U.S.N.										

B.M.S. College of Engineering, Bengaluru-560019

Autonomous Institute Affiliated to VTU

June 2025 Semester End Main Examinations

Programme: B.E. **Semester: VI**

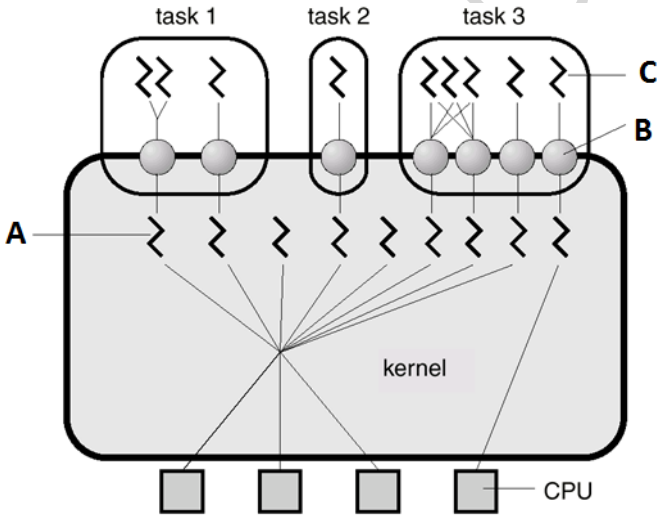
Branch: Biotechnology **Duration: 3 hrs.**

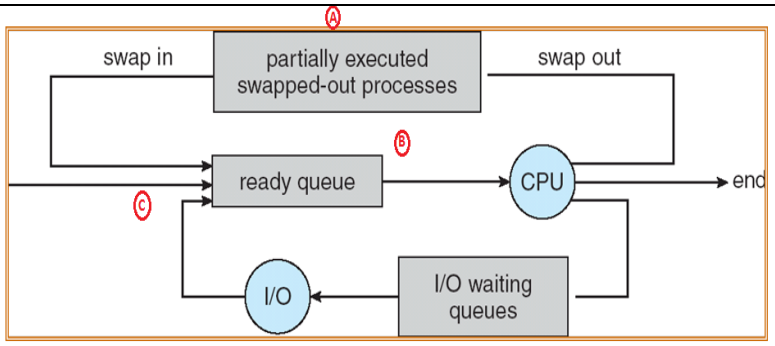
Course Code: 23BT4PCBCA / 22BT4PCBCA **Max Marks: 100**

Course: Basics of Computer Applications

Instructions: 1. Answer any FIVE full questions, choosing one full question from each unit.
2. Missing data, if any, may be suitably assumed.

Important Note: Completing your answers, compulsorily draw diagonal cross lines on the remaining blank pages. Revealing of identification, appeal to evaluator will be treated as malpractice.

		UNIT - I	CO	PO	Marks
1	a)	Discuss the various services provided by the operating system.	CO1	PO	05
	b)	What is a thread? Examine the diagram and recommend the types of threads used at points A, B, and C that can improve CPU utilization and enhance throughput for process execution. 	CO1	PO	05
	c)	Write a shell script that generates a menu from a predefined list of items, allowing the user to choose an option and execute the corresponding command.	CO1	PO	05
	d)	Explain the meaning of the following Linux file permission and show how to modify file permissions accordingly: -rwxr-xr--	CO1	PO	05
		OR			
2	a)	Examine the diagram and identify the type of scheduler applied at points A, B, and C that would optimize CPU utilization and maximize throughput.	CO1	PO	06

						
		b)	Describe with suitable example any eight Linux commands.	***CO1***	***PO***	**08**
		c)	Explain the concept of a process in an operating system. Discuss the different process states and support your explanation with a process state transition diagram.	***CO1***	***PO***	**06**
			UNIT - II			
	3	a)	The Prescriptions-R-X pharmacy chain has offered you a lifetime supply of medicines in exchange for designing their database. Based on the information collected, consider the following requirements: a. Patients are identified by P_Id, and their name, address, and age must be stored. b. Doctors are identified by D_Id, with recorded attributes including name, specialty, and years of experience. c. Pharmaceutical companies are identified by name and address, and each has a phone number. d. For each drug, record the trade name and formula. Each drug is marketed by one pharmaceutical company, and the trade name uniquely identifies a drug within that company's products. e. Pharmacies have a name, address, and phone number. f. Each patient has a primary physician, and every doctor has at least one patient. g. Pharmacies sell multiple drugs, each with a specific price that may vary between pharmacies. A drug can be sold by multiple pharmacies at different prices. h. Doctors prescribe drugs to patients. A doctor can prescribe one or more drugs to several patients, and a patient may receive prescriptions from multiple doctors. Each prescription includes a date and quantity. Create an Entity-Relationship (ER) model that accurately represents these requirements.	***CO3***	***PO2***	**10**

