Instructions for use of network files

This zipped folder should contain 3 files:

1. Instructions.doc (this file)
2. Arabidopsis_predicted_interactome.cys
3. Arabidopsis_predicted_interactome.osp

To use the network files, download the following software

1: For Arabidopsis_predicted_interactome.cys

Cytoscape, current version (2.5.0 at the time of this publication)

http://www.cytoscape.org/

It is platform independent (MAC/WIN/LINUX), however requires JAVA SE5 or SE6, which can be downloaded from:

http://java.sun.com/javase/downloads/index.jsp

Launch cytoscape, select file-open and browse to where you have saved the Arabidopsis_predicted_interactome.cys file. Open as a cytoscape type file. This should take a minute or two, then give you a big splatterball of all predicted interactions, and a few smaller networks of proteins not connected to the big ball. To find your protein of interest, use select-node-by name or from a file (a simple text file listing all the proteins you want to find). To then find interacting partners of these proteins use select-node-first neighbors of selected nodes. Use filters to limit your selection to specific confidence quality, subcellular compartment, or hub size. Save your subnet of interesting proteins using file-new-network-from selected nodes, all edges. Cytoscape is a powerful tool, but requires a little getting used to. There is a manual available from the home website http://www.cytoscape.org/manual/Cytoscape2_5Manual.html

2: For Arabidopsis_predicted_interactome.osp

Osprey, current version 1.2 is available from http://www.thebiogrid.org/ and will work with MAC (OSX), Win32, or Linux.

Launch osprey and use file-open-standard, then browse to where you have saved Arabidopsis_predicted_interactome.osp, and let it load. Use find (binoculars symbol) to select gene of interest, then use tools on lower left to set depth (start with depth 1) and minimum number of connections (to look only at hubs). Might want to try switching off arrowheads and labels, and changing colors to suit your needs. Click on a node (protein) and read the information on the left panel for TAIR based description.

The osprey program is simpler, and with fewer options, but easier to use. The manual can be found here: http://biodata.mshri.on.ca/osprey/OspreyHelp/index.html