

GUJARAT TECHNOLOGICAL UNIVERSITY**BE SEM-VIII Examination May 2012****Subject code: 180305****Subject Name: Bioinformatics****Date : 08/05/2012****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) List and explain branches of Bioinformatics. **07**
(b) Define Bioinformatics? Discuss the scope of bioinformatics. **07**

- Q.2** (a) What are the categories of database in NCBI? Explain Gene Expression Database. **07**
(b) Differentiate *BankIT* and *Sequin* tools for sequence submission to NCBI. **07**

OR

- (b) Write PERL program to display the complement of the given DNA sequence. **07**

- Q.3** (a) What are the methods available for alignment of pairs of sequences? Explain Dot Matrix Method. **07**
(b) What are the common usages of Multiple Sequence Alignment (MSA)? **07**

OR

- Q.3** (a) What is Gene Prediction? Explain Extrinsic method of Gene prediction. **07**
(b) Which are the reasons, affecting the accuracy of Gene Prediction? **07**

- Q.4** (a) Explain the levels of protein structures. **07**
(b) List the applications of comparative modeling in protein modeling. **07**

OR

- Q.4** (a) Explain Monte Carlo Method to compute pathways and thermodynamics properties of bio-macromolecules. **07**
(b) Differentiate *Steepest Descent Method* and *Conjugate Gradient Method*. **07**

- Q.5** (a) Compare *Smith-Waterman* and *Needleman-Wunsch* algorithm. **07**
(b) Explain Model Refinement in protein modeling. **07**

OR

- Q.5** (a) Explain the limitations of secondary structure prediction. **07**
(b) Explain applications of Hidden Markov Models for Gene finding. **07**
