



VIT

Vellore Institute of Technology
(Deemed to be University under section 3 of UGC Act, 1956)

REG.NO.:

**SCHOOL OF COMPUTER SCIENCE AND ENGINEERING
CONTINUOUS ASSESSMENT TEST - II
WINTER SEMESTER 2024-2025**

SLOT: A2+TA2

Programme Name & Branch : B.Tech Computer Science and Engg
Course Code and Course Name : BCSE204L (Design and Analysis of Algorithms)
Faculty Name(s) : ALL
Class Number(s) : ALL
Date of Examination : 16-03-2025
Exam Duration : 90 minutes **Maximum Marks: 50**

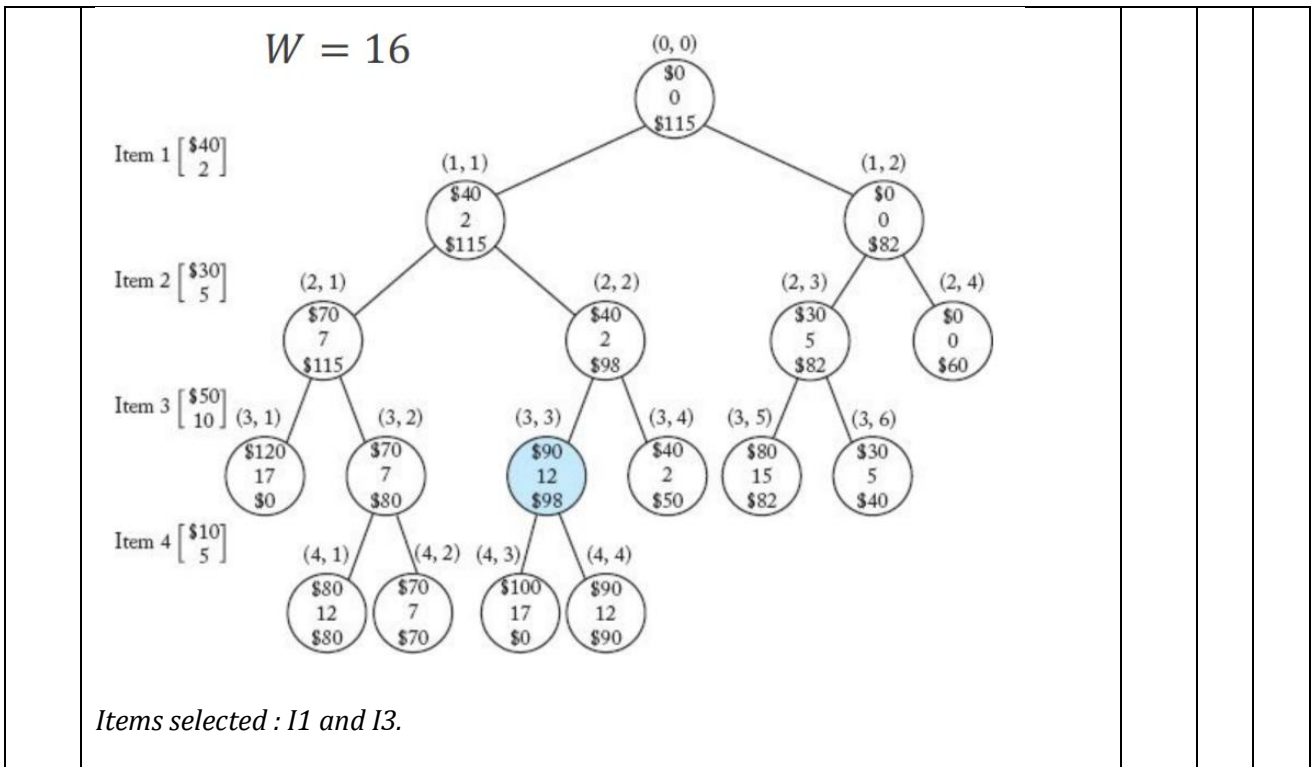
General instruction(s):

- Answer All Questions
- M - Max mark; CO – Course Outcome; BL – Blooms Taxonomy Level (1 – Remember, 2 – Understand, 3 – Apply, 4 – Analyse, 5 – Evaluate, 6 – Create)
- Course Outcomes
 CO2 - Demonstrate the major algorithm design paradigms.
 CO3 - Explain major graph algorithms, string matching and geometric algorithms along with their analysis

