

# Package ‘gespeR’

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**Description** Estimates gene-specific phenotypes from off-target confounded RNAi  
screens. The phenotype of each siRNA is modeled based on on-targeted and  
off-targeted genes, using a regularized linear regression model.

**License** GPL-3

**URL** <http://www.cbg.ethz.ch/software/gespeR>

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'gespeR-class.R' 'gespeR-concordance.R' 'gespeR-functions.R'  
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gespeR-package	2
annotate.gsp	4
as.data.frame,Phenotypes-method	5
as.data.frame.concordance	6
c,Phenotypes-method	7
concordance	8
dim,Phenotypes-method	9
gespeR-class	9
gsp	11
join	12
lasso.rand	13
loadValues	14
na.rem	15
path<-	16
Phenotypes-class	16
plot.concordance	18
plot.gespeR	19
plot.Phenotypes	19
rbo	20
scores	21
simData	22
stability	22
stability.selection	23
stabilityfits	24
target.relations	24
TargetRelations-class	25
values	26
[,Phenotypes,ANY,ANY,ANY-method	27
[,TargetRelations,ANY,ANY,ANY-method	28
<b>Index</b>	<b>29</b>

gespeR-package

*Package: Gene-Specific Phenotype Estimator***Description**

This package provides a model to deconvolute off-target confounded RNAi knockdown phenotypes, and methods to investigate concordance between ranked lists of (estimated) phenotypes. The regularized linear regression model can be fitted using two different strategies. (a) Cross-validation over regularization parameters optimising the mean-squared-error of the model and (b) stability selection of covariates (genes) based on a method by Nicolai Meinshausen et al.

**Author(s)**

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## References

Fabian Schmich et. al, Deconvoluting Off-Target Confounded RNA Interference Screens (2014).

## See Also

[gespeR](#)

## Examples

```
# Read phenotypes
phenos <- lapply(LETTERS[1:4], function(x) {
  sprintf("Phenotypes_screen_%s.txt", x)
})
phenos <- lapply(phenos, function(x) {
  Phenotypes(system.file("extdata", x, package="gespeR"),
             type = "SSP",
             col.id = 1,
             col.score = 2)
})
phenos
plot(phenos[[1]])

# Read target relations
tr <- lapply(LETTERS[1:4], function(x) {
  sprintf("TR_screen_%s.rds", x)
})
tr <- lapply(tr, function(x) {
  TargetRelations(system.file("extdata", x, package="gespeR"))
})
tr[[1]]
tempfile <- paste(tempfile(pattern = "file", tmpdir = tempdir()), ".rds", sep="")
tr[[1]] <- unloadValues(tr[[1]], writeValues = TRUE, path = tempfile)
tr[[1]]
tr[[1]] <- loadValues(tr[[1]])
tr[[1]]

# Fit gespeR models with cross validation
res.cv <- lapply(1:length(phenos), function(i) {
  gespeR(phenotypes = phenos[[i]],
        target.relations = tr[[i]],
        mode = "cv",
        alpha = 0.5,
        ncores = 1)
})
summary(res.cv[[1]])
res.cv[[1]]
plot(res.cv[[1]])

# Extract scores
ssp(res.cv[[1]])
gsp(res.cv[[1]])
head(scores(res.cv[[1]]))
```

```

# Fit gespeR models with stability selection
res.stab <- lapply(1:length(phenos), function(i) {
  gespeR(phenotypes = phenos[[i]],
        target.relations = tr[[i]],
        mode = "stability",
        nbootstrap = 100,
        fraction = 0.67,
        threshold = 0.75,
        EV = 1,
        weakness = 0.8,
        ncores = 1)
})
summary(res.stab[[1]])
res.stab[[1]]
plot(res.stab[[1]])

# Extract scores
ssp(res.stab[[1]])
gsp(res.stab[[1]])
head(scores(res.stab[[1]]))

# Compare concordance between stability selected GSPs and SSPs
conc.gsp <- concordance(lapply(res.stab, gsp))
conc.ssp <- concordance(lapply(res.stab, ssp))

pl.gsp <- plot(conc.gsp) + ggtitle("GSPs\n")
pl.ssp <- plot(conc.ssp) + ggtitle("SSPs\n")

if (require(grid)) {
  grid.newpage()
  pushViewport(viewport(layout = grid.layout(1, 2) ) )
  print(pl.gsp, vp = viewport(layout.pos.row = 1, layout.pos.col = 1))
  print(pl.ssp, vp = viewport(layout.pos.row = 1, layout.pos.col = 2))
} else {
  plot(pl.gsp)
  plot(pl.ssp)
}

