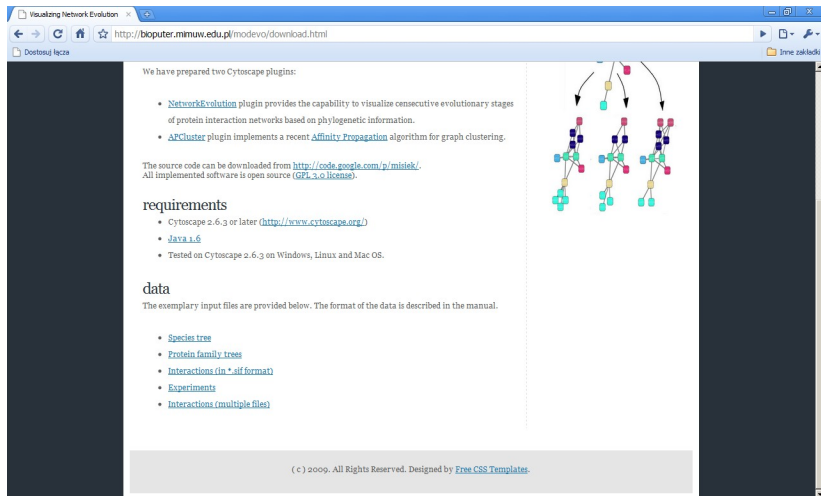


Example demonstrating how to use both  
APCluster and the Network Evolution plugin for  
evolutionary analysis.

# Download plugins and sample data from: <http://bioputer.mimuw.edu.pl/modevo>



Visualizing Network Evolution

http://bioputer.mimuw.edu.pl/modevo/download.html

Dostosuj łączę

We have prepared two Cytoscape plugins:

- [NetworkEvolution](#) plugin provides the capability to visualize consecutive evolutionary stages of protein interaction networks based on phylogenetic information.
- [APCluster](#) plugin implements a recent [Affinity Propagation](#) algorithm for graph clustering.

The source code can be downloaded from <http://code.google.com/p/misieki/>. All implemented software is open source ([GPL 3.0 license](#)).

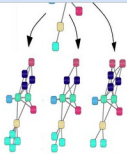
### requirements

- Cytoscape 2.6.3 or later (<http://www.cytoscape.org/>)
- [Java 1.6](#)
- Tested on Cytoscape 2.6.3 on Windows, Linux and Mac OS.

### data

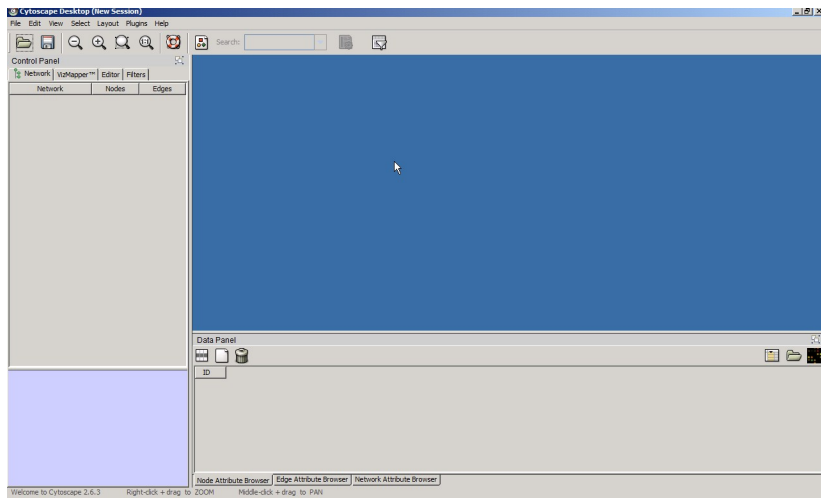
The exemplary input files are provided below. The format of the data is described in the manual.

