NTNU – Trondheim
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Department of Biology

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

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Date Signature

Exam Questions BI3019 – 2013 - Systems Biology

Your answers should typically be at least ¼ page of written text.
One question can be skipped (optional)

1. You have performed a microarray experiment and you now need to analyse the result file. Describe the benefits of using a pathway-based analysis method, and provide three tools (names + short description) that are available for such an analysis.

2. Describe what is meant with the name 'phenome'; explain how phenome information is obtained; and describe how this type of information can be integrated with other 'omics' data and what can you learn from it about gene function.

3. Describe an example of Next Generation Sequencing, or 'deep sequencing', and discuss how it may replace microarray technology for the analysis of gene expression.

4. Provide three arguments for using a systems biology approach to biological discovery, rather than a more common reductionist approach.

5. Discuss the issue of 'network robustness', describe how it arises from particular network characteristics, and how evolution may have designed these networks.

6. Why are 'standard data exchange formats' important; name three exchange formats and describe in what context these are used: types of information, databases and tools.

7. Describe the Gene Ontology, describe three of its structural characteristics and discuss its importance for the analysis of experimental data sets.

8. You have performed a microarray experiment that resulted in a list of 100 significantly regulated genes. Provide a step-by-step description how you can find evidence for overrepresentation of specific gene classes in Cytoscape, and discuss the important statistical decisions to consider in this analysis.

9. Compare Boolean modelling, Ordinary Differential Equation modelling and Stochastic modelling with respect to various strengths and weaknesses: for instance the amount of data that you need, the type of data, the size of the models that you can use these for and provide arguments concerning which of these approaches you would chose if you would have a network map with 50 components.

10. You have a pathway model from the Panther database, explain what your approach would be to identify new pathway proteins from a variety of public resources, and discuss how you can ensure that the new proteins would be good candidates for experimental validation.

11. Describe three ways to make use of multiple independent sources of data, and explain how integration of such data 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.

12. You are working in the field of 'cell cycle control', and you are especially interested in how the cell cycle process can become deregulated and result in unlimited growth / cancer. Describe the steps you would take to support your project with modelling in CellDesigner, and the resources that you have available to build a model.

13. Provide brief descriptions of the REACTOME knowledge base, the KEGG knowledge base and the ENSEMBL genome browser. You may consider for instance the type of knowledge in these resources, the functionality provided and the integration of the knowledge bases with other resources.