M.E. Second Semester (Digital Electronics) (Part Time / Full Time) (C.G.S.- New) 13234: Elective-II: Bio-Informatics: 2 UMEF 5 / 4 UMEP 3

P. Pages: 2 Time: Three Hours

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Tin	ne : Th	ree Hours	ts : 80
	Not	es: 1. Assume suitable data wherever necessary. 2. Diagrams and chemical equations should be given wherever necessary. 3. Illustrate your answer necessary with the help of neat sketches.	
1.	a)	What is bioinformatics? Explain the scope of bioinformatics in detail.	6
	b)	Explain the categories of research in bioinformatics.	7
		OR	
2.	a)	Explain the characteristics of Bioinformatics database.	7
	b)	Describe the application of bioinformatics.	6
3.	a)	Explain Gene expressing database in brief?	6
	b)	Describe the methods from for searching from protein sequence databases?	7
	-	OR	
4.	a)	Explain three databases exchange and update data on a daily basis with neat schematic diagram?	7
	b)	Explain protein sequence databases?	6
5.	a)	Describe the CATH data formats? What is main classification level of CATH.	7
	b)	Briefly give reasons why MMDB would yield different structural neighbours from other classification methods.	7
		OR	-
.	a)	Describe the enzyme pathways databases.	7
	b)	Explain the information retrieval system to obtain data from databases.	7
i.	a)	Explain phylogenetic tree with neat sketch.	7
	þ)	Explain similarities and differences between BLAST and FASTA tools for sequence alignment.	6

OR

a)	Which are the tools available for data submission in GenBank? Explain any one.	7
b) .	Define Data Mining. Explain Data Mining operations in context of a larger knowledge discovery process.	6
a)	Describe the classification of algorithm.	7
b)	Explain the Biological algorithm.	6
	OR	
a)	Explain the functions of probabilistic algorithm.	6
b)	Discuss the algorithm and bioinformatics software for different bioinformatics task.	7
a)	How PAM matrix was developed? How will you choose the best PAM scoring matrix for detecting sequence similarity.	7
b)	Differentiate between Ab-Initio and Heuristic methods of protein structure prediction?	7
	OR	
a)	Explain Similarity based approach to Gene prediction.	7
b)	Briefly discuss the various method of protein structure prediction.	7
	b) a) b) a) b) a)	b) Define Data Mining. Explain Data Mining operations in context of a larger knowledge discovery process. a) Describe the classification of algorithm. b) Explain the Biological algorithm. OR a) Explain the functions of probabilistic algorithm. b) Discuss the algorithm and bioinformatics software for different bioinformatics task. a) How PAM matrix was developed? How will you choose the best PAM scoring matrix for detecting sequence similarity. b) Differentiate between Ab-Initio and Heuristic methods of protein structure prediction? OR a) Explain Similarity based approach to Gene prediction.

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