ABSTRACT

Summary: Cytoscape is a popular bioinformatics package for biological network visualization and data integration. Version 2.8 introduces two powerful new features—Custom Node Graphics and Attribute Equations—which can be used jointly to greatly enhance Cytoscape’s data integration and visualization capabilities. Custom Node Graphics allow an image to be projected onto a node, including images generated dynamically or at remote locations. Attribute Equations provide Cytoscape with spreadsheet-like functionality in which the value of an attribute is computed dynamically as a function of other attributes and network properties.

Availability and implementation: Cytoscape is a desktop Java application released under the Library GNU Public License (LGPL). Binary install bundles and source code for Cytoscape 2.8 are available for download from http://cytoscape.org.

Contact: smoot@ucsd.edu

Received and revised on September 24, 2010; accepted on October 23, 2010

2 INTEGRATED VISUALIZATION

2.1 Custom node graphics

A key function of Cytoscape is to allow diverse types of attribute data to be visualized on the nodes and edges of a biological network. Scalar data can be linked to simple visualization properties such as node color, shape, or size as node and edge attributes. To represent multivariate data associated with a node, Cytoscape can control the visualization of each node using a custom graphical image (since version 2.3) through a programming API. Version 2.8 introduces the ability for non-programmers to specify images through the Cytoscape GUI and to map these images to nodes using Cytoscape’s standard VizMapper interface.

Using this new feature, images are loaded using a standard file browser or by dragging and dropping them into a pool of available images maintained by Cytoscape. For cases involving large numbers of custom images, Cytoscape also allows images to be loaded as node attributes by providing a Uniform Resource Locator (URL) address for each image. Given a URL, Cytoscape will try to read that URL and generate an image for display. Images can be mapped to nodes using Cytoscape’s VizMapper framework, which connects the visualization properties of the network to attribute data. Placement and sizing of images can also be directly controlled within Cytoscape.

In addition to rich, multivariate visualizations (Fig. 1A and B), images enable shading, highlights and other aesthetic effects to be applied to nodes (Fig. 1C) to further enhance network visualization.

2.2 Equations

The Cytoscape Attribute Browser provides a tabular view of data that have been loaded into Cytoscape and attached to nodes, edges or networks. To improve the ability of users to manipulate attribute data
As a first example illustrating the joint use of Custom Node Graphics and Equations, we integrate networks of protein interactions with the visualizations of the known protein structures. This can be accomplished in Cytoscape v2.8 by constructing a URL that points to an image of the 3D structure of a protein and then mapping that image to a node in the network. We begin by creating a data attribute called ‘pdbID’ and, for each node, we populate the value of this attribute with a valid protein name in the Protein Data Bank (http://www.pdb.org). We then create a new string attribute, which we name ‘imageURL’. We then write the following equation for the imageURL attribute:

\[
\text{imageURL} = \text{"http://www.rcsb.org/pdb/images/"} \& \text{SpdBID}\text{"_bio_500.jpg?bioNum=1"}
\]

This equation is copied to all nodes via an option in the right-click menu of the Attribute Browser. For each node, Cytoscape interprets the SpdBID variable using the corresponding pdbID attribute value and concatenates the resulting strings into a valid URL. We then use the Cytoscape VizMapper to map the imageURL attribute to a Custom Graphics visual property. As described in Section 2.1, this visual property interprets the URL and loads the image it points to. Following this procedure produces rich network visualizations such as those seen in Figure 1D and E.

A second example that demonstrates the use of both new features is the GLINECHART function available from the GoogleChartFunctions plugin (available in the Plugin Manager). This function uses the Google Visualization API (http://code.google.com/apis/visualization) to dynamically generate a URL to an image. For instance, if a user has time course data (values [1.1, 2.3, 1.7, 0.6]) for an experiment stored in an attribute named ‘timeCourse’, the following function call will produce a URL of a line chart image of the data with a F-axis range of 0–3:

\[
\text{GLINECHART}(0,3,\text{timeCourse})
\]

This function evaluates to a URL, which in turn is interpreted by the VizMapper as a node image, resulting in integrated network visualizations such as those shown in Figure 1A and B.

### 3 CONCLUSION

Custom node graphics provide a new tool for non-programmers that allows rich new network visualizations to be created that integrate large and complex datasets. Equations provide a powerful mechanism for data transformation within Cytoscape. Together, these features can be used to embed rich visualizations of data within the nodes of large networks.

### ACKNOWLEDGEMENTS

Our team would like to acknowledge the the Ideker Laboratory and the core Cytoscape development team.

**Funding:** National Institutes of Health (grant numbers: GM070743, P01HG005062).

**Conflict of Interest:** none declared.

### REFERENCES


