3DScape: three dimensional visualization plug-in for Cytoscape

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ABSTRACT

Summary: 3DScape is the first plug-in which enables three-dimensional network visualization in Cytoscape. The extra dimension is useful in accommodating, visualizing, and distinguishing larger networks with multiple crossing connections. Special features in 3DScape include 3D layout algorithms, mapping onto 3D models and animation effects on a series of expression data.

Availability: http://www.rendware.com or http://www.rendware.info

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1 INTRODUCTION

Cytoscape (Shannon *et al.*, 2003) is a freely available open source platform providing two-dimensional biological network analysis and visualization for biologists. However, with the rapid growth in the quantity of experimental data, it lacks the capability to show the larger-scale and more complex networks. By transferring to a three-dimensional (3D) platform, the extra space offers more flexibility for hierarchical and layered representation. Though a few applications are available for 3D network visualization, such as BioLayout (Enright *et al.*, 2001), Tulip (Auber, 2003), Arena3D (Pavlopoulos *et al.*, 2008), FORG3D (Paananen *et al.*, 2009) the lack of community support has hindered their widespread use. Moreover, many of them suffer performance drawbacks when displaying large networks. Although there is Cytoscape's 3D plug-in using Processing library (http://processing.org) under development, it's not yet released. Therefore, we developed 3DScape, a fast 3D Cytoscape plug-in implemented in C++ and wrapped for Java. By employing VTK (Schroeder *et al.*, 2003), a hardware-accelerated 3D graphics library based on OpenGL, networks with several thousand nodes can be rendered in real time.

2 IMPLEMENTATION

2.1 Visualization of Three-dimensional Networks

The 3DScape plug-in is used to convert an opened network to a 3D view (Fig. 1a). The conversion retains the color, size, and shape of nodes from the existing network view if user has specified to retain them. After conversion, a cube-like placement of nodes is generated. The drawing can be easy manipulated using the mouse. Basic operations include: rotation, pan and zoom of the graph. On selecting nodes or edges, the Node/Edge Attribute Browser panel shows the attributes of nodes or edges (Fig. 1b). Node can be searched by their identifier in a search box built in 3DScape. If the node exists, it will be highlighted and centered in the scene.

2.2 Three-dimensional Layout Algorithms

The layout algorithms are used to generate meaningful and aesthetic drawings of biological networks. Currently, there is Fruchterman-Reingold (Fruchterman *et al.*, 1991), Fast Multipole Multilevel Method (FM3) (Hachul *et al.*, 2004), and Span Tree algorithms available for 3D graph layout. The first two algorithms are force-directed. They act by balancing the repulsive force between nodes and attractive force from the edge. After several rounds of movement and annealing, they generate aesthetically pleasing graph layouts with all edges of nearly equal length. The Fruchterman-Reingold algorithm was built in VTK, and has been modified to show up in the 3D space. However, due to its O(N3) complexity and poor local minima (http://en.wikipedia.org), it is only suitable for graphs of medium size (up to several hundred nodes). Hereby we incorporated the FM3 algorithm, which was initially implemented in OGDF (http://www.ogdf.net), for large graph layout. In this approach, the graph is partitioned into subgraphs. Forces are only calculated within the scope of subgraphs, so that the final graph layout can be obtained in O(NlogN+E) runtime. This means both the detail and a global view can be obtained. The Span Tree algorithm was also built in VTK, but it is only suitable for displaying a network with a tree structure (Fig. 1c).

2.3 Time-course Expression Data Animation

Cytoscape supports the mapping of gene expression data to node color, label, and border thickness. With VistaClara (Kincaid *et al.*, 2008) plug-in installed, the user can distinguish expression intensities from a heat map themed node color scheme. It also creates an animated view of the network for displaying the changes over time in a series of experiments. In our implementation, we allow the user to explore expression data in a more efficient manner. The user sees not only colored nodes, but also a gradient of colored edges of heat map colors (Fig. 1d). For studies of the dynamics of a system, the user either clicks the play button or drags the time point widget through the slider bar to create a dynamic view of expression data.

2.4 Mapping Biological Networks to 3D Models

3DScape provides an approach for visualizing and understanding the interactions between molecules in a biological context. There is a Cytoscape plug-in called Cerebral (Barsky *et al.*, 2007) generates subcellular localized layout in a 2D canvas. By migrating to a 3D space, 3DScape presents these interactions in a more realistic, intuitive manner. Using the VTK's model importers, user can import 3DS or Wavefront file into the scenario. There are plant/animal cell and human body models included in 3DScape (Fig. 1e,f), networks can be easily mapped onto these models by providing corresponding localizations (e.g., mitochrion, nuclear membrane, knee, etc.).

