Package ‘viper’

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**aecdf**

*Approximate empirical commulative distribution function*

**Description**

This function generates an empirical null model that computes a normalized statistics and p-value.

**Usage**

```r
aecdf(dnull, symmetric = FALSE, n = 100)
```

**Arguments**

- `dnull` Numerical vector representing the null model.
- `symmetric` Logical, whether the distribution should be treated as symmetric around zero and only one tail should be approximated.
- `n` Integer indicating the number of points to evaluate the empirical cumulative probability function.

**Value**

Function with two parameters, `x` and `alternative`.

---

**approxk2d**

*approxk2d*

**Description**

This function uses a Gaussian kernel to estimate the joint density distribution at the specified points.

**Usage**

```r
approxk2d(x, gridsize = 128, pos = x)
```

**Arguments**

- `x` Matrix of x and y points.
- `gridsize` Number or vector indicating the size of the grid where to estimate the density.
- `pos` Matrix of coordinates to evaluate the density.

**Value**

Vector of density estimates.
Examples

```r
x <- rnorm(500)
y <- x+rnorm(500)
kde2 <- approxk2d(cbind(x, y))
plot(x, y, pch=20, col=hsv(0, kde2/max(kde2), 1))
```

aracne2regulon

Regulon object generation from ARACNe results

Description

This function generates a regulon object from ARACNe results and the corresponding expression dataset.

Usage

```r
aracne2regulon(afile, eset, gene = FALSE, format = c("adj", "3col"), verbose = TRUE)
```

Arguments

- `afile` Character string indicating the name of the ARACNe network file
- `eset` Either a character string indicating the name of the expression-dataset file, a ExpressionSet object or a gene expression matrix with genes (probes) in rows and samples in columns
- `gene` Logical, whether the probes should be collapsed at the gene level
- `format` Character string, indicating the format of the aracne file, either adj for adjacency matrices generated by aracne, or 3col when the interactome is represented by a 3 columns text file, with regulator in the first column, target in the second and mutual information in the third column
- `verbose` Logical, whether progression messages should be printed in the terminal.

Value

Regulon object

See Also

`msviper`, `viper`

Examples

```r
data(bcellViper, package="bcellViper")
adjfile <- file.path(find.package("bcellViper"), "aracne", "bcellaracne.adj")
regul <- aracne2regulon(adjfile, dset)
print(regul)
```
Regulon object generation from ARACNe results corrected by cnv

Description

This function generates a regulon object from ARACNe results and the corresponding expression dataset when correction for CNV have been applied.

Usage

aracne2regulon4cnv(afile, eset, regeset, gene = FALSE, format = c("adj", "3col"), verbose = TRUE)

Arguments

- **afile**: Character string indicating the name of the ARACNe network file
- **eset**: Either a character string indicating the name of the expression-dataset file, a ExpressionSet object or a gene expression matrix with genes (probes) in rows and samples in columns, where the expression was corrected by CNV
- **regeset**: Either a character string indicating the name of the expression-dataset file, a ExpressionSet object or a gene expression matrix with genes (probes) in rows and samples in columns
- **gene**: Logical, whether the probes should be collapsed at the gene level
- **format**: Character string, indicating the format of the aracne file, either adj for adjacency matrixes generated by aracne, or 3col when the interactome is represented by a 3 columns text file, with regulator in the first column, target in the second and mutual information in the third column
- **verbose**: Logical, whether progression messages should be printed in the terminal.

Value

Regulon object

See Also

msviper, viper

Examples

data(bcellViper, package="bcellViper")
adjfile <- file.path(find.package("bcellViper"), "aracne", "bcellaracne.adj")
regul <- aracne2regulon(adjfile, dset)
print(regul)
**aREA**

analytic Rank-based Enrichment Analysis

**Description**

This function performs wREA enrichment analysis on a set of signatures

**Usage**

```r
aREA(eset, regulon, method = c("auto", "matrix", "loop"), minsize = 20, cores = 1, wm = NULL, verbose = FALSE)
```

**Arguments**

- `eset` Matrix containing a set of signatures, with samples in columns and traits in rows
- `regulon` Regulon object
- `method` Character string indicating the implementation, either auto, matrix or loop
- `minsize` Integer indicating the minimum allowed size for the regulons
- `cores` Integer indicating the number of cores to use (only 1 in Windows-based systems)
- `wm` Optional numeric matrix of weights (0; 1) with same dimension as eset
- `verbose` Logical, whether a progress bar should be shown

**Value**

List of two elements, enrichment score and normalized enrichment score

---

**as.dist.signatureDistance**

Distance matrix from signatureDistance objects

**Description**

This function transforms a signatureDistance object into a dist object

**Usage**

```r
## S3 method for class 'signatureDistance'
as.dist(m, diag = FALSE, upper = FALSE)
```

**Arguments**

- `m` signatureDistance object
- `diag` parameter included for compatibility
- `upper` parameter included for compatibility
Value

