Seat No./Enrollment No.: _____

GUJARAT TECHNOLOGICAL UNIVERSITY
BACHELOR OF ENGINEERING – SEMESTER 5 – EXAMINATION – SUMMER 2026

Subject Code: 3150407 **Date: 09/06/2026**

Subject Name: Fundamentals and Applications of Bioinformatics

Time: 02:30 PM TO 05:00 PM **Total Marks: 70**

Instructions:

1. **Attempt all questions.**
2. **Make suitable assumptions wherever necessary.**
3. **Figures to the right indicate full marks.**
4. **Simple and non-programmable scientific calculators are allowed.**

Q.1	**(a)**	Mention any three aims of Bioinformatics.	**03**
	(b)	Briefly discuss the present scenario of Bioinformatics in India.	**04**
	(c)	Explain Biological Sequence Databases with reference to NCBI, EMBL, DDBJ, and PIR.	**07**
Q.2	**(a)**	Define MMDB and its use.	**03**
	(b)	Differentiate between CDD and Gene3D	**04**
	(c)	Explain how CATH and SCOP databases contribute to understanding protein structure and evolution.	**07**
		OR	
Q.2	**(c)**	Describe the Needleman–Wunsch algorithm for global sequence alignment.	**07**
Q.3	**(a)**	Explain the concept of gaps and penalties in alignment.	**03**
	(b)	Explain PAM and BLOSUM matrices.	**04**
	(c)	Explain the working of BLAST as a heuristic method.	**07**
		OR	
Q.3	**(a)**	Differentiate between global and local alignment.	**03**
	(b)	Give one heuristic method for sequence alignment.	**04**
	(c)	Explain the importance and interrelationship of PDB, MMDB, CDD, and Gene3D in bioinformatics.	**07**
Q.4	**(a)**	Mention two applications each of CATH and SCOP	**03**
	(b)	What is molecular phylogeny?	**04**
	(c)	Explain the methods of phylogenetic analysis and factors affecting their reliability.	**07**
		OR	
Q.4	**(a)**	Define a dot plot in sequence analysis.	**03**
	(b)	Differentiate between phenotypic and molecular phylogeny.	**04**
	(c)	Describe the importance and applications of molecular viewers in structural bioinformatics.	**07**
Q.5	**(a)**	What is gene prediction?	**03**
	(b)	Describe the workflow of molecular simulation in bioinformatics.	**04**

(c) Explain the role of structural bioinformatics in drug discovery **07**

OR

Q.5 **(a)** Name two graphics or visualization capabilities provided by Python/Biopython. **03**

(b) Give two differences between NGS and traditional Sanger sequencing. **04**

(c) Explain how Python and Biopython can be integrated to automate the retrieval, analysis, and visualization of DNA sequence data from biological databases such as NCBI. **07**

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