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Brainware University
Barasat, Kolkata -700125**Term End Examination 2025-2026****Programme – B.Tech.(BT)-2024****Course Name – Bioinformatics****Course Code - BTB40201A****(Semester IV)****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) State the approximate number of protein-coding genes in humans.
 - a) 5,000
 - b) 10,000
 - c) 20,000–25,000
 - d) 100,000
- (ii) Locate the database that stores three-dimensional protein structures.
 - a) UniProt
 - b) Protein Data Bank
 - c) MEDLINE
 - d) GenBank
- (iii) Interpret the significance of non-coding DNA revealed by the HGP.
 - a) Non-coding DNA has regulatory and functional roles
 - b) Non-coding DNA codes for enzymes
 - c) Non-coding DNA has no biological importance
 - d) Non-coding DNA is absent in humans
- (iv) Shotgun DNA sequencing involves which key step?
 - a) RNA synthesis
 - b) Random fragmentation followed by assembly
 - c) Direct sequencing of whole genome
 - d) Protein translation
- (v) Similarity observed in aligned sequences often indicates:
 - a) Random chance
 - b) Homology due to common ancestry
 - c) Sequence contamination
 - d) Experimental error
- (vi) Why is dynamic programming computationally expensive?
 - a) Evaluates all possible alignment paths
 - b) Requires experimental validation
 - c) Uses large databases
 - d) Uses visualization tools
- (vii) What does an outgroup help determine in a phylogenetic tree?
 - a) Root and direction of evolution
 - b) Branch length
 - c) Sequence length
 - d) Bootstrap value
- (viii) Which type of tree explicitly shows evolutionary distance using branch lengths?

- a) Phylogram
 c) Cladogram
 (ix) Which method is most appropriate for large datasets without assuming a molecular clock?
 a) Neighbour-Joining
 c) Cladistics
 (x) Homology modeling is based on the assumption that:
 a) All proteins are unique
 c) Folding is random
 (xi) Fold recognition is particularly useful when sequence similarity is:
 a) Absent
 c) Low but structural folds are conserved
 (xii) CASP is important because it:
 a) Benchmarks structure prediction methods
 c) Aligns proteins
 (xiii) Why is energy minimization a prerequisite for docking and MD simulations?
 a) To calculate entropy
 c) To remove steric clashes and stabilize geometry
 (xiv) Why are tools like RasMol and SwissPDB Viewer important for beginners?
 a) They generate force fields
 c) They provide intuitive structure visualization and analysis
 (xv) Why is QSAR considered a powerful tool in lead optimization?
 a) It replaces synthesis
 c) It predicts structure
- b) Dendrogram
 d) Unrooted tree
 b) Maximum parsimony
 d) UPGMA
 b) Structure determines sequence
 d) Similar sequences have similar structures
 b) Very high
 d) Irrelevant
 b) Stores structures
 d) Predicts sequences
 b) To add solvent molecules
 d) To predict binding affinity
 b) They predict QSAR
 d) They perform docking
 b) It ignores chemistry
 d) It correlates molecular features with biological activity

Group-B

(Short Answer Type Questions)

3 x 5=15

2. Interpret why different phylogenetic methods may produce different tree topologies. (3)
3. Demonstrate how a Ramachandran plot is used to assess protein model quality. (3)
4. List any three major applications of bioinformatics. (3)
5. Illustrate the role of gap penalties in sequence alignment scoring. (3)
6. Evaluate the role of molecular recognition principles in achieving drug selectivity. (3)

OR

Critically assess the impact of CADD on reducing drug discovery cost and time. (3)

Group-C

(Long Answer Type Questions)

5 x 6=30

7. Evaluate the applications of PSI-BLAST in detecting distant homologs. (5)
8. Examine how Newick format facilitates phylogenetic tree storage and exchange. (5)
9. Explain the principles of X-ray crystallography and NMR spectroscopy in protein structure determination. (5)
10. Describe the Human Genome Project highlighting its goals, major findings, and impact. (5)
11. Summarize the complete workflow of shotgun DNA sequencing with emphasis on alignment. (5)
12. Analyze the role of energy minimization and molecular dynamics in refining protein structures. (5)

OR

Analyze how molecular graphics tools support rational drug design workflows. (5)