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# SBGNViz.as 1.0 User's Guide

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# 1. Introduction

SBGNViz.as is an ActionScript [1] based visualization tool specific to pathways represented in Systems Biology Graphical Notation (SBGN) [2] Process Description (PD) Notation [3]. The tool is built by extending the CytoscapeWeb [4] data visualization tool for the visualization of SBGN PD pathways. This document shows the features available in SBGNViz.as.

The notation used in SBGNViz.as is shown through legends. The node legend can be displayed using "Node Legend" under the Legend menu (Figure 1).

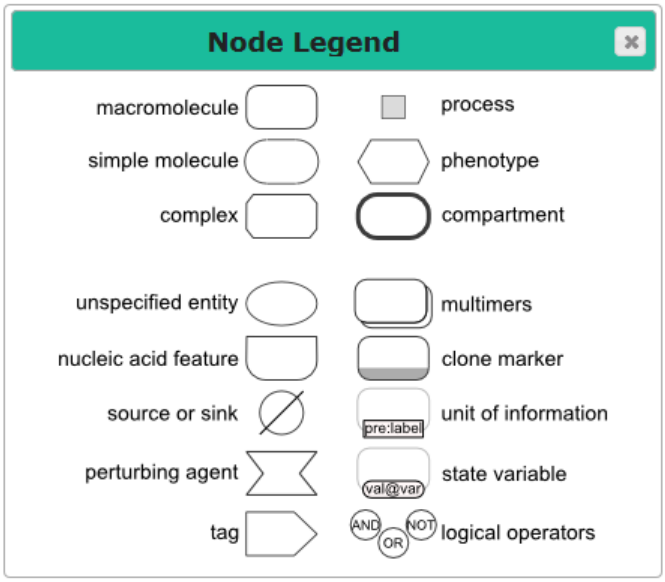


Figure 1 Node legend for process description diagrams in SBGN

Similarly, the interaction legend can be displayed using the "Interaction Legend" under the Legend menu (Figure 2).

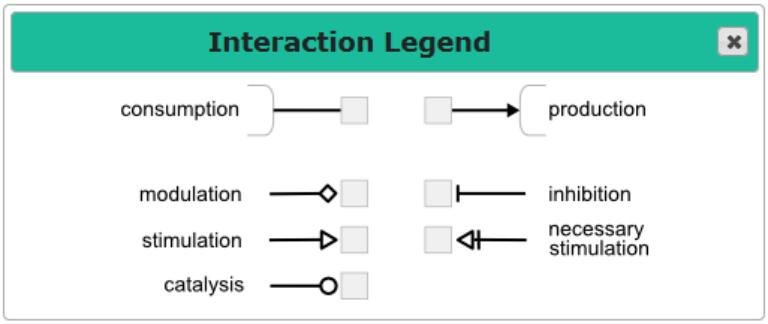


Figure 2 Interaction legend for process description diagrams in SBGN

The User Guide of SBGNViz.as (this document) can be opened up on a new browser tab using "How to Use" under the Help menu.

In summary, SBGNViz.as comes with usual zoom-scroll and move capabilities inherited from Cytoscape.js. In addition, automatic layout and context sensitive highlighting capabilities are provided by the tool as described later. Unlike most other pathway visualization tools, SBGNViz.as has full support for compound structures (i.e., molecular complexes and compartments), handling them during interactive editing operations such as move and when re-calculating layout. Finally, the tool supports inspection of macro-molecules through a dynamic connection to BioGene [6].

# 2. Loading and Saving SBGN Models

## 2.1. Load an SBGN Model

You can load files that contain SBGN-PD graphs for visualization via the "Load …" button under the File menu. A file dialog will appear in order to upload the desired file.

## 2.2. Sample SBGN Models

SBGNViz.as comes with a number of sample SBGN-PD graphs to view, available under the File menu.

