Package ‘GENE.E’

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Type Package
Title Interact with GENE-E from R
Version 1.14.0
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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

R topics documented:

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Description

R interface to get selection from GENE-E.

Usage

from.genee(url='http://localhost:998')
to.gene

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

```r
# not run
# z = from.genee();
```

Description

R interface to view a matrix in GENE-E

Usage

```r
to.genee(mdat, row.annotations=NULL, column.annotations=NULL, show.rownames=T, show.colnames=T, row.hclust=NULL, column.hclust=NULL, url=
```

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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