```

---

annotate.gsp

*annotate.gsp*

---

## Description

Query Biomart HGNC symbols for the entrez identifiers of estimated GSPs. Currently, only implemented for species "hsapiens".

## Usage

```
## S4 method for signature 'Phenotypes'
```

```
annotate.gsp(object, organism = "hsapiens")  
  
## S4 method for signature 'gespeR'  
annotate.gsp(object, organism = "hsapiens")
```

### Arguments

object	A <a href="#">gespeR</a> or <a href="#">Phenotypes</a> object
organism	String indicating the biomaRt organism

### Value

data.frame containing gene identifier, gene symbol and phenotypic score

### Author(s)

Fabian Schmich

### See Also

[gsp](#)  
[ssp](#)  
[scores](#)

### Examples

```
data(stabilityfits)  
gspA <- gsp(stabilityfits$A)  
## Not run:  
  annotate.gsp(gspA)  
  
## End(Not run)
```

---

as.data.frame,Phenotypes-method

*Convert Phenotypes object to a data.frame*

---

### Description

Convert Phenotypes object to a data.frame

### Usage

```
## S4 method for signature 'Phenotypes'  
as.data.frame(x)
```

**Arguments**

x                    A [Phenotypes](#) object

**Value**

A data.frame

**Author(s)**

Fabian Schmich

**Examples**

```
phenos <- Phenotypes(system.file("extdata", "Phenotypes_screen_A.txt", package = "gespeR"),
  type = "SSP",
  col.id = 1,
  col.score = 2)
as.data.frame(phenos)
```

---

as.data.frame.concordance

*Coerce method*

---

**Description**

Coerce method

**Usage**

```
## S3 method for class 'concordance'
as.data.frame(x, ...)
```

**Arguments**

x                    concordance object  
...                  additional arguments

**Value**

data.frame

**Author(s)**

Fabian Schmich

---

c,Phenotypes-method    *Concatenate Phenotypes objects*

---

## Description

Concatenate Phenotypes objects

## Usage

```
## S4 method for signature 'Phenotypes'  
c(x, ..., recursive = FALSE)
```

## Arguments

x	A <a href="#">Phenotypes</a> object
...	additional <a href="#">Phenotypes</a> objects
recursive	recursive

## Value

A concatenated [Phenotypes](#) object

## Author(s)

Fabian Schmich

## Examples

```
phenos.a <- Phenotypes(system.file("extdata", "Phenotypes_screen_A.txt", package = "gespeR"),  
  type = "SSP",  
  col.id = 1,  
  col.score = 2)  
phenos.b <- Phenotypes(system.file("extdata", "Phenotypes_screen_B.txt", package = "gespeR"),  
  type = "SSP",  
  col.id = 1,  
  col.score = 2)  
c(phenos.a, phenos.b)
```

---

 concordance

*Evaluate the concordance between Phenotype objects*


---

### Description

Measures include the correlation ( $\rho$ ) between pairs of phenotypes for the same gene, the rank biased overlap (**rbo**) of the top and bottom of ranked lists, and the Jaccard index (J) of selected genes.

