

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

Autonomous Institute Affiliated to VTU

June 2025 Semester End Main Examinations

Programme: B.E.

Branch: BIOTECHNOLOGY

Course Code: 23BT6PESYB / 22BT6PESYB

Course: SYSTEMS BIOLOGY

Semester: VI

Duration: 3 hrs.

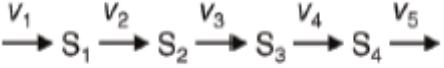
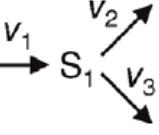
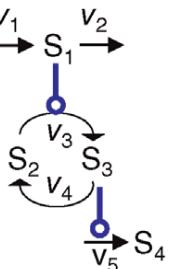
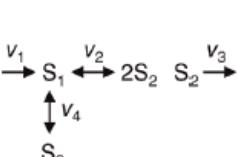
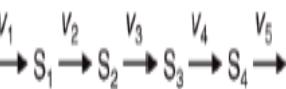
Max Marks: 100

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

UNIT - I			CO	PO	Marks
1	a)	<p>Given a biochemical network in which each species allosterically inhibits the production of the other, formulate the model equations for species S_1 and S_2. Illustrate the dynamic behavior of the system as it approaches steady state.</p> <pre> graph TD v1((v1)) --> S1[S1] S1 --> v2((v2)) v2 --> S2[S2] S2 --> v3((v3)) v3 --> S1 v4((v4)) --> S2 S2 --> v2 S1 --> v3 S2 --> v4 </pre>	CO2	PO3	05
	b)	<p>Evaluate the accuracy of the finite difference approach by approximating the absolute sensitivity coefficient using the given equation at the nominal value of $V_{max} = 5$ mM/min. Calculate approximations with $\Delta p_0 = 0.2$ (5% deviation) and $\Delta p_0 = 0.04$ (1% deviation). Data: $V_0=4$ mM/min and $K_m=1.5$.</p> $\frac{ds^{ss}}{dp} \approx \frac{s^{ss}(p_0 + \Delta p_0) - s^{ss}(p_0)}{\Delta p_0}$	CO2	PO3	05
	c)	Demonstrate the dynamic model to design an engineered genetic toggle switch.	CO2	PO3	10
OR					
2	a)	Demonstrate how a dynamic model can be used to investigate the origin of oscillations in the NF- κ B signaling pathway that drives the expression of cellular response genes.	CO2	PO3	10
	b)	<p>Consider the network</p> $\xrightarrow{k_1} S_1 \xrightarrow{k_2} S_2 \xrightarrow{k_3}$ <p>Suppose that the degradation rate $k_3 = 4$ mM/min has been measured directly, and that observations are made in two conditions, but only the pooled concentration of S_1 and S_2 can be</p>	CO2	PO 3	10

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.

		<p>measured. Perform a least square fit for the following two conditions. Compare and contrast between condition (i) and (ii)</p> <ol style="list-style-type: none"> Suppose that in the control condition $S_1^{\text{obs}} + S_2^{\text{obs}} = 6 \text{ mM}$, while in the experimental condition, the production rate k_1 has been reduced by 90% and the resulting observation is $S_1^{\text{obs}} + S_2^{\text{obs}} = 0.6 \text{ mM}$. Suppose that in the control condition $S_1^{\text{obs}} + S_2^{\text{obs}} = 6 \text{ mM}$, while in the experimental condition, the production rate k_2 has been reduced by 90% and the resulting observation is $S_1^{\text{obs}} + S_2^{\text{obs}} = 18 \text{ mM}$. 			
		UNIT - II			
3	a)	Describe how different model reduction strategies can be applied to streamline a biochemical model, especially in the context of a branched metabolic or signaling pathway	<i>CO2</i>	<i>PO3</i>	10
	b)	Using a schematic representation, distinguish between identifiable and non-identifiable parameters in the context of parameter identifiability analysis based on maximum likelihood estimation. Highlight how identifiable parameters can be uniquely estimated from the data, whereas non-identifiable parameters lead to ambiguity due to insufficient or redundant information.	<i>CO2</i>	<i>PO3</i>	10
		OR			
4	a)	Perform the quasi-steady state and quasi-equilibrium approximation for the following simple model of upper glycolysis	<i>CO2</i>	<i>PO3</i>	10
	b)	Illustrate how the cross-validation technique can be applied to identify overfitting in a predictive model.	<i>CO2</i>	<i>PO3</i>	10
		UNIT - III			
5	a)	<p>Consider the following metabolic network reactions and answer the following:</p> <ol style="list-style-type: none"> How many reactions are present in the network? Construct the stoichiometric matrix for the given reactions. Determine the elementary flux modes (or simply flux modes) involving metabolites i and ii. Identify all possible metabolic pathways or routes that the system can take based on the reactions. 	<i>CO2</i>	<i>PO3</i>	10
	i.	$ \begin{array}{ccccccc} & & & & & & \\ & \xleftarrow{v_1} & & \xrightarrow{v_2} & \xleftarrow{v_3} & & \\ S_0 & & S_1 & & S_2 & & S_3 \\ & \updownarrow v_4 & & & & & \\ & & S_4 & & & & \end{array} $	ii.	$ \begin{array}{ccccccc} & & & & & & \\ & \xleftarrow{v_1} & & \xleftarrow{v_2} & \xleftarrow{v_3} & & \\ S_0 & & S_1 & \leftrightarrow & S_2 & \leftrightarrow & S_3 \\ & \updownarrow v_4 & & & & & \\ & & S_4 & & & & \end{array} $	

