

GUJARAT TECHNOLOGICAL UNIVERSITY**MCA SEM-V Examination- Dec.-2011****Subject code: 650015****Date: 21/12/2011****Subject Name: Bioinformatics(Bio-I)****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)** Attempt following in detail. **04+03**
- 1) What is Mutation ? Explain various types of mutation.
 - 2) Explain UPGMA Algorithm.
- (b)** Why do we use dynamic programming algorithm for pairwise sequence alignment problems but not for multiple alignment. **07**
- Q.2 (a)** Write a short note on. **04+03**
- 1) GenBank
 - 2) Gap penalty
- (b)** What is Bioinformatics ? Explain scope and importance of bioinformatics and explain challenges in information processing. **07**
- OR**
- (b)** Differentiate the following. **03+04**
- 1) Global alignment V/S Local alignment.
 - PAM v/s BLOSUM.
- Q.3 (a)** What is Multiple Sequence Alignment? Explain progressive methods of multiple alignment with example. **07**
- (b)** Attempt in detail **04+03**
- 1) Explain BLAST algorithm
 - 2) Explain X-RAY crystallography.
- OR**
- Q.3 (a)** Explain Watson and Crick's structure of DNA. **07**
- (b)** Explain CATH, SCOP and Unique protein structure data sets. **07**
- Q.4 (a)** How to Annotating and Analyzing whole genome sequence **07**
- (b)** Explain Protein resource databases. **07**
- OR**
- Q.4 (a)** What are Neural Network? How they are useful in predicting a Gene structure. **07**
- (b)** What is database ? Which types of Database used in Bioinformatics and explain Flat-File database in detail. **07**
- Q.5 (a)** What is Data-Mining ? Explain collection of Data-Mining techniques. **07**
- (b)** Explain Database searching with Smith-Waterman Dynamic programming method. **07**
- OR**
- Q.5 (a)** Explain phylogenetic tree with Distance, Parsimony and Likelihood based algorithm. **07**
- (b)** Explain Central Dogma of molecular biology with neat diagram. **07**
