

# Visualizing and Analyzing Biological Network Data in Cytoscape 2.1

*Cytoscape* is an open source software project for integrating biomolecular interaction networks with high-throughput expression data and other molecular states into a unified conceptual framework. Although applicable to any system of molecular components and interactions, Cytoscape is most powerful when used in conjunction with large databases of protein-protein, protein-DNA, and genetic interactions that are increasingly available for humans and model organisms. Cytoscape's software Core provides basic functionality to lay out and query networks; to visually integrate networks with expression profiles, phenotypes, and other molecular states; and to link networks to databases of functional annotations. The Core is extensible through a straightforward plugin architecture, allowing rapid development of additional computational analyses and features. Cytoscape core functionality and interesting new plugins will be demonstrated and discussed.

Highlighted plugins will include:

- *cPath Plugin* - enables Cytoscape users to query, retrieve and visualize interactions retrieved from the cPath protein-protein interaction database.
- *Agilent Literature Search Plugin* - is a meta-search tool for automatically querying multiple text-based search engines in order to aid biologists faced with the daunting task of manually searching and extracting associations among genes/proteins of interest.
- *Active Modules Plugin* - enables Cytoscape to search for significant networks, or active subnetworks, as described in *Bioinformatics*. 2002 Jul;18 Suppl 1:S233-40.
- *MCODE Plugin* - finds clusters (highly interconnected regions) in any network loaded into Cytoscape.
- *Motif Finder Plugin* runs a Gibbs sampling motif detector on sequences corresponding to the selected nodes in the current network.

The Cytoscape project is an ongoing collaboration between the Institute for Systems Biology, University of California, San Diego, Memorial Sloan-Kettering Cancer Center and the Institut Pasteur. Funding for Cytoscape is provided by a federal grant from the U.S. National Institute of General Medical Sciences (NIGMS) of the National Institutes of Health (NIH). Corporate funding is provided through a contract from Unilever PLC.

## Major application area

Systems Biology

## Platform requirements

Cytoscape requires Java 1.4.2 and higher versions of the Java runtime, and runs on platforms supporting current JVMs. Unix/Linux, Mac OS X and Windows are fully supported and tested.

## Availability/license

Cytoscape is developed and released under the GNU Lesser General Public License (LGPL).

## How to obtain the software

For more information about Cytoscape, including downloading of current releases, user documentation, etc., please visit: <http://www.cytoscape.org>

## References

Shannon P, Markiel A, Ozier O, Baliga NS, Wang JT, Ramage D, Amin N, Schwikowski B, Ideker T. Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Res*. 2003 Nov;13(11):2498-504.