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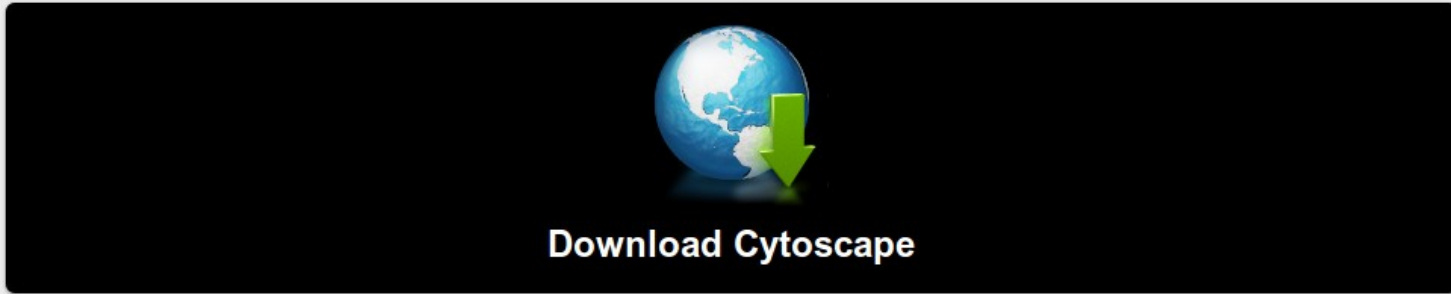
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Platform Specific Installers

⬇ Mac OS X

⬇ Windows 32bit

⬇ Windows 64bit

⬇ Linux

Archived Distribution Files

⬇ Zip Archive (for Windows)

⬇ GZIP Archive (for Mac/Unix Systems)

Source Distributions

⬇ Zipped Source Archive

Older Versions

⬇ 2.1

⬇ 2.2

⬇ 2.3.0

⬇ 2.3.1

⬇ 2.3.2

⬇ 2.4.0

⬇ 2.4.1

⬇ 2.5.0

⬇ 2.5.1

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Cytoscape Online Tutorials

To get you started with Cytoscape: Getting Started Guide

The Cytoscape Online Tutorials from cytoscape.org have been moved here and updated for use with version 2.4.

- Basic Tutorials
  - Getting Started, Filters & Editor, Fetching External Data, Web Services Clients, Expression Analysis
- Advanced Tutorials
  - Literature Searching, Gene Ontology Annotation, Modules and Complexes, and Web Services

A Cytoscape tutorial series of lectures, videos, and exercises can be found at http://www.csc.fi/english/research/sciences/bioscience/Courses_and_events/cytoscape/index_html. Note that the videos require RealPlayer to view.

Presentations and Lecture Slides

Please feel free to use these lecture slides for your own presentations about Cytoscape.

- Print this Cytoscape Handout for your lectures
- CytoscapeAndR2_16_4_09.ppt A presentation on Cytoscape in general and a specific plugin R2 (by Piet Molenaar, partly based on slides by Tero Aittokallio)
- 2008 Systems Biology Conference Demos and Case Studies
- ISMB 2005 Tutorial
- BMES 2005 Tutorial
- Data Integration with Cytoscape at EMBL-EBI Biological Networks: Reconstruction, Analysis, and Modelling (May 5 & 6 2009)
  - Use Mondrian Cytoscape Web Start as a demonstration
  - LaTeX file, Makefile, included EPS files, and lecture notes as TeX comments
    - Requires beamer to be installed
    - EPS diagrams made with OmniGraffle
- Cytoscape 2.x Developers Tutorial
- Clusters and Groups Presentation
- 2010 Cytoscape Retreat User Tutorial
- EmblHeidelbergCytoscapeCourseSept2010

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3. Layouts
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5. Network Visualization
6. Competitive Landscape (Under Construction)

Software applications

- Cytoscape in Java. Freely available (open-source)
- NodeXL in C#/.Net. Freely available (open-source) extension to Excel 2007 adds social network analysis and visualization features.
- GenoLink. Free executable for academic use.
- ONDEX. Open source.
- Network Workbench A Large-Scale Network Analysis, Modeling and Visualization Toolkit for Biomedical, Social Science and Physics Research
- VisANT - Java biological analysis software
- Graphviz - Graph Visualization Software
- Pajek - Graph visualization and analysis software. Popular among social science community.
- OSPREY - Biological network visualization software.
- UCINET - De facto standard network analysis tool in social science. (commercial software)
- Vizster - Social network visualization software
- WilmaScope - Java3D application which creates real time 3d animations of dynamic graph structures.
- NAViGaTOR - Network Analysis, Visualization, & Graphing TORonto
- BioLayout Express3D - 3D Java graph visualization
- Walrus - Java3D directed graph visualization
- ProViz - protein interaction network visualization tool built using TULIP C++ graph library
- PIMWalker - Java based PSI-MI protein interaction network visualizer
- GUESS - Java graph exploration system
- InFlow - Commercial Software for Social Network Analysis & Organizational Network Analysis
- NetMiner - Commercial social network analysis software
- GraphExplore - Free Java network visualizer