Q. No	Question	M	CO	BL															
1.	Consider the following items that can be added to the knapsack with a capacity of 16 kgs. Solve and obtain the optimal solution using the branch-and-bound FIFO method. Use variable and fixed representation to create the state space tree and differentiate between the representations. Note: Variable representation refers to the binary variables (0 or 1) that determine whether an item is included or excluded from the knapsack, while fixed representation refers to the predetermined, unchanging data associated with each item, such as its weight and value. <table border="1" style="margin: 10px auto; width: 50%;"> <thead> <tr> <th>Item</th> <th>I1</th> <th>I2</th> <th>I3</th> <th>I4</th> </tr> </thead> <tbody> <tr> <td>Profit</td> <td>\$40</td> <td>\$30</td> <td>\$50</td> <td>\$10</td> </tr> <tr> <td>Weight (in kg)</td> <td>2</td> <td>5</td> <td>10</td> <td>5</td> </tr> </tbody> </table>	Item	I1	I2	I3	I4	Profit	\$40	\$30	\$50	\$10	Weight (in kg)	2	5	10	5	10	2	3
Item	I1	I2	I3	I4															
Profit	\$40	\$30	\$50	\$10															
Weight (in kg)	2	5	10	5															



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2. Consider the following gene sequence:

AGCTTAGCTGAGCTAGCTAGCTGAGCTGCTAG

where Adenine (A), Cytosine (C), Guanine (G), and Thymine (T) are the four bases in DNA. During analysis, assume that the following pattern often occurs: GCTAG (in HIV disease) and GAGCTG (in lung cancer disease) in the sequence. Identify the disease sequence that occurs more frequently by using the KMP string matching technique. Make the LPS table for the two patterns that are being considered. Give the steps for building the table.

Answer Key:

LPS table - 1 mark each

Finding the pattern using KMP string matching algorithm- 4 marks each

Failure function:

j	0	1	2	3	4
P[j]	G	C	T	A	G
f(j)	0	0	0	0	1

AGCTTAGCTGAGCTAGCTAGCTGAGCTGCTAG

Pattern GCTAG occurs twice

3 3

10

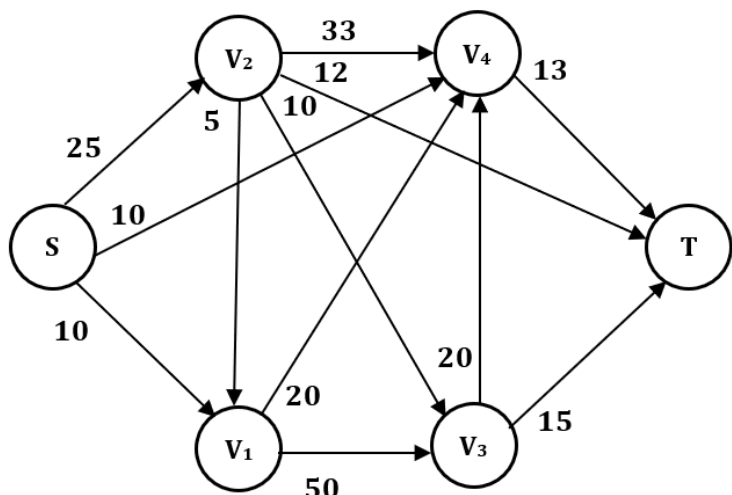
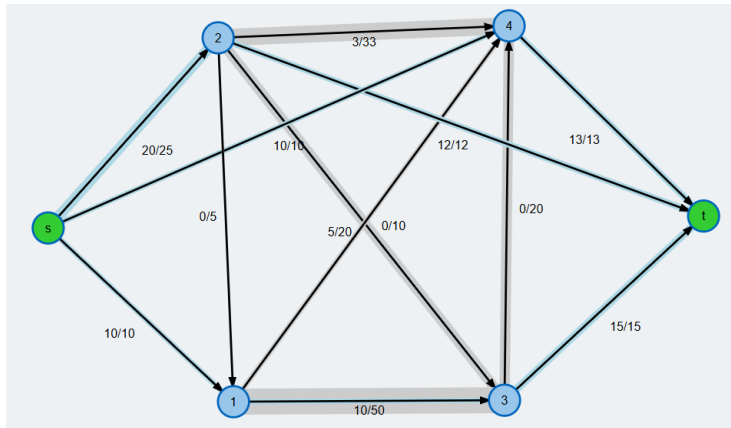