- [Species tree](#)
- [Protein family trees](#)
- [Interactions \(in \\*.sif format\)](#)
- [Experiments](#)
- [Interactions \(multiple files\)](#)

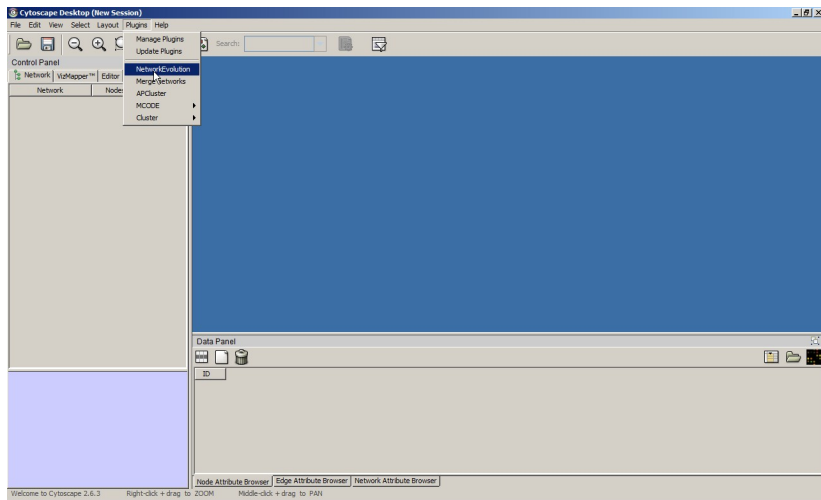


(c) 2009. All Rights Reserved. Designed by [Free CSS Templates](#).

Copy jar\* files to the plugins folder in Cytoscape directory and run Cytoscape



# Activate plugins by selecting them from the Cytoscape plugins menu



# Select the Network Evolution plugin tab

The screenshot displays the Cytoscape Desktop application window titled "Cytoscape Desktop (New Session)". The interface includes a menu bar (File, Edit, View, Select, Layout, Plugins, Help), a toolbar with icons for file operations and search, and a central workspace area that is currently blank and blue. On the left side, the "Control Panel" is visible, with the "Network Evolution" tab selected. Below the tabs are buttons for "New", "Update", and "Clean", followed by "Mapping" and "Show network" buttons. Further down are "Refresh interactions", "Help", and "Show log" buttons. At the bottom left, there is a "Colors of families" table with columns for "Family name" and "Color". At the bottom right, the "Data Panel" is visible, showing a table with a column labeled "ID". The status bar at the bottom of the window contains the text: "Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN".

Control Panel

VoMapper™ | Editor | Filters | **Network Evolution**

New Update Clean

Mapping Show network

Refresh interactions Help Show log

Colors of families

Family name	Color
-------------	-------

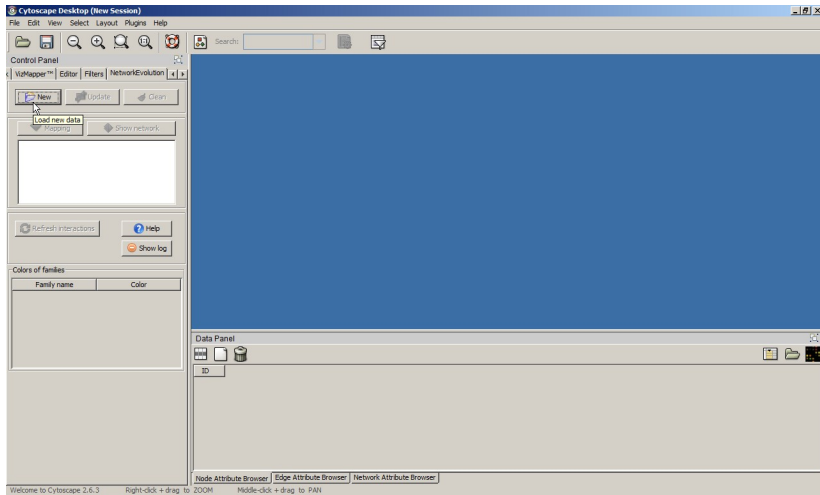
Data Panel

ID
----

Node Attribute Browser | Edge Attribute Browser | Network Attribute Browser

Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN

Click "New" to open the data loading panel.



Choose the species tree file "sp\_tree.txt", and click "Load". You should see the loaded species tree.

