

# README

## Cytoscape Navigation Basics

Cytoscape networks are navigated using the mouse. Click and hold the right mouse button while dragging to zoom in and out of the network. Click and hold the middle mouse button while dragging to pan around the network from left to right and top to bottom. Most nodes/wedges are clickable with the left mouse button, which shows additional information in the bottom panel. For more information on Cytoscape, please see the Cytoscape user manual at <http://www.cytoscape.org>

## About the Networks

Collins et al	Consolidated PE	Interactions are scored with the PE score, and complexes predicted using the MCL algorithm at inflation 3.1, on interactions with PE $\geq 3.19$ .
Pu et al	Gavin MCL Reclustered	Interactions published by Gavin et al (scored with socio-affinity index) are clustered using MCL at inflation 2.9.
Gavin et al	Gavin Original	Original published network & predicted complexes from Gavin et al. Interactions scored with socio affinity index, and complexes predicted using hierarchical clustering.
Krogan et al	Krogan Original	Original published network & predicted complexes from Krogan et al. Interactions scored using supervised machine learning, and complexes predicted with MCL at inflation 1.9
Pu et al	Krogan PE	A new interaction network was derived from the raw TAP/MS Krogan dataset, and scored with the PE score. Complexes were predicted using MCL at inflation 2.3.
Pu et al	Gavin PE	Interactions from Gavin et al were rescored with the PE score, and complexes predicted using MCL at inflation 2.7.
Mewes et al	MIPS Complexes	Complexes published by the Munich Information Centre for Protein Sequences (MIPS).

## Post-processing

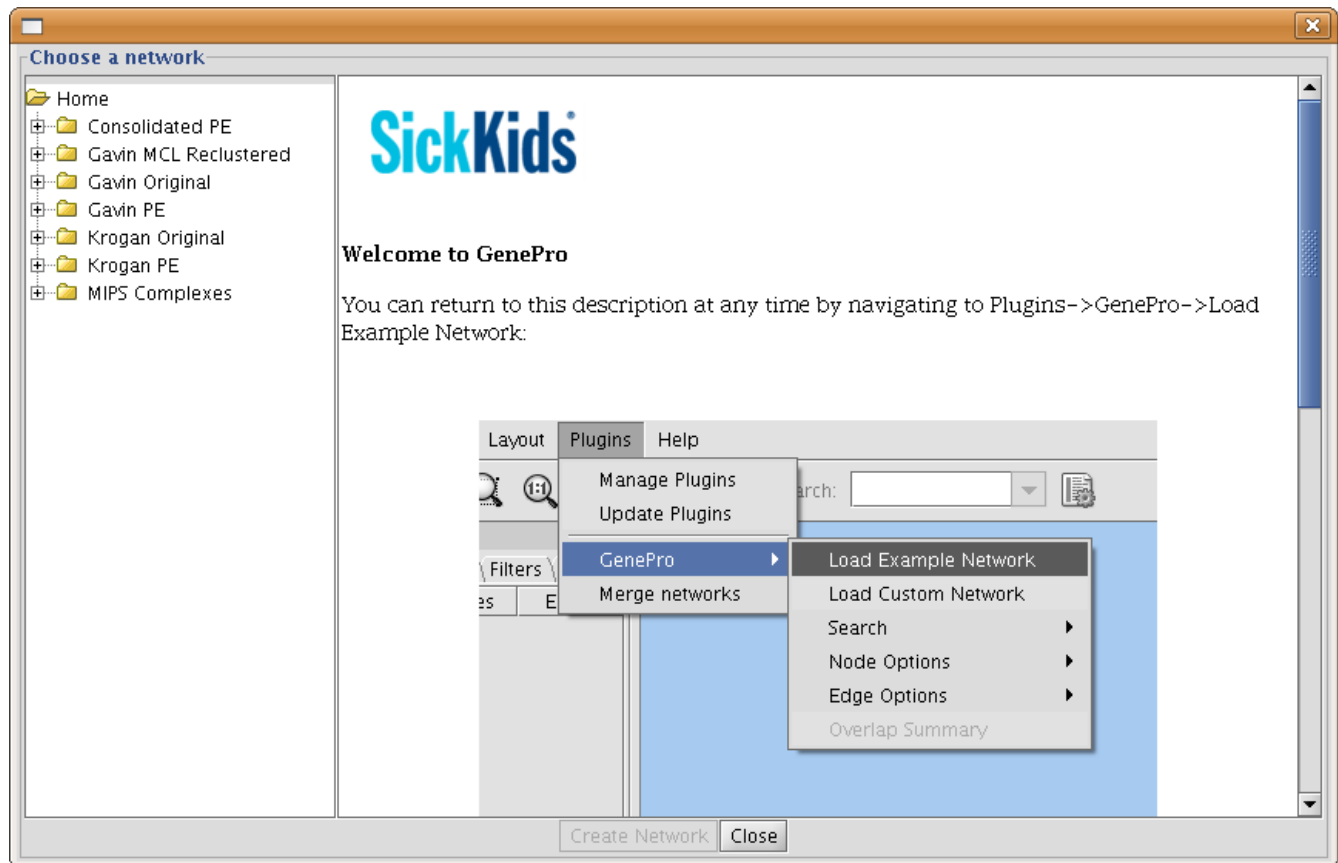
The MCL graph clustering algorithm fully partitions the interaction network into distinct clusters. This does not reflect biological reality, where proteins can be shared between complexes. After clustering, a post-processing step can be employed to introduce shared components indicated visually in GenePro with an edge. If a component of an MCL-predicted complex is found to have many interactions with an adjacent cluster, the post-processing step will add that protein to the adjacent cluster. For full details, see Pu et al (Proteomics 2007).

