NTNU – Trondheim
Norwegian University of Science and Technology

Department of Biology

Examination paper for BI3019
Systems Biology: Resources, standards and tools

Academic contact during examination: Martin Kuiper

Phone: 91897322

Examination date: 4 June 2015

Examination time (from-to): 9:00 – 13:00

Permitted examination support material: Dictionary of English

Other information: Credits 7.5

Language: English

Number of pages: 3

Checked by:

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Date   Signature

Exam Questions BI3019 – 4 June 2015 - Systems Biology

Your answers should typically be at least ½ page of written text.
One question can be skipped (optional)

1. Describe three ways to integrate data about an experimental system, and explain how integration helps you to obtain more and better information about a biological system. Consider in your answer for instance high throughput data, orthology, and knowledge bases.

2. Describe what is meant with the name 'interactome'; describe how interactome information can be generated (mention technologies as well as experimental designs) and explain how this type of information can be integrated with other 'omics' data.

3. Describe the STRING database, explain how it is built, discuss the different types of data that it contains, and describe analysis methods that STRING supports.

4. Describe the four steps of systems biology and provide for each of these steps examples of what this means in practice. You may use a drawing to illustrate these steps.

5. Describe the network shown in the figure below (left panel), focusing on how well network nodes are connected. Describe what is shown in the two graphs to the right of it and discuss what analysis method has been used to produce these graphs, and how they can help to understand the network.
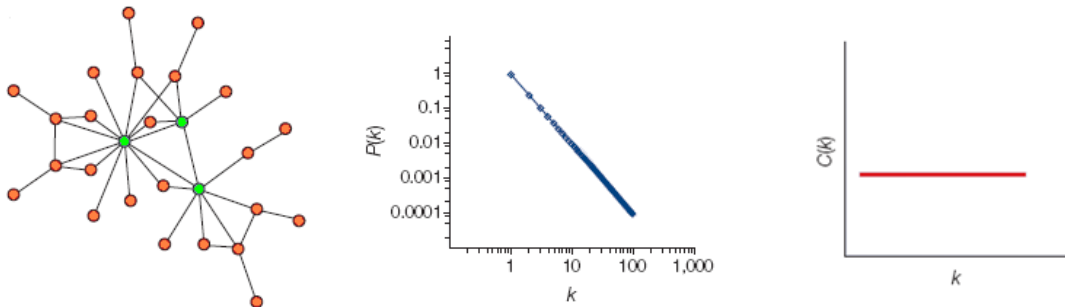
6. Data exchange languages include PSI-MI, BioPAX, and SBML. Checklists include MIAME, MIAPE and MIRIAM. Discuss similarities and differences between exchange languages and checklists, how they relate to each other and how they can help in analysing experimental data.

7. What is an 'Ontology'? Provide an example of an ontology and describe at least 3 different ways in which ontologies can be used, in the analysis of experimental data.

8. You have performed an experiment that resulted in a gene expression dataset. Describe three different software tools and analysis strategies that would give you information about pathways that are perturbed by your experiment.

9. You study the process of cell cycle control. Discuss the arguments to use either Boolean modelling or Ordinary Differential Equation modelling for supporting your research, discuss the amounts and types of data that you need for these different approaches, and argue which modelling approach you prefer to use.

10. You have a set of 75 genes that prove to be significantly perturbed by your experiment. Describe step by step how you would use the Cytoscape plugin BiNGO for understanding the biological processes affected by your experiment.

11. Compare text mining with text curation, describe the differences, and discuss how these two approaches can be used together for building knowledge bases.

12. Describe what you know about the General Systems Theory, and why it has laid the foundation for Systems Biology as we practice it today.

13. Provide brief descriptions of the IntAct database, the REACTOME database base and the KEGG database. You may consider for instance the type of data/knowledge in these resources, the functionality provided and the integration of information in these databases with information from other resources.