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Daffodil International University

Faculty of Science & Information Technology

Department of Computer Science & Engineering

Midterm Examination, Fall 2025

Course Code: CSE115

Course Title: Introduction to Biology & Chemistry for Computation

Level: L1 Term: T1 Batch:70

Time: 01:30 Hrs. **Marks: 25**

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.	A research team in an environmental lab is working to make pollution analysis faster and more reliable. They plan to use chromatography to separate pollutants from samples like water and air extracts and link the system to a Distributed Control System (DCS) for automated control.		[5]	CO2
	a)	**Analyze** how chromatography helps in separating and detecting pollutants, and explain how integrating a DCS could make the overall process more efficient through automation.		
2.	Sofia, a molecular biology student, is studying a double-stranded helical molecule found in dividing animal cells. Each strand has a sugar–phosphate backbone with the bases adenine, thymine, cytosine, and guanine. Her supervisor mentions that before cell division, this molecule produces an identical copy of itself using its existing strands as templates.		*[5]*	*CO1*
	a)	**Identify** the biological process her supervisor is referring to, and **describe** how it occurs with appropriate diagrams.		
3.	You are part of a bioinformatics research team studying a mutating viral strain. To understand its evolution and identify potential drug targets, you must compare two related DNA sequences to map their shared ancestry and divergence. Your goal is to find the most comprehensive alignment that accounts for every nucleotide from the beginning to the end of both sequences. Given the two DNA sequences: • S1 = GACTAG • S2 = CACAGT And the following scoring scheme: • **Match = +2 Mismatch = −1 Gap = −2**		[7]	CO3

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	a)	**Apply** a suitable algorithm to construct the optimal end-to-end alignment for these two sequences and calculate the final alignment score.		
4.		A research team is studying how a group of closely related organisms have changed over time from a single common ancestor. After comparing their DNA sequences, the team uses a computational method to build a phylogenetic tree that shows how each group gradually diverged from the original lineage. The software provides the following Newick format output: (((A,B),(C,D)),(E,(F,G))); **Examine** the given Newick format, **classify** the type of tree representation, draw the corresponding phylogenetic tree, and explain how the organisms are evolutionarily related.	[5]	CO2
	b)	**Analyze** your constructed phylogenetic tree and identify the main features such as clade, root, lineage, taxa, and dichotomy. Label these parts on the tree and explain what each of these terms means in the context of the tree.	[3]	