Enrolment No./ Seat No.: _____

GUJARAT TECHNOLOGICAL UNIVERSITY

POST GRADUATE DIPLOMA IN BIOINFORMATICS - SEMESTER – I EXAMINATION – WINTER - 2025

Subject Code: 1310104 **Date: 29-12-2025**

Subject Name: Bioinformatics

Time: 10:30 AM TO 01:00 PM **Total Marks: 70**

Instructions:

1. **Attempt all questions.**
2. **Make suitable assumptions wherever necessary.**
3. **Figures to the right indicate full marks.**
4. **Draw neat and clean diagrams as required.**

Q.1 **Write a note on following** **(Marks-10X2=20)**

1. Primary vs. Secondary Databases in Bioinformatics.
2. Evaluate the importance of sequence file formats in bioinformatics workflows. Discuss challenges in converting formats.
3. Substitution Scores and Gap Penalties in Sequence Alignment.
4. Ramachandran Plot and its significance in structural biology.
5. Limitations of BLAST for sequence similarity searches in large, repetitive genomes.
6. DNA Barcoding and its limitations.
7. The role of molecular mechanics in the prediction of ligand binding affinity for drug design.
8. Principles of Homology Modeling.
9. The significance of scoring matrices like PAM and BLOSUM in sequence alignment.
10. Explain the key features of the Molecular Modelling Database (MMDB) and its applications in bioinformatics.

Q.2 **Answer the following (Any 2 out of 3)** **(Marks-2X10=20)**

1. Explain the concept of multiple sequence alignment. Discuss methods such as ClustalW and MUSCLE.
2. Analyze the process of phylogenetic tree construction using Maximum Likelihood and Neighbor-Joining methods.
3. Design an experimental workflow for receptor-ligand interaction analysis in structure-based drug design.

Q.3 **Answer the following (Any 6 out of 8)** **(Marks-6X5=30)**

1. Evaluate the role of Protein Data Bank (PDB) in structural biology research.
2. Compare and contrast the Chou-Fasman and GOR methods for protein secondary structure prediction.
3. Evaluate the computational challenges of building a phylogenetic tree using Maximum Likelihood methods for large datasets.
4. Propose an approach for analyzing microarray data to identify differentially expressed genes.
5. Critically assess the role of CASP in advancing protein structure prediction methods.
6. Discuss the integration of transcriptomics and proteomics data in systems biology.

7. Interpret a Ramachandran map and its implications for protein folding.
8. Develop a QSAR model to predict the biological activity of a new compound.

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