Package ‘GENE.E’

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Type Package

Title Interact with GENE-E from R

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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

R topics documented:

`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();
```

`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.
```

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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