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Graphviz - Graph Visualization Software

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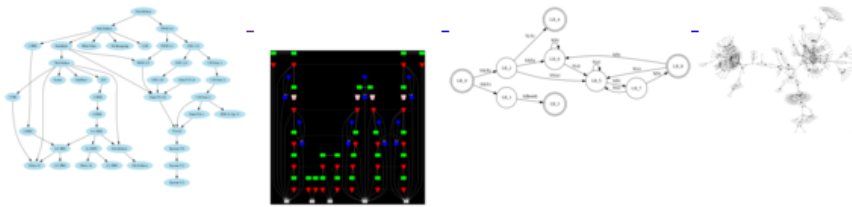
Graph Visualization

Graph visualization is a way of representing structural information as diagrams of abstract graphs and networks. Automatic graph drawing has many important applications in software engineering, database and web design, networking, and in visual interfaces for many other domains.

Graphviz is open source graph visualization software. It has several main graph layout programs. See the gallery for some sample layouts. It also has web and interactive graphical interfaces, and auxiliary tools, libraries, and language bindings.

The Mac OS X edition of Graphviz, by Glen Low, won two 2004 Apple Design Awards.

The Graphviz layout programs take descriptions of graphs in a simple text language, and make diagrams in several useful formats such as images and SVG for web pages, Postscript for inclusion in PDF or other documents; or display in an interactive graph browser. (Graphviz also supports GXL, an XML dialect.)

Graphviz has many useful features for concrete diagrams, such as options for colors, fonts, tabular node layouts, line styles, hyperlinks, and custom shapes.

In practice, graphs are usually generated from an external data sources, but they can also be created and edited manually, either as raw text files or within a graphical editor. (Graphviz was not intended to be a Visio replacement, so it is probably frustrating to try to use it that way.)

Roadmap

dot - ``hierarchical'' or layered drawings of directed graphs. The layout algorithm aims edges in the same direction (top to bottom, or left to right) and then attempts to avoid edge crossings and reduce edge length.

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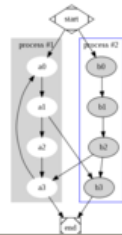
PAJEK WIKI

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Trace: » network_analysis » start

Pajek Wiki

This Wiki is about program Pajek and (large) network analysis and visualization.

Most of its content is provided by authors of Pajek and the Wiki users can only read it.

The logged-in users can create/edit pages in Questions and Answers area and in User's Comments area. They can also join the Pajek mailing list and discuss their ideas or problems on it.

To login you need a **user name** and a **password**. To get them you click on login in the toolbox and then register - the password will be sent to you by e-mail.

The rules for writing Wiki pages are described on Syntax page.

Some trusted users will be promoted to **writer**s. They will be allowed to create/edit on pages with

edit: writer

at the bottom of the page - such as for example events, introduction and selected topics.

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ClusterMakerRecipe		complexes, protein families, functional relationships and view in biological context	ClusterMakerDemo	Allan	??	
7	CyOogPowerGraphAnalysisRecipe		1. explore functional relationships 2. get sequence similarities that are otherwise hidden by low scoring from homology networks	CyOogAbstract	Matthias	??	
8	CommunityStructureLayoutRecipe		find community structures in large biological networks, which may infer protein complexes and biological pathways.	CommunityStructureLayout	Allan	??	
9	DomainGraphRecipe, NetworkAnalyzerRecipe	*Multi-level Network Analysis*	Which splice variants influence the structure of ppi networks	DomainGraph, NetworkAnalyzer	Dorothea	??	
10	StructureVizRecipe		Expand the network by incorporating lower level structure and function	StructureVizDemo	Allan	??	will require some familiarization with Chimera. Perhaps show a slide about the interconnection with SubGeneViewer (splice variation to domain)? Side benefit is to show how plugins written completely independently can interoperate with each other to answer a biological question.
11	WikiPathwaysRecipe	*Pathway Curation, Storing and Exporting Images*	Storing and expanding knowledge of biological networks	WikiPathwaysPathVisio	Thomas	??	

To Do

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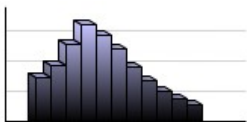
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NetworkAnalyzer Download

You can download NetworkAnalyzer using Cytoscape's Plugin Manager. Set the following URL as a download site:

http://med.bioinf.mpi-inf.mpg.de/netanalyzer/download.xml

If you are not experienced with Cytoscape, take a look at the NetworkAnalyzer installation tutorial.

_____

NetworkAnalyzer includes the JFreeChart chart drawing library version 1.0.6. The source code is contained in the following two files:

- jfreechart-1.0.13.zip
- jcommon-1.0.16.zip

The above files are NOT required in order to run NetworkAnalyzer.

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