	b)	In pharmacokinetics, the decay of a drug in the body often follows first-order kinetics, where the rate of elimination is directly proportional to the drug concentration. Write a MATLAB code to represent first order kinetics of drug used to model drug elimination.	CO2	PO3	05
	c)	Write a MATLAB code to represent Michelis Menten Kinetics represented by the reaction $S+E \leftrightarrow ES \leftrightarrow E+P$ for any K_m and V_{max} values.	CO2	PO3	05
		OR			
6	a)	What is a flux cone? Determine the flux cone for the following on the basis of vectors of kernel matrix K. a) A higher dimensional system with $r\text{-Rank}(N)=4$ b) An unbranched reaction chain of arbitrary length  c) A metabolic network  d) Consider the metabolic network given in c and answer the following i. Compute the stoichiometric matrix. ii. Formulate the ODE. iii. Compute the possible vectors of kernel matrix k.	CO2	PO3	10
	b)	Consider the following metabolic networks and answer the following for each network: a. Construct the stoichiometric matrix (N). b. Determine the number of reactions and compute the rank of the stoichiometric matrix (rank(N)). c. Formulate the corresponding ordinary differential equations (ODEs) for each stoichiometrically active (SA) metabolite. d. Compute the kernel matrix (K) and list its possible basis vectors i.  ii.  iii. 	CO2	PO3	10

UNIT - IV																																																																					
7	a)	Design and demonstrate a state transition diagram to represent a given state of a species.	<i>CO3</i>	<i>PO1, 5</i>	05																																																																
	b)	Discuss the features of KEGG database.	<i>CO1</i>	<i>PO</i>	05																																																																
	c)	Discuss the major features of Cell Designer tool to build a model and COPASI tool for simulation and analysis for biochemical networks and their dynamics.	<i>CO3</i>	<i>PO1, 5</i>	10																																																																
OR																																																																					
8	a)	Design a SBGN diagram and develop a model in BIOPAX format for AKT pathway	<i>CO3</i>	<i>PO1, 5</i>	10																																																																
	b)	Discuss the features of Reactome database.	<i>CO3</i>	<i>PO1, 5</i>	05																																																																
	c)	Design and demonstrate an entity-relation diagram to represent the gene regulation and transcription of a gene.	<i>CO3</i>	<i>PO1, 5</i>	05																																																																
UNIT - V																																																																					
9	a)	Consider the following model for Upper Glycolysis and answer the following	<i>CO4</i>	<i>PO2</i>	10																																																																
		<p>Reaction scheme for Upper Glycolysis:</p> $ \begin{array}{ccccccc} & \xrightarrow{V_1} & \text{Glucose} & \xrightarrow{V_2} & \text{Gluc6P} & \xleftarrow{V_3} & \text{Fruc6P} \\ & & \downarrow & & \downarrow & & \downarrow \\ & & \text{ATP ADP} & \xrightarrow{V_7} & \text{ATP ADP} & \xrightarrow{V_4} & \text{Pi} \\ & & \uparrow & & \uparrow & & \uparrow \\ & & V_5 & & V_6 & & V_7 \end{array} $																																																																			
		<p>a) Compute the stoichiometric matrix. b) How many reactions are there and what is the rank(N)? c) Formulate the ordinary differential equations to develop system biology model. d) Plot the dynamic behavior of the model. e) Compute the possible vectors of kernel matrix K.</p> <p>Flux and concentration control coefficients for the above model are represented in grey scale. Analyze the following grey scale diagram and interpret the flux and concentration control coefficients for the upper glycolysis model.</p>																																																																			
		<p>(a)</p> <table border="1"> <tr><td>\vec{C}</td><td>J_1</td><td>J_2</td><td>J_3</td><td>J_4</td><td>J_5</td><td>J_6</td><td>J_7</td></tr> <tr><td></td><td>V_1</td><td>V_2</td><td>V_3</td><td>V_4</td><td>V_5</td><td>V_6</td><td>V_7</td></tr> <tr><td></td><td colspan="7"> </td></tr> <tr><td></td><td colspan="7"> </td></tr> </table> <p>(b)</p> <table border="1"> <tr><td>\vec{C}</td><td>J_1</td><td>J_2</td><td>J_3</td><td>J_4</td><td>J_5</td><td>J_6</td><td>J_7</td></tr> <tr><td></td><td>V_1</td><td>V_2</td><td>V_3</td><td>V_4</td><td>V_5</td><td>V_6</td><td>V_7</td></tr> <tr><td></td><td colspan="7"> </td></tr> <tr><td></td><td colspan="7"> </td></tr> </table>	\vec{C}	J_1	J_2	J_3	J_4	J_5	J_6	J_7		V_1	V_2	V_3	V_4	V_5	V_6	V_7																	\vec{C}	J_1	J_2	J_3	J_4	J_5	J_6	J_7		V_1	V_2	V_3	V_4	V_5	V_6	V_7																			
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	b)	<p>Illustrate the sequential steps involved in a signaling pathway cascade that begins with receptor activation by an external stimulus. Use a schematic diagram to explain how the signal is transmitted through intracellular components to elicit a specific cellular response.</p> <p style="text-align: center;">OR</p>	<i>CO4</i>	<i>PO2</i>	10
10	a)	<p>How can we mathematically model the Aspartate-derived Threonine biosynthesis pathway to study the flux regulation and feedback inhibition by lysine, methionine, and threonine? Derive the system of ordinary differential equations (ODEs) representing the dynamics of each metabolite in the pathway, and use appropriate kinetic expressions for enzyme-catalyzed reactions, including the feedback-inhibited rate law for AK I and III.</p>	<i>CO4</i>	<i>PO2</i>	10
	b)	<p>Develop the signal transduction cascades for the following, accompanied by schematic diagrams:</p> <ol style="list-style-type: none"> MAP kinase cascade. The phosphorelay mechanism in the yeast HOG signaling pathway 	<i>CO4</i>	<i>PO2</i>	10