The screenshot shows the Cytoscape Desktop interface. The main window is titled "Cytoscape Desktop (New Session)". The menu bar includes File, Edit, View, Select, Layout, Plugins, and Help. The Control Panel on the left has tabs for VizMapper™, Editor, Filters, and NetworkEvolution. Below these are buttons for New, Update, and Clean. A Mapping section shows a tree structure with ROOT: 3 and Fungi: 3. Below that are buttons for Refresh interactions, Help, and Show log. A table for Colors of families is also visible.

The Data loading panel is open, showing tabs for Species tree, Protein family trees, Interactions, and Experiments. The Species tree tab is active, and the Load tree button is highlighted. The file path is C:\Users\mizek\Documents\sp\_tree.txt. The loaded tree structure is displayed in a list:

- ROOT: 3
  - Fungi: 3

At the bottom of the Data loading panel, there are buttons for Show log and Close. The status bar at the bottom of the Cytoscape window displays "Welcome to Cytoscape 2.6.3" and navigation instructions: "Right-click + drag to ZOOM Middle-click + drag to PAN".

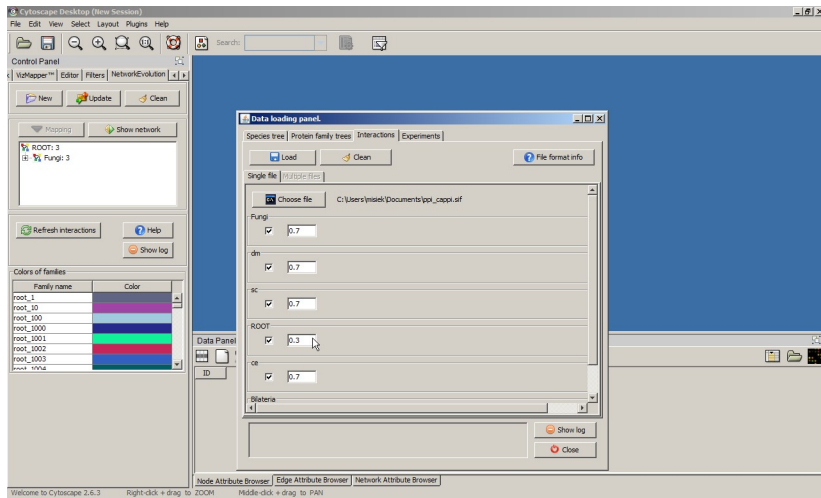
Change the tab to "Protein family trees" and do the same for protein family tree data (protein\_trees.txt file).

The screenshot shows the Cytoscape Desktop interface with a "Data loading panel" window open. The panel has tabs for "Species tree", "Protein family trees", "Interactions", and "Experiments". The "Protein family trees" tab is selected. It contains a "Choose file" button, a "Load" button, and a "File format info" button. The file path is "C:\Users\masek\Documents\protein\_trees.txt". Below this is a table with the following data:

Species name	Proteins count	Interactions count
Fungi	4425	0
dm	5999	0
sc	3371	0
ROOT	1435	0
ce	6119	0
Bacteria	6342	0

At the bottom of the panel are "Show log" and "Close" buttons. The main Cytoscape window shows a "Control Panel" with "Mapping" and "Show network" buttons, and a "Colors of families" table with columns for "Family name" and "Color". The status bar at the bottom indicates "Welcome to Cytoscape 2.6.3" and provides navigation instructions: "Right-click + drag to ZOOM" and "Middle-click + drag to PAN".

Change tab to "Interactions". Load data from file with interactions in sif format: "ppi\_cappi.sif". Select the cutoff value and choose file. Change the cutoff for ROOT network to 0.3!



The screenshot shows the Cytoscape Desktop interface with the "Data loading panel" open. The "Interactions" tab is selected. The "Single file" section shows the file path "C:\Users\nisiel\Documents\ppi\_cappi.sif". The "Cutoff" values for different taxonomic groups are as follows:

Taxonomic Group	Cutoff Value
Fungi	0.7
dm	0.7
sc	0.7
ROOT	0.3
ce	0.7

The "Data Panel" on the left shows a tree structure with "ROOT: 3" and "Fungi: 3". The "Colors of families" table is also visible:

Family name	Color
root_1	Blue
root_10	Purple
root_100	Green
root_1000	Dark Blue
root_1001	Cyan
root_1002	Red
root_1003	Dark Green
root_1004	Light Blue

At the bottom of the window, there are tabs for "Node Attribute Browser", "Edge Attribute Browser", and "Network Attribute Browser". The status bar at the very bottom provides instructions: "Welcome to Cytoscape 2.6.3", "Right-click + drag to ZOOM", and "Middle-click + drag to PAN".