## About GenePro

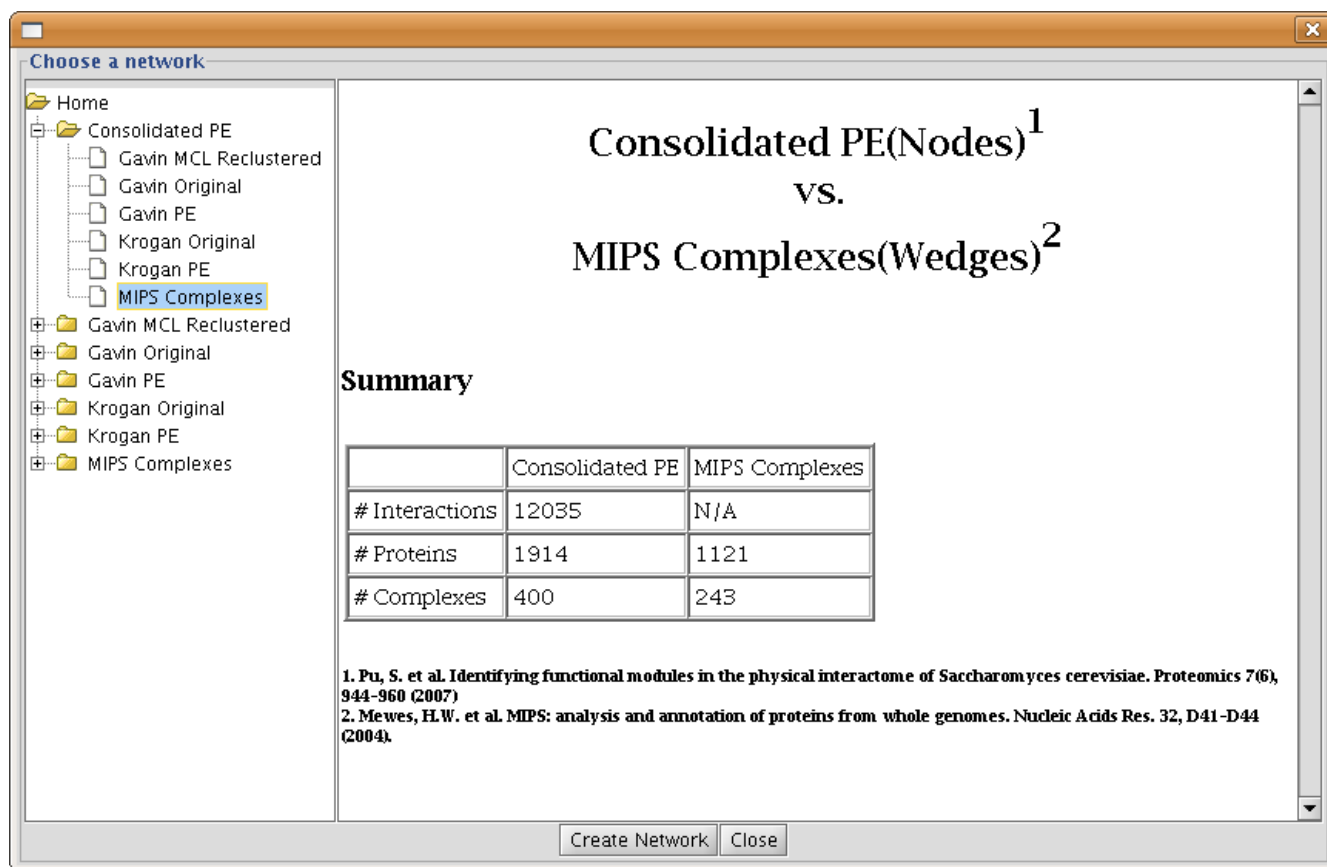
GenePro is a visualization plugin for the Cytoscape (<http://www.cytoscape.org>) environment. It enables the hierarchical organization of the display, so that at low resolution complexes can be viewed as nodes and at higher resolution, complex components (proteins) are viewed as nodes. Comparisons between networks are facilitated using pie nodes which visually indicate overlap between complexes between the two networks.

