NTNU – Trondheim
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Department of Biology

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

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Exam Questions BI3019 – 18 December 2015 - Systems Biology

Your answers should typically be at least ½ page of written text.
You may skip one of the 13 questions (optional)

1. Systems biology is sometimes called 'integrative biology'. Describe some of the different types of data, information and knowledge (collectively called: 'data') that can be integrated, and explain how such data integration can help you to obtain more and better understanding of a biological system. Discuss in your answer not only the different types of data that are available for this, but also where you can obtain these data.

2. Describe what is meant with the name 'phenome'; describe how phenome information can be generated: mention experimental designs and approaches as well as ways to describe such information (e.g. in the form of tables, or if you could use ontologies for this). Explain how this type of information can be integrated with other 'omics' data.

3. Describe the IntAct database, explain what its purpose is, how it is built, what data formats, data standards and data exchange mechanisms IntAct uses, and discuss the different types of information (biological components and their relationships) that it contains.

4. The Gene Ontology is important for the analysis of experimental results, for instance a set of regulated genes. Explain at least three characteristics of the Gene Ontology, describe a software tool that you could use to analyse your gene set, and provide a step-by step description of how you would do the analysis, using the most up-to-date version of the gene ontology annotation.

5. Pathway-based analysis can provide a useful help in analysing an omics dataset. Describe three different pathway-based analysis possibilities using either free or commercial software tools, and provide in short the steps that you would follow for such analyses.

6. Network-based analysis as for instance with Cytoscape does not allow you to easily understand what the effects of perturbations are on a system. For this you need to use mathematical simulation tools. Describe at least two tools that are available for this, explain how you would create a model or import a model from a public repository and mention what kind of information you would be able to obtain from model simulations.

7. You have downloaded a large protein-protein interaction network from a public database. Describe how you would use Cytoscape to perform a graph-based analysis of this network (using NetworkAnalyzer). Explain some of the results that you would expect to see in this analysis, focusing on network structure and node connectivity. You may use drawings in your explanation.

8. When are genes 'orthologous'? Explain how gene orthology can help you to gain insight in the function of a gene. Compare the information that you can expect from orthology and another form of homology: paralogy.

9. You have 3 genes that are very significantly upregulated in a microarray dataset. Describe how you can find out what is known about their function, and whether those genes are related to each other, using the iHOP web tool.

10. You are interested in analysing the results from a microarray experiment. You decide to analyse the data by overlaying it on a protein-protein interaction network. Describe how you can get access to such a network, what your criteria would be to select such data from public resources, and how you would perform a joint analysis with microarray data using Cytoscape and some of its apps.

11. Argue why you need a systems biology approach rather than a purely reductionist approach in order to understand the function of a biological process of an organism. You may refer to 'General Systems Theory', 'causation' and 'emergent behaviour', in your answer.

12. Give an example of a Next Generation Sequencing technology, explain the technology and discuss how it may replace microarray technology for the analysis of gene expression.

13. Describe the GeneMANIA resource, describe what types of information it contains, and how you may use it to get more insight into a particular experimental result.