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## LGI Network Modelling & Visualization – V0.95

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### Executive Summary

This manual provides a step-by-step guide to run the developed program. It also illustrates the possible output and how to use them to analyze the results.

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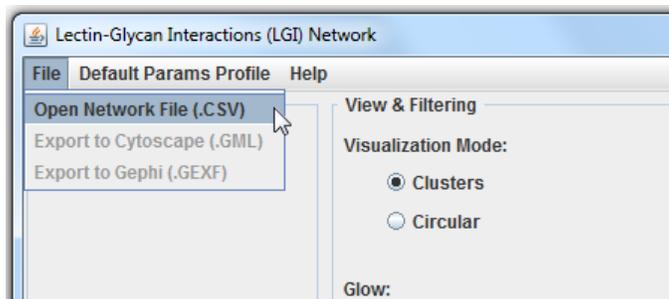
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## Installation Requirements

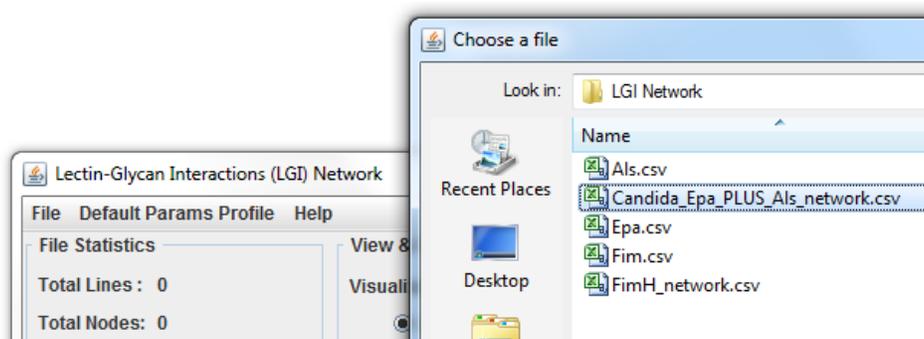
- Java Runtime Environment version 1.6 or higher

## Open a new LGI network data file

Click the File option in the top menu, and then click the Open Network File (.CSV) option and the sub-menu:

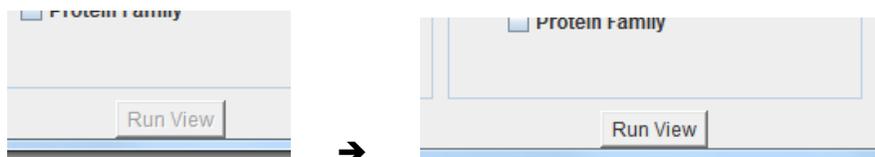


Select one of the network data files and ignore the binding data files:



a progress bar will visualize the processing of the file.

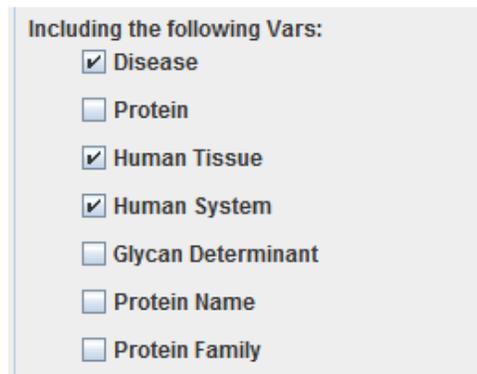
The binding strength data (i.e. Als.csv, Epa.csv, Fim.csv, or any other) should be located in the same folder as the network data files. If the network data file and the binding strength data files are correct, the Run View button will become enabled.



Once the button becomes enabled, select one among several visualization choices.

## Network Information to Visualize

There are seven different types of nodes involved available for the network visualization, namely: *Disease*, *Protein*, *Human Tissue*, *Human System*, *Glycan Determinant*, *Protein Name*, and *Protein Family*. They should be selected depending on the type of study to perform. Although all the nodes are involved in the analysis, the visualization should be customized depending on the aim.