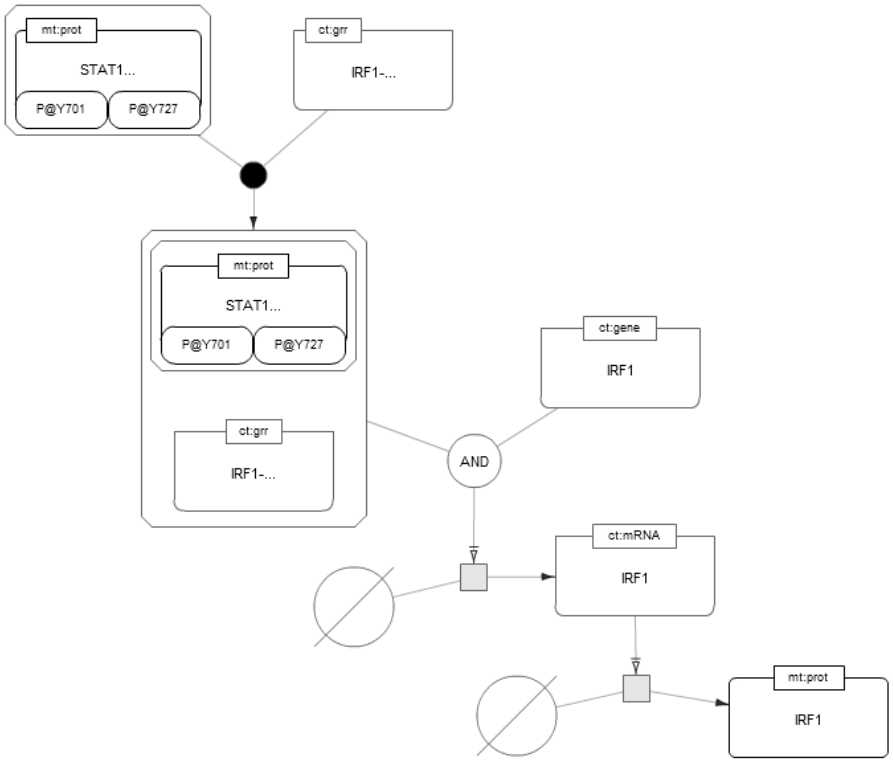


Figure 3 An example sample biological network in SBGN PD notation as rendered by SBGNViz.as

## 2.3. Save as SBGN Model

"Save …" button available under the File menu exports the current network (including both topology and geometry) in SBGN-ML format to a file on your computer. You can name the file as you wish using the file dialog.

### 2.4. Save as Image

"Save as Image" available under the File menu lets you export the current network visualized on the canvas to an image file. Currently PNG and PDF image formats are supported.

## 3. Editing of Diagrams

Since SBGNViz.as is built using Cytoscape Web, it inherits the library's zoom and scroll facilities.

The layout of a currently viewed SBGN model may be changed by the user by performing usual drag operations on nodes/molecules. In addition, the user may ask for recalculation of layout. Since most layout algorithms rely on initial random positioning, a recall of layout may result in a better looking drawing.

### 3.1. Deleting Selected Objects

In case you're not interested in a certain set of nodes and/or edges, you may delete them from the current model by simply selecting them and deleting them using "Delete Selected" under the Edit menu.

### 3.2. Perform Automatic Layout

If the user is not happy with the current layout, an automatic layout could be performed to optimize the layout of the currently viewed model. The layout algorithm used here is a modified version of CoSE (Compound Spring Embedder) algorithm [5].

