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Daffodil International University

Faculty of Science & Information Technology
Department of Computer Science & Engineering
Mid Examination, Spring 2026
Course Code: CSE115
Course Title: Introduction to Biology and Chemistry for Computation
Level: 1 Term: 1 Batch: 71

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 pharmaceutical quality control laboratory needs to analyze trace-level impurities present in liquid drug samples. To improve accuracy and reduce human intervention, the laboratory plans to use chromatography integrated with a computer-based automated control system.			CO 2
	a)	Explain how chromatography can be used to separate and identify chemical impurities from complex samples step by step.	[5]	
2.	Rafi is observing cells under a microscope during a biology experiment. He notices that before cell division, a double-stranded molecule inside the nucleus duplicates itself. Each strand contains a sugar–phosphate backbone and nitrogenous bases arranged in a specific complementary pattern.			CO 1
	a)	Name the biological molecule and the cellular process responsible for this duplication.	[2]	
	b)	Describe the major steps involved in this process, including the role of enzymes, with the help of a neat labeled diagram.	[3]	
3.	You are working as a bioinformatics analyst studying genetic similarity between two bacterial strains. To understand their evolutionary relationship, you decide to perform a complete end-to-end sequence alignment. Given the sequences: • S1 = ATGCTA • S2 = AGCTTA Scoring scheme: Match = +2 Mismatch = –1 Gap = –2			CO 3
	a)	Identify the most appropriate sequence alignment algorithm for this task.	[1]	
	b)	Construct the scoring matrix, perform traceback with appropriate	[4]	

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		alignment.		
	c)	Calculate the final alignment score.	[2]	
4.	A biologist studies five species (A, B, C, D, E). After sequencing a gene, she computes the pairwise genetic distances (smaller = more similar). Distance Matrix A B C D E A 0 4 6 8 8 B 4 0 6 8 8 C 6 6 0 4 4 D 8 8 4 0 2 E 8 8 4 2 0			CO 2
	a)	Calculate the distance matrices and draw the UPGMA tree step by step.	[5+3]	

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