

**GUJARAT TECHNOLOGICAL UNIVERSITY**  
**BE – SEMESTER–VIII • EXAMINATION – SUMMER • 2014**

**Subject Code: 180305****Date: 27-05-2014****Subject Name: Bioinformatics****Time: 10:30 am - 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.

- Q.1** (a) Define the following terms: **07**
- |                      |                    |
|----------------------|--------------------|
| i. Proteomics        | ii. Bioinformatics |
| iii. Transcriptomics | iv. Genomics       |
| v. Codons            | vi. Metabolomics   |
| vii. Glycomics       |                    |
- (b) List the advantages and limitations of HMM for biological sequence analysis. **07**
- Q.2** (a) Explain the various features of biological databases. **07**
- (b) Explain the classification schema of biological databases. **07**
- OR**
- (b) Discuss the sequence submission tools to NCBI. **07**
- Q.3** (a) Can one use the same scoring matrix for nucleic acid and protein sequence alignment? Justify your answer. **07**
- (b) What are the common usages of Multiple sequence alignment? List the various methods for MSA implementation. **07**
- OR**
- Q.3** (a) Mention the differences between content sensor and signal sensor. **07**
- (b) What are the methods of computational gene prediction? Discuss any one in detail. **07**
- Q.4** (a) How do you predict the 3D structure of proteins by homology modeling? **07**
- (b) Explain the various levels of protein structure. **07**
- OR**
- Q.4** (a) What are the fundamental differences between the following two pairs of minimization techniques? a). Steepest descent Newton-Raphson, b) Steepest descent and conjugate gradient. **07**
- (b) Explain the Monte Carlo methodology to compute pathways and thermodynamic properties of bio-macromolecules. **07**
- Q.5** (a) Write a program to read a DNA sequence from a file and then ask the user to enter the query sequence and then look for the query in DNA sequence file. **07**
- (b) Write a program to enter a three codon and display its corresponding amino acid. When a user gives a wrong input display an appropriate error message. **07**
- OR**
- Q.5** (a) Why is gene prediction difficult? **07**
- (b) List the various methods of protein secondary structure prediction and explain any one method. **07**

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