### Usage

```
concordance(..., min.overlap = 10, cor.method = "spearman", rbo.p = 0.98,
            rbo.k = NULL, rbo.mid = 0, uneven.lengths = TRUE)
```

### Arguments

<code>...</code>	The phenotypes to be evaluated for concordance
<code>min.overlap</code>	The minimum number of overlapping genes required
<code>cor.method</code>	A character string indicating which correlation coefficient is to be computed
<code>rbo.p</code>	The weighting parameter for rank biased overlap (rbo) in [0, 1]. High p implies strong emphasis on top ranked elements
<code>rbo.k</code>	The evaluation depth for rank biased overlap extrapolation
<code>rbo.mid</code>	The mid point to split a ranked list, e.g. in order to split positive and negative scores choose mid=0
<code>uneven.lengths</code>	Indicator if lists have uneven lengths

### Value

A [concordance](#) object with the following elements:

<code>pair.test</code>	Indicator of compared phenotypes
<code>cor</code>	The correlation between pairs of phenotypes for the same gene
<code>rbo.top</code>	The rank biased overlap of genes evaluated at the top of the ranked list
<code>rbo.bottom</code>	The rank biased overlap of genes evaluated at the bottom of the ranked list
<code>jaccard</code>	The Jaccard index of selected genes

### Author(s)

Fabian Schmich

### See Also

[Phenotypes](#)  
[plot.concordance](#)  
[rbo](#)



### Examples

```
data(stabilityfits)
conc <- concordance(gsp(stabilityfits$A), gsp(stabilityfits$B),
  gsp(stabilityfits$C), gsp(stabilityfits$D))
plot(conc)
```

---

`dim,Phenotypes-method` *Dimension of a [Phenotypes](#) object*

---

### Description

Dimension of a [Phenotypes](#) object

### Usage

```
## S4 method for signature 'Phenotypes'
dim(x)
```

### Arguments

x [Phenotypes](#) object

### Value

Dimension of the [Phenotypes](#) object

### Author(s)

Fabian Schmich

---

`gespeR-class` *gespeR*

---

### Description

Class that represents a `gespeR` model. It contains a SSP [Phenotypes](#) and [TargetRelations](#) representing a siRNA knockdown experiment. When the model is fitted, it additionally contains estimated GSP [Phenotypes](#).

**Usage**

```
gespeR(phenotypes, target.relations, ...)

## S4 method for signature 'Phenotypes,TargetRelations'
gespeR(phenotypes, target.relations,
       mode = c("cv", "stability"), alpha = 0.5, nbootstrap = 100,
       fraction = 0.67, threshold = 0.9, EV = 1, weakness = 0.8,
       ncores = 1, ...)

## S4 method for signature 'numeric,Matrix'
gespeR(phenotypes, target.relations, ...)
```

**Arguments**

phenotypes	The siRNA-specific phenotypes. Single object for univariate phenotypes and list of <a href="#">Phenotypes</a> objects for multivariate phenotypes.
target.relations	The siRNA-to-gene target relations
...	Additional arguments
mode	The mode of covariate selection ("cv" or "stability")
alpha	The <a href="#">glmnet</a> mixing parameter
nbootstrap	The number of bootstrap samples
fraction	The fraction for each bootstrap sample
threshold	The selection threshold
EV	The expected value of wrongly selected elements
weakness	The weakness parameter for randomised lasso
ncores	The number of cores for parallel computation

**Value**

A [gespeR](#) object

**Slots**

SSP	The observed siRNA-specific phenotypes
GSP	The deconvoluted gene-specific phenotypes
target.relations	The siRNA-to-gene target relations, e.g. predicted by TargetScan
is.fitted	An indicator whether the <a href="#">gespeR</a> model was fitted
model	The fitted regularized linear regression model

**Author(s)**

Fabian Schmich

**See Also**

[gespeR-package](#)  
[plot.gespeR](#)  
[gsp](#)  
[ssp](#)  
[scores](#)  
[stability](#)  
[target.relations](#)

**Examples**

```
phenos <- Phenotypes(system.file("extdata", "Phenotypes_screen_A.txt", package = "gespeR"),
  type = "SSP",
  col.id = 1,
  col.score = 2)
trels <- TargetRelations(readRDS(system.file("extdata", "TR_screen_A.rds", package = "gespeR")))
res <- gespeR(phenotypes = phenos,
  target.relations = trels,
  mode = "stability",
  nbootstrap = 100,
  fraction = 0.67,
  threshold = 0.75,
  EV = 1,
  weakness = 0.8,
  ncores = 1)
gsp(res)
```

---

`gsp`

*Retrieve GSPs and SSPs from [gespeR](#) objects*

---

**Description**

Retrieve GSPs and SSPs from [gespeR](#) objects

**Usage**

```
gsp(object)

## S4 method for signature 'gespeR'
gsp(object)

ssp(object)

## S4 method for signature 'gespeR'
ssp(object)
```