Object of class dist

Description

This function integrates the bootstrap msviper results

Usage

`bootstrapmsviper(mobj, method = c("mean", "median", "mode"))`

Arguments

- `mobj`: msviper object
- `method`: Character string indicating the method to use, either mean, median or mode

Value

msviper object

See Also

`msviper`

Examples

```r
data(bcellViper, package="bcellViper")
sig <- bootstrapTtest(dset, "description", c("CB", "CC"), "N")
mra <- msviper(sig, regulon)
plot(mra, cex=.7)
```
bootstrapTtest  
**Bootstrapped signature by t-test**

**Description**

This function generates a bootstrapped signature matrix by t-test

**Usage**

```r
bootstrapTtest(x, ...)  
## S4 method for signature 'matrix'
bootstrapTtest(x, y, per = 100, seed = 1,  
cores = 1, verbose = TRUE)  
## S4 method for signature 'ExpressionSet'
bootstrapTtest(x, pheno, group1, group2,  
per = 100, seed = 1, verbose = TRUE)
```

**Arguments**

- `x`: Matrix containing the test dataset
- `...`: Additional parameters added to keep compatibility
- `y`: Matrix containing the reference dataset
- `per`: Integer indicating the number of permutations
- `seed`: Integer indicating the seed for the permutations, 0 for disable it
- `cores`: Integer indicating the number of cores to use (set to 1 in Windows-based systems)
- `verbose`: Logical whether progress should be reported
- `pheno`: Character string indicating the phenotype data to use
- `group1`: Vector of character strings indicating the category from phenotype pheno to use as test group
- `group2`: Vector of character strings indicating the category from phenotype pheno to use as control group

**Value**

Matrix of z-scores with genes in rows and permutations in columns

**See Also**

- `msviper`
Examples

```r
data(bcellViper, package="bcellViper")
d1 <- exprs(dset)
sig <- bootstrapTtest(d1[, 1:10], d1[, 11:20], per=100)
dim(sig)
plot(density(sig[1907, ]))
data(bcellViper, package="bcellViper")
sig <- bootstrapTtest(dset, "description", "CB", "N", per=100)
dim(sig)
plot(density(sig[1907, ]))
```

Description

This function performs a viper analysis with bootstraps.

Usage

```r
bootstrapViper(eset, regulon, nes = TRUE, bootstraps = 10, 
eset.filter = FALSE, adaptive.size = TRUE, minsize = 20, 
mvws = 1, cores = 1, verbose = TRUE)
```

Arguments

- **eset**: ExpressionSet object or Numeric matrix containing the expression data, with samples in columns and genes in rows.
- **regulon**: Object of class regulon.
- **nes**: Logical, whether the enrichment score reported should be normalized.
- **bootstraps**: Integer indicating the number of bootstraps iterations to perform. Only the scale method is implemented with bootstraps.
- **eset.filter**: Logical, whether the dataset should be limited only to the genes represented in the interactome.
- **adaptive.size**: Logical, whether the weighting scores should be taken into account for computing the regulon size.
- **minsize**: Integer indicating the minimum number of targets allowed per regulon.
- **mvws**: Number or vector indicating either the exponent score for the metaViper weights, or the inflection point and trend for the sigmoid function describing the weights in metaViper.
- **cores**: Integer indicating the number of cores to use (only 1 in Windows-based systems).
- **verbose**: Logical, whether progression messages should be printed in the terminal.
Value

A list containing a matrix of inferred activity for each regulator gene in the network across all samples and the corresponding standard deviation computed from the bootstrap iterations.

See Also

viper

Examples

data(bcellViper, package="bcellViper")
d1 <- exprs(dset)
res <- viper(d1[, 1:50], regulon, bootstraps=10) # Run only on 50 samples to reduce computation time
dim(d1)
d1[1:5, 1:5]
regulon
dim(res$nes)
res$nes[1:5, 1:5]
res$sd[1:5, 1:5]

comNames

Combinatorial annotation

Description

This function converts combinatorial annotations

Usage

comNames(x, annot)

Arguments

x Character vector of gene name combinations, where the combinations are separated by –
annot Vector of gene names with geneID as names attribute

Value

Converted annotations

See Also

msvipер
distMode

Mode of continuous distributions

Description
This function computes the mode for continuous distributions

Usage
```r
distMode(x, adj = 1)
```

Arguments
- `x` Numeric data vector
- `adj` Number indicating the adjustment for the kernel bandwidth

