



NTNU – Trondheim
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Department of Biology

Examination paper for BI3019

Systems Biology: Resources, standards and tools

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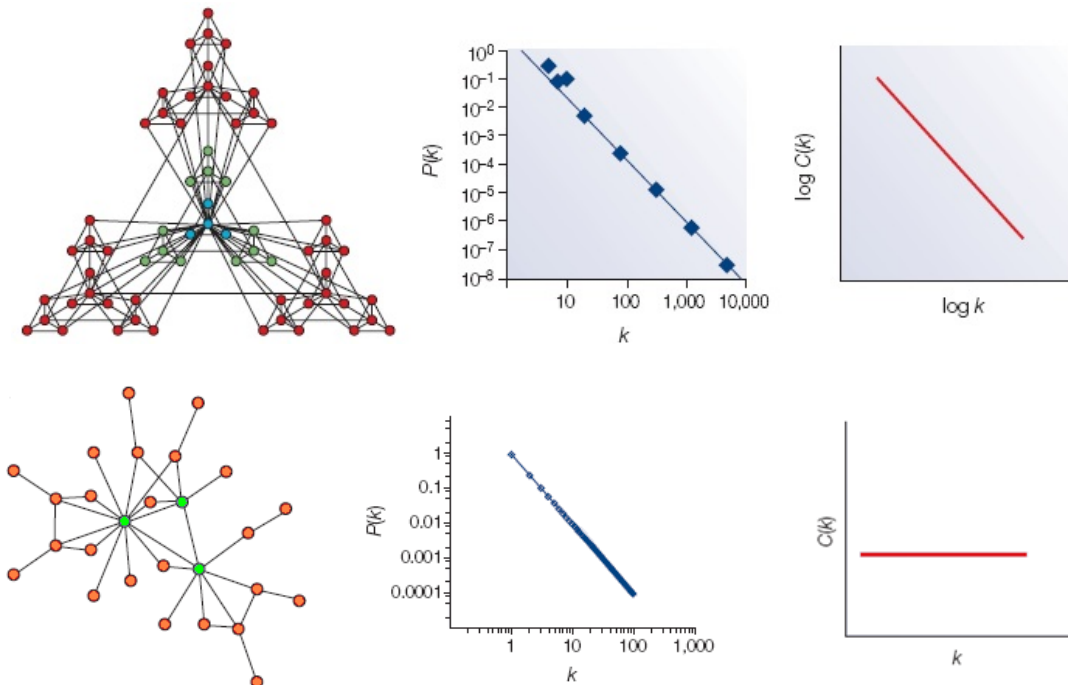
Date

Signature

Exam Questions BI3019 – 29 November 2017 - Systems Biology

Your answers should typically be at least ½ page of written text.

1. Describe at least 4 different types of edges, or relationships, that can be used in a Cytoscape network, and explain for each of them how you can use it to understand the biological relations between the genes or proteins in your network.
2. Describe the Gene Ontology, describe three of its structural characteristics (including its graph structure) and discuss its importance for the analysis of experimental data sets.
3. Both Leroy Hood and Hiroaki Kitano have described different steps that can be followed in a Systems Biology approach. Describe four steps that can be used in a repeating cycle, and how they can be used to gain a better understanding of a biological system.
4. Discuss the two networks shown below, and compare them using the network metrics shown in the graphs on the right. Consider in your answer the node degree, clustering coefficient and the existence of network modules.



5. 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.
6. Describe the GeneMANIA tool, describe what types of information it contains, and how you may use it to get more insight into an experimental dataset.
7. 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.
8. You have built a biological network in Cytoscape. Describe step by step how you would further expand this network with a large protein-protein interaction dataset related to cancer, obtained from a public resource. Describe how you can compare your network with the larger network.
9. Describe what is meant with the name 'transcriptome'; describe at least two technologies that you can use to generate transcriptome information and explain how this type of information can be integrated with other 'omics' data.
10. Name two different pathway databases; describe how they are constructed, what types of pathways they cover and how they can be used to help you analyse and understand a biological network that you are studying.
11. 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 they have a shared biological function, using text mining resources like iHOP or LitInspector.
12. Compare the two Cytoscape apps BiNGO and ClueGO and describe at least 3 similarities and 3 differences between these tools.