Seat No.: _____ Enrolment No._____

GUJARAT TECHNOLOGICAL UNIVERSITY

M.SC. INDUSTRIAL BIOTECHNOLOGY(IB) /POST GRADUATE DIPLOMA IN BIOINFORMATICS (DB) - SEMESTER - 1 EXAMINATION - WINTER - 2023

Subject Code:1310104 **Date: 15 Dec 2023**

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. Significance of sequence annotation in Bioinformatics
2. Role and importance of primary databases in molecular biology research.
3. Distinguish Protein Data Bank (PDB) and Molecular Modelling Database (MMDb) in terms of content and usage in Bioinformatics.
4. Impact of low complexity regions and repetitive elements on sequence alignment accuracy.
5. Gap penalties in sequence alignment, and how do they affect the alignment results?
6. Concept of bootstrapping and its role in assessing the reliability of phylogenetic trees.
7. Significance of the Ramachandran map in the context of protein structure validation and quality assessment.
8. Structural and functional significance of specific phi, and psi torsion angles in proteins.
9. Fundamental concepts of molecular mechanics and force fields in molecular modeling
10. Multiple sequence alignment and its application in Bioinformatics

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

1. Describe homology based and ab initio gene prediction workflow in prokaryotes and eukaryotes.
2. Explain the key steps involved in phylogenetic analysis, including alignment, tree building, and tree evaluation.
3. Describe any one heuristic based sequence alignment method used in Bioinformatics

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

1. Analyze the impact of different substitution matrices (e.g., BLOSUM, PAM) on sequence alignment results and discuss when to use each one.
2. Evaluate the impact and global initiatives associated with DNA barcoding, such as the Consortium for Barcode of Life (CBOL).
3. Evaluate the impact of 3-D structure visualization and molecular modeling in advancing structural biology research.
4. Define microarray data analysis and its significance in genomics research.
5. Define Interactomics and Fluxomics and their significance in studying biological systems.

6. Describe Genbank file format and FASTA file format.

7 Explain the difference between next generation sequencing and chain termination reaction method of DNA sequencing.

8 Which method is most appropriate to build evolutionary tree of strains from single species and why?

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