



18053



BRAINWARE UNIVERSITY

Term End Examination 2025-2026

Programme – M.Sc.(BT)-2024

Course Name – Bioinformatics

Course Code - MBT30210

(Semester III)

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Brainware University
Barasat, Kolkata -700125

Full Marks : 60

Time : 2:30 Hours

[The figure in the margin indicates full marks. Candidates are required to give their answers in their own words as far as practicable.]

Group-A

(Multiple Choice Type Question)

1 x 15=15

1. Choose the correct alternative from the following :

- (i) Indicate the application of bioinformatics used in analyzing RNA expression levels across different conditions.
 - a) Genomic Sequencing
 - b) Proteomics
 - c) Transcriptomics
 - d) Phylogenetics
- (ii) Name the repository established in 1971 for storing three-dimensional protein structures.
 - a) GenBank
 - b) EMBL
 - c) Protein Data Bank
 - d) SWISS-PROT
- (iii) Classify the following databases based on their primary focus: PDB.
 - a) Protein Sequences
 - b) Protein Structures
 - c) Nucleotide Sequences
 - d) Metabolic Pathways
- (iv) Decide which algorithm is used for predicting protein-ligand binding affinity.
 - a) AutoDock Vina
 - b) Glide
 - c) GOLD
 - d) FlexX
- (v) Decide which database is the best choice for storing whole-genome sequences.
 - a) ENSEMBL
 - b) NCBI GenBank
 - c) DDBJ
 - d) UCSC Genome Browser
- (vi) Decide which method is best for predicting protein secondary structure.
 - a) Chou-Fasman
 - b) GOR
 - c) PSIPRED
 - d) HMMTOP
- (vii) Decide which of the following bioinformatics tools is best suited for protein sequence alignment.
 - a) BLAST
 - b) ClustalW
 - c) FASTA
 - d) HMMER
- (viii) Decide which of the following is an unsupervised machine learning method used in bioinformatics.

- a) K-means
c) Random Forest
- b) SVM
d) Naive Bayes
- (ix) Choose the most accurate method for RNA-Seq data normalization.
- a) TPM
c) RPKM
- b) FPKM
d) DESeq
- (x) Indicate the main purpose of the Protein Data Bank (PDB).
- a) To store DNA sequences
c) To store protein family classifications
- b) To store 3D structures of proteins
d) To store bibliographic references
- (xi) Identify the secondary database that provides information on protein families, domains, and functional sites.
- a) ProSite
c) Protein Data Bank
- b) UniProtKB/Swiss-Prot
d) PInTFDB
- (xii) Define what a gap represents in sequence alignment.
- a) A region of high similarity
c) An insertion or deletion event in one of the sequences
- b) A mismatch between aligned residues
d) A region with no sequence data
- (xiii) Determine what each cell in the alignment matrix represents in dynamic programming for sequence alignment.
- a) The score for aligning the corresponding subsequences up to that point
c) The number of gaps in the sequences
- b) The final alignment scores
d) The total number of matching residues between sequences
- (xiv) Choose the correct statement about the Dot Matrix method.
- a) It guarantees an optimal alignment
c) It is a visual method that can be computationally intensive
- b) It requires a scoring matrix
d) It is faster than dynamic programming methods
- (xv) Indicate the key assumption behind homology modeling.
- a) Proteins with similar sequences have similar structures.
c) Protein structures evolve independently of their sequences.
- b) All proteins fold in a predictable manner regardless of sequence.
d) Protein folding depends entirely on solvent interactions.

Group-B

(Short Answer Type Questions)

3 x 5=15

2. Write the key features of the EMBL file format. (3)
3. Distinguish the affine gap penalty function from constant and linear gap penalties. (3)
4. Describe the interactions that stabilize tertiary structures in proteins. (3)
5. Explain the role of bioinformatics in genomic data management and analysis. (3)
6. Explain the challenges of structural analysis using PDB. (3)

OR

Analyze the role of UniProt in protein research. (3)

Group-C

(Long Answer Type Questions)

5 x 6=30

7. Describe the applications of bioinformatics in proteomics and functional genomics, emphasizing the importance of these fields in biological research. (5)
8. Summarize the process of protein identification in proteomics. (5)
9. Evaluate the main features and functions of the Protein Data Bank (PDB) and its significance in the field of structural biology. (5)
10. Report and describe the bioinformatics tools available for structural class prediction and modeling. (5)

11. Compare and contrast globular proteins and integral membrane proteins in terms of their structural characteristics and functions. How do their environments influence their structural features? (5)
12. Analyze the applications of metabolomics in disease diagnosis. (5)
- OR**
- Analyze the role of quantitative proteomics. (5)

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