(Optional) Change tab to experiments, choose appropriate file (ppi\_exp.txt) and load.

Cytoscape Desktop (New Session)

File Edit View Select Layout Plugins Help

Control Panel

VizMapper™ Editor Filters NetworkEvolution

New Update Clean

Mapping Show network

ROOT: 3  
Fungi: 3

Refresh interactions Help

Show log

Colors of families

Family name	Color
root_1	Dark Purple
root_10	Light Purple
root_100	Light Blue
root_1000	Dark Blue
root_1001	Light Green
root_1002	Light Red
root_1003	Dark Red
root_1004	Light Blue

Data loading panel

Species tree Protein family trees Interactions Experiments

Choose file Load Clean File format info

C:\Users\msiek\Documents\ppi\_exp.txt

Data Panel

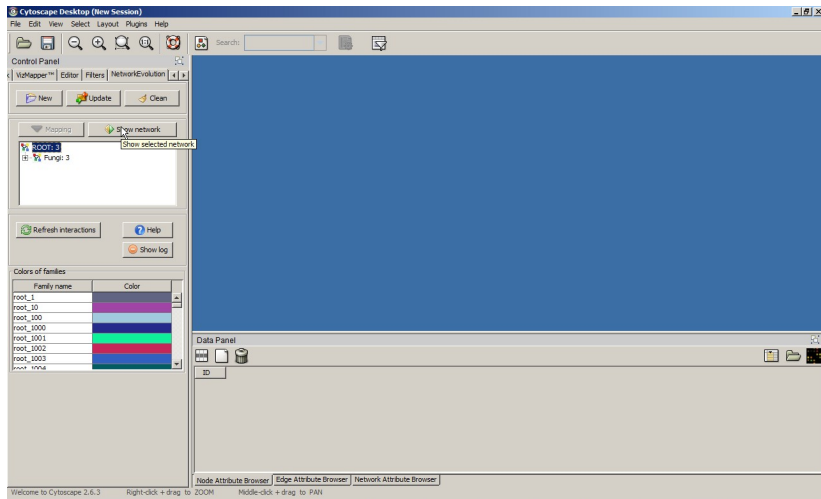
ID

Show log Close

Node Attribute Browser Edge Attribute Browser Network Attribute Browser

Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN

Select ancestral network "ROOT" on the species tree, and click the "Show network" button. The ancestral PPI network will be shown.



The screenshot shows the Cytoscape Desktop interface. The main window is titled "Cytoscape Desktop (New Session)". The top menu bar includes File, Edit, View, Select, Layout, Plugins, and Help. Below the menu bar is a toolbar with icons for file operations and search. The left sidebar contains a "Control Panel" with tabs for "VizMapper™", "Editor", "Filters", and "NetworkEvolution". The "NetworkEvolution" tab is active, showing a tree view with "ROOT" selected and "Fungi: 3" below it. A tooltip "Show selected network" is visible over the "Show network" button. Below the tree view are buttons for "New", "Update", and "Clean". Further down are "Refresh interactions" and "Help" buttons, and a "Show log" button. At the bottom of the sidebar is a "Colors of families" table.

Family name	Color
root_1	Blue
root_10	Purple
root_100	Dark Blue
root_1000	Light Blue
root_1001	Cyan
root_1002	Red
root_1003	Green
root_1004	Orange

The main workspace is currently empty and blue. The bottom of the interface has a "Data Panel" with an "ID" field and three browser tabs: "Node Attribute Browser", "Edge Attribute Browser", and "Network Attribute Browser". The status bar at the very bottom reads: "Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN".

