

Package ‘gespeR’

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Title Gene-Specific Phenotype EstimatorR

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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.

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

Collate 'Phenotypes-class.R' 'TargetRelations-class.R'
'gespeR-class.R' 'gespeR-concordance.R' 'gespeR-functions.R'
'gespeR-generics.R' 'gespeR-methods.R' 'gespeR-package.R'

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Contents

| | |
|--|-----------|
| 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 |
| Index | 29 |

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 gespeR or Phenotypes 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 Phenotypes object |
| ... | additional Phenotypes 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 (ρ) 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 <code>mid=0</code> |
| <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 Phenotypes 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 glmnet 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 gespeR 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 glmnet |

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 TargetRelations object or gespeR 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

Usage

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

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

Arguments

| | |
|--------|--|
| object | A TargetRelations 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 (ρ) 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 concordance |
| ... | Additional parameters for plot |

Value

Boxplots of concordance measures

Author(s)

Fabian Schmich

| | |
|-------------|---|
| plot.gespeR | <i>Plot method for gespeR objects</i> |
|-------------|---|

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 | <i>Plot method for Phenotype objects</i> |
|-----------------|--|

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 gespeR or Phenotypes 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 lasso.rand |

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 Phenotypes 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 TargetRelations 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.gspeR, 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