

Norges teknisk-naturvitenskapelige universitet
Institutt for Biologi
Norwegian University of Science and Technology
Department of Biology



EKSAMENSOPPGAVE I BI3019:
Systems Biology: Resources, standards and tools

EXAMINATION IN BI3019:
Systems Biology: Resources, standards and tools

Faglig kontakt under eksamen/Contact person/Subject teacher during exam:

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Eksamensdato/Date: 27. May 2013

Eksamenstid/Number of hours: 4

Studiepoeng/Credits: 7.5

Tillatte hjelpemidler/Permitted aids: Dictionary for English

Språkform/Languages:

bokmål: No

nynorsk: No

engelsk: Yes

Antall sider vedlegg/attachment: 2

Sensurdato/Grades to be announced on: 17. June 2013

Exam Questions BI3019 – Spring 2013 - Systems Biology
QUESTIONS HAVE EQUAL WEIGHT

1. Describe the different steps that you would take in a systems biology approach to study a biological problem, and discuss their relevance by giving examples.

2. What is meant with the term ‘emergent behavior’, in a systems biology context.

3. Describe the process of text mining, and discuss examples of how it can be applied. This should also include a discussion of particular tools that are available, or are based on text mining.

4. What is meant with the term ‘phenomics’, and how would you build a phenomics dataset for yeast.

5. Describe the use of transcription microarrays and compare their application (advantages/disadvantages) relative to next generation sequencing technology.

6. List three major knowledge bases and describe for each one how you would use it to perform typical tasks in a Systems Biology approach.

7. What is the significance of the observation that biological networks show scale free characteristics; describe one mechanism that explains why evolution favored the development of scale free systems.

8. Why are checklists like MIAME important for Systems Biology.

9. What is an ontology, describe at least three of its characteristics and provide an example.

10. Describe the use of BiNGO, discuss the important things to consider in the analysis, and how to interpret the results.

11. Describe the benefits of performing an integrated analysis of transcriptome and proteome data, rather than an independent analysis of these individual datasets.

12. Compare Stochastic and Ordinary Differential Equation based modeling with respect to the amount of data that you need, the type of data, and the results that you may get from these types of modeling.

13. What is the Systems Biology Graphical Notation and what is it important for.

14. Compare Cytoscape and CellDesigner with respect to their use for network and pathway based analysis.

Your answers should typically be at least $\frac{1}{4}$ page of written text.