

341 Introduction to Bioinformatics:

Biological Networks

Tutorials 4 and 5 -- February 18 and 25, 2010

1. In this exercise you will be comparing protein interaction data for a small family of proteins called glutaredoxins.
 - a) Go to the Saccharomyces genome database (SGD) at www.yeastgenome.org and identify the five glutaredoxin genes found in this organism. List the gene names, all aliases, the systematic names, and a brief description for each gene.
 - b) Identify the interactions for each glutaredoxin identified by Ito and coworkers. Go to their web site at <http://itolab.cb.k.u-tokyo.ac.jp/Y2H/> and download the full data file. From this file, draw an interaction map that illustrates all interactions identified for each glutaredoxin in this experiment. Identify name or function of each gene product.
 - c) Identify the interactions for each glutaredoxin identified by Uetz and coworkers. Go to their web site at http://depts.washington.edu/sfields/yp_interactions/twohybrid_interaction_data.xls. Try to identify the interactions and draw an interaction map for each glutaredoxin in this experiment. Identify name or function for each gene product.
 - d) Compare the interactions that you identified from the original data sets. Where are overlaps or differences? Discuss the reason for possible discrepancies.
 - e) For this exercise you will take preliminary look at the Cytoscape network visualization tool. To download Cytoscape on your computer go to www.cytoscape.org and follow the instructions for installation. To download the Cytoscape-formatted interaction data for Grx2, go to SGD and click the "Batch download" link on the left side of the page. Enter Grx2 under "Option 1", select "physical interactions", and then submit. Follow the instructions for downloading the file. Start Cytoscape, in the "File-load-Network" menu, enter the file name of the interaction file that you downloaded from SGD. Under the "Layout" Menu, select "Apply Spring Embedded Layout – all nodes". Find Grx2 in this network. To which nodes is it connected? What is this protein and what is its function. Compare what you see in the Cytoscape network to what you have identified from the Ito and Uetz data, respectively. What is the most highly connected node in the Cytoscape network? Using the functional description for the protein from SGD, provide a biological explanation for this highly connected node.