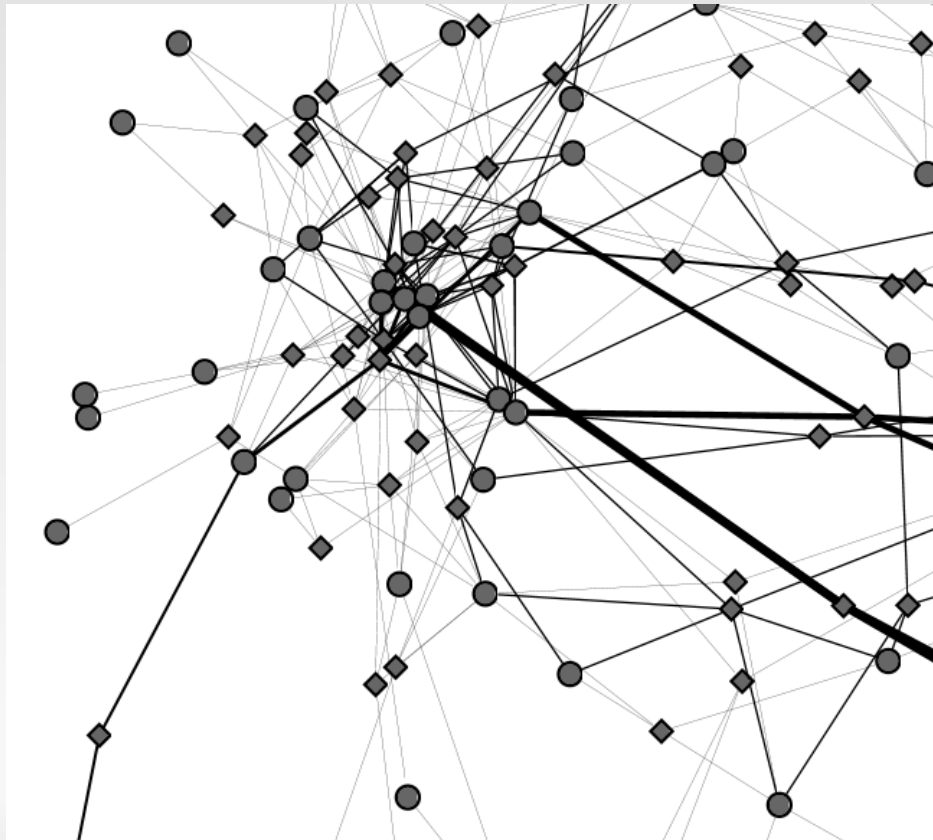


# FluxViz – Cytoscape Plugin



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Group seminar  
Berlin 01|02|10