Go to the APCluster plugin tab. Refresh "Edge weight attribute" and choose "Probability"

The screenshot displays the Cytoscape Desktop interface with the APCluster plugin active. The Control Panel on the left is configured as follows:

- Parameters:
  - Edge weight attribute: DEFAULT (dropdown menu)
  - Number of iterations: 10 (input field)
  - Stop criterion: Probability (dropdown menu)
  - Preference: 0.500 (input field)
  - Lambda: 0.5 (input field)
  - Add noise:
  - Log transform edge weights:
- Output attributes:
  - Cluster ID: cluster\_id (input field)
  - Center ID: center\_id (input field)
- Graph mode:
  - Undirected edges
  - Directed edges
- Buttons: Advanced options, Start
- Highlight centers: (dropdown menu)
- Network | Preferences | Lambda | Clusters (tabs)
- Buttons: Delete row, Details

The main window shows a dense network graph with many nodes and edges. The Data Panel at the bottom is empty, showing only an ID column header. The status bar at the bottom indicates: Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN

Check "Log transform...", to transform probabilities to –similarities.

The screenshot displays the Cytoscape Desktop interface for a new session. The main window is titled "Cytoscape Desktop (New Session)" and contains a menu bar (File, Edit, View, Select, Layout, Plugins, Help) and a toolbar. The "Control Panel" is active, showing the "APCluster" tab. The "Parameters" section includes:

- Edge weight attribute: Probability
- Number of iterations: 500
- Stop criterion: 50
- Preference: 0.474
- Lambda: 0.5
- Add noise:
- Log transform edge weights:  (highlighted by a mouse cursor)

The "Output attributes" section shows "Cluster ID" and "Center ID" both set to "cluster\_id". The "Graph mode" is set to "Undirected edges". A "Start" button is visible. Below the parameters, there are tabs for "Network", "Preferences", "Lambda", and "Clusters". The "Network" tab is active, showing a "Delete row" button and a "Details" button. The main workspace displays a dense network graph with many nodes and edges, labeled "ROOT". The "Data Panel" at the bottom shows a table with a single column labeled "ID". The status bar at the bottom indicates "Welcome to Cytoscape 2.6.3" and provides instructions for zooming and panning.

Run the algorithm.

The screenshot displays the Cytoscape Desktop interface during a network clustering process. The main window, titled "Cytoscape Desktop (New Session)", shows a dense network graph with nodes of various colors and numerous edges. A dialog box titled "Clustering completed." is overlaid on the graph, providing the following information:

- Description: Performing Affinity Propagation
- Status: Iteration: 77, number of clusters: 287
- Progress: A progress bar showing approximately 77% completion.

The dialog box includes "Close" and "Cancel" buttons. In the background, the Cytoscape interface is visible, including the Control Panel on the left with the "APCluster" plugin selected. The "Parameters" section shows settings for "Probability", "Number of iterations" (500), "Stop criterium" (50), "Preference" (0.474), and "Lambda" (0.5). The "Output attributes" section shows "cluster\_id" and "center\_id". The "Graph mode" section has "Undirected edges" selected. The "Data Panel" at the bottom is currently empty.

# The algorithm will converge.

The screenshot shows the Cytoscape Desktop interface with a network graph and a dialog box. The dialog box, titled "Clustering complete", contains the following information:

- Description: Per
- Status: Cer
- Progress: [Progress bar]
- Algorithm converged after: 78 iterations

The dialog box also has "Close", "Cancel", and "OK" buttons.

The main window shows the Control Panel on the left with the following settings:

- Edge weight attribute: Probability
- Number of iterations: 500
- Stop criterium: 50
- Preference: 0,474
- Lambda: 0,5
- Add noise:
- Log transform edge weights:

The Data Panel at the bottom shows a table with the following data:

Network	Preferences	Lambda	Clusters
ROOT	0,474	0,5	287

At the bottom of the window, there are navigation instructions: "Welcome to Cytoscape 2.6.3", "Right-click + drag to ZOOM", and "Middle-click + drag to PAN".

Choose "Group Attribute Layout" and select "cluster\_id" as the attribute.

The screenshot shows the Cytoscape Desktop interface. The 'Layout' menu is open, and the 'Group Attribute Layout' option is selected. A sub-menu is visible, showing 'All Nodes' and 'Selected Nodes Only' options, with 'cluster\_id' selected under 'All Nodes'. The 'Data Panel' at the bottom shows a table with columns for 'Network', 'Preferences', 'Lambda', and 'Clusters'. The 'ROOT' network is selected, and the 'Preferences' column shows '0,474' and '0,5'. The 'Clusters' column shows '287'. The 'Node Attribute Browser' is also visible at the bottom.

