

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.

License GPL-2

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

VignetteBuilder knitr

biocViews ThirdPartyClient

NeedsCompilation no

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from.genee	<i>from.genee</i>
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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();
```

<code>to.genee</code>	<i>to.genee</i>
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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, ...)
```

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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