		b)	Create a Retail Store database with the following entities: Customers (Customer_ID, Name, Email, City, Phone) Purchases (Purchase_ID, Customer_ID, Product, Amount) Write SQL queries for the following tasks: i. Create the RetailStore database. ii. Create tables for Customers and Purchases with the given attributes. iii. Insert 4 records into each table. iv. Add a NOT NULL constraint on Customer_ID in the Customers table. v. Define primary key constraints on Customer_ID (Customers) and Purchase_ID (Purchases). vi. Add a CHECK constraint to ensure Amount is greater than 100. vii. Display details of all customers who have made at least one purchase. viii. Display details of customers from cities "New York", "Los Angeles", and "Chicago" with purchases between 500 and 2000. ix. Create a new table purchase_summary and insert records from Purchases where Amount is between 1000 and 5000.	***CO2***	***PO1***	**10**
			OR			
	4	a)	Create a Hospital_Management database with two entities: Patients and Appointments, having the following attributes: Patients (Patient_ID, name, DOB, city, contact) Appointments (Appointment_ID, Patient_ID, Doctor_name, Appointment_date, Fee) Write SQL queries for the following tasks: a. Insert 4 records into both the Patients and Appointments tables. b. Modify the tables to add primary key constraints on Patient_ID (Patients) and Appointment_ID (Appointments). c. Add a CHECK constraint to ensure the Fee is greater than 1000. d. Create a view from the Appointments table showing Appointment_ID and Fee. e. Display details of all patients who have scheduled at least one appointment. f. Display details of patients from the cities Delhi, Mumbai, and Chennai whose appointment fee is between 2000 and 5000. g. Alter the Patients table to add a new column for email. h. Remove the DOB column from the Patients table. i. Update the contact number to '9988776655' for the patient named 'Sita'. j. Create a new table appointment_summary and insert records from Appointments where the fee is between 3000 and 7000.	***CO2***	***PO1***	**14**

		b)	A flight database is used to manage information about an airline's fleet, flights, and seat reservations. Develop an ER model for this flight database based on the following requirements: a. The airline owns one or more airplanes. b. Each airplane is identified by a unique registration number, has a model number, and a seating capacity to accommodate one or more passengers. c. Each flight has a unique flight number, departure and destination airports, along with scheduled departure and arrival dates and times. d. Every flight is operated by a single airplane. e. Passengers have first names, last names, and a unique email address. f. Passengers can reserve seats on flights.	***CO3***	***PO2***	**06**
			UNIT - III			
	5	a)	In molecular biology, obtaining the reverse complement of a DNA sequence is vital for identifying gene orientation and designing primers. As part of a research group specializing in DNA sequence analysis, create a Perl script that automates the process of generating the reverse complementary strand.	***CO2***	***PO1***	**04**
		b)	Outline the various data types used in Perl, illustrating each with relevant examples.	***CO2***	***PO1***	**06**
		c)	In computational biology, nucleotide sequences are frequently processed for motif detection, alignment, and analysis. As part of a sequence manipulation tool, write a Perl script that accomplishes the following tasks on an array of nucleotides: a. Initialize an array of nucleotides: A, T, G, C, A. b. Remove the first element of the array and append it to the end, then print the updated array. c. Delete two elements starting after the first element, then print the array in reverse order and display its remaining length. d. Insert elements 'G' and 'T' after the second element of the array and print the updated array. e. Remove the last element of the array and insert it at the beginning, then print the final array.	***CO2***	***PO1***	**10**
			OR			
	6	a)	You are developing a payroll management script for a small company. Write a Perl program that performs the following tasks on employee salary data: i. Initialize a hash with five employees names as keys and their salaries as values. ii. Add a new employee and their salary to the existing hash. iii. Check if a specific employee is present in the payroll system. iv. Remove an employee's record from the payroll when they leave the company. v. Retrieve and display the salary of a particular employee when requested.	***CO2***	***PO1***	**10**