Control Panel

Editor | Filters | NetworkEv | Settings...

Parameters

Edge weight attribute: yFiles

Number of iterations: 50

Stop criterion: JGraph Layouts

Preference: 0,474

Lambda: 0,5

Add noise:

Log transform edge weights:

Output attributes

Cluster ID: cluster\_id

Center ID: center\_id

Graph mode

Undirected edges  Directed edges

Advanced options Start

Highlight centers center\_id

Network	Preferences	Lambda	Clusters
ROOT	0,474	0,5	287

Delete row Details

ROOT

Attribute Circle Layout

Edge-weighted Spring Embedded

Hierarchical Layout

Circular Layout

Inverted Self-Organizing Map Layout

Group Attributes Layout

Grid Layout

Force-Directed Layout

Degree Sorted Circle Layout

Spring Embedded

Edge-weighted Force directed (Biolayout)

All Nodes cluster\_id

Selected Nodes Only center\_id

Data Panel

ID
root_604
root_66
root_649
root_1229
root_515
root_952
root_365
root_472
root_1226

Node Attribute Browser Edge Attribute Browser Network Attribute Browser

Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN

Select and zoom into a fragment of the clustered network.

The screenshot displays the Cytoscape Desktop interface for a new session. The main window shows a network graph with a red box highlighting a specific cluster of nodes. The interface is divided into several panels:

- Control Panel:** Contains various settings for the network simulation, including parameters and output attributes.
- Parameters:** Includes fields for Edge weight attribute (Probability), Number of iterations (500), Stop criterium (50), Preference (0.474), and Lambda (0.5). There are also checkboxes for Add noise and Log transform edge weights.
- Output attributes:** Shows Cluster ID (cluster\_id) and Center ID (center\_id).
- Graph mode:** Offers options for Undirected edges and Directed edges.
- Advanced options:** Includes a Start button and a Highlight centers dropdown menu set to center\_id.
- Data Panel:** A table showing the current network configuration.

Network	Preferences	Lambda	Clusters
ROOT	0,474	0,5	287

At the bottom of the interface, there are buttons for Node Attribute Browser, Edge Attribute Browser, and Network Attribute Browser. A footer message reads: "Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN".

Choose one of the clusters, go to the Network Evolution plugin tab and select species from the tree.

The screenshot shows the Cytoscape Desktop interface with the Network Evolution plugin. The main window displays a network graph with nodes and edges. The left sidebar contains the Control Panel with tabs for Editor, Filters, NetworkEvolution, and APCluster. The NetworkEvolution tab is active, showing a tree view of species clusters. The Data Panel at the bottom right displays a list of node IDs.

Control Panel: Editor | Filters | NetworkEvolution | APCluster

Mapping of selected proteins on networks

Family name	Color
root_1	
root_10	
root_100	
root_1000	
root_1001	
root_1002	
root_1003	
root_1004	

Data Panel

10
root_1099
root_907
root_726
root_1353
root_848
root_102
root_652
root_931

Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN

Click the "Mapping" button to project selected cluster onto target species.

The screenshot displays the Cytoscape Desktop interface. The main window shows a network graph with nodes of various colors (purple, green, red, yellow, pink) and edges. Several smaller windows are open, showing different views of the network, including a 'MAP\_ROOT\_OR\_sc\_1' window and a 'MAP\_ROOT\_OR\_sc\_2' window. The interface includes a menu bar (File, Edit, View, Select, Layout, Plugins, Help), a toolbar, and a control panel on the left. The control panel has tabs for 'Editor', 'Filters', 'NetworkEvolution', and 'APCluster'. Below these are buttons for 'New', 'Update', and 'Clean'. The 'Mapping' section is active, showing a tree view of the network structure with folders for 'Fungi: 3', 'Blateria: 2', and 'sc\_EXP: 0'. A 'Refresh interactions' button and a 'Help' button are also present. At the bottom, there is a 'Data Panel' with a table of family names and colors, and a 'Node Attribute Browser' section.

Family name	Color
root_1	Purple
root_10	Purple
root_100	Purple
root_1000	Purple
root_1001	Green
root_1002	Red
root_1003	Red
root_1004	Red

Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN