Xi'an Jiaotong-Liverpool University



PAPER CODE	EXAMINER	DEPARTMENT	TEL
INT102	Jia WANG	Intelligent Science	9047

2nd SEMESTER 2023/24 EXAMINATIONS(RESIT)

BACHELOR DEGREE - Year 2

ALGORITHMIC FOUNDATIONS AND PROBLEM SOLVING

TIME ALLOWED: 2.5 Hours

INSTRUCTIONS TO CANDIDATES

READ THE FOLLOWING CAREFULLY:

- 1. The paper consists of Part I and Part II. Answer all questions in both parts.
- 2. Answer all questions in Part I using the Multiple-Choice Answer Sheet. Please read the instructions on the Multiple-Choice Answer Sheet carefully and use a 2B pencil to mark the Multiple-Choice Answer Sheet. If you change your mind, be sure to erase the mark you have made. You may then mark the alternative answer.
- 3. Answer all questions in Part II using the answer booklet.
- 4. Enter your name and student ID No. on BOTH the Multiple-Choice Answer Sheet and the answer booklet.
- 5. At the end of the examination, be absolutely sure to hand in BOTH the answer booklet AND the Multiple-Choice Answer Sheet.
- 6. All answers must be in English.

THIS PAPER MUST NOT BE REMOVED FROM THE EXAMINATION ROOM

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4. Finding the nth Fibonacci number.

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PART II

Question 1 (10 marks)

- 1. Describe what a decision problem is and what an optimisation problem is.
- 2. Describe what a P problem is and what a NP problem is. 3
- 3. For each problem below, state whether it is a P problem or NP-complete problem.
 - 1. Vertex Cover Problem. NPC 1 2. Finding minimum spanning tree (MST) in a weighted undirected graph 1 3. 0/1 Knapsack problem. 1 NPC

Question 2 (20 marks)

Consider the problem of searching for genes in DNA sequences using Horspool's algorithm. A DNA sequence is represented by a text on the alphabet {A, C, G, T}, and the gene or a gene segment is a pattern.

Construct the shift table for the following gene segment. *10*

TCCTATTCTT

Apply Horspool's algorithm to locate the pattern in the following DNA sequence. *10*

TTATAGATCTGGTATTCTTTATAGATCTCCTATTCTT

2. Algorithm Harsper (sequence common), Patient to many // Input: two string 1) output: the first place the pattern appears n= sequence slength m= partition's length shift table c fattern to ... m-1], X) for it m-1 to n-1 do k = 0 while [K==m && Sequence [i-k] == Partlem [m-1-k]) do if k== m then
Yethin i=mt/ else i = i + shift able (pattorn [0---m-1], Portlern [m-1-lc])

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