



Roll No.											
----------	--	--	--	--	--	--	--	--	--	--	--

# PRESIDENCY UNIVERSITY

## BENGALURU

### Mid - Term Examinations – October 2025

**Date:** 09-10-2025

**Time:** 09.30am to 11.00am

<b>School:</b> SOCSE	<b>Program:</b> COMPUTER SCIENCE AND ENGINEERING	
<b>Course Code:</b> CSE3507	<b>Course Name:</b> Algorithms in Computational Biology	
<b>Semester:</b> V	<b>Max Marks:</b> 50	<b>Weightage:</b> 25%

<b>CO - Levels</b>	<b>CO1</b>	<b>CO2</b>	<b>CO3</b>	<b>CO4</b>	<b>CO5</b>
<b>Marks</b>	<b>14</b>	<b>36</b>	---	---	---

**Instructions:**

- (i) *Read all questions carefully and answer accordingly.*
- (ii) *Do not write anything on the question paper other than roll number.*

#### Part A

**Answer ALL the Questions. Each question carries 2marks.**

**5Q x 2M=10M**

<b>1</b>	Describe the fundamental components that define an algorithm, including its structure, clarity, and effectiveness in solving a problem.	<b>2 Marks</b>	<b>L2</b>	<b>CO1</b>
<b>2</b>	Interpret how to write a pandas DataFrame to a CSV file in Python while excluding the index column. Provide the relevant syntax and reasoning.	<b>2 Marks</b>	<b>L2</b>	<b>CO1</b>
<b>3</b>	Distinguish between Comparative ImmunoProfiling and the Consecutive Integer Problem. List four differences in their domain, purpose, data type, and analytical method.	<b>2 Marks</b>	<b>L2</b>	<b>CO2</b>
<b>4</b>	Summarize two practical strategies used to address NP-complete problems when exact polynomial-time solutions are not feasible. Include one example for each.	<b>2 Marks</b>	<b>L2</b>	<b>CO2</b>
<b>5</b>	Interpret the pattern of four consecutive odd integers using algebraic expressions, and determine a set whose sum equals 136.	<b>2 Marks</b>	<b>L2</b>	<b>CO2</b>

## Part B

### Answer the Questions.

**Total Marks 40M**

<b>6.</b>	<b>a.</b>	Summarize how the merge sort algorithm is implemented in Python. Interpret how its divide-and-conquer strategy organizes data during sorting.	<b>10 Marks</b>	<b>L2</b>	<b>CO1</b>
-----------	-----------	---	-----------------	-----------	------------

**Or**

<b>7.</b>	<b>a.</b>	Describe how binary search operates on a sorted list. Interpret why its time complexity is more efficient than linear search, using Python to illustrate the process.	<b>10 Marks</b>	<b>L2</b>	<b>CO1</b>
-----------	-----------	---	-----------------	-----------	------------

<b>8.</b>	<b>a.</b>	Interpret the concept of asymptotic analysis by describing its key ideas, standard notations, and core properties. Illustrate how it is performed using a relevant example, and explain its role in evaluating algorithmic efficiency.	<b>10 Marks</b>	<b>L2</b>	<b>CO2</b>
	<b>b.</b>	Explain the process of identifying and proving that a problem is NP-complete. What are the key steps involved, and why is this classification important.	<b>5 marks</b>	<b>L2</b>	<b>CO2</b>

**Or**

<b>9.</b>	<b>a.</b>	Explain how a custom Fibonacci-like sequence can be generated starting from two user-defined numbers. How does this differ from the traditional Fibonacci sequence? Illustrate the output for the first 10 terms when the starting numbers are 5 and 8.	<b>10 Marks</b>	<b>L2</b>	<b>CO2</b>
	<b>b.</b>	Explain the concept of Polynomial-Time Reducibility. Why is it important in computational complexity theory, and how can one reduce a problem A to another problem B in polynomial time.	<b>5 marks</b>	<b>L2</b>	<b>CO2</b>

<b>10.</b>	<b>a.</b>	Explain how DNA fragments are used in Comparative ImmunoProfiling (CIP) to reconstruct biological sequences through overlap analysis. Then, apply the overlap rule ( $\geq 5$ bases) to the fragments below to identify valid links, build the longest chain, reconstruct the full sequence by trimming overlaps, and justify any exclusions.  F <sub>1</sub> : GATCGTACGA  F <sub>2</sub> : TACGATCGGA  F <sub>3</sub> : ATCGGATACC	<b>10Marks</b>	<b>L2</b>	<b>CO2</b>
------------	-----------	--	----------------	-----------	------------

		F <sub>4</sub> : GGATACCGTT  F <sub>5</sub> : ACCGTTAGCA			
	<b>b.</b>	Outline the main procedures of Heap Sort using pseudocode. Interpret how the heap structure supports efficient sorting operations.	<b>5 Marks</b>	<b>L2</b>	<b>CO 2</b>
<b>Or</b>					
<b>11.</b>	<b>a.</b>	Interpret the TSP-based DNA assembly approach by writing an algorithm that uses suffix-prefix overlap as edge cost. Apply this algorithm to the fragments below to determine an efficient traversal order and reconstruct the final DNA sequence.  F <sub>1</sub> : GATCGTACGA  F <sub>2</sub> : TACGATCGGA  F <sub>3</sub> : ATCGGATACC  F <sub>4</sub> : GGATACCGTT  F <sub>5</sub> : ACCGTTAGCA	<b>10 Marks</b>	<b>L2</b>	<b>CO 2</b>
	<b>b.</b>	Demonstrate your understanding of Radix Sort by writing its pseudocode. Interpret how the algorithm processes digits to achieve sorting.	<b>5 marks</b>	<b>L2</b>	<b>CO 2</b>