**Arguments**

object            A [gespeR](#) object

**Value**

A [Phenotypes](#) object of GSPs and SSPs, respectively

**Author(s)**

Fabian Schmich

**See Also**

[annotate.gsp](#)  
[scores](#)

**Examples**

```
data(stabilityfits)
gsp(stabilityfits$A)
ssp(stabilityfits$B)
```

---

*join*

*join*

---

**Description**

Join a [TargetRelations](#) object and a [Phenotype](#) object

**Usage**

```
join(targets, phenotypes)
```

```
## S4 method for signature 'TargetRelations,Phenotypes'
join(targets, phenotypes)
```

**Arguments**

targets            A [TargetRelations](#) object.  
phenotypes        A [Phenotypes](#) object.

**Value**

List containing the matched targets and phenotypes

**Author(s)**

Fabian Schmich

**Examples**

```
phenos <- Phenotypes(system.file("extdata", "Phenotypes_screen_A.txt", package = "gespeR"),
  type = "SSP",
  col.id = 1,
  col.score = 2)
trels <- TargetRelations(readRDS(system.file("extdata", "TR_screen_A.rds", package = "gespeR")))
phenos <- phenos[1:17]
stripped_down <- join(targets = trels, phenotypes = phenos)
```

lasso.rand

*Randomized Lasso***Description**

Based on Meinshausen and Buehlmann (2009)

**Usage**

```
lasso.rand(x, y, weakness = 1, subsample = 1:nrow(x), dfmax = (ncol(x) +
  1), lambda = NULL, standardize = FALSE, intercept = FALSE, ...)
```

**Arguments**

x	The design matrix
y	The response vector
weakness	The weakness parameter
subsample	The data subsample (default: none)
dfmax	The maximum number of degrees of freedom
lambda	The regularisation parameter
standardize	Indicator, whether to standardize the design matrix
intercept	Indicator, whether to fit an intercept
...	Additional arguments to <a href="#">glmnet</a>

**Value**

A [glmnet](#) object

**Author(s)**

Fabian Schmich

**Examples**

```
y <- rnorm(50)
x <- matrix(runif(50 * 20), ncol = 20)
lasso.rand(x = x, y = y)
```

---

loadValues *Methods for values of [TargetRelations](#) objects*

---

### Description

Load, unload or write to file the values of a [TargetRelations](#) object

### Usage

```
loadValues(object)

## S4 method for signature 'TargetRelations'
loadValues(object)

## S4 method for signature 'gespeR'
loadValues(object)

unloadValues(object, ...)

## S4 method for signature 'TargetRelations'
unloadValues(object, writeValues = TRUE,
             overwrite = FALSE, path = NULL)

## S4 method for signature 'gespeR'
unloadValues(object, writeValues = TRUE,
             overwrite = FALSE, path = NULL)

writeValues(object, ...)

## S4 method for signature 'TargetRelations'
writeValues(object, overwrite = FALSE)
```

### Arguments

object	A <a href="#">TargetRelations</a> object or <a href="#">gespeR</a> object
...	Additional arguments
writeValues	Indicator, whether to write values
overwrite	Indicator, wheter to overwrite values if file exists at path
path	The path to write out values

### Value

A [TargetRelations](#) object or [gespeR](#) object

### Author(s)

Fabian Schmich

**Examples**

```
data(stabilityfits)
## Not run:
loadValues(stabilityfits$A)

## End(Not run)
```

---

na.rem	<i>Remove NA/Inf values from phenotype vectors</i>
--------	--

---

**Description**

Remove NA/Inf values from phenotype vectors

**Usage**

```
na.rem(object)

## S4 method for signature 'Phenotypes'
na.rem(object)
```

**Arguments**

object            A [Phenotypes](#) object

**Value**

A [Phenotypes](#) object without NA scores values

**Author(s)**

Fabian Schmich

**Examples**

```
phenos <- Phenotypes(system.file("extdata", "Phenotypes_screen_A.txt", package = "gespeR"),
  type = "SSP",
  col.id = 1,
  col.score = 2)
na.rem(phenos)
```

path<- *path*

---

**Description**

Set the path of a [TargetRelations](#) object object

**Usage**

```
path(object) <- value
```

```
## S4 replacement method for signature 'TargetRelations,character'  
path(object) <- value
```

