

# GenePattern

**Module name:** HierarchicalClusteringViewer  
**Description:** Views hierarchial trees.  
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**Release:** 1.0

Reads in files in Eisen's tree view format and displays hierarchial trees.

## References:

Eisen, MB, Spellman PT, Brown PO, Botstein D. (1998) Cluster analysis and display of genome-wide expression patterns. Proc. Natl. Acad. Sci. USA 95:14863-14868.

## Parameters:

Name	Description
cdt.filename	Clustered data table (TreeView cdt file)
gtr.filename	Gene Tree file (TreeView gdt file)
atr.filename	Array Tree file (TreeView atr file)
className	edu.mit.genome.gp.ui.hclviewer.CdtParser

**Return Value:** An R list with components:

1. Stdout: the "stdout" text output from running the program.
2. Stderr: the "stderr" text output from running the program.

## Platform dependencies:

<b>Task type:</b>	Visualizer
<b>CPU type:</b>	any
<b>OS:</b>	any
<b>Java JVM level:</b>	1.3
<b>Language:</b>	Java
<b>Support files:</b>	gp-common.jar, hclviewer.jar, jargs.jar, ij.jar

**Native command line:** <java> <java\_flags>-cp gp-common.jar:hclviewer.jar:jargs.jar:ij.jar  
edu.mit.genome.gp.ui.hclviewer.CdtParser<cdt.filename> <gtr.filename> <atr.filename>