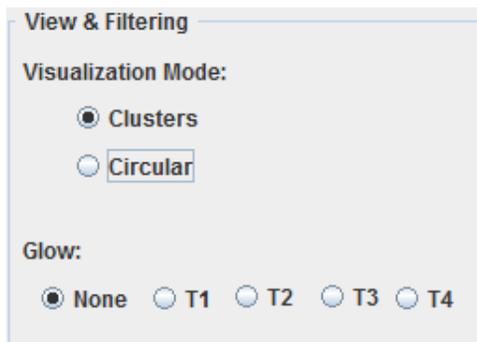
Including the following Vars:

- Disease
- Protein
- Human Tissue
- Human System
- Glycan Determinant
- Protein Name
- Protein Family

Any possible combination of the different types of nodes can be selected for visualization. However, the more nodes are involved in the visualization, the more crowded and difficult to interpret the visualization will be for large networks.

## Network Visualization Options

There are several possible ways to visualize the network, each one for different purposes. Two visualization modes are available to select: Clusters and Circular visualization modes.



View & Filtering

Visualization Mode:

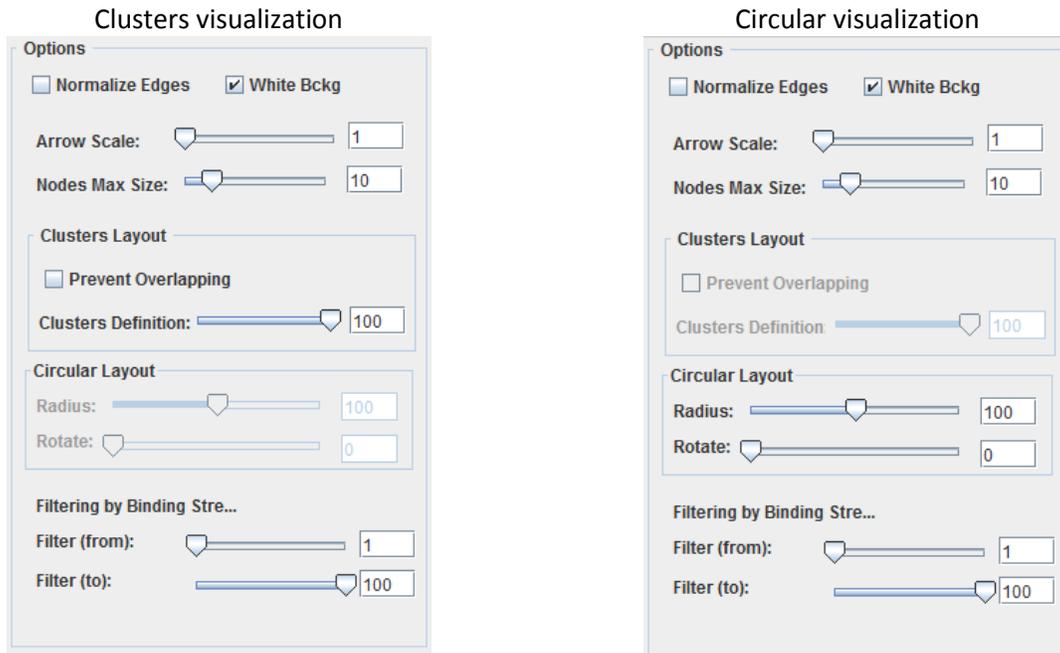
- Clusters
- Circular

Glow:

- None
- T1
- T2
- T3
- T4

clicking on the radio button allows changing between the different visualization modes. In addition, glowing effects can be achieved in four different configurations to highlight the proximity of node's types.

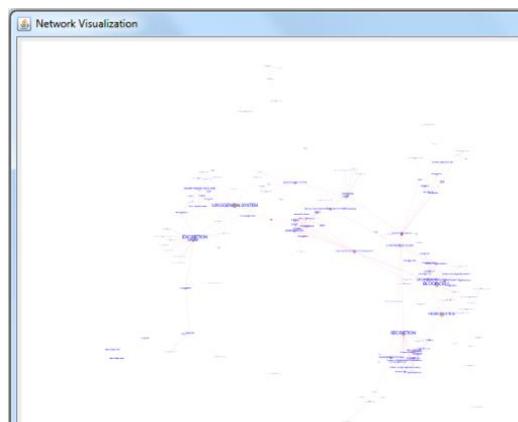
Some of the Options parameters are common the different possible visualizations.



