

Exercises:

Networks and Interactions

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In this practical we will use free, web-based resources to construct networks from gene lists. In doing so, we will be able to visualise interactions between genes in gene lists, and possibly gain further understanding of the pathways that may be of interest to our research.

Exercise 1: Network construction and exploration using geneMANIA

You should find a file called “yeast_genes.txt” in your Data folder. This list contains 33 genes from which we will construct a network.

- Navigate to geneMANIA in a web browser (<http://www.genemania.org/>, or search for ‘genemania’).
- Copy and paste the gene names from the file into GeneMania. A drop down selection of species should appear when you click on the human icon (our data is from yeast - *Saccharomyces cerevisiae*).

The constructed multiple network should appear.

- Use the options buttons on the left of the screen to change the layout to circular, vertical and back to the default.
- Select the More options/3 dot icon at the top of the screen, navigate to the advanced options and change the max resultant genes to 20. Re-run the analysis.
This will add in any extra genes (up to the max number selected) that were not in your original query set, but that GeneMania believes are related. The original genes are displayed as striped nodes.
- Change the options so that the ‘predicted’ and ‘co-localisation’ networks are no longer shown in the multiple network.
- What are the 5 most significantly enriched functions?
- Highlight genes from the most significantly enriched function in the network.
- Manually move the nodes of the network until you are happy with the layout.
- Save the image of the network.
- Save the interaction information so that we could import the network into other programs, such as Cytoscape, for manipulation and analysis.

Exercise 2 – Network exploration using STRING

Now we will construct a network of the same genes using STRING.

- Navigate to STRING in a web browser (<http://string-db.org/>, or search for ‘string network’).
- Select the Multiple proteins options from the menu on the left, enter the genes and run the analysis.
- In the settings menu, look at the evidence, confidence and action views of the network.
- Going back to the evidence view, change it so that only data/interactions coming from experiments, databases and co-expression studies are shown.
- Have a look at the analysis option to see which ontology categories are most highly enriched.
- In the parameters, update the required confidence score to 0.7 and reconstruct the network.
- Set the max number of interactors to 20, does this make the network clearer? If not remove these additional nodes.
- Double click on a node to view more information
- Remove any disconnected nodes.
- Save your favourite view of the network as an SVG file.
- Save the network interaction data.