

Package ‘gscreend’

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Type Package

Title Analysis of pooled genetic screens

Version 1.24.0

Description Package for the analysis of pooled genetic screens (e.g. CRISPR-KO). The analysis of such screens is based on the comparison of gRNA abundances before and after a cell proliferation phase. The gscreend packages takes gRNA counts as input and allows detection of genes whose knockout decreases or increases cell proliferation.

License GPL-3

Encoding UTF-8

LazyData false

Depends R (>= 3.6)

Imports SummarizedExperiment, nloptr, fGarch, methods, BiocParallel, graphics

Suggests knitr, testthat, rmarkdown, BiocStyle

VignetteBuilder knitr

RoxygenNote 7.2.3

biocViews Software, StatisticalMethod, PooledScreens, CRISPR

URL <https://github.com/imkeller/gscreend>

BugReports <https://github.com/imkeller/gscreend/issues>

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Author Katharina Imkeller [cre, aut],
Wolfgang Huber [aut]

Maintainer Katharina Imkeller <k.imkeller@dkfz.de>

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assignGeneData	<i>Calculate gene rank</i>
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Description

Calculate gene rank

Usage

assignGeneData(object, alpha_cutoff)

Arguments

- | | |
|--------------|--|
| object | PoolScreenExp object |
| alpha_cutoff | alpha cutoff for alpha-RRA (default: 0.05) |

Value

object

calculateIntervalFits *Calculate fit parameters for every subset of data*

Description

Calculate fit parameters for every subset of data

Usage

```
calculateIntervalFits(object, quant1, quant2)
```

Arguments

object	PoolScreenExp object
quant1	lower quantile for least quantile of squares regression (default: 0.1)
quant2	upper quantile for least quantile of squares regression (default: 0.9)

Value

object

calculateLFC *Calculate log fold changes*

Description

Calculate log fold changes

Usage

```
calculateLFC(object)
```

Arguments

object	PoolScreenExp object
--------	----------------------

Value

object

calculatePValues	<i>Calculate p-values</i>
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Description

Calculate p-values

Usage

```
calculatePValues(object)
```

Arguments

object	PoolScreenExp object
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Value

object

createPoolScreenExp	<i>Create PoolScreenExp Experiment</i>
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Description

Create PoolScreenExp Experiment

Usage

```
createPoolScreenExp(data)
```

Arguments

data	Input data object containing gRNA level data (SummarizedExperiment)
------	---

Value

object PoolScreenExp object

Examples

```
raw_counts <- read.table(
  system.file('extdata', 'simulated_counts.txt',
    package = 'gscreeend'),
  header=TRUE)

counts_matrix <- cbind(raw_counts$library0, raw_counts$R0_0, raw_counts$R1_0)

rowData <- data.frame(sgRNA_id = raw_counts$sgrna_id,
  gene = raw_counts$Gene)

colData <- data.frame(samplename = c('library', 'R1', 'R2'),
```

```
timepoint = c('T0', 'T1', 'T1'))

library(SummarizedExperiment)
se <- SummarizedExperiment(assays=list(counts=counts_matrix),
  rowData=rowData, colData=colData)

# create a PoolScreenExp experiment
pse <- createPoolScreenExp(se)
```

`createPoolScreenExpFromSE`*Create PoolScreenExp Experiment from summarized experiment*

Description

Create PoolScreenExp Experiment from summarized experiment

Usage

```
createPoolScreenExpFromSE(data)
```

Arguments

data	SummarizedExperiment object containing gRNA level data
------	--

Value

object

`defineFittingIntervals`*Calculate interval limits for splitting data into subsets*

Description

Calculate interval limits for splitting data into subsets

Usage

```
defineFittingIntervals(object)
```

Arguments

object	PoolScreenExp object
--------	----------------------

Value

object

fit_least_quantile	<i>Fit paramters for skew normal distribution</i>
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Description

Fit paramters for skew normal distribution

Usage

```
fit_least_quantile(LFC, quant1, quant2)
```

Arguments

LFC	logarithmic fold changes of gRNA counts
quant1	lower quantile for least quantile of squares regression (default: 0.1)
quant2	upper quantile for least quantile of squares regression (default: 0.9)

Value

fit_skewnorm

GeneData	<i>GeneData: set and retrieve GeneData of PoolScreenExp</i>
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Description

GeneData: set and retrieve GeneData of PoolScreenExp

Usage

```
GeneData(x)
```

Arguments

x	PoolScreenExp object
---	----------------------

Value

Gene slot of the object

Examples

```
# import a PoolScreenExp object that has been generated using
# RunGscreen()
pse_an <- readRDS(
  system.file('extdata', 'gscreen_analysed_experiment.RData',
    package = 'gscreen'))

GeneData(pse_an)
```

`GeneData, PoolScreenExp-method`*Accessor function for the Gene slot of the PoolScreenExp class*

Description

Accessor function for the Gene slot of the PoolScreenExp class

Usage

```
## S4 method for signature 'PoolScreenExp'  
GeneData(x)
```

Arguments

x PoolScreenExp object

Value

Gene slot of the object

Examples

```
# import a PoolScreenExp object that has been generated using  
# RunGscreenend()  
pse_an <- readRDS(  
  system.file('extdata', 'gscreend_analysed_experiment.RData',  
  package = 'gscreend'))  
  
GeneData(pse_an)
```