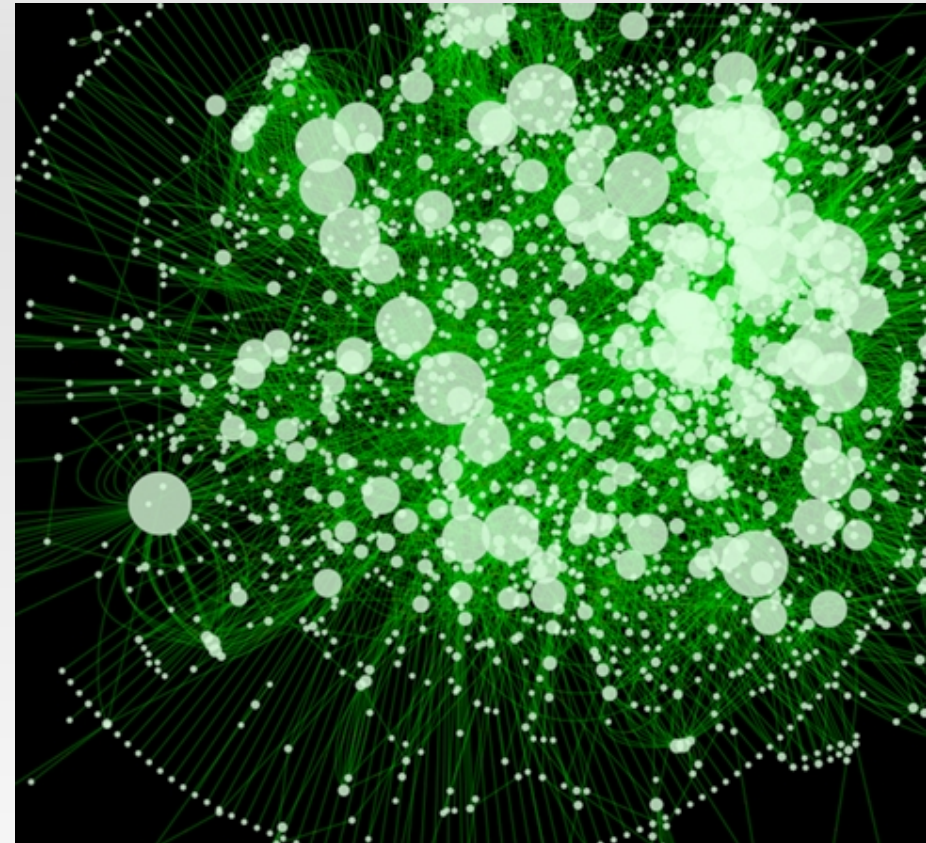
# Outline

- Cytoscape
- FluxViz
- Further Plugins
  - SBMLReader2
  - PositionReuse
  - HepatoBase Connection



# Cytoscape

- open source software for **visualizing** molecular interaction networks
  - **integrating** gene expression profiles and other state data
  - general platform for complex network analysis and visualization
  - Additional features as plugins



<http://www.cytoscape.org/>

# FluxViz

- Plugin for visualization of flux distributions
  - FBA in biochemical reaction networks
  - frontend for FASIMU
- Features
  - full Cytoscape functionality (filters, additional visual mappings, ...)
  - cycle through flux distributions
  - visualize flux containing subgraph
  - export vector and scalar images

# FluxViz installation I

- 2 Click solution
  - Download fluxviz.jar
  - Move in PluginFolder
  - Control over version

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[SourceForge.net](#) > [Find Software](#) > FluxViz Plugin for Cytoscape

 **FluxViz Plugin for Cytoscape** Beta by [matthiascoenig](#)

[Summary](#) | [Files](#) | [Support](#) | [Develop](#)

 The FluxViz Cytoscape plugin integrates the visualization of flux distributions in Cytoscape.

[Download Now!](#)  
fluxviz-v0.1.beta.jar (1.1 MB)  OR [View all files](#) 

[View screenshots](#)

<http://fluxvizplugin.sourceforge.net>

**Features:**

- cycle through flux distributions
- visualize the flux containing subgraph in the full network context
- export flux modes as vector or scalar images
- mapping of additional network information

