U.S.N.										

B.M.S. College of Engineering, Bengaluru-560019

Autonomous Institute Affiliated to VTU

January / February 2025 Semester End Main Examinations

Programme: B.E. **Semester: VI**
Branch: Biotechnology **Duration: 3 hrs.**
Course Code: 22BT6PCGAP **Max Marks: 100**
Course: GEONEMICS & PROTEOMICS

Instructions: 1. Answer any FIVE full questions, choosing one full question from each unit.
2. Missing data, if any, may be suitably assumed.

Important Note: Completing your answers, compulsorily draw diagonal cross lines on the remaining blank pages. Revealing of identification, appeal to evaluator will be treated as malpractice.

			UNIT-I	*CO*	*PO*	Marks
1	a)		Enumerate the principle and steps of Illumina sequencing.	*CO* 1	*PO1, 5,12*	**8**
	b)		Elucidate the steps of automated method of fluorescent sequencing.	*CO* 1	*PO1, 5,12*	**7**
	c)		Identify the sequencing technology depicted in the following image and write the principle of the technique. 	*CO* 1	*PO1, 5,12*	**5**
			OR			
2	a)		Identify the next gen sequencing method involving emission of light as a signal for sequence and involving luciferase. Write its principle and mechanism of working with a neat diagram	CO 1	PO1, 5,12	**10**
	b)		Compare and contrast all generation sequencing technologies			**10**
			UNIT-II			
3	a)		Elucidate how Fluorescent *in situ* hybridisation (FISH) technique helps in mapping of genes and its applications	*CO* 2	*PO1, 5,12*	**10**
	b)		Elaborate on the principle and steps of optical mapping technique.	*CO* 2	*PO1, 5,12*	**10**
			OR			

	4	a)	A plasmid digested with Hpa1 results in one band of 26kb. When digested with HindIII, there are four bands: 13kb, 6kb, 4kb, and 3kb. A combination digest with Hpa1 and HindIII results in 7kb, 6kb, 4kb and 3kb. Construct a map of the plasmid.	CO 2	PO1,5,12	**10**
		b)	Develop a strategy for denovo genome assembly based on NGS sequence data. List any five software tools that are being used for sequence assembly	CO 2	PO1,5,12	**10**
			UNIT-III			
	5	a)	RNA sequencing (RNA-Seq) uses the capabilities of high-throughput sequencing methods to provide insight into the transcriptome of a cell. Elucidate the principle and steps involved in RNA Seq.	*CO* 3	*PO5,12*	**10**
		b)	Enlist the steps and disadvantages of DNA microarray technique.	*CO* 3	*PO5,12*	**10**
			OR			
	6	a)	What is SNP profiling? Write the steps of the technique	*CO* 3	*PO1*	**10**
		b)	Elaborate on the principle and steps of differential display PCR technique.	*CO* 3	*PO1*	**10**
			UNIT-IV			
	7	a)	What is the importance of phosphoproteome in proteomics? Write how mass spectrometry can be used for the analysis of phosphoproteome.	*CO* 3	*PO5,12*	**10**
		b)	Elucidate the steps of peptide mass fingerprinting	*CO* 3	*PO5,12*	**10**
			OR			
	8	a)	Elaborate on the method of the Isotope Coded Affinity Tagging (ICAT) used in quantitative proteomic analysis.	*CO* 3	*PO5,12*	**10**
		b)	Write the steps of 2-D gel electrophoresis.	*CO* 3	*PO5,12*	**10**
			UNIT-V			
	9	a)	What is yeast two-hybrid system? Write how the technique is used in identifying protein-protein interactions.	*CO*4	*PO1,12*	**10**
		b)	Illustrate with a neat labelled diagram the principle and working of Surface Plasmon Resonance technique.	*CO*4	*PO1,12*	**10**
			OR			
	10	a)	Design a strategy for identifying the interacting partners of a protein using antibodies with neat figures.	CO4	PO1,12	10
		b)	Illustrate with a neat labelled diagram the principle and working of AFM technique. Add a note on its applications.	CO4	PO1,12	10

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