



HierarchicalClusteringViewer Documentation

Module name: HierarchicalClusteringViewer
Description: Views hierarchial trees.
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Release: 1.1

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 gtr file)
atr.filename	Array Tree file (TreeView atr file)

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:

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

Native command line: <java> <java_flags> -cp <libdir>gp-common.jar<path.separator><libdir>hclviewer.jar<path.separator><libdir>jargs.jar<path.separator><libdir>ij.jar<path.separator><libdir>colt.jar<path.separator><libdir>trove.jar<path.separator><libdir>file_support.jar edu.mit.genome.gp.ui.hclviewer.CdtParser <cdt.filename> <gtr.filename> <atr.filename>