Cytoscape 2.1 Features

22 February 2005

*Cytoscape 2.1 is the latest release of the open source bioinformatics software platform for **visualizing** molecular interaction networks and **integrating** these interactions with gene expression profiles and other state data.*

The 2.1 release of Cytoscape includes: major performance improvements for loading, manipulating and managing large networks; new layout and visual attribute operations; support for new external data formats; usability improvements; and bug fixes.

Performance Improvements

Optimization and Run-Time Performance Improvements
Performance Optimization of Graph Model
- Large graphs are now supported (>100K nodes, edges, depending on system)
- The 2.1 release features significant performance improvements for graph loading, creation, and miscellaneous graph operations (> 2 - 10x improvements for some operations)

New Features and Functionality

VizMapper
Node label color control has been added.

Graph Model and Operations
New layout features are available, providing new operations on selected nodes:
- Layout selected nodes
- Rotate selected nodes

External Data Support
A direct cPath Interface is available via a new cPath plug-in.

cPath is a freely available, open-source protein-protein interaction database from Memorial Sloan-Kettering Cancer Center. Using cPath, a researcher can search for specific protein-protein interaction records, inspect matching records, and export them to a third-party database or visualization application, such as Cytoscape. More information about cPath is available at http://www.cbio.mskcc.org/cpath

Support for new data import and export formats has been added:
- GEO SOFT
- PSI-MI Level 1

Usability Improvements

Headless mode operation is now supported.

Headless mode allows users to now run their own Cytoscape processing/analysis jobs without creating the GUI and user interaction components or requiring user intervention.

New Progress Bar Manager/Threading Control/Task Framework.

Progress Bar and Task control has been added for the following longer-running operations:
- Load Operations
  - SIF files
  - GML Files
  - Node Attributes
  - Edge Attributes
  - Expression Data
- Save Operations
  - SIF files
  - GML files
  - Node Attributes
  - Edge Attributes
- Layout
  - Spring Embedded Layout
  - y-Layouts
- Visual Attributes/VizMap

A new Threading/Task Framework and associated GUI components have been added to the Cytoscape core architecture which allows for visual feedback and user control for longer-running tasks. A progress bar API is available for communicating activity and status to users for operations which formerly blocked the GUI, thereby improving usability and perceived performance of the application. Many load, save, and layout operations now utilize the Threading/Task Framework.

On-line Help System
- On-line help and content for Cytoscape
- On-line help framework for plug-in developers

An on-line help system supporting topic-based, indexed, context-sensitive and full-text search is now available. The on-line help system is based on JavaHelp

technology, and supports the standard on-line help conventions, including "F1" (function key F1) and Help menu activated help system invocation. Current help content is derived and indexed from the Cytoscape 2.1 User Manual.

<u>Documentation</u>

Technical Documentation

- Updated User Documentation
- Updated and expanded Developer Documentation, including new JavaDoc format API documentation for Cytoscape classes

The 2.1 release of Cytoscape includes updates to the user and developer documentation. Updated APIs and more complete "JavaDoc"'s capturing new, changed and deprecated APIs introduced by the core changes in the Cytoscape 2.1 release are included for developers and plug-in writers.

<u>Core Plug-Ins</u>

Five "core" plug-ins are bundled and distributed with Cytoscape 2.1. These plug-ins offer fundamental operations of value to many users, and are included in the basic distribution.

Plug-In Name	JAR file	Description
Filter	filter.jar	Provides filtering functionality; adds filter icon, filters menu and filtering dialog box
yFiles Layouts	yLayouts.jar	Provides yFiles layouts functionality; adds yFiles submenu to layout menu Layouts provided: • Circular • Organic • Hierarchic • Random • MirrorX • MirrorY • Orthogonal
Align	control.jar	Provides alignment/distribution functionality; adds align menu item to layout menu and align/distribute dialog box
Hierarchical Layout	HierarchicalLayout.jar	Provides hierarchical layout functionality; adds hierarchical layout menu item to layout menu

Plug-In Name	JAR file	Description
Web Search	yeast-context.jar	Provides graph object-based general web search functionality; launches Google search against selected node or edge name
Yeast context-sensitive menu	yeast-context.jar	Provides Yeast-specific web search capabilities

Table 1. Core Plug-ins