`normalizePoolScreenExp`*Normalize raw count*

Description

Normalize raw count

Usage

```
normalizePoolScreenExp(object)
```

Arguments

object PoolScreenExp object

Value

object

plotModelParameters	<i>Plot model parameters from the fitting</i>
---------------------	---

Description

Plot model parameters from the fitting

Usage

```
plotModelParameters(object)
```

Arguments

object	PoolScreenExp object
--------	----------------------

Value

plot

Examples

```
# import a PoolScreenExp object that has been generated using
# RunGscreen()
pse_an <- readRDS(
  system.file('extdata', 'gscreen_analysed_experiment.RData',
    package = 'gscreen'))
plotModelParameters(pse_an)
```

plotReplicateCorrelation	<i>Plot replicate correlation</i>
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Description

Plot replicate correlation

Usage

```
plotReplicateCorrelation(object, rep1 = "R1", rep2 = "R2")
```

Arguments

object	PoolScreenExp object
rep1	Name of replicate 1
rep2	Name of replicate 2

Value

replicate_plot

Examples

```
# import a PoolScreenExp object that has been generated using RunGscreen()
pse_an <- readRDS(
  system.file('extdata', 'gscreen_analysed_experiment.RData',
    package = 'gscreen'))
plotReplicateCorrelation(pse_an, rep1 = 'R1', rep2 = 'R2')
```

PoolScreenExp-class	<i>Class to store pooled CRISPR screening experiment</i>
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Description

The poolScreenExp class is an S4 class used to store sgRNA and gene related data as well as parameters necessary for statistical model.

Slots

sgRNAData A SummarizedExperiment containing the data related to sgRNAs.

FittingIntervals A vector defining the limits of the intervals used for fitting of null model.

LFCModelParameters A vector of parameters estimated when fitting the null model.

GeneData SummarizedExperiment containing the data related to genes.

FittingOptions A named list with options for fitting: IntervalFraction - fraction of sgRNAs used in every fitting interval (default 0.1), alphaCutoff - alpha cutoff for alpha RRA algorithm (default: 0.05).

ResultsTable	<i>Extract a results table</i>
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Description

Extract a results table

Usage

```
ResultsTable(object, direction = "negative")
```

Arguments

object	PoolScreenExp object
direction	Whether the table should contain information on positive or negative fold changes ['negative' 'positive']

Value

plot

Examples

```
# import a PoolScreenExp object that has been generated using
# RunGscorend()
pse_an <- readRDS(
  system.file('extdata', 'gscorend_analysed_experiment.RData',
    package = 'gscorend'))
ResultsTable(pse_an, direction = 'negative')
```

RunGscorend	<i>run gscorend</i>
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Description

run gscorend

Usage

```
RunGscorend(object, quant1 = 0.1, quant2 = 0.9, alphacutoff = 0.05)
```

Arguments

object	PoolScreenExp object
quant1	lower quantile for least quantile of squares regression (default: 0.1)
quant2	upper quantile for least quantile of squares regression (default: 0.9)
alphacutoff	alpha cutoff for alpha-RRA (default: 0.05)

Value

object

Examples

```
raw_counts <- read.table(
  system.file('extdata', 'simulated_counts.txt',
    package = 'gscorend'),
  header=TRUE)

# Create the PoolScreenExp to be analyzed
counts_matrix <- cbind(raw_counts$library0, raw_counts$R0_0, raw_counts$R1_0)

rowData <- data.frame(sgRNA_id = raw_counts$sgrna_id,
  gene = raw_counts$Gene)

colData <- data.frame(samplename = c('library', 'R1', 'R2'),
  timepoint = c('T0', 'T1', 'T1'))

library(SummarizedExperiment)
se <- SummarizedExperiment(assays=list(counts=counts_matrix),
  rowData=rowData, colData=colData)

pse <- createPoolScreenExp(se)
```

```
# Run Analysis
pse_an <- RunGscrend(pse)
```

sgRNAData

*sgRNAData: set and retrieve sgRNAData of PoolScreenExp***Description**

sgRNAData: set and retrieve sgRNAData of PoolScreenExp

Usage

sgRNAData(x)

Arguments

x PoolScreenExp object

Value

sgRNA slot of the object

Examples

```
# import a PoolScreenExp object that has been generated using
# RunGscrend()
pse_an <- readRDS(
  system.file('extdata', 'gscrend_analysed_experiment.RData',
    package = 'gscrend'))

sgRNAData(pse_an)
```

sgRNAData,PoolScreenExp-method

*Accessor function for the sgRNA slot of the PoolScreenExp class***Description**

Accessor function for the sgRNA slot of the PoolScreenExp class

Usage

```
## S4 method for signature 'PoolScreenExp'
sgRNAData(x)
```

Arguments

x PoolScreenExp object

Value

sgRNA slot of the object

Examples

```
# import a PoolScreenExp object that has been generated using
# RunGscreen()
pse_an <- readRDS(
  system.file('extdata', 'gscreend_analysed_experiment.RData',
    package = 'gscreend'))

sgRNAData(pse_an)
```

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