Seat No.:	Enrolment No.
Seat No	Emoniem No

GUJARAT TECHNOLOGICAL UNIVERSITY

BE - SEMESTER-VII • EXAMINATION – WINTER • 2014

	•	Code: 170406 Date: 29-11-20	14
Ti	•	Attempt all questions. Make suitable assumptions wherever necessary.	70
Q.1	(a) (b)	Explain Homology modeling with all steps. What is the importance of progressive alignment for evolutionary studies?	07 07
Q.2	(a) (b)	Discuss <i>GOR –IV</i> and <i>Chau-Fasman</i> methods of protein structure predictions. State the applications of Bio Informatics in various fields. OR	07 07
	(b)	How bioinformatics helps in drug discovery?	07
Q.3	(a)	What are the methods of building phylogenic trees? Compare all of them over each other keeping in view its efficiency.	07
	(b)	Give the main features of DBGET and SRS. OR	07
Q.3	(a) (b)	Where and how global and local alignements differ? Explain. Justify the statement: "Simulation facilitates molecular docking".	
Q.4	(a) (b)	Explain CLUSTALW/X and compare it with BLAST and FASTA. Elaborate on Computer-aided Drug designing. OR	07 07
Q.4	(a) (b)	Define networking. Mention the role of TCP/IP protocol. State clearly how and where does multiples sequence alignements help?	
Q.5	(a) (b)	How do the functions of proteins can be predicted? Write a note on any one of specialized genome database. OR	
Q.5	(a) (b)	Mention about the difficulties in molecular modeling. Define: conserved domains, paralogous sequence, cladogram, rooted tree, genomics, evolution, motifs.	07 07
