

Package ‘phantom’

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Title Gene Set Pareto Heterogeneity Analysis of Time-Course Gene Expression Data

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Description Pareto front based statistical tool for detecting heterogeneity in gene sets and biological modules from time-course data.

License GPL-2

Encoding UTF-8

LazyData true

Depends R (>= 3.0.1)

Imports Rcpp (>= 0.12.3), NMF (>= 0.20.6), MASS (>= 7.3-35), RColorBrewer (>= 1.1-2), gplots (>= 2.16.0)

LinkingTo Rcpp, RcppArmadillo

RoxygenNote 6.0.1.9000

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation yes

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baylor.module	<i>baylor gene modules</i>
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Description

This data set gives the a geneset list of baylor modules

Usage

baylor.module

Format

A large list containing 260 gene sets.

Source

baylor modules

emory.geneset	<i>emory genesets</i>
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Description

This data set gives a geneset list of emory gene sets

Usage

emory.geneset

Format

A large list containing 346 gene sets.

Source

emory genesets from MSigDB

geneset.names	<i>Print all geneset names in geneset list</i>
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Description

This function allows user to print all the geneset names in the loaded geneset list such that user can find the specific query_geneset name for run.phantom function.

Usage

```
geneset.names(geneset_list = NULL)
```

Arguments

`geneset_list` User provided genesets list loaded by `load.geneset()`. Phantom package provides four geneset lists from different resources: kegg, reactome, emory geneset and baylor modules. These genesets can be obtained with `data()`, e.g. `data(kegg.geneset)`

Examples

```
## load in the demo geneset in phantom package
data("reactome.geneset")

## store all the geneset names in one vector
g.names = geneset.names(reactome.geneset)
```

kegg.geneset	<i>kegg genesets</i>
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Description

This data set gives a geneset list of 186 kegg gene sets

Usage

```
kegg.geneset
```

Format

A large list containing 186 gene sets.

Source

kegg genesets from MSigDB

load.data	<i>Load data function</i>
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Description

This function allows user to load in the time-course gene differential expression data in a format that can be used by run.phantom and run.phantom.batch functions.

Usage

```
load.data(filename)
```

Arguments

filename	the time-course gene differential expression data file path and name on user's local machine
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load.geneset	<i>Load geneset function</i>
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Description

This function allows user to load in the genesets in a format that can be used by run.phantom and run.phantom.batch functions.

Usage

```
load.geneset(geneset_file)
```

Arguments

geneset_file	the genesets data file path and name on user's local machine
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reactome.geneset	<i>reactome genesets</i>
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Description

This data set gives the a geneset list of reactome gene sets

Usage

```
reactome.geneset
```

Format

A large list containing 674 gene sets.

Source

reactome genesets from MSigDB

run.phantom	<i>Run phantom analysis</i>
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Description

This function allows user to run individual geneset heterogeneity analysis with phantom

Usage

```
run.phantom(data = NULL, geneset_list = NULL, query_geneset = NULL,
            ncluster = 2, nsample = 1000)
```

Arguments

data	User provided time-course data loaded by load.data()
geneset_list	User provided genesets list loaded by load.geneset(). Phantom package provides four geneset lists from different resources: kegg, reactome, emory geneset and baylor modules. These genesets can be obtained with data(), e.g. data(kegg.geneset)
query_geneset	The name of a geneset user wants to analysis. This geneset should be from the geneset_list designated by geneset_list parameter
ncluster	The number of clusters within a geneset user wants to use to identify the heterogeneity of this geneset.
nsample	The times of random sampling that is used to build the NULL distribution for parato front analysis.

Examples

```
## load in the demo data and geneset in phantom package
data("time.course.data")
data("reactome.geneset")

## store the analysis result in an object
obj = run.phantom(data = time.course.data, geneset_list = reactome.geneset,
                  query_geneset = 'REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES',
                  ncluster = 2, nsample = 1000)
```

<code>run.phantom.batch</code>	<i>Run phantom batch analysis</i>
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Description

This function allows user to run batch analysis of a full geneset list with phantom, and download the identified heterogeneous genesets

Usage

```
run.phantom.batch(data = NULL, geneset_list = NULL, maxncluster = 5,
                  nsample = 1000, report_pval = 0.05, report_nmin = 5,
                  output_dir = file.path("./phantom_result"))
```

Arguments

<code>data</code>	User provided time-course data loaded by <code>load.data()</code>
<code>geneset_list</code>	User provided genesets list loaded by <code>load.geneset()</code> . Phantom package provides four geneset lists from different resources: kegg, reactome, emory geneset and baylor modules. These genesets can be obtained with <code>data()</code> , e.g. <code>data(kegg.geneset)</code>
<code>maxncluster</code>	The maximum number of clusters within a geneset user wants to test with. All numbers from 1 to <code>ncluster</code> will be tested and an optimal cluster number will be selected to identify the heterogeneity of this geneset.
<code>nsample</code>	The times of random sampling that is used to build the NULL distribution for parato front analysis.
<code>report_pval</code>	The maximum p value of a geneset that will be reported as a significant heterogeneous geneset. Genesets with p value larger than <code>report_pval</code> will not be reported
<code>report_nmin</code>	The minimum size of subcluster in a geneset that will be reported as a significant heterogeneous geneset.
<code>output_dir</code>	The directory where user wants to put the phantom batch analysis results

Examples

```
## load in the demo data and geneset in phantom package
data("time.course.data")
data("kegg.geneset")

## store the analysis result in an object
## Not run: obj = run.phantom.batch(data = time.course.data, geneset_list = kegg.geneset,
maxncluster = 5, nsample = 1000, report_pval = 0.05, report_nmin = 5,
output_dir = file.path(getwd(), '/phantom_result'))
## End(Not run)
```

time.course.data	<i>A sample time.course.data with 15 time points</i>
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Description

This data set gives a sample of time-course gene differential expression data, designated by t statistics of symptomatic samples versus asymptomatic samples gene expression across 15 time points.

Usage

```
time.course.data
```

Format

A large matrix containing the t statistics of 11745 genes across 15 time points

Source

publications

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