Package ‘GENE.E’

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Type Package
Title Interact with GENE-E from R
Version 1.15.0
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Author Joshua Gould
Maintainer Joshua Gould <jgould@broadinstitute.org>
Depends R (>= 2.7.0), rhdf5 (>= 2.8.0), RCurl (>= 1.6-6)
Imports rhdf5, RCurl
Suggests RUnit, BiocGenerics, knitr, golubEsets (>= 1.0)
SystemRequirements GENE-E software.
Description Interactive exploration of matrices in GENE-E.
License GPL-2
URL http://www.broadinstitute.org/cancer/software/GENE-E
VignetteBuilder knitr
biocViews ThirdPartyClient
NeedsCompilation no

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from.genee from.genee

Description
R interface to get selection from GENE-E.

Usage
from.genee(url='http://localhost:9998')
to.genee

Arguments
url GENE-E URL.

Details
Gets selection from GENE-E. If no rows or columns are selected, the full dataset is returned.

Value
List containing row.annotations, column.annotations, and matrix.

Examples
# not run
# z = from.genee();

to.genee

description
R interface to view a matrix in GENE-E

Usage

Arguments
mdat a matrix.
row.annotations a data frame containing row annotations.
column.annotations a data frame containing column annotations.
show.rownames Whether to show the row names of the matrix in GENE-E.
show.colnames Whether to show the column names of the matrix in GENE-E.
row.hclust An object of class hclust to show in GENE-E. If provided, the matrix and annotations will be reordered to reflect the tree produced by the clustering process.
column.hclust An object of class hclust to show in GENE-E. If provided, the matrix and annotations will be reordered to reflect the tree produced by the clustering process.
url GENE-E URL.

Details
R interface to GENE-E.
Examples

# not run
# z = matrix(rnorm(30),nrow=5,ncol=6);
# row.names(z) <- LETTERS[1:NROW(z)];
# colnames(z) <- LETTERS[1:NCOL(z)];
# row.annotations <- data.frame(y=1:5, char = I(letters[1:5]))
# L3 <- LETTERS[1:3]
# column.annotations <- data.frame(y=1:6, char = I(letters[1:6]), fac=sample(L3, 6, replace=TRUE))
# to.genee(z, row.annotations, column.annotations, column.hclust=hclust(dist(t(z))));
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