**Release Date:** 2010-01-29

**Topic:** [Visualization, Bio-Informatics](#)

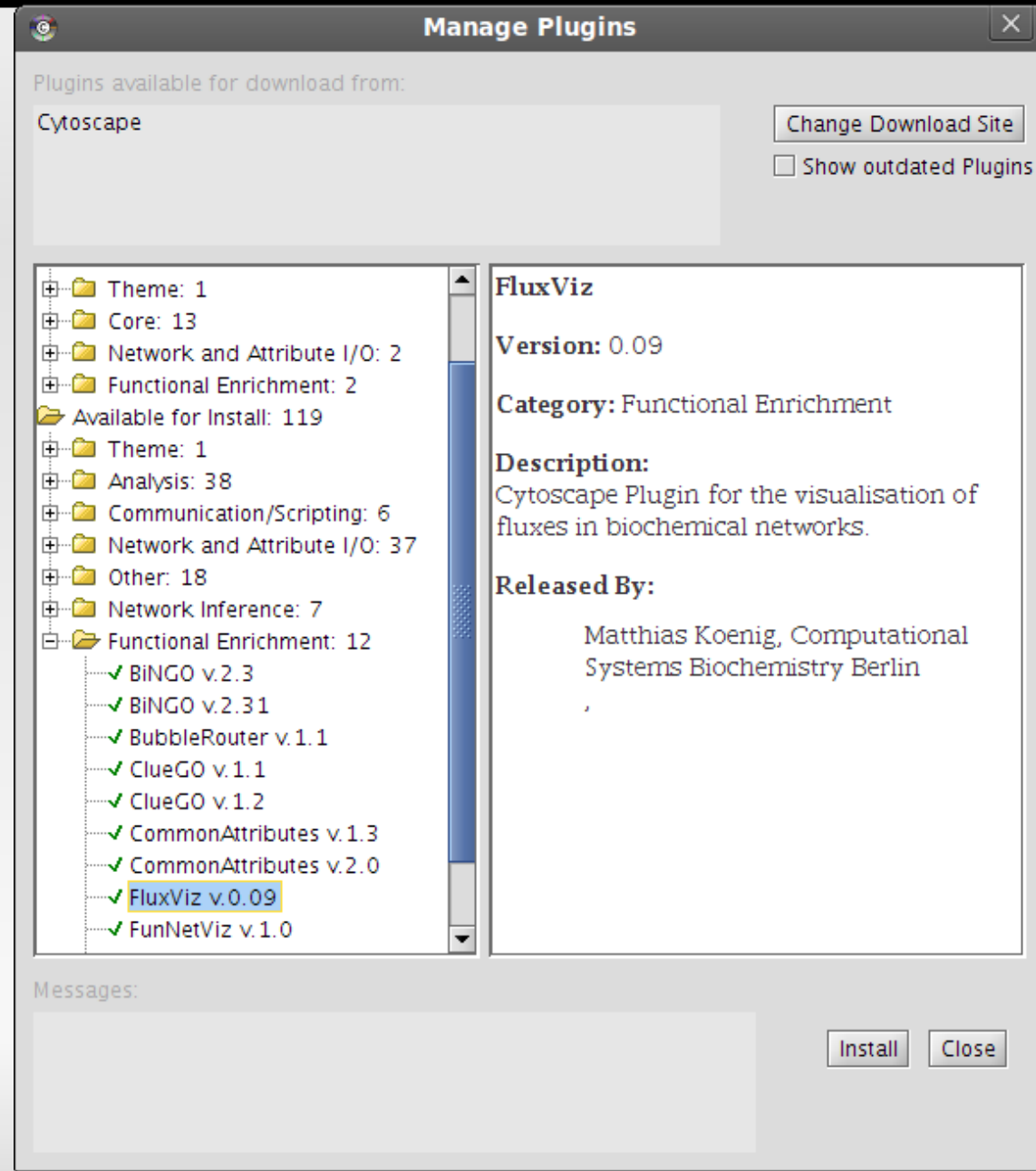
**Operating System:** [OS Independent \(Written in an interpreted language\)](#)

