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: VII**

Branch: Biotechnology **Duration: 3 hrs.**

Course Code: 22BT7PEGIN **Max Marks: 100**

Course: Genome Informatics

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)	How does the chemical process in pyrosequencing contribute to nucleotide detection?	CO1	PO 1	7
	b)	What factors might contribute to the differences in read accuracy between Illumina and Ion Torrent sequencing?	CO1	PO 1	7
	c)	How would you assess the trade-offs between sequencing cost, speed, and accuracy across different NGS technologies?	CO1	PO 1	6
		OR			
2	a)	If a sequencing lab is constrained by budget but requires high accuracy, which sequencing method would be most suitable? Justify your choice.	CO1	PO5	6
	b)	Why do short-read sequencing technologies face challenges in genome assembly?	CO1	PO5	6
	c)	Design a flowchart comparing the workflow of three NGS techniques based on their core principles.	CO1	PO5	8
		UNIT - II			
3	a)	How would you adjust the assembly pipeline if your dataset contains a high number of sequencing errors?	CO1	PO5	7
	b)	What would be the consequences of ignoring sequence read correction methods in genome assembly?	CO1	PO5	6
	c)	What role do genome browsers play in analyzing large-scale sequencing data?	CO1	PO5	7
		OR			
4	a)	Why is De Novo Genome Assembly considered more challenging than reference-based assembly?	CO1	PO5	7
	b)	What are the advantages and limitations of various NGS data preprocessing methods?	CO1	PO5	7
	c)	Propose a strategy to improve genome assembly quality using current sequencing technologies.	CO1	PO5	6

			UNIT - III			
	5	a)	Why is genome assembly often compared to solving a complex puzzle?	*CO2*	*PO2*	**6**
		b)	How would you decide whether to use the Overlap Graph Approach or the De Bruijn Graph Approach for a given dataset?	*CO2*	*PO2*	**6**
		c)	If you were to design a new genome assembly algorithm, what key features would you include?	*CO2*	*PO2*	**8**
			OR			
	6	a)	What are the strengths and weaknesses of Greedy Algorithms in genome assembly?	*CO2*	*PO2*	**7**
		b)	What preprocessing steps would you recommend before applying the Overlap Layout Consensus (OLC) method?	*CO2*	*PO2*	**7**
		c)	Given an NGS dataset, what criteria would you use to determine the most suitable assembly algorithm?	*CO2*	*PO2*	**6**
			UNIT - IV			
	7	a)	How does RNA-seq contribute to biomarker discovery in cancer research?	*CO3*	*PO2*	**7**
		b)	If given an RNA-seq dataset from prostate cancer patients, how would you identify key differentially expressed genes?	*CO3*	*PO2*	**7**
		c)	Propose a study using NGS to investigate microRNAs in a specific type of cancer.	*CO3*	*PO2*	**6**
			OR			
	8	a)	How effective is targeted sequencing compared to whole-genome sequencing in identifying cancer mutations?	*CO3*	*PO2*	**7**
		b)	What are the implications of high-throughput RNA interference screens for personalized cancer therapy?	*CO3*	*PO2*	**8**
		c)	How does the integration of NGS with clinical oncology impact early cancer diagnosis and treatment?	*CO3*	*PO2*	**5**
			UNIT - V			
	9	a)	How does NGS facilitate the identification of polymorphisms in neuropsychiatric disorders?	*CO4*	*PO1*	**5**
		b)	What are the major challenges in using NGS for early disease diagnosis?	*CO4*	*PO1*	**6**
		c)	Develop a workflow for using NGS in personalized medicine for neuroinflammatory diseases.	*CO4*	*PO1*	**9**
			OR			
	10	a)	How would you use NGS to detect genetic variations linked to Alzheimer's disease?	*CO4*	*PO1*	**5**
		b)	How do different sequencing strategies compare in their ability to detect genetic markers for Parkinson's disease?	*CO4*	*PO1*	**6**
		c)	How can NGS contribute to precision medicine approaches in neurodegenerative disorders?	*CO4*	*PO1*	**9**

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