



## HierarchicalClusteringViewer Documentation

**Module name:** HierarchicalClusteringViewer  
**Description:** Hierarchical clustering viewer that reads cdt, atr, and gtr files.  
**Author:** Joshua Gould (Broad Institute), gp-help@broad.mit.edu

### Summary:

Reads in files in Eisen's tree view format and displays hierarchical trees. At least one of gtr filename and atr filename files is required. A cdt file is always required.

Coloring of nodes in the dendrogram is supported. The color of the selected node in the sample dendrogram can be set by selecting View > Sample Dendrogram Color. Similarly to set the color for the feature tree, select View > Feature Dendrogram Color.

The HierarchicalClusteringViewer module displays expression values in a heat map format where the largest values are displayed as the reddest (hot), the smallest values are displayed as the bluest (cool), and intermediate values are a lighter color of either blue or red. This is a very convenient way to display three-dimensional data (samples, genes, and expression values).

Users have a number of options regarding the appearance of the heat map that can be set by selecting the Options item in the View menu. Users can choose between radio buttons for Relative and Global color schemes. The relative choice causes the colors for expression values to be scaled as a function of the number of standard deviations relative to the mean for each row. The global choice scales values using the minimum and maximum values in the dataset. To display the color legend, select the Legend item from the View menu. Users can choose whether to show or hide row names and descriptions and column names from the display by deselecting the corresponding check box. The row and column size fields control the size of each element in the heat map. The show grid checkbox controls whether a grid is drawn around each element.

Users can save the color gram image to a file by selecting File > Save Image. Choices for the output file format are bmp, jpeg, png, and tiff.

The File > Save Dataset item allows the user to create new data sets that contain only a subset of the features and/or samples of the original data set.

You can visually inspect the profile of each feature across each sample by selecting the desired features in the heat map and then choosing View > Profile item.

Users can enter their own annotations of features and view these annotations via a color-coding mechanism by selecting File > Open Feature List(s). Accepted file formats are gmt, gmx, and grp. Similarly, users can annotate samples by opening a cls file.

Affymetrix probe set identifiers can be interactively annotated from genomic databases such as GenBank, UniGene, SwissProt, LocusLink, and Gene Ontology using GeneCruiser. GeneCruiser (<http://www.broad.mit.edu/cancer/genecruiser/>) maintains a database of regularly updated mappings between microarray probes and other genomic databases.

# GenePattern

## Parameters

cdt.filename	Clustered data table (TreeView cdt file)
gtr.filename	Gene Tree file (TreeView gtr file)
atr.filename	Array Tree file (TreeView atr file)

## Platform Dependencies

**CPU Type:** any  
**OS:** any  
**Language:** Java  
**Java JVM Level:** 1.4