## Instructions:

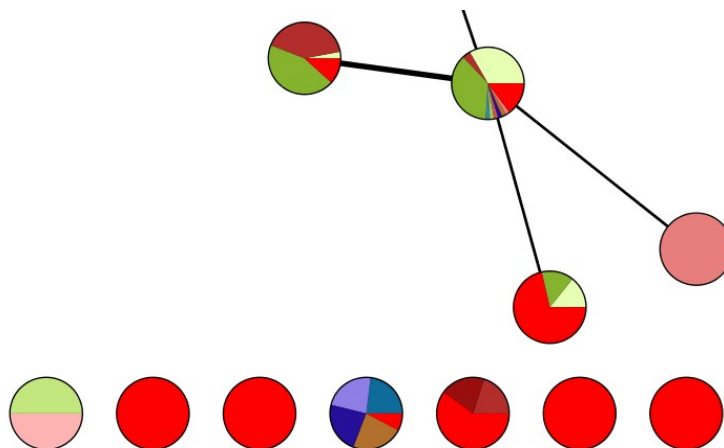
This version of GenePro will display network comparisons between the networks identified above and discussed in the review. After clicking the link to launch Cytoscape, the following dialog will appear:



On the left side is listed the primary network for comparison. The primary network will be displayed as nodes (corresponding to predicted complexes) and edges (corresponding to shared components) within Cytoscape. Upon expanding one of the primary networks in this tree, a second network can be chosen for comparison. This second network will be mapped onto the primary network, so that each node in the primary network displays a small pie-graph, indicating the extent of overlap between that complex and a complex within the secondary network.



After selecting a primary and secondary network, click 'Create Network' to create the network. For example, in the above screenshot, we have selected the consolidated PE network of Collins et al as the primary network, and the MIPS complexes as the secondary network. A portion of the resulting network is shown below:



Thus the two colours in the lower left node indicate that the components (proteins) of this predicted complex from Collins et al are distributed between two MIPS complexes. The red colour is reserved, and indicates the fraction (if any) of complex components that are not identified in the secondary network (in this case, the MIPS complexes). Edges by default represent components that are shared

between complexes, with the thickness of the edge proportional to the number of shared components.

Various options are available under the plugins->GenePro menu. The option for variable sized nodes can be useful, as with this option nodes are sized proportional to the number of components they contain. Another frequently used option is Search, which allows genes, wedges, or nodes to be located.

Complete documentation and a downloadable standalone version is available on the GenePro website, at <http://genepro.ccb.sickkids.ca>