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	<p>Failure function:</p> <table border="1" data-bbox="300 394 668 560"> <tr><td>j</td><td>0</td><td>1</td><td>2</td><td>3</td><td>4</td><td>5</td></tr> <tr><td>P[j]</td><td>G</td><td>A</td><td>G</td><td>C</td><td>T</td><td>G</td></tr> <tr><td>f(j)</td><td>0</td><td>0</td><td>1</td><td>0</td><td>0</td><td>1</td></tr> </table> <p>AGCTTAGCTGAGCTAGCTAGCTGAGCTGCTAG Pattern GAGCTG occurs once</p> <p>Hence, the HIV disease sequence occurs often.</p> <p>Step by step visualization can be done at: https://cmeps-people.ok.ubc.ca/ylocet/DS/KnuthMorrisPratt.html</p>	j	0	1	2	3	4	5	P[j]	G	A	G	C	T	G	f(j)	0	0	1	0	0	1			
j	0	1	2	3	4	5																			
P[j]	G	A	G	C	T	G																			
f(j)	0	0	1	0	0	1																			
3.	<p>Given a weighted directed graph, apply the Floyd-Warshall algorithm to compute the shortest paths between all pairs of nodes. After obtaining the distance matrix, construct the predecessor matrix to store the intermediate nodes along the shortest paths.</p> <p>Using this predecessor matrix, determine the paths for the following node pairs: a) From node A to node D b) From node D to node B</p> <div data-bbox="576 1200 975 1570" data-label="Diagram"> </div> <p>Final Answer:</p> <pre> vertex_labels = ["A", "B", "C", "D", "E"] shortest_paths = [[0, -2, 2, 1, -3], [7, 0, 4, 3, -1], [19, 17, 0, 5, 11], [14, 12, 11, 0, 6], [8, 6, 5, 9, 0],] </pre> <p>Predecessor Matrix</p>	A	3	3																					



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	<p> $\begin{matrix} & 0 & A & B & B & B \\ E & 0 & B & B & B \\ E & A & 0 & C & D \\ E & A & E & 0 & D \\ E & A & E & B & 0 \end{matrix}$ </p> <p> Path from A to D: A->B-> D Total path cost: 1 Path from D to B: D->E->A->B Total path cost: 12 </p>			
<p>4.</p>	<p>For the given graph that represents a water treatment plant with various stations, calculate the total network flow of the plant using the Ford Fulkerson algorithm. For every augmenting path selected, the residual graph must be clearly drawn.</p>  <p>Final max flow: 40</p> 	<p>10</p>	<p>3</p>	<p>3</p>
<p>5.</p>	<p>From the given set of points, $\{(6, 1), (3, 3), (7, 5), (1, 2), (0, 5)\}$, create possible line segments so that the points are not repeated. Calculate $d_1, d_2, d_3,$ and d_4 for the</p>	<p>10</p>	<p>3</p>	<p>2</p>



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created line segments and check according to SEGMENT_INTERSECT procedure if they straddle each other or are collinear. Every step in the intersection process shall be shown.

Set of points	directions d1, d2, d3, d4		
(6,1) (3,3) (7,5)	(1,2) 1 2 2 0	onsegment	Collinear Yes
(6,1) (7,5) (3,3)	(1,2) 2 2 2 0	No	
(6,1) (1,2) (3,3)	(7,5) 1 1 1 0	No	
Next Set of points	directions d1, d2, d3, d4		
(6,1) (3,3) (7,5)	(0,5) 1 0 2 2	No	
(6,1) (7,5) (3,3)	(0,5) 2 2 0 1	No	
(6,1) (0,5) (3,3)	(7,5) 0 1 1 2	onsegment	Collinear Yes
Next Set of points	directions d1, d2, d3, d4		
(7,5) (3,3) (1,2)	(0,5) 0 1 1 1	No	
(7,5) (1,2) (3,3)	(0,5) 0 1 1 2	onsegment	Collinear Yes
(7,5) (0,5) (3,3)	(1,2) 2 2 0 1	No	
Next Set of points	directions d1, d2, d3, d4		
(7,5) (6,1) (1,2)	(0,5) 1 1 1 1	No	
(7,5) (1,2) (6,1)	(0,5) 2 1 1 2	Yes	
(7,5) (0,5) (6,1)	(1,2) 2 2 1 1	No	
Next Set of points	directions d1, d2, d3, d4		
(3,3) (6,1) (1,2)	(0,5) 1 0 1 1	No	
(3,3) (1,2) (6,1)	(0,5) 2 1 0 2	onsegment	Collinear Yes
(3,3) (0,5) (6,1)	(1,2) 0 2 1 1	No	

