[Maximum Marks: 80

M.Sc. Part-I Semester-II (CBCS Scheme) Examination BIOINFORMATICS

(Techniques in Bioinformatics)

Paper-VIII

Note :- (1) ALL questions are compulsory and carry equal marks. (2) Draw suitable diagram wherever necessary. Describe: Primary nucleotide sequence database with an example. Need of derived databases. CATH as a structure database. (d) INTERPRO OR Primary protein sequence data with an example. PRINTS as a derived database. Genome databases STS as a repository for genomic sequences.

Time: Three Hours]

2.	Explain:			4.	What is genome rearrangement? Describe in detail the
	(a)	Any one algorithm used for searching seque	ence pattem. 4		common rearrangement events in unichromosomal and multichromosomal genomes. 16
	(b)	Scan prosite	4		OR
	(c)	Role of Bioinformatics in identification genes.	4	What is Permutation? Describe in detail the role of signed unsigned and transformation of permutation in genom rearrangement.	
	(d)	SNP database.	4	5	
	OR .		٥.	 Define DNA Microarray. Explain different databases and tools used in DNA microarray analysis. 	
	(p)	Any one algorithm used for generation of profiles.	neration of sequence 4		OR
	(q)	PHI-BLAST	4		Describe in detail normalization of microarray data. Explain their role in detecting differential gene expression and correlation of gene expression data to biological process.
	(r)	HMMer	4		
	(s)	Role of Bioinformatics in gene expression	on profiling. 4		
3.	Describe:				
	(a)	CPG Islands	4		
	(b)	Gibbs sampling technique	4		
	(c)	Gene prediction in Prokaryotes	4		
	(d)	Spliced Alignment.	4		
	OR				
	(p)	Reverse gene finding	4		
	(q)	Gene prediction in Eukaryotes	4		
	(r)	DNA Linguistics	4		
	(s)	HMM in gene prediction.	4		

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(Contd.)

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