

# Package ‘gscreend’

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**Type** Package

**Title** Analysis of pooled genetic screens

**Version** 1.27.0

**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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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 squares regression (default: 0.1)
quant2	upper quantile for least squares regression (default: 0.9)

**Value**

object

---

calculateLFC *Calculate log fold changes*

---

**Description**

Calculate log fold changes

**Usage**

```
calculateLFC(object)
```

**Arguments**

object	PoolScreenExp object
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**Value**

object

---

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

**Description**

Calculate p-values

**Usage**

```
calculatePValues(object)
```

**Arguments**

object            PoolScreenExp object

**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 = 'gscreend'),
  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`     *Fit parameters for skew normal distribution*

---

**Description**

Fit parameters 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`     *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', '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  
# RunGscreeend()  
pse_an <- readRDS(  
  system.file('extdata', 'gscreeend_analysed_experiment.RData',  
  package = 'gscreeend'))  
  
GeneData(pse_an)
```

---

normalizePoolScreenExp

*Normalize raw count*

---

**Description**

Normalize raw count

**Usage**

```
normalizePoolScreenExp(object)
```

**Arguments**

object                PoolScreenExp object

**Value**

object

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

---

ResultsTable     *Extract a results table*

---

**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
# RunGscreeend()
pse_an <- readRDS(
  system.file('extdata', 'gscreeend_analysed_experiment.RData',
    package = 'gscreeend'))
ResultsTable(pse_an, direction = 'negative')
```

---

RunGscreeend	<i>run gscreeend</i>
--------------	----------------------

---

**Description**

run gscreeend

**Usage**

```
RunGscreeend(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 = 'gscreeend'),
  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 <- RunGscreeend(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
# RunGscreeend()
pse_an <- readRDS(
  system.file('extdata', 'gscreeend_analysed_experiment.RData',
  package = 'gscreeend'))

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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