Package 'GENE.E'

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Type Package

Title Interact with GENE-E from R

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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.

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URL http://www.broadinstitute.org/cancer/software/GENE-E

VignetteBuilder knitr

biocViews ThirdPartyClient

R topics documented:

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from.genee	*from.genee*

Description

R interface to get selection from GENE-E.

Usage

```
from.genee(url=http://localhost:9998)
```

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();
```

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to.genee	*to.genee*

Description

R interface to view a matrix in GENE-E

Usage

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

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 anno-
                      tations 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 anno-
                      tations 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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