

Package ‘phantasus’

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Title Visual and interactive gene expression analysis

Version 1.0.2

Description Phantasus is a web-application for visual and interactive gene expression analysis. Phantasus is based on Morpheus – a web-based software for heatmap visualisation and analysis, which was integrated with an R environment via OpenCPU API. Aside from basic visualization and filtering methods, R-based methods such as k-means clustering, principal component analysis or differential expression analysis with limma package are supported.

URL <https://genome.ifmo.ru/phantasus>,
<https://artyomovlab.wustl.edu/phantasus>

BugReports <https://github.com/ctlab/phantasus/issues>

Depends R (>= 3.5)

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DifferentialExpression, PrincipalComponent

Imports ggplot2, protolite, Biobase, GEOquery, Rook, htmltools,
httpuv, jsonlite, limma, opencpu, assertthat, methods, httr,
rhdf5, utils, parallel, stringr, fgsea, svglite

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calcPCA	<i>Principal Component Analysis.</i>
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Description

calcPCA calculates PCA-matrix for the given ExpressionSet and returns this matrix encoded to JSON.

Usage

```
calcPCA(es, columns = c(), rows = c(), replacena = "mean")
```

Arguments

es	an ExpressionSet object, should be normalized
columns	list of specified columns' indices (optional)
rows	list of specified rows' indices (optional)
replacena	method for replacing NA values (mean by default)

Value

json with full description of the plot for plotly.js

Examples

```
## Not run:  
data(es)  
calcPCA(es)  
  
## End(Not run)
```

`checkGPLs`*Check possible annotations for GEO Dataset.*

Description

checkGPLs returns GPL-names for the specified GEO identifier.

Usage

```
checkGPLs(name)
```

Arguments

name String, containing GEO identifier of the dataset.

Value

Vector of filenames serialized in JSON format. If there is only one GPL for that dataset, the function will return name.

Examples

```
## Not run:  
checkGPLs('GSE27112')  
checkGPLs('GSE14308')  
  
## End(Not run)
```

`checkPreloadedNames`*Check names inside preloaded file*

Description

checkPreloadedNames checks names of ExpressionSets that are included in file name

Usage

```
checkPreloadedNames(name)
```

Arguments

name String, containing filename. Assuming that in the directory with preloaded files preloadedDir exists file filename.rda with list of ExpressionSets ess.

Value

Vector of names serialized in JSON format.

createES

Create ExpressionSet.

Description

createES function produces an ExpressionSet object from given data, and exports it to global scope.

Usage

```
createES(data, pData, varLabels, fData, fvarLabels)
```

Arguments

data	Gene expression matrix.
pData	Matrix with phenotypical data.
varLabels	Names of phenoData columns.
fData	Matrix with feature data.
fvarLabels	Names of featureData columns.

Value

produced ExpressionSet object

Examples

```
## Not run:
data <- matrix(1:15, 5, 3)
pData <- c("A", "B", "C")
varLabels <- "cat"
fData <- c("p", "r", "s", "t", "u")
fvarLabels <- "id"
createES(data, pData, varLabels, fData, fvarLabels)

## End(Not run)
```

es

*Example dataset***Description**

Small slice from GSE27112-GPL6103 for runnable examples.

Usage

```
data(es)
```

Format

An object of class ExpressionSet with 20 rows and 5 columns.

Examples

```
## Not run:
data(es)
performKmeans(es, k = 2)

## End(Not run)
```

getES

*Load ExpressionSet by GEO identifier***Description**

getES return the ExpressionSet object(s) corresponding to GEO identifier.

Usage

```
getES(name, type = NA, destdir = tempdir(),
      mirrorPath = "https://ftp.ncbi.nlm.nih.gov")
```

Arguments

name	String, containing GEO identifier of the dataset. It should start with 'GSE' or 'GDS' and can include exact GPL to annotate dataset, separated with dash ('-') from the identifier.
type	Type of the dataset: 'GSE' or 'GDS'. If not specified, the function will take first three letters of name variable as type.
destdir	Directory for caching loaded Series and GPL files from GEO database.
mirrorPath	URL string which specifies the source of matrices.

Value

List of ExpressionSet objects, that were available by given in name variable GEO identifier.

