Name:

Enrolment No:

UPES
End Semester Examination, December 2023

Course: Systems Biology **Semester : V**
Program: B.Tech Biotechnology **Duration : 3 Hours**
Course Code: HSBT3005 **Max. Marks: 100**

Instructions: Attempt all questions

S. No.	**Section A** **Short answer questions/ MCQ/T&F** **(20Qx1.5M= 30 Marks)**	**Marks**	**COs**
Q 1	What is the primary goal of systems biology? a. To study individual molecules in isolation b. To understand the complex interactions within biological systems c. To focus exclusively on genetics d. To develop new pharmaceutical drugs	1.5	CO1
Q 2	Which of the following is not a key component of systems biology? a. Data analysis and modeling b. Reductionism c. Experimental validation d. Integration of biological information	1.5	CO1
Q 3	Which term refers to the study of how genes are turned on or off in response to different signals or conditions? a. Structural biology b. Functional genomics c. Comparative genomics d. Synthetic biology	1.5	CO1
Q 4	In a systems biology approach, what is the significance of "crosstalk" between different omics fields? a. It indicates a lack of integration in the research. b. It represents communication between cells. c. It reveals how different biological components interact and influence each other. d. It describes the competition for funding in biological research.	1.5	CO1
Q 5	What is the role of a cofactor in enzyme-catalyzed reactions? a. It is a competitive inhibitor of the enzyme. b. It enhances the substrate binding affinity of the enzyme. c. It is an alternative name for an enzyme. d. It increases the enzyme's turnover number.	1.5	CO2

Q 6	What is the primary function of NAD+ (nicotinamide adenine dinucleotide) in biochemical pathways? a. To serve as a substrate in ATP synthesis b. To transfer high-energy electrons during redox reactions c. To stabilize enzyme-substrate complexes d. To act as a structural component of enzymes	1.5	CO2
Q 7	Which of the following is an example of post-transcriptional gene regulation in eukaryotes? a. DNA methylation b. Histone acetylation c. Alternative splicing d. Promoter binding	1.5	CO2
Q 8	What is the term for a small RNA molecule that can regulate gene expression by binding to mRNA and preventing its translation? a. siRNA (small interfering RNA) b. miRNA (microRNA) c. lncRNA (long non-coding RNA) d. snRNA (small nuclear RNA)	1.5	CO2
Q 9	Which of the following is an example of epigenetic regulation of gene expression? a. Alternative splicing b. DNA methylation c. Translation initiation d. Exon skipping	1.5	CO3
Q 10	In eukaryotes, how do miRNAs achieve specificity in targeting specific mRNAs for regulation? a. By binding to a wide range of mRNA sequences b. By perfectly complementary base-pairing with the target mRNA c. By recognizing specific sequences in the 5' cap of the target mRNA d. By partial base-pairing with the target mRNA, often involving the 3' UTR	1.5	CO3
Q 11	What term describes the metabolic pathway that breaks down fatty acids into acetyl-CoA through a series of beta-oxidation reactions? a. Glycolysis b. Gluconeogenesis c. Fatty acid oxidation d. Citric acid cycle	1.5	CO3
Q 12	Gene Ontology (GO) is a widely used resource for annotating genes and gene products. What are the three main branches of GO that categorize gene functions? a. Cellular compartment, molecular function, and gene expression b. Structural domains, metabolic pathways, and transport processes c. Biological process, cellular component, and molecular function	1.5	CO3

	d. Transcription factors, kinases, and ligand binding		
Q 13	In pathway analysis using tools like DAVID, what does the term "enrichment score" represent? a. The statistical significance of a gene's expression level b. The percentage of genes in a dataset that are annotated to a specific pathway c. The degree to which a set of genes is overrepresented in a particular pathway d. The expression level of a gene in a given biological sample	1.5	CO4
Q 14	In pathway analysis, what is the primary goal of identifying "significant pathways"? a. To determine the shortest pathways in a network b. To identify pathways with the highest number of genes c. To understand the biological processes that are most relevant to a specific dataset d. To predict the regulatory genes in a pathway	1.5	CO4
Q 15	Gene Ontology terms often include hierarchical relationships between more general and more specific terms. What type of structure does this represent? a. Directed acyclic graph (DAG) b. Linear regression model c. Hierarchical tree structure d. Correlation matrix	1.5	CO4
Q 16	Which mathematical modeling technique is used to analyze the behavior of genes in biological networks and predict their interactions? a. Structural equation modeling b. Network analysis c. Multiple regression analysis d. Time series analysis	1.5	CO4
Q 17	StochSim is a software tool used for stochastic modeling in systems biology. What does "stochastic modeling" refer to in this context? a. Modeling based on deterministic equations b. Modeling that ignores random fluctuations in biological systems c. Modeling that takes into account probabilistic events and random variability d. Modeling of only simple linear systems	1.5	CO5
Q 18	Which of the following software tools is best suited for simulating the behavior of a large-scale biochemical network with stochastic interactions between molecules? a. eCell b. Virtual Cell c. StochSim d. BioNetS	1.5	CO5

