



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. <i>DNA, Replication</i>	[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]	

		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			CO 2
	A B C D E A04688 B40688 C66044 D88402 E88420			
	a)	Calculate the distance matrices and draw the UPGMA tree step by step.	[5+3]	

A T G C U T A

A U G C T T A

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U G C T U A

A G C T T A

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Signature