

# Package ‘gscreend’

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**Type** Package

**Title** Analysis of pooled genetic screens

**Version** 1.10.0

**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

**VignetteBuilder** knitr

**RoxygenNote** 6.1.1

**biocViews** Software, StatisticalMethod, PooledScreens, CRISPR

**URL** <https://github.com/imkeller/gspreend>

**BugReports** <https://github.com/imkeller/gspreend/issues>

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createPoolScreenExp    *Create PoolScreenExp Experiment*

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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 = 'gscreen'),
  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)
```

---

GeneData

*GeneData: set and retrieve GeneData of PoolScreenExp*

---

## 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', 'gscreend_analysed_experiment.RData',
package = 'gscreend'))

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  
# RunGscreened()  
pse_an <- readRDS(  
  system.file('extdata', 'gscreened_analysed_experiment.RData',  
  package = 'gscreened'))  
  
GeneData(pse_an)
```

---

plotModelParameters    *Plot model parameters from the fitting*

---

**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  
# RunGscreened()  
pse_an <- readRDS(  
  system.file('extdata', 'gscreened_analysed_experiment.RData',  
  package = 'gscreened'))  
plotModelParameters(pse_an)
```

---

plotReplicateCorrelation  
*Plot replicate correlation*

---

**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    *Class to store pooled CRISPR screening experiment*

---

**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).

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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
# RunGscreen()
pse_an <- readRDS(
  system.file('extdata', 'gscreen_analysed_experiment.RData',
  package = 'gscreen'))
ResultsTable(pse_an, direction = 'negative')
```

---

RunGscreend	<i>run gscreend</i>
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---

### Description

run gscreend

### Usage

```
RunGscreend(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 = 'gscreend'),  
  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 <- RunGscreend(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
# RunGscreen()
pse_an <- readRDS(
  system.file('extdata', 'gscreen_analysed_experiment.RData',
    package = 'gscreen'))

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', 'gscreen_analysed_experiment.RData',
    package = 'gscreen'))

sgRNAData(pse_an)
```

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