Examples

```
## Not run:
  getES('GSE14308', type = 'GSE', destdir = 'cache')
  getES('GSE27112')

## End(Not run)
getES('GDS4922')
```

getGDS

Load ExpressionSet from GEO Datasets

Description

getGDS return the ExpressionSet object corresponding to GEO Dataset identifier.

Usage

```
getGDS(name, destdir = tempdir(),
  mirrorPath = "https://ftp.ncbi.nlm.nih.gov")
```

Arguments

name	String, containing GEO identifier of the dataset. It should start with 'GSE' or 'GDS' and can include exact GPL to annotate dataset, separated with dash ('-') from the identifier.
destdir	Directory for caching loaded Series and GPL files from GEO database.
mirrorPath	URL string which specifies the source of matrices.

Value

ExpressionSet object wrapped in list, that was available by given in name variable GEO identifier.

Examples

```
getGDS('GDS4922')
```

getGSE

Load ExpressionSet from GEO Series

Description

getGSE return the ExpressionSet object(s) corresponding to GEO Series Identifier.

Usage

```
getGSE(name, destdir = tempdir(),
  mirrorPath = "https://ftp.ncbi.nlm.nih.gov")
```

Arguments

name	String, containing GEO identifier of the dataset. It should start with 'GSE' or 'GDS' and can include exact GPL to annotate dataset, separated with dash ('-') from the identifier.
destdir	Directory for caching loaded Series and GPL files from GEO database.
mirrorPath	URL string which specifies the source of matrices.

Value

List of ExpressionSet objects, that were available by given in name variable GEO identifier.

Examples

```
## Not run:
  getGSE('GSE14308', destdir = 'cache')
  getGSE('GSE27112')

## End(Not run)
  getGSE('GSE53986')
```

gseaPlot

Returns path to an svg file with enrichment plot

Description

Returns path to an svg file with enrichment plot

Usage

```
gseaPlot(fData, fvarLabels, rankBy, selectedGenes, width, height)
```

Arguments

fData	list of annotation columns
fvarLabels	vector of column names
rankBy	name of the numeric column used for gene ranking
selectedGenes	indexes of selected genes (starting from one, in the order of fData)
width	width of the image (in inches)
height	height of the image (in inches)

Value

path to an svg file

limmaAnalysis *Differential Expression analysis.*

Description

limmaAnalysis performs differential expression analysis from limma package and returns a ProtoBuf-serialized resulting de-matrix.

Usage

```
limmaAnalysis(es, rows = c(), columns = c(), fieldValues)
```

Arguments

es	ExpressionSet object. It should be normalized for more accurate analysis.
rows	Vector of specified rows' indices (optional).
columns	Vector of specified columns' indices (optional).
fieldValues	Vector of comparison values, mapping categories' names to columns/samples (must be equal length with columns' vector if specified).

Value

Name of the file containing serialized de-matrix.

Examples

```
## Not run:
data(es)
limmaAnalysis(es, fieldValues = c("A", "A", "A", "B", "B"))

## End(Not run)
```

loadGEO *Load GEO Dataset.*

Description

loadGEO returns the file with serialized ExpressionSet using ProtoBuf, parsed from data downloaded from GEO by identifier.

Usage

```
loadGEO(name, type = NA)
```

Arguments

name	String, containing GEO identifier of the dataset. It should start with 'GSE' or 'GDS' and can include exact GPL to annotate dataset, separated with dash ('-') from the identifier.
type	Type of the dataset: 'GSE' or 'GDS'. If not specified, the function will take first three letters of name variable as type.

Value

File with ProtoBuf-serialized ExpressionSet-s that were downloaded by this identifier. For GSE-datasets there can be multiple annotations, so in file will be a list mapping name with GPL to ExpressionSet.

Examples

```
## Not run:
  loadGEO("GSE27112")
  loadGEO("GDS4922")

## End(Not run)
```

loadPreloaded	<i>Load GEO Dataset.</i>
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Description

loadPreloaded returns the file with serialized ExpressionSets using ProtoBuf, that were preloaded on server.

Usage

```
loadPreloaded(name, exactName = NULL)
```

Arguments

name	String, containing filename. Assuming that in the directory with preloaded files preloadedDir exists file filename.rda with list of ExpressionSets ess.
exactName	If you know, that inside file is object with name exactName, you can specify it to load only this object. Otherwise, whole file will be loaded.