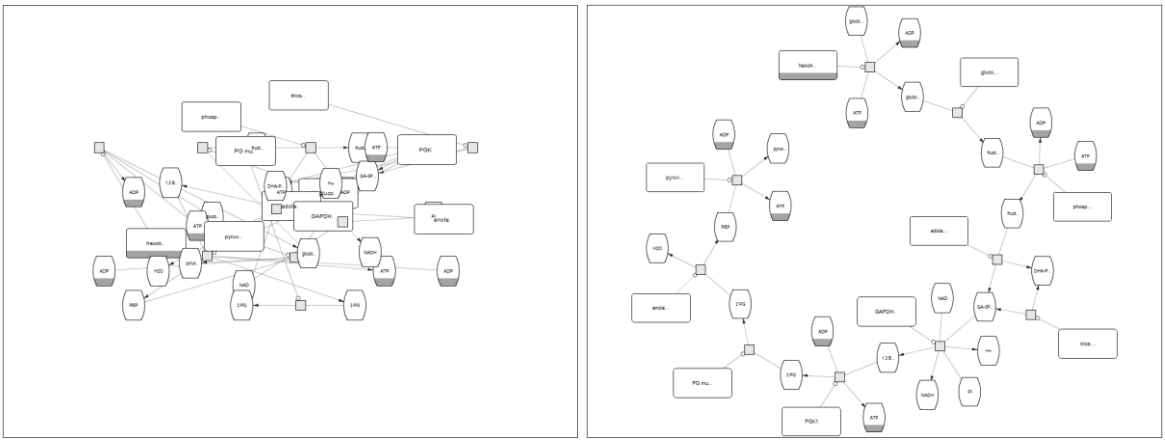

Figure 4 The same SBGN PD diagram randomly laid out (left) and automatically layout performed by SBGNViz.as (right)

### 3.3. Layout Properties

When clicked, this menu item opens a pop-up window named "Layout Properties". Properties on this window modify the parameters used during automatic layout. After you set the desired values by clicking the "Save" button, succeeding layout operations will use the new values of these parameters. For more information on these parameters, please refer to Cytoscape Web documentation [4].

## 4. Highlighting

### 4.1. Highlight Neighbors

This operation highlights the neighbors of selected node on the canvas.

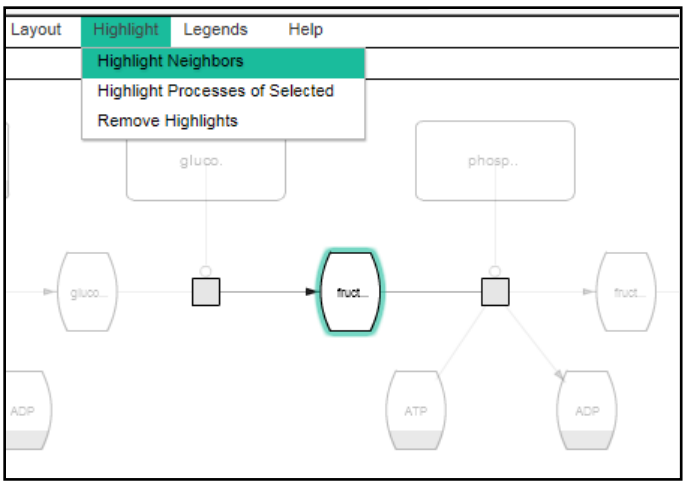


Figure 5 A sample highlight of the neighbors of a simple molecule

### 4.2. Highlight Processes of Selected

This operation highlights the processes that selected node participates in.