**Arguments**

object	A <a href="#">TargetRelations</a> object
value	A string defining the path

**Value**

A [TargetRelations](#) object with set path

**Author(s)**

Fabian Schmich

**Examples**

```
treIs <- TargetRelations(readRDS(system.file("extdata", "TR_screen_A.rds", package = "gespeR")))  
path(treIs) <- "/dev/null"
```

---

Phenotypes-class *Phenotypes*

---

**Description**

Class used to represent various types of phenotypes, e.g. from siRNA-specific (SSP) or estimated gene-specific phenotypes (GSP).



**Usage**

```

Phenotypes(phenotypes, ...)

## S4 method for signature 'character'
Phenotypes(phenotypes, type = c("SSP", "GSP"),
  sep = "\t", col.id = 1, col.score = 2)

## S4 method for signature 'cellHTS'
Phenotypes(phenotypes, channel, sample)

## S4 method for signature 'Matrix'
Phenotypes(phenotypes, ids = NULL, pnames = NULL,
  type = c("SSP", "GSP"))

```

**Arguments**

phenotypes	The phenotypes as numeric vector, path to a .txt file with two columns (1: identifiers, 2: values), or a cellHTS object
...	Additional arguments
type	The type of phenotype (GSP, SSP)
sep	The separator string
col.id	Column number for the siRNA identifiers
col.score	Column number(s) for the phenotype score
channel	The cellHTS channel identifier
sample	The cellHTS sample index
ids	The siRNA/gene identifiers
pnames	The phenotype identifiers

**Value**

A [Phenotypes](#) object

**Slots**

type	The type of represented phenotypes (i.e., "SSP" or "GSP")
ids	The entity identifiers (i.e., siRNA or gene ids)
pnames	The phenotype names
values	The phenotypic values

**Author(s)**

Fabian Schmich

**See Also**

[plot.Phenotypes](#)  
[join](#)  
[gsp](#)  
[ssp](#)  
[scores](#)  
[concordance](#)

**Examples**

```
phenos <- Phenotypes(system.file("extdata", "Phenotypes_screen_A.txt", package = "gespeR"),  
  type = "SSP",  
  col.id = 1,  
  col.score = 2)
```

---

plot.concordance	<i>Plot concordance</i>
------------------	-------------------------

---

**Description**

Plots boxplots of concordance evaluated between multiple Phenotype objects. Measures include the correlation ( $\rho$ ) between pairs of phenotypes for the same gene, the rank biased overlap (rbo) of the top and bottom of ranked lists, and the Jaccard index (J) of selected genes.

**Usage**

```
## S3 method for class 'concordance'  
plot(x, ...)
```

**Arguments**

x	The data of class <a href="#">concordance</a>
...	Additional parameters for plot

**Value**

Boxplots of concordance measures

**Author(s)**

Fabian Schmich

---

plot.gespeR                      *Plot method for [gespeR](#) objects*

---

**Description**

Plot method for [gespeR](#) objects

**Usage**

```
## S3 method for class 'gespeR'  
plot(x, ...)
```

**Arguments**

x                      A [gespeR](#) object  
...                    Additional paramters for plot

**Value**

Histogram of SSPs or GSPs

**Author(s)**

Fabian Schmich

---

plot.Phenotypes                  *Plot method for [Phenotype](#) objects*

---

**Description**

Plot method for [Phenotype](#) objects

**Usage**

```
## S3 method for class 'Phenotypes'  
plot(x, ...)
```

**Arguments**

x                      A [Phenotypes](#) object  
...                    Additional arguments for plot

**Value**

Histogram of scores `phenos <- Phenotypes(system.file("extdata", "Phenotypes_screen_A.txt", package = "gespeR"), type = "SSP", col.id = 1, col.score = 2) plot(phenos)`

**Author(s)**

Fabian Schmich

---

**rbo***Rank biased overlap (Webber et al., 2010)*

---

**Description**

Evaluates the rank biased overlap (rbo) of two ranked lists based on formula based on (32) from "A Similarity Measure for Indefinite Rankings" (Webber et al.). Two ranked lists with high rbo are very similar, whereas low rbo indicates dissimilar lists. rbo ranges between 0 and 1. In this method the extrapolated version of rbo is implemented.