**License:** [GNU General Public License \(GPL\)](#)

**Intended Audience:** [Science/Research](#)

# FluxViz Installation II

- 1 Click solution
  - Cytoscape Plugin Manager
  - Automatic Updates

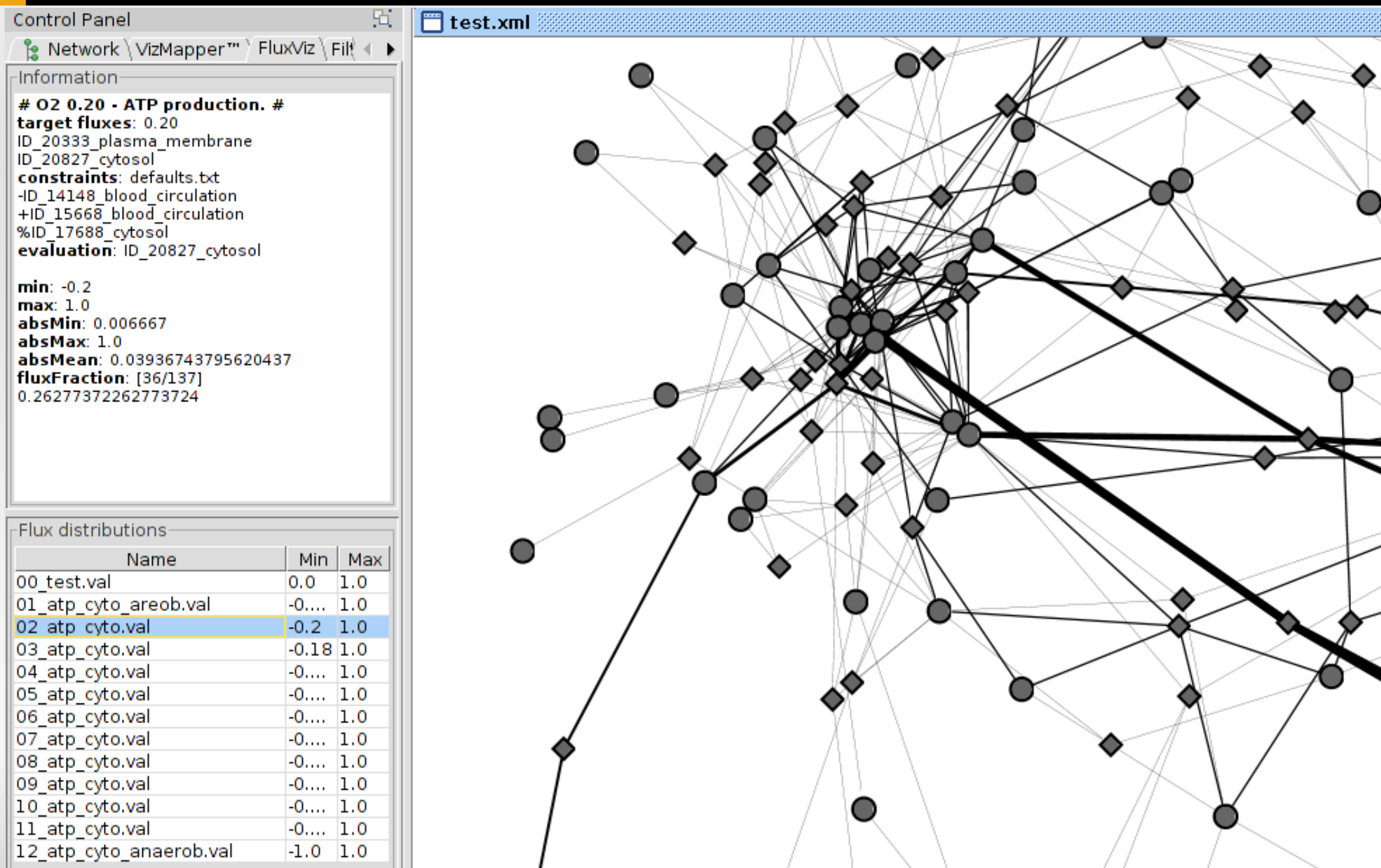


# Usage example

- Installation
- Loading example data
  - Standard example
  - Erythrocyte network
  - Hepatocyte Core network
- Export of images



# Examples





## Information

[Help Tutorial](#) | [JavaDoc](#) | [Contact](#)**1. Select Network for visualisation**

FluxViz works on the current NetworkView.

**2. Load val files**

Load flux distribution via \*.val files.

**3. Load sim file [optional]**

FASIMU simulation information can be integrated with the flux data.

**4. Export SVG [optional]**

Select val file for Flux visualisation and export as svg.

## Flux subnetworks

## Flux distributions

Name	Min	Max
00_test.val	0.0	1.0
01_atp_cyto_areob.val	-0....	1.0
02_atp_cyto.val	-0.2	1.0
03_atp_cyto.val	-0....	1.0
04_atp_cyto.val	-0....	1.0
05_atp_cyto.val	-0....	1.0
06_atp_cyto.val	-0....	1.0
07_atp_cyto.val	-0....	1.0
08_atp_cyto.val	-0....	1.0
09_atp_cyto.val	-0....	1.0
10_atp_cyto.val	-0....	1.0
11_atp_cyto.val	-0....	1.0
12_atp_cyto_anaerob.val	-1.0	1.0

