

## Cytoscape Phylogenetic Tree Plugin v1.0

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The phylogenetic tree plugin for Cytoscape allows users to visualize phylogenetic trees in the Cytoscape environment. Trees can be imported into Cytoscape and manipulated like any other network. Information stored in the tree can be accessed using the network, node and edge attributes.

### **Supported formats:**

Currently the plugin can import phylogenetic trees that are in the **Phylip/Newick** format and the **phyloXML** format. Details about these formats can be obtained from their webpages (<http://evolution.genetics.washington.edu/phylip/newicktree.html>) and (<http://www.phyloxml.org/>) respectively.

### **Layouts:**

The plugin provides the following layouts for displaying phylogenetic trees:

**Cladograms - Rectangular, Slanted, Radial and Circular**

**Phylograms - Rectangular, Slanted, Radial and Circular**

The phylogram layouts position nodes in the network view based on the distances defined in the tree. It is highly recommended to use the phylogram layouts only for phylogenetic trees that have branch lengths defined, otherwise they may not be easy to visualize.

If edges in the layout appear too close together or too far apart, they can be scaled by entering an appropriate value for the edge scaling factor under **Settings** in the layout menu.

### **Visual Styles:**

The plugin provides two visual styles under the VizMapper designed specifically for trees.

phyлотree\_DepthwiseColor colors nodes and edges in the tree in a continuous gradient reflecting the number of ancestors between the node and the root of the tree. The lighter the color of the node, the greater the number of ancestors existing between it and the root.

phyлотree\_DepthwiseSize also colors nodes and edges similar to the phyлотree\_DepthwiseColor. Additionally, it also changes the sizes of nodes to reflect the number of ancestors between the node and the root of the tree. The smaller the node, the greater the number of ancestors existing between it and the root.

### **Usage:**

To import a phylogenetic tree into the Cytoscape, go to "**Phylogenetic tree...**"

under **File->Import**. Select the format of the tree to be imported and click on "..." to browse to the file. Please ensure that the format selected matches the format of the file selected. Click OK to begin importing the file.

The tree is a valid tree, it will automatically be displayed with the slanted cladogram layout and the phylotree\_DepthwiseSize layout. You may select a new layout from the **Layout->Phylotree Layouts** menu.

In order to change visual style, click on the **VizMapper** tab on the panel to the left and select a visual style from the drop down list.

### **Troubleshooting:**

1. The tree imports without error but the network view displays only a black screen.
  - The tree is actually being displayed correctly, but because of its large size, the view has been zoomed out considerably. You may try zooming into the tree or selecting a different visual style if you would prefer to visualize the entire tree at the current zoom level.
2. Nodes overlap in the phylotree\_DepthwiseSize visual style.
  - This can occur if nodes are placed too close to each other. This problem can be remedied by changing the scale of the network view from the Layout->Scale menu.