**Usage**

```
rbo(s, t, p, k = floor(max(length(s), length(t))/2), side = c("top",  
"bottom"), mid = NULL, uneven.lengths = TRUE)
```

**Arguments**

s	List 1
t	List 2
p	Weighting parameter in [0, 1]. High p implies strong emphasis on top ranked elements
k	Evaluation depth for extrapolation
side	Evaluate similarity between the top or the bottom of the ranked lists
mid	Set the mid point to for example only consider positive or negative scores
uneven.lengths	Indicator if lists have uneven lengths

**Value**

rank biased overlap (rbo)

**Author(s)**

Fabian Schmich

**See Also**[concordance](#)**Examples**

```
a <- rnorm(26)  
b <- rnorm(26)  
names(a) <- names(b) <- LETTERS  
rbo(a, b, p = 0.95)
```

---

scores	<i>scores</i>
--------	---------------

---

## Description

Return a named vector of phenotype scores

## Usage

```
## S4 method for signature 'Phenotypes'  
scores(object)
```

```
## S4 method for signature 'gespeR'  
scores(object, type = c("GSP", "SSP"))
```

## Arguments

object	A <a href="#">gespeR</a> or <a href="#">Phenotypes</a> object
type	The type of phenotype scores (GSP, SSP)

## Value

A named vector of scores for each phenotype identifier

## Author(s)

Fabian Schmich

## See Also

[gespeR](#)

[Phenotypes](#)

## Examples

```
data(stabilityfits)  
scores(stabilityfits$A)
```

---

simData	<i>Example data: Simulated phenotypes and target relations for 4 screens (A, B, C, D)</i>
---------	---

---

### Description

The data set contains simulated data for four screens. Each screen consists of a phenotype vector and target relations between siRNAs and genes, i.e. which siRNA binds which genes (on- and off-targets). The size of each simulated screen is  $N = 1000$  siRNAs  $\times$   $p = 1500$  genes. SSPs are generated by first defining GSPs and multiplying the true GSPs with the sampled target relation matrices. For sampling the GSPs, we set the number of effect genes to 5 from  $\text{Normal}(0, 3)$ . Target relation matrices are simulated by sampling the number of off-targets per siRNA from  $\text{Normal}(3e-2 * N, 3e-3 * N)$  and the strength of off-targets is sampled from  $\text{Beta}(2, 5)$ . On-target components are set to 0.75.

### Details

The code used to simulate the data can be found in `system.file("example", "data_simulation.R", package="gespeR")`

### Examples

```
pheno.a <- Phenotypes(system.file("extdata", "Phenotypes_screen_A.txt", package="gespeR"),
  type = "SSP", col.id = 1, col.score = 2)
targets.a <- TargetRelations(system.file("extdata", "TR_screen_A.rds", package="gespeR"))
```

---

stability	<i>stability</i>
-----------	------------------

---

### Description

Retrieve a [Phenotypes](#) object with stability values from a [gespeR](#) object.

### Usage

```
stability(object)

## S4 method for signature 'gespeR'
stability(object)
```

### Arguments

object            A [gespeR](#) object

### Value

A [Phenotypes](#) object of SSPs

**Author(s)**

Fabian Schmich

**Examples**

```

phenos <- Phenotypes(system.file("extdata", "Phenotypes_screen_A.txt", package = "gespeR"),
  type = "SSP",
  col.id = 1,
  col.score = 2)
trels <- TargetRelations(readRDS(system.file("extdata", "TR_screen_A.rds", package = "gespeR")))
res <- gespeR(phenotypes = phenos,
  target.relations = trels,
  mode = "stability",
  nbootstrap = 100,
  fraction = 0.67,
  threshold = 0.75,
  EV = 1,
  weakness = 0.8,
  ncores = 1)
stab <- stability(res)
ans <- merge(as.data.frame(gsp(res)), as.data.frame(stability(res)), by = "ID")
colnames(ans)[2:3] <- c("Phenotype", "Stability")
ans[order(ans$Stability, decreasing = TRUE),]

```

---

stability.selection     *Stability Selection*

---

**Description**

Based on Meinshausen and Buehlmann (2009)

**Usage**

```

stability.selection(x, y, fraction = 0.5, threshold = 0.75, EV = 1,
  nbootstrap = 100, weakness = 1, intercept = FALSE, ncores = 1, ...)