		b)	In genetic studies, converting DNA sequences into their corresponding protein sequences is essential for identifying functional genes and predicting protein structures. As part of a bioinformatics project focused on coding region analysis, write a Perl script that: i. Takes a DNA sequence as input. ii. Translates the input DNA sequence into the matching protein sequence based on the standard genetic code, beginning translation from the first nucleotide.	***CO2***	***PO1***	**10**
			UNIT - IV			
	7	a)	You are a data scientist working for a biotech company aiming to predict enzyme activity based on experimental conditions like pH level and temperature. To demonstrate this, you decide to create simulated data that models the relationship between these factors and enzyme activity. Write a Python program to simulate this scenario and complete the following tasks: a. Generate a dataset representing enzyme activity as a function of pH and temperature. b. Split the dataset into training and testing subsets for model validation. c. Train a polynomial regression model on the training data to learn how pH and temperature influence enzyme activity. d. Assess the model's performance using the test data. e. Use the trained model to predict enzyme activity under new pH and temperature conditions.	***CO3***	***PO2***	**10**
		b)	Write a Python script to compute the Reynolds number (NRe) and determine whether the flow is laminar or turbulent based on the calculated value.	***CO3***	***PO2***	**05**
		c)	You are a bioinformatician analyzing the relationship between enzyme concentration and reaction rate in an experiment. Write a Python program to generate a linear regression plot using the following data, where x is enzyme concentration (in micromolar) and y is reaction rate (in micromoles per minute): x = [0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0] y = [2.1, 4.3, 6.1, 7.9, 10.2, 12.0, 13.8, 15.7]	***CO3***	***PO2***	**05**
			OR			
	8	a)	Design a mathematical model to simulate how an epidemic spreads through a population of susceptible individuals.Your model should include the following components: a. Define model equations. b. Implement the model in code. c. Create an update function to compute state transitions. d. Run simulations over a specified time frame. e. Record simulation outputs at each step. f. Plot and analyze results to compare scenarios.	***CO3***	***PO2***	**10**
		b)	Write a Python program to calculate the Body Mass Index (BMI) given a person's weight (in kilograms) and height (in meters), and classify the BMI into categories such as underweight and obese.	***CO3***	***PO2***	**05**

		c)	Write a Python program that takes coefficients a,b,c as input and computes the roots of the quadratic equation $ax^2+bx+c=0$. The program should display the real or complex roots accordingly.	***CO3***	***PO2***	**05**
			UNIT - V			
	9	a)	You are modeling a simple drug metabolism system in the human body. The drug is metabolized by the liver into a byproduct called Metabolite. This reaction follows mass-action kinetics. Write MATLAB code to perform the following steps: a. Create a biochemical model involving two species: Drug and Metabolite. b. Define a reaction representing the conversion of Drug into Metabolite. c. Add the species Drug and Metabolite to the model. d. Set the initial amount of Drug to 50 units. e. Create a kinetic law object for the reaction. f. Set the name of the rate constant parameter used in the kinetic law. g. Define the kinetic law to follow mass-action kinetics. h. Add a rate constant parameter (k_metabolism) to the kinetic law. i. Simulate the model over a reasonable time span (e.g., 0 to 10 hours). j. Plot the simulation results to observe how Drug decreases and Metabolite increases over time.	***CO3***	***PO2***	**10**
		b)	As part of a biomedical signal processing task, you are simulating the periodic nature of a heartbeat signal. Generate data points for one complete cycle of a sine wave to mimic the heart rhythm. Let the x-values represent time in radians ranging from 0 to 4π with an interval of 0.1. Plot the sine wave to visualize how the simulated heartbeat varies over time.	***CO3***	***PO2***	**05**
		c)	You are analyzing the daily temperature variations and humidity levels in a greenhouse to optimize plant growth. Write a program to plot the temperature (sinusoidal pattern) and humidity (cosine pattern) on the same graph over a 24-hour period, with data points every 0.5 hours. Make sure to include legends for both temperature and humidity curves to distinguish them clearly.	***CO3***	***PO2***	**05**
			OR			
	10	a)	Using Matlab Simbiology toolbox, simulate the glucose insulin response for normal subject and for a type-2 diabetic patient considering a single meal dose of 75grams of glucose.	***CO3***	***PO2***	**10**
		b)	Plot the sine(x) function where x ranges from 0 to 2π with a differential of $\pi/20$ over three different ranges like x, x- $\pi/2$ and x- π using different line styles, colours, and markers.	***CO3***	***PO2***	**05**
		c)	Create a matrix with the following values using Matlab and extract a sub matrix for the following. a. Last two rows and 2^{nd} column b. 3^{rd} row with all columns c. 1^{st} two rows with 2^{nd} and 3^{rd} column.	***CO3***	***PO2***	**05**

			$\begin{bmatrix} 1 & 8 & -10 \\ -4 & 2 & 4 \\ -5 & 2 & 8 \end{bmatrix}$			

******