

Assignment-2

ECHELON INSTITUTE OF TECHNOLOGY

Department of Computer Application BIO-INFORMATICS (BCA-DS-314)

Course: BCA-DS-314

Date of Issue: 23th April, 2025

Course Unit included: 3st & 4nd

Session: 2024-25

Semester: 6TH

Date of Submission: 28th April, 2025

Assignment Number: 2st

Max. Marks: 20

CO-1: - Students will learn to use bioinformatics tools and databases for sequence analysis.

CO-2: - They will also be able to predict secondary and tertiary structures of proteins.

Q.N.	Question	CO	Revised Bloom's Taxonomy Level	Marks
Q1	a. Define Big-O Notation and explain its significance in bioinformatics algorithms.	CO-3	RBTL-1	4
	b. Differentiate between iterative and recursive algorithms with a suitable biological example.			
Q2	a. Explain the difference between biological algorithms and computer algorithms with relevant examples.	CO-3	RBTL-1	4
	b. Discuss the change problem and its relevance to bioinformatics.			
Q3	a. Describe recursive algorithms. Provide an example relevant to sequence alignment.	CO-3	RBTL-1	4
	b. What are the key design techniques used in creating efficient bioinformatics algorithms?			
Q4	a. Write the use and syntax of the following Unix commands: <code>ls</code> , <code>cat</code> , <code>rm</code> , <code>uniq</code> .	CO-4	RBTL-2	4

	b. Describe the function of the <code>grep</code> command and provide two biological applications.			
Q5	a. What are scalar and array variables in Perl? Give examples of each.	CO-4	RBTL-2	4
	b. Explain Perl regular expressions with one example. How are they useful in bioinformatics?			