3 DISCUSSION

We have integrated VTK and Cytoscape in 3DScape. The 3D perspective not only guarantees the user a greater experience in visualization, but also offers more insight into Cytoscape networks. However, the operations of graph are limited in VTK. For example, user can not drag vertices or edges in the graph to set locations. Therefore, in the future, we would like to add these functionalities. Moreover, it is necessary to set up an automatic layout algorithm for helping nodes localized to corresponding positions of the 3D models, and thereby making the biological network more meaningful.

ACKNOWLEDGEMENTS

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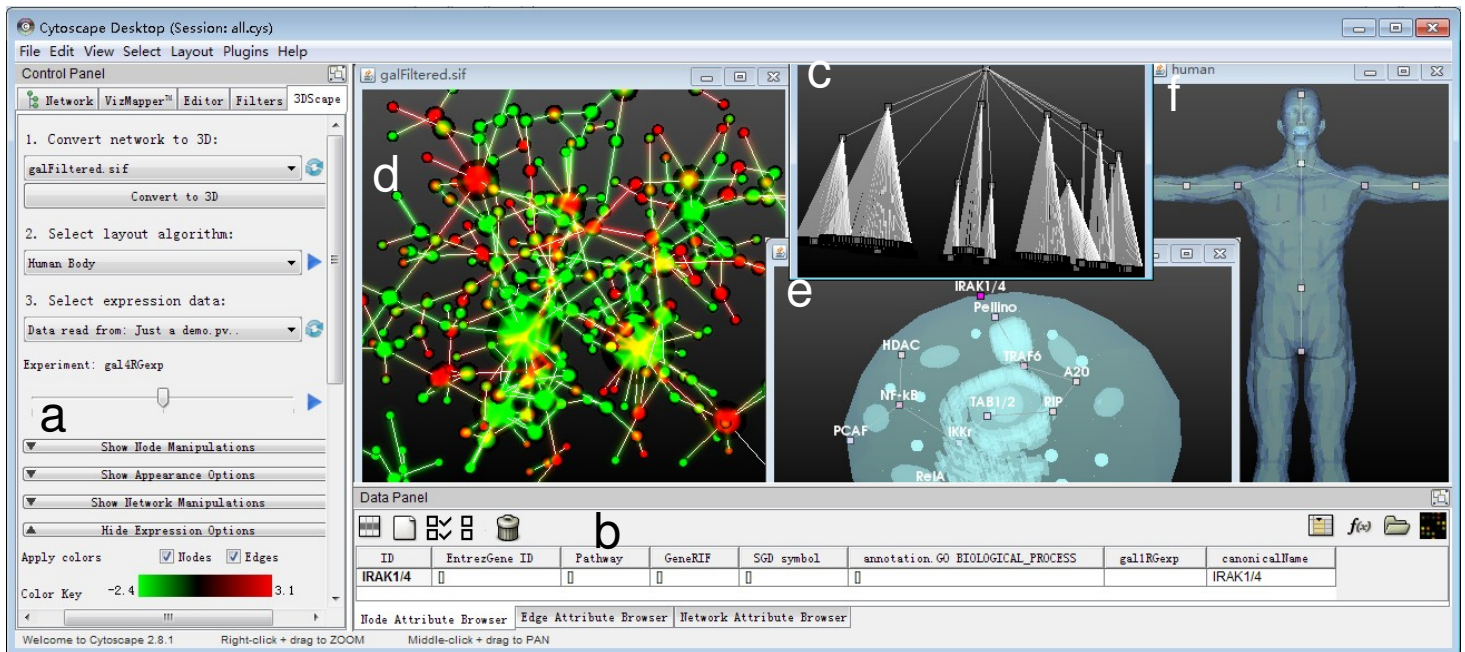
Fig. 1. Running 3DScape plug-in in Cytoscape. (a) 3DScape control panel; (b) Selected nodes/edges are listed in Attribute Browser; (c) Displaying hierarchical data using Span Tree layout; (d) Test data converted into 3D view, layout using the Fruchterman-Reingold algorithm, expression changes are rendered in glowing edges; (e) Partial NF-kB signaling pathways in a 3D cell context; (f) Partial meridian network mapped on to human body.