```

**Arguments**

x	The design matrix
y	The response vector
fraction	The fraction for each bootstrap sample
threshold	The selection threshold
EV	The expected value of wrongly selected elements
nbootstrap	The number of bootstrap samples
weakness	The weakness parameter for randomised lasso
intercept	Indicator, whether to fit an intercept
ncores	The number of cores for parallel computation
...	Additional arguments to <a href="#">lasso.rand</a>

**Value**

A list containing selected covariates with frequencies, and the fitted model

**Author(s)**

Fabian Schmich

---

stabilityfits	<i>Example fits for phenotypes from simulated screening data A, B, C and D</i>
---------------	--

---

**Description**

The data set contains four fitted gespeR models using stability selection from the four simulated screens.

**Examples**

```
data(stabilityfits)
```

---

target.relations	<i>target.relations</i>
------------------	-------------------------

---

**Description**

Retrieve siRNA-to-gene target relations from a [gespeR](#) object.

**Usage**

```
target.relations(object)

## S4 method for signature 'gespeR'
target.relations(object)
```

**Arguments**

object            A [gespeR](#) object

**Value**

A [TargetRelations](#) object

**Author(s)**

Fabian Schmich



**Examples**

```
data(stabilityfits)
target.relations(stabilityfits$A)
```

---

TargetRelations-class *TargetRelations*

---

**Description**

Class used to represent siRNA-to-gene on- and off-target relations for a knockdown library and a set of genes.

**Usage**

```
TargetRelations(targets)

## S4 method for signature 'character'
TargetRelations(targets)

## S4 method for signature 'Matrix'
TargetRelations(targets)
```

**Arguments**

targets            Path to a .rds target relations matrix file or [Matrix](#) object

**Value**

A [TargetRelations](#) object

**Slots**

siRNAs The siRNA identifiers  
genes The gene identifiers (Entrez)  
path The path to and .rds [TargetRelations](#) file  
is.loaded An indicator if target relations values are loaded  
values The quantitative target relation values between siRNAs and genes

**Author(s)**

Fabian Schmich

**See Also**

[join](#)  
[loadValues](#)  
[unloadValues](#)  
[writeValues](#)  
[values](#)  
[path<-](#)

**Examples**

```
trels <- TargetRelations(readRDS(system.file("extdata", "TR_screen_A.rds", package = "gespeR")))
```

---

values	<i>values</i>
--------	---------------

---

**Description**

Retrieve the numeric values from a [TargetRelations](#) or [Phenotypes](#) object

**Usage**

```
values(object)  
  
## S4 method for signature 'TargetRelations'  
values(object)  
  
## S4 method for signature 'Phenotypes'  
values(object)
```

**Arguments**

object            A [TargetRelations](#) or [Phenotypes](#) object

**Value**

A [Matrix](#) object

**Author(s)**

Fabian Schmich

## Examples

```
trels <- TargetRelations(readRDS(system.file("extdata", "TR_screen_A.rds", package = "gespeR")))
values(trels)[1:5, 1:5]
phenos <- Phenotypes(system.file("extdata", "Phenotypes_screen_A.txt", package = "gespeR"),
  type = "SSP",
  col.id = 1,
  col.score = 2)
values(phenos)
```

---

[,Phenotypes,ANY,ANY,ANY-method

*Subsetting for Phenotype objects.*

---

## Description

Subsetting for Phenotype objects.

