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Daffodil International University

Faculty of Science & Information Technology

Department of Computer Science and Engineering

Final Examination, Spring 2024

Course Code: CSE 115, Course Title: Introduction to Biology and Chemistry for Computation

Level: 1 Term: 1 Batch: 66

Time: 02:00 Hours **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.	I. Define mutation. Write down the different type of mutation with example. II. Given dataset: Suppose you are searching for a character T and the outcome is GTTT. Calculate the selectivity and sensitivity.	[5] [5]	CO1
2.	Biological database searching is a key aspect of bioinformatics, involving querying specialized databases to retrieve biological data such as DNA sequences, protein sequences, and gene annotations. Researchers use tools like BLAST and FASTA to search for similarities between sequences. For the following sequences apply step by step FASTA algorithm to gain insights into genetic functions, evolutionary relationships, and disease mechanisms.	[10]	CO3
3.	I. As a biologist, if you were given a biological sequence for compressing using the Burrows-Wheeler Transform (BWT), what would be the steps for the given sequence : GTTACTATCC II. From the BWT extracted from (I), apply LF mapping to it to regenerate the original sequence and prove that they are same.	[5] [5]	CO1
4.	Pairwise sequence alignment is a technique used to compare two sequences (such as DNA, RNA, or protein) to identify similarities and differences. The process involves aligning the sequences in a way that maximizes the number of matched characters and minimizes gaps and mismatches. I. Apply local alignment for the given sequences (mention the algorithm name). II. Calculate the score showing back tracing path.	 [5] [5]	CO3

Query: MAGNESIUMCHLORIDE	Target: MILKOFMAGNESIA

A	T	G	C	T	T	A	T
G	T	T	T	A	A	G	C

S1: CTTGTTATT S2: TTTCATATT	Given that: Match: +8, Mismatch: -3, Gap: -5