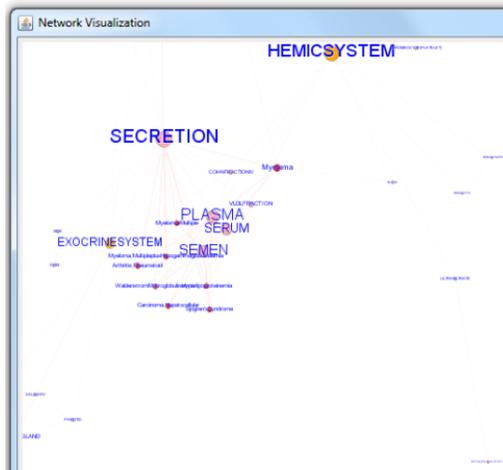
Some of the common options are the background color, the nodes and arrows size, and the filtering options to hide irrelevant nodes in big networks.

## Network Visualization Panel

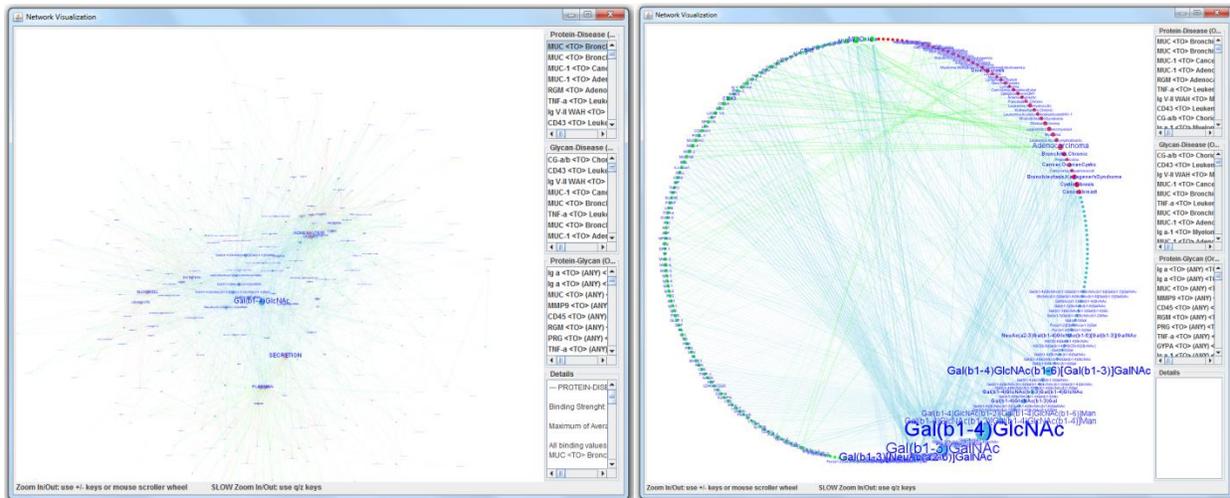
Once the visualization mode has been selected, the next step is to click on the Run View button. This action will open a new window displaying the LGI network:



The visualization panel allows interacting with the network by zooming in/out in order to see the relevant information. The keys + or – (or mouse scroll alternatively) allows to zoom in or out, respectively; the keys q or z (lower case) allows to slowly zoom in or out:



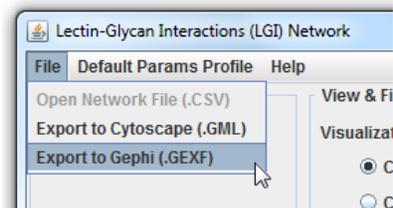
the same visualization window provides three panels in the right side, allowing a detailed inspection of the computed edge values, for both visualization modes:



the different edge values calculation can be detailed by selecting the edge of interest from the list; as consequence, the Details box will display the corresponding data.

## Export network data to other formats

In addition, once the network has been visualized, an option to export the network other formats becomes available in the File option of the top menu, then click Export to Cytoscape (.GML) or click Export to Gephi (.GEXF)



This option allows using the network data, including the node's relevance and edge values estimated using the LGI network program, for visualization in other visualization programs such as Gephi or Cytoscape.

Next, a dialog box will appear asking for the filename to save, and suggesting a file extension depending on the selected format to export.