Name: **Enrolment No:**	

UPES

End Semester Examination, December 2024

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 central goal of systems biology? a) Study individual cellular components b) Model and understand the interaction of biological systems as a whole c) Develop new laboratory techniques d) Analyze DNA sequences	1.5	CO1
Q 2	What does the Michaelis constant (Km) represent in enzyme kinetics? a) Maximum reaction rate b) Substrate concentration at half-maximum velocity c) Energy required for activation d) Total enzyme concentration	1.5	CO1
Q 3	Which of the following is not a factor determining the activity of an enzyme? a) Association with regulatory protein b) Feedback regulation c) Allosteric regulation d) Nucleotides	1.5	CO1
Q 4	Epigenetic modifications include: a) Changes in DNA sequence b) Post-translational modifications of proteins c) DNA methylation and histone modifications d) RNA editing	1.5	CO1
Q 5	Explain the significance of the pentose phosphate pathway in cellular metabolism.	1.5	CO1
Q 6	The Reactome database is primarily used to study: a) Genomics data b) Biochemical reactions and pathways c) Epigenetic regulation	1.5	CO2

	d) Microbial diversity		
Q 7	Annotation of metabolic genes in prokaryotic genomes often relies on: a) Ribosome profiling b) Homology-based methods c) Polymerase Chain Reaction (PCR) d) Single-cell sequencing	1.5	CO2
Q 8	Functional annotation of hypothetical genes can be improved by: a) Pathway-based approaches b) PCR analysis c) Flow cytometry d) Northern blotting	1.5	CO2
Q 9	What is a primary metabolic pathway? a) Pathways associated with antibiotic production b) Pathways essential for cell survival and growth c) Pathways involved in toxin production d) Pathways restricted to non-coding regions	1.5	CO2
Q 10	The study of organism-specific metabolic pathways can help in: a) Constructing phylogenetic trees b) Identifying novel enzymes and biocatalysts c) Developing RNA vaccines d) Determining ribosome structures	1.5	CO2
Q 11	Which computational tool is essential for pathway optimization? a) RAST b) Flux Balance Analysis (FBA) c) RNA-Seq d) Western blot	1.5	CO3
Q 12	Which technique is typically used to study the kinetics of enzyme-catalyzed reactions in *E. coli*? a) Michaelis-Menten kinetics b) Western blotting c) RNA-seq d) PCR amplification	1.5	CO3
Q 13	Which of the following is a key assumption in flux balance analysis (FBA)? a) The system is always in equilibrium b) Fluxes are assumed to be constant across all conditions c) Reaction fluxes are constrained by metabolic network stoichiometry d) Only aerobic conditions are considered	1.5	CO3
Q 14	Which of the following types of networks is essential for understanding cell signaling? a) Regulatory networks b) Neural networks	1.5	CO3

	c) Metabolic networks d) Pathogen-host interaction networks		
Q 15	Neural networks in systems biology are used to: a) Predict brain activity based on cellular interactions b) Model metabolic networks c) Predict the structure of proteins d) Understand gene regulatory networks	1.5	CO3
Q 16	The combination of E. coli genome sequencing with metabolic network modeling allows for: a) A better understanding of genetic diseases b) Improved fermentation and bioproduction processes c) Identification of cancer biomarkers d) Prediction of protein-protein interactions	1.5	CO4
Q 17	What does SBML stand for? a) System Biology Markup Language b) Standard Biological Modeling Language c) Synthetic Biology Markup Language d) Systematic Biology Model Language	1.5	CO4
Q 18	Virtual Cell is an open-source software primarily used for: a) Modeling biological reaction kinetics b) Network analysis c) Gene expression profiling d) DNA sequencing	1.5	CO4
Q 19	In the lac operon model, the repressor protein binds to which region to inhibit transcription? a) Operator b) Promoter c) Enhancer d) Terminator	1.5	CO4
Q 20	In the lambda phage switch model, the Cro protein favors the transition to: a) Lysogenic cycle b) Lytic cycle c) DNA replication d) Transcription of the lac operon	1.5	CO4
Section B: Short-Answer Questions (4Qx5M=20 Marks)			
Q 1	Define the role of computational modeling in systems biology. How does it aid in interpreting data from various omics technologies?	5	CO1
Q 2	Discuss pathway databases that help to predict metabolic capabilities in an organism? Explain with reference to a specific pathway.	5	CO2

Q 3	How can flux balance analysis (FBA) guide the engineering of metabolic pathways?	5	CO3
Q 4	Explain the concept of Gene Ontologies (GO) and their importance in understanding gene functions and biological pathways.	5	CO4
	Section C: Case study (2Qx15M=30 Marks)		
Q 1	In a recent study, a research team utilized systems biomedicine to identify biomarkers associated with breast cancer. The approach involved integrating genomic, proteomic, and metabolomic data to create a comprehensive model of the disease's biological processes. Using bioinformatics tools and pathway analysis software, the team mapped the interactions between key molecules and identified potential therapeutic targets. Additionally, they focused on identifying genetic mutations that contribute to cancer progression and explored how these mutations affect metabolic pathways, gene expression, and protein activity. Based on your understanding of systems biology, answer the following questions: A) Explain the role of integrating genomic, proteomic, and metabolomic data in systems biomedicine for cancer research. B) Discuss the significance of bioinformatics tools and pathway analysis software in identifying potential therapeutic targets for breast cancer? List any two such tools. C) Mention the potential benefits and challenges of using systems biomedicine to identify biomarkers for early breast cancer detection.	15 marks (5 marks each)	CO3
Q 2	A pharmaceutical company is using a systems pharmacology approach to develop a new drug for Alzheimer's disease. The company uses computational models to predict how the drug will interact with various biological pathways involved in neurodegeneration. In addition, they are investigating the pharmacokinetics and pharmacodynamics of the drug to determine the optimal dosage and treatment schedule. Based on your understanding of systems biology, answer the following questions: A) Define systems pharmacology, and how is it applied to drug discovery? Explain the significance of pharmacokinetics and pharmacodynamics in drug development. B) How does computational modeling help in the design of drugs for complex diseases like Alzheimer's? C) List challenges that might arise when applying systems pharmacology in the development of Alzheimer's drugs?	15 marks (5 marks each)	CO4

	How can personalized medicine be integrated into systems pharmacology for Alzheimer's treatment?		
Section D: Long-Answer Questions (2Qx10M=20 Marks)			
Q 1	A) Explain key steps of genome regulation. Discuss the concept of epigenetic regulation of gene expression. B) Discuss the role of microRNAs (miRNAs) in post-transcriptional regulation? Explain the mechanism of RNA-induced silencing complex (RISC).	5+5 marks	CO2
Q 2	Write the applications of flux analysis in metabolic engineering for industrial bioprocesses. How can flux balance analysis be combined with transcriptomics to enhance pathway predictions?	10 marks	CO4