Q 19	Quantitative modeling of E. coli metabolism often involves the use of metabolic flux analysis. What does "metabolic flux" refer to in this context? a. The rate of substrate utilization in a bacterial culture b. The flow of water through bacterial cell membranes c. The rate of chemical reactions within metabolic pathways d. The distribution of bacteria in a colony	1.5	CO5
Q 20	Which type of modeling approach is commonly used to predict the impact of gene deletions or mutations on E. coli metabolism? a. Genome sequencing b. Structural biology analysis c. Constraint-based modeling d. Protein structure prediction	1.5	CO5
Section B **(4Qx5M=20 Marks)**			
Q 1	Explain the significance of omics technologies in the field of systems biology.	5	CO1
Q 2	Describe the main features and functionalities of pathway databases like DAVID, Gene Ontology, and Pathway Miner	5	CO2
Q 3	Discuss how genome-scale models can be used to predict cellular behavior under different growth conditions, nutritional environments, or genetic perturbations.	5	CO3
Q 4	Describe the key features and tools provided by eCell for simulating and visualizing cellular processes.	5	CO4
Section C: Case study **(2Qx15M=30 Marks)**			
Q 1	Consider a scenario where a medical team is faced with a challenging case of a newly diagnosed diabetes patient. The patient's condition is complex, as it involves the interplay of genetic factors, lifestyle choices, and the gut microbiome. The team decides to employ GSMs to develop a personalized approach to manage the patient's diabetes effectively. The model predicts the patient's optimal dietary choices and exercise routines for blood glucose control, considering individual genetic variations. It identifies key metabolic pathways and potential drug targets for developing personalized pharmaceutical interventions. This helps healthcare professionals track the patient's progress and make informed decisions about treatment adjustments. Based on your understanding of GSM, answer the following questions	15 marks (5 marks each)	CO2

	A) What types of data should be collected and integrated to create the personalized genome-scale model for the diabetes patient in this case? B) Explain the process of constructing a personalized genome-scale model. Discuss how personalized GSM provides valuable insights into the patient's diabetes management:		
Q 2	Metabolic pathway analysis is a powerful tool in biotechnology, allowing researchers to manipulate and optimize cellular processes. Enzyme engineering involves the modification of enzymes to enhance their catalytic properties. Imagine a biotechnology company that specializes in the production of a high-value compound, such as a biofuel, pharmaceutical precursor, or specialty chemical. They are facing challenges in optimizing the metabolic pathway responsible for compound production. Several strategies can be employed to enhance the efficiency of the pathway such as modify enzymes within the pathway to improve their catalytic efficiency, maintain low substrate and product concentrations to alleviate feedback inhibition and maintain reaction equilibrium, utilize enzyme inhibitors or genetic modifications to mitigate the effects of feedback inhibition, etc. Based on your understanding of metabolic pathway analysis, answer the following questions: A) Explain how the company identifies bottlenecks or limitations within the pathway that hinder efficient compound production. What analytical methods or data are used for this? B) Explain the strategies used to optimize the overall metabolic pathway. C) How might this optimized pathway impact the production of the target compound in various applications?	15 marks (5 marks each)	CO4
Section D **(2Qx10M=20 Marks)**			
Q 1	a) Explore the synergy between omics technologies, biochemical kinetics, and genome regulation in systems biology. b) Describe how quantitative data from omics can be integrated with biochemical kinetic models to create comprehensive models of biological systems.	**10**	**CO3**
Q 2	a) Highlight the challenges in mathematical representation and network analysis in cell biology, such as data integration, model validation, and parameter estimation. b) Reflect on the potential impact of advances in mathematical modeling and network analysis on fields like cancer biology, drug development, and regenerative medicine.	**10**	**CO5**