Trouth Ray Songh

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT TEST-3 EXAMINATION- Dec-2017

B. Tech (7th Semester) Bioinformatics

	B. Tech (/ Semes	ster) Bioinformatics		
	COURSE CODE: 14B1WBI732	MAX	X. MARKS: 35	
	COURSE NAME: Computational Systems Biology			
	COURSE CREDITS: 3		MAX. TIME: 2 hours	
	Q1. Discuss the following models of TRN with suitable example:		(2x3 = 6 Marks)	
	a) Boolean Model b) Continuous	Model c) Single mo	c) Single molecule model	
	Q2. Explain the following with a reference points towards any real biological system: $(2x3 = 6 \text{ Marks})$			
)	a) Biological toggle switches b) Reverse eng	gineering		
	c) Temporal expression in network motifs			
	Q3. Discuss system and its basic properties. How a biological system evolve? Explain your views with			
	the justification of network based computations and	parameters.	(3 Marks)	
	Q4. Explain the G protein life cycle and describe the ODEs for the same.		(2 Marks)	
	Q5. What is a phosphorelay system and what is the difference between this and phosphorylation system?			
			(2 Marks)	
	Q6. What are the three levels of abstraction in metabolic networks?		(2 Marks)	
	Q7. Compare and contrast metabolic network with s	signal transduction.	(2 Marks)	
	Q8. Define stoichiometric coefficients with example.		(2 Marks)	
	Q9. How many vectors and matrices are involved in describing a metabolic network mathematically?			
			(2 Marks)	
	Q10. What are the different layers of information required in a genome scale metabolic network			
	reconstruction?		(2 Marks)	
	Q11. What is the problem with carbon chemistry and metabolic network reconstruction		n? (2 Marks)	
Q12. What are the assumptions of Flux Balance A		alysis?	(2 Marks)	
	Q13. Define the following:		(0.5x4=2 Marks)	
	a) Flux cone	b) Objective Function		
	c) Constraint based modeling d) Lower and upp		s of flux	