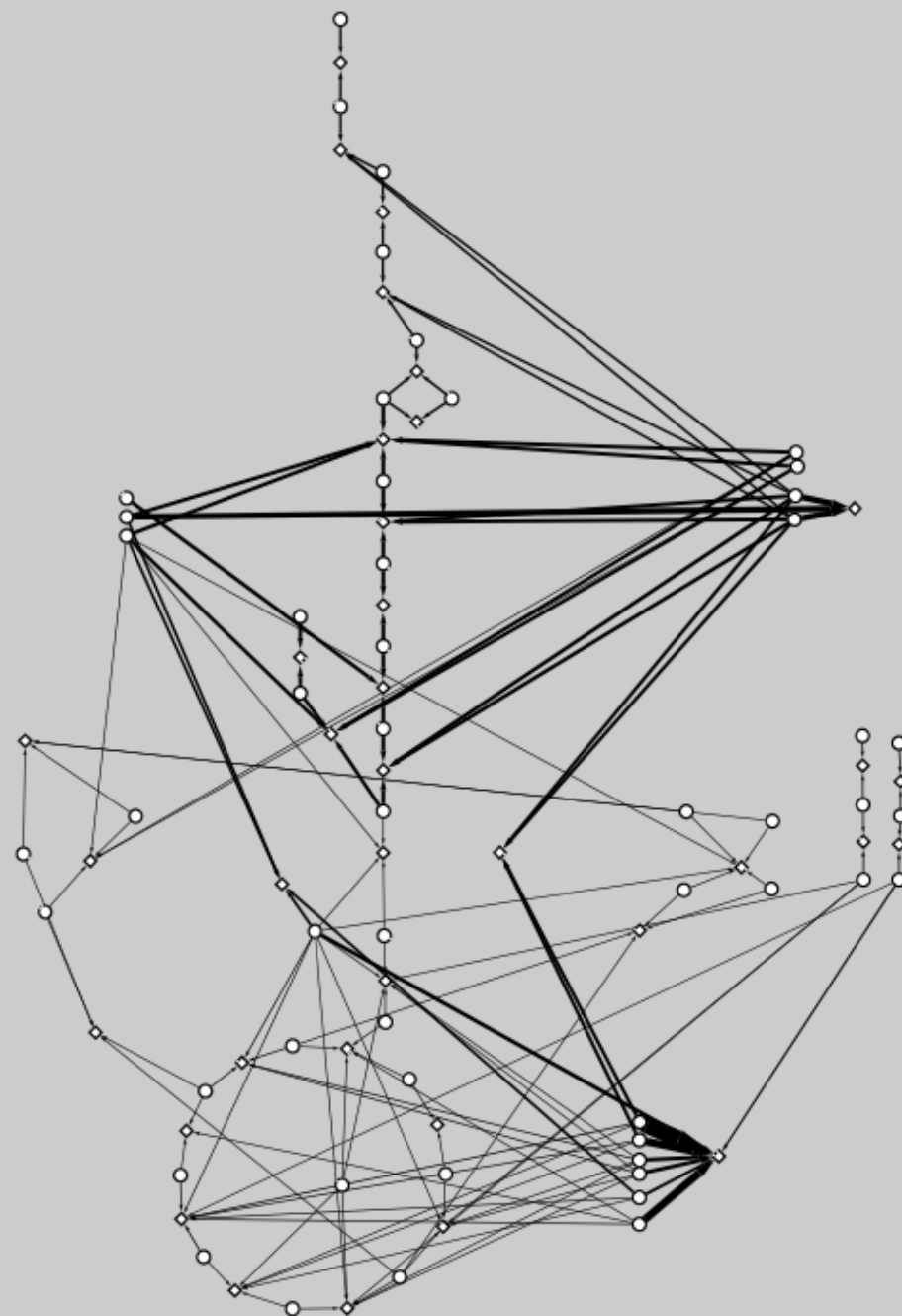
## Settings

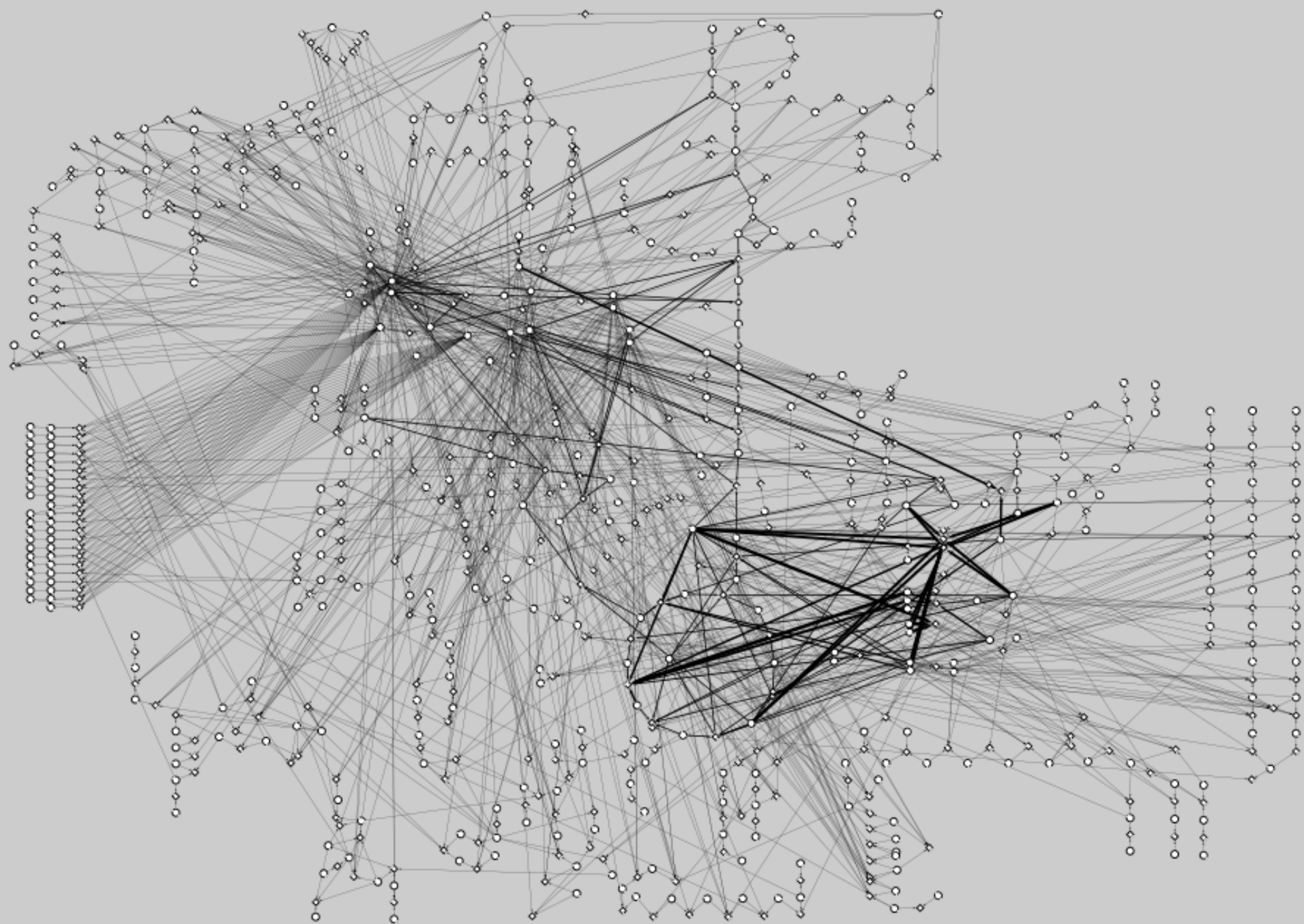
Load val

Load sim

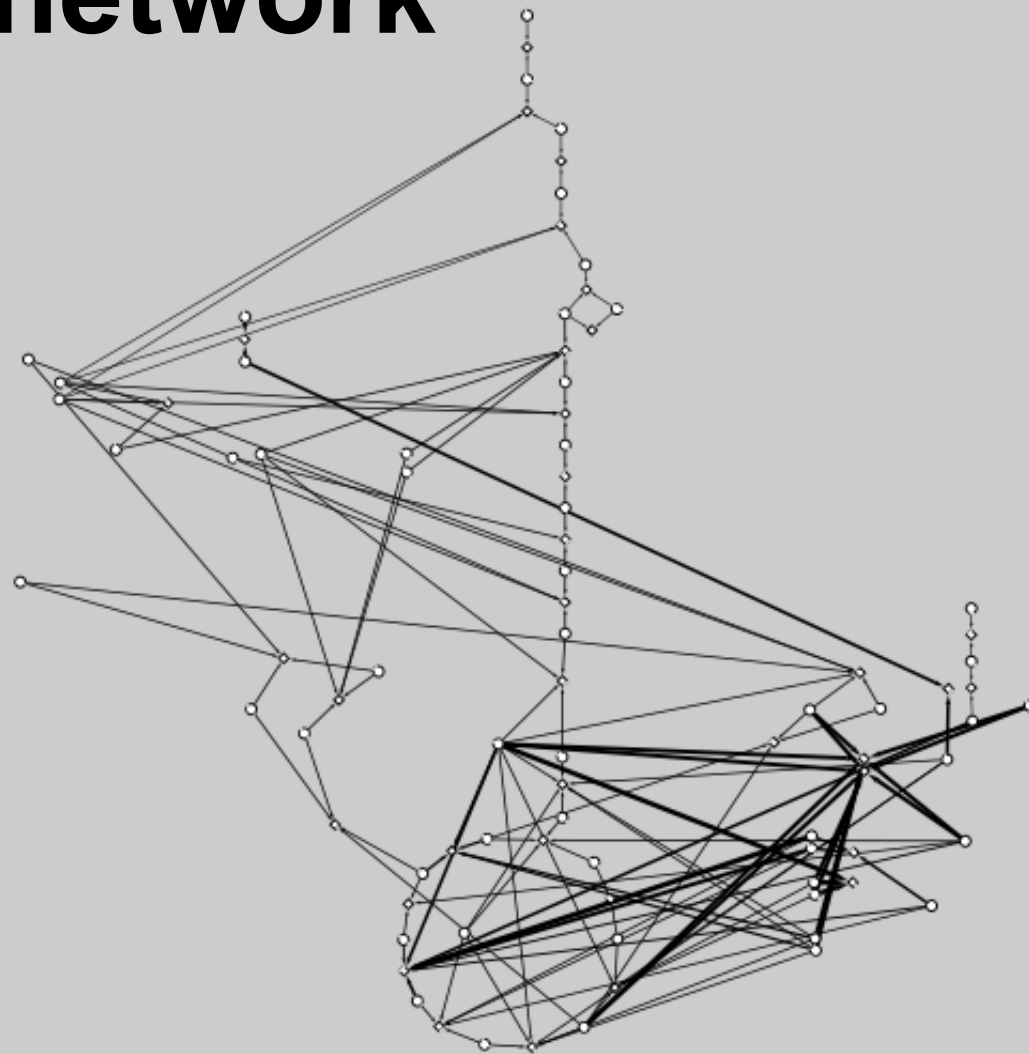
Export SVG

Help

☐ Flux subnetwork



# Flux subnetwork



# Further plugins

- SBMLReader2 [finished]
  - New SBML parser for Cytoscape with support of all SBML versions and all node and edge attributes
  - <http://sourceforge.net/projects/sbmlreader2/>
- PositionalData [starting]
  - Reuse of layouts
  - Compartments
- HepatoBase integration [usage case]
  - SQL queries

# References

- FluxViz <http://sourceforge.net/projects/fluxvizplugin/>  
<http://www.charite.de/sysbio/people/koenig/>
- SBMLReader2 <http://sourceforge.net/projects/sbmlreader2/>
- Cytoscape <http://www.cytoscape.org/>
- Cytoscape plugins  
[http://chianti.ucsd.edu/cyto\\_web/plugins/index.php](http://chianti.ucsd.edu/cyto_web/plugins/index.php)
- FASIMU <http://www.bioinformatics.org/fasimu/>