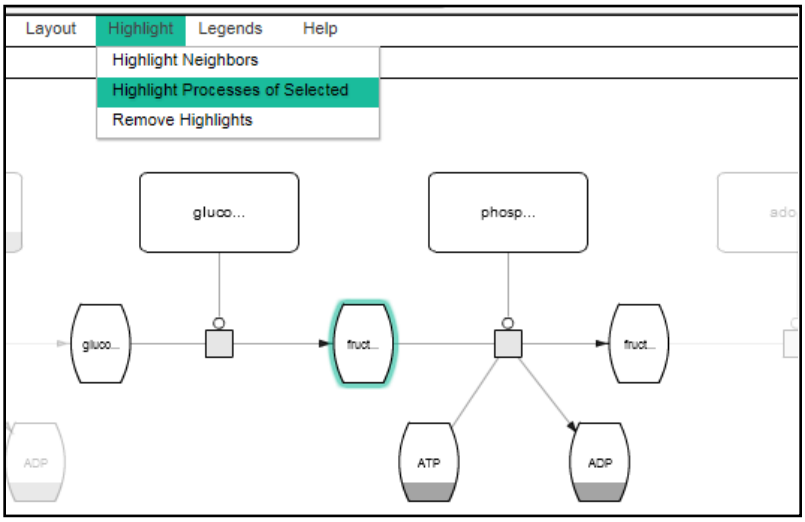


Figure 6 A sample highlight of the processes of selected; in this example selected simple molecule is involved in two processes, which are highlighted.

### 4.3. Remove Highlights

This operation removes any previous highlights on the canvas.

## 5. Inspecting Genes

SBGNViz.as also provides an interface to BioGene with cross-links to learn more about the function of the associated gene. As an example, Figure 7 shows the properties of GRB2 in a pop-up window on double click of the gene.

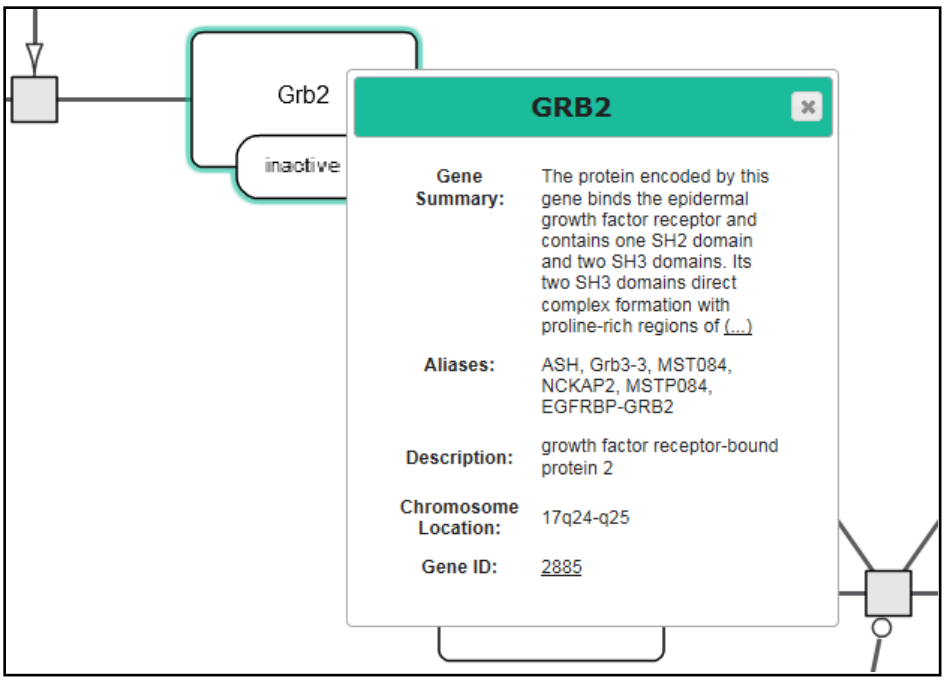


Figure 7 Properties of GRB2 as collected from BioGene

## 6. References


[1] ActionScript, http://www.adobe.com/devnet/actionscript.html.

[2] Systems Biology Graphical Notation, http://www.sbgn.org/.

[3] SBGN Process Description Notation, http://www.sbgn.org/images/5/56/Sbgn_PD-level1-user-public.pdf.

[4] Cytoscape Web, http://cytoscapeweb.cytoscape.org/.

[5] U. Dogrusoz, E. Giral, A. Cetintas, A. Civril, and E. Demir, "A Layout Algorithm For Undirected Compound Graphs", Information Sciences, 179, pp. 980-994, 2009.

[6] BioGene, http://cbio.mskcc.org/biogene/index.html.