNA molecules from DNA

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13. Which component is strictly part of a Microprocessor System Unit, excluding peripherals?
(A) Keyboard
(B) Monitor
(C) CPU
(D) Printer

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14. How does a 2D array differ from a 1D array in a programming language like C++?
(A) A 2D array stores characters only
(B) A 2D array has rows and columns
(C) A 2D array stores only integers
(D) A 2D array cannot store multiple values

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15. Which type of bond characterizes the primary structure of DNA?
(A) Hydrogen bond
(B) Ionic bond
(C) Phosphodiester bond
(D) Disulfide bond
