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Daffodil International University

Faculty of Science & Information Technology

Department of Computer Science & Engineering

Final Examination, Summer 2026

Course Code: CSE115, Course Title: Introduction to Biology & Chemistry for Computation

Level: 1 Term: 1 Batch: 72

Time: 02:00 Hrs **Marks: 40**

Answer ALL Questions

[The figures in the right margin indicate the full marks and corresponding course outcomes. All portions of each question must be answered sequentially.]

1.		The Human Genome Project was completed using a specific sequencing method which requires Bacteria cells.		CO2
	a)	Identify the sequencing method and list its positive and negative sides.	[3]	
	b)	Break down the steps of the mentioned sequencing method with diagrams.	[7]	
2.		A team developed a system for cancer diagnosis. 700 inputs were given to the system, out of which 300 were actually negative. 10 positive and 5 negative inputs were misdiagnosed.They will also apply a rapid sequence alignment, given, query sequence: ATAAGCAT and target sequence:CCGATGCGCTTA.		CO3
	a)	Compute the Confusion Matrix and precision of diagnosis.	[3]	
	b)	Apply the 1-tuple variation of the mentioned rapid alignment algorithm.	[7]	
3.		A researcher is working with four taxa. First he wants to calculate the number of possible rooted phylogenetic trees. Then he will find out the Newick format of the final rooted tree utilizing the UPGMA algorithm. Given below is the p-distance matrix.		CO3
	a)	Calculate the number of possible rooted trees.	[3]	
	b)	Compute the Newick format for the tree constructed based on the jukes-cantor method. The tree construction process has to be demonstrated.	[7]	
4.		A DNA sequence ATATCAC needs to be transformed to aid compression for storage. Proper transformation allows compression, efficient storage and retrieval of DNA sequences.		CO3
	a)	Apply the appropriate transformation method step by step to generate output.	[7]	
	b)	Compute the original input from the transformed output for verification.	[3]	

	A	B	C
B	0.3		
C	0.4	0.45	
D	0.6	0.5	0.74