

# Package ‘GENE.E’

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**Type** Package

**Title** Interact with GENE-E from R

**Version** 1.1.0

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**biocViews** ConnectTools

**Depends** R (>= 2.7.0), h5r (>= 1.4.1), RCurl (>= 1.6-6)

**Imports** h5r, 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

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`from.genee`*from.genee*

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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();
```

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`to.genee`*to.genee*

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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, row.h
```

**Arguments**

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