Value

File with ProtoBuf-serialized ExpressionSet-s that were loaded from specified file.

performKmeans	<i>K-means clusterisation.</i>
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Description

performKmeans returns a vector of corresponding clusters for each gene from a given Expression-Set.

Usage

```
performKmeans(es, columns = c(), rows = c(), k, replacena = "mean")
```

Arguments

es	ExpressionSet object.
columns	List of specified columns' indices (optional), indices start from 0
rows	List of specified rows' indices (optional), indices start from 0
k	Expected number of clusters.
replacena	Method for replacing NA values in series matrix (mean by default)

Value

Vector of corresponding clusters, serialized to JSON.

Examples

```
## Not run:
data(es)
performKmeans(es, k = 2)

## End(Not run)
```

```
preloadedDirExists    Check existence of phantasiaPreloadedDir
```

Description

preloadedDirExists checks if there is specified directory with preloaded files.

Usage

```
preloadedDirExists()
```

Value

Boolean value.

```
read.gct              Reads ExpressionSet from a GCT file.
```

Description

Only versions 1.2 and 1.3 are supported.

Usage

```
read.gct(gct, ...)
```

Arguments

gct	Path to gct file
...	additional options for read.csv

Value

ExpressionSet object

Examples

```
read.gct(system.file("extdata", "centers.gct", package = "phantasus"))
```

reparseCachedESs	<i>Reparse cached expression sets from GEO.</i>
------------------	---

Description

The function should be used on phantasus version updates that change behavior of loading datasets from GEO. It finds all the datasets that were cached and runs ‘getES’ for them again. The function uses cached Series and other files from GEO.

Usage

```
reparseCachedESs(destdir, mirrorPath = "https://ftp.ncbi.nlm.nih.gov")
```

Arguments

destdir Directory used for caching loaded Series files from GEO database.
mirrorPath URL string which specifies the source of matrices.

Value

vector of previously cached GSE IDs

Examples

```
reparseCachedESs(destdir=tempdir())
```

servePhantasus	<i>Serve phantasus.</i>
----------------	-------------------------

Description

servePhantasus starts http server handling phantasus static files and opencpu server.

Usage

```
servePhantasus(host = "0.0.0.0", port = 8000,  
staticRoot = system.file("www/phantasus.js", package = "phantasus"),  
cacheDir = tempdir(), preloadedDir = NULL, openInBrowser = TRUE)
```

Arguments

host	Host to listen.
port	Port to listen.
staticRoot	Path to static files with phantanus.js (on local file system).
cacheDir	Full path to cache directory.
preloadedDir	Full path to directory with preloaded files.
openInBrowser	Boolean value which states if application will be automatically loaded in default browser.

Value

Running instance of phantanus application.

Examples

```
## Not run:
servePhantanus()

## End(Not run)
```

shinyGAMAnalysis	<i>Constructs data frame with gene annotations and submits it into Shiny GAM web-server</i>
------------------	---

Description

Constructs data frame with gene annotations and submits it into Shiny GAM web-server

Usage

```
shinyGAMAnalysis(fData, fvarLabels)
```

Arguments

fData	list of annotation columns
fvarLabels	vector of column names

Value

URL for Shiny GAM

subsetES	<i>Subsets es, if rows or columns are not specified, all are retained</i>
----------	---

Description

Subsets es, if rows or columns are not specified, all are retained

Usage

```
subsetES(es, columns = c(), rows = c())
```

Arguments

es	ExpressionSet object.#'
columns	List of specified columns' indices (optional), indices start from 0#'
rows	List of specified rows' indices (optional), indices start from 0

Value

'es''s subset

write.gct	<i>Saves ExpressionSet to a GCT file (version 1.3).</i>
-----------	---

Description

Saves ExpressionSet to a GCT file (version 1.3).

Usage

```
write.gct(es, file, gzip = FALSE)
```

Arguments

es	ExpressionSet object to save
file	Path to output gct file
gzip	Whether to gzip apply gzip-compression for the output file#'
...	additional options for read.csv

Value

Result of the closing file (as in 'close()' function')

Examples

```
es <- read.gct(system.file("extdata", "centers.gct", package = "phantasus"))
out <- tempfile(fileext = ".gct.gz")
write.gct(es, out, gzip=TRUE)
```

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