

GUJARAT TECHNOLOGICAL UNIVERSITY**BE - SEMESTER-VII • EXAMINATION – WINTER • 2014****Subject Code: 170406****Date: 29-11-2014****Subject Name: Bio Informatics****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) Explain Homology modeling with all steps. **07**
(b) What is the importance of progressive alignment for evolutionary studies? **07**
- Q.2** (a) Discuss *GOR-IV* and *Chau-Fasman* methods of protein structure predictions. **07**
(b) State the applications of Bio Informatics in various fields. **07**
- OR**
- (b) How bioinformatics helps in drug discovery? **07**
- Q.3** (a) What are the methods of building phylogenetic trees? Compare all of them over each other keeping in view its efficiency. **07**
(b) Give the main features of DBGET and SRS. **07**
- OR**
- Q.3** (a) Where and how global and local alignments differ? Explain. **07**
(b) Justify the statement: "Simulation facilitates molecular docking". **07**
- Q.4** (a) Explain CLUSTALW/X and compare it with BLAST and FASTA. **07**
(b) Elaborate on Computer-aided Drug designing. **07**
- OR**
- Q.4** (a) Define networking. Mention the role of TCP/IP protocol. **07**
(b) State clearly how and where does multiples sequence alignments help? **07**
- Q.5** (a) How do the functions of proteins can be predicted? **07**
(b) Write a note on any one of specialized genome database. **07**
- OR**
- Q.5** (a) Mention about the difficulties in molecular modeling. **07**
(b) Define: conserved domains, paralogous sequence, cladogram, rooted tree, genomics, evolution, motifs. **07**