## Usage

```
## S4 method for signature 'Phenotypes,ANY,ANY,ANY'
x[i, j, ..., drop = TRUE]
```

## Arguments

x	A <a href="#">Phenotypes</a> object
i	The subsetting indices for siRNAs
j	Subsetting indices for multivariate phenotypes
...	Additional parameters
drop	Drop Redundant Extent Information

## Value

A [Phenotypes](#) object

## Author(s)

Fabian Schmich

---

[,TargetRelations,ANY,ANY,ANY-method

*Subsetting for TargetRelations objects.*

---

## Description

Subsetting for TargetRelations objects.

## Usage

```
## S4 method for signature 'TargetRelations,ANY,ANY,ANY'  
x[i, j, ..., drop = TRUE]
```

## Arguments

x	A <a href="#">TargetRelations</a> object
i	The row subsetting indices (siRNAs)
j	The column subsetting indeces (genes)
...	Additional parameters
drop	Drop Redundant Extent Information

## Value

A [TargetRelations](#) object

## Author(s)

Fabian Schmich

# Index

- \* **package**
  - gespeR-package, 2
- [,Phenotypes,ANY,ANY,ANY-method, 27
- [,TargetRelations,ANY,ANY,ANY-method, 28
  
- annotate.gsp, 4, 12
- annotate.gsp,gespeR-method (annotate.gsp), 4
- annotate.gsp,Phenotypes-method (annotate.gsp), 4
- as.data.frame,Phenotypes-method, 5
- as.data.frame.concordance, 6
  
- c,Phenotypes-method, 7
- concordance, 8, 8, 18, 20
  
- dim,Phenotypes-method, 9
  
- gespeR, 3, 5, 10–12, 14, 19, 21, 22, 24
- gespeR (gespeR-class), 9
- gespeR,numeric,Matrix-method (gespeR-class), 9
- gespeR,Phenotypes,TargetRelations-method (gespeR-class), 9
- gespeR-class, 9
- gespeR-package, 2
- gespeRpkg (gespeR-package), 2
- glmnet, 10, 13
- gsp, 5, 11, 11, 18
- gsp,gespeR-method (gsp), 11
  
- join, 12, 18, 26
- join,TargetRelations,Phenotypes-method (join), 12
  
- lasso.rand, 13, 23
- loadValues, 14, 26
- loadValues,gespeR-method (loadValues), 14
  
- loadValues,TargetRelations-method (loadValues), 14
  
- Matrix, 25, 26
  
- na.rem, 15
- na.rem,Phenotypes-method (na.rem), 15
  
- path<-, 16
- path<-,TargetRelations,character-method (path<-), 16
  
- Phenotypes, 5–10, 12, 15, 17, 19, 21, 22, 26, 27
- Phenotypes (Phenotypes-class), 16
- Phenotypes,cellHTS-method (Phenotypes-class), 16
- Phenotypes,character-method (Phenotypes-class), 16
- Phenotypes,Matrix-method (Phenotypes-class), 16
- Phenotypes-class, 16
- plot.concordance, 8, 18
- plot.gespeR, 11, 19
- plot.Phenotypes, 18, 19
  
- rbo, 8, 20
  
- scores, 5, 11, 12, 18, 21
- scores,gespeR-method (scores), 21
- scores,Phenotypes-method (scores), 21
- simData, 22
- ssp, 5, 11, 18
- ssp (gsp), 11
- ssp,gespeR-method (gsp), 11
- stability, 11, 22
- stability,gespeR-method (stability), 22
- stability.selection, 23
- stabilityfits, 24
  
- target.relations, 11, 24

target.relations, gespeR-method  
    (target.relations), 24

TargetRelations, 9, 12, 14, 16, 24–26, 28

TargetRelations  
    (TargetRelations-class), 25

TargetRelations, character-method  
    (TargetRelations-class), 25

TargetRelations, Matrix-method  
    (TargetRelations-class), 25

TargetRelations-class, 25

  

unloadValues, 26

unloadValues (loadValues), 14

unloadValues, gespeR-method  
    (loadValues), 14

unloadValues, TargetRelations-method  
    (loadValues), 14

  

values, 26, 26

values, Phenotypes-method (values), 26

values, TargetRelations-method (values),  
    26

  

writeValues, 26

writeValues (loadValues), 14

writeValues, TargetRelations-method  
    (loadValues), 14