Value
Number

Examples
```r
data(bcellViper, package="bcellViper")
d1 <- exprs(dset)
mean(d1[1,])
median(d1[1,])
distMode(d1[1,])
plot(density(d1[, 1]))
abline(v=c(mean(d1[, 1]), median(d1[, 1]), distMode(d1[, 1])), col=c("green", "red", "blue"))
legend("topleft", c("Mean", "Median", "Mode"), col=c("green", "red", "blue"), lwd=4)
```

fcvarna

Variance of columns for arrays with NA values

Description
This function computes the variance by columns ignoring NA values

Usage
```r
fcvarna(x)
```

Arguments
- `x` Numeric matrix
Value

1-column matrix with the variance by column results

Examples

data(bcellViper, package="bcellViper")
tmp <- exprs(dset)[, 1:10]
tmp[round(runif(100, 1, length(tmp)))] <- NA
fcvarna(tmp)

filterColMatrix  Filter for columns of a matrix with no loss of col and row names

Description

This function filters the columns of a matrix returning always a two dimensional matrix

Usage

filterColMatrix(x, filter)

Arguments

x  Matrix
filter Logical or numerical index of columns

Value

Matrix

filterCV  Coefficient of variation filter

Description

This function filter redundant probes based on the highest coefficient of variation

Usage

filterCV(expset, ...)

## S4 method for signature 'matrix'
filterCV(expset)

## S4 method for signature 'ExpressionSet'
filterCV(expset)
**Arguments**

- **expset** Expression set or Matrix containing the gene expression data, with samples in columns and probes in rows. The `colnames` attribute should contain the sample names and the `rownames` attribute should contain the unique geneIDs

- Additional parameters added to keep compatibility

**Value**

CV filtered dataset

**Examples**

```r
data(bcellViper, package="bcellViper")
d1 <- exprs(dset)
tmp <- rownames(d1)
tmp[round(runif(10, 1, length(tmp)))] <- tmp[1]
rownames(d1) <- tmp
dim(d1)
d1 <- filterCV(d1)
dim(d1)
```

---

**Description**

This function filters the rows of a matrix returning always a two dimensional matrix

**Usage**

```r
filterRowMatrix(x, filter)
```

**Arguments**

- **x** Matrix

- **filter** Logical or numerical index of rows

**Value**

Matrix
frcv  
**Coefficient of variations for rows**

**Description**
This function computes the coefficient of variation (CV) by rows.

**Usage**
```
frcv(x)
```

**Arguments**
- `x` Numeric matrix

**Value**
1-column matrix with the coefficient of variation by row results

**Examples**
```
data(bcellViper, package="bcellViper")
tmp <- exprs(dset)[1:10,]
tmp[round(runif(100, 1, length(tmp)))] <- NA
frcv(tmp)
```

frvarna  
**Variance of rows for arrays with NA values**

**Description**
This function computes the variance by rows ignoring NA values.

**Usage**
```
frvarna(x)
```

**Arguments**
- `x` Numeric matrix

**Value**
1-column matrix with the variance by row results

**Examples**
```
data(bcellViper, package="bcellViper")
tmp <- exprs(dset)[1:10,]
tmp[round(runif(100, 1, length(tmp)))] <- NA
frvarna(tmp)
```
Examples

```r
data(bcellViper, package="bcellViper")
tmp <- exprs(dset)[1:10,]
tmp[round(runif(100, 1, length(tmp)))] <- NA
frvarna(tmp)
```

Description

This function performs a Proportionally Weighted Enrichment Analysis on groups of gene-sets.

Usage

```r
groupPwea3(rlist, groups, nullpw = NULL, alternative = c("two.sided", "less", "greater"), per = 0, minsize = 5, cores = 1, verbose = TRUE)
```

Arguments

- `rlist`: Named vector containing the scores to rank the expression profile or matrix where columns contain bootstrapped signatures.
- `groups`: List of gene-sets (regulons), each component is a list of two vectors: `TFmode` containing the TFMoA index (-1; 1) and `likelihood` containing the interaction relative likelihood.
- `nullpw`: Numerical matrix representing the null model, with genes as rows (geneID as rownames) and permutations as columns.
- `alternative`: Character string indicating the alternative hypothesis, either `two.sided`, `greater` or `less`.
- `per`: Integer indicating the number of permutations for the genes in case `nullpw` is omitted.
- `minsize`: Integer indicating the minimum size for the regulons.
- `cores`: Integer indicating the number of cores to use (only 1 in Windows-based systems).
- `verbose`: Logical, whether progression messages should be printed in the terminal.

Value

A list containing four matrices:

- `es`: Enrichment score.
- `nes`: Normalized Enrichment Score.
- `size`: Regulon size.
- `p.value`: Enrichment p.value.
integrateSignatures  

**Description**

This function integrates signatures represented as columns in the input matrix using self-weighting average.

**Usage**

```r
integrateSignatures(signature, score = 1)
```

**Arguments**

- **signature**
  Numeric matrix containing the signatures as z-scores or NES, genes in rows and signatures in columns
- **score**
  Number indicating the exponent score for the weight

**Value**

Vector containing the integrated signatures

**Examples**

```r
data(bcellViper, package="bcellViper")
sig <- bootstrapTtest(dset, "description", "CB", "N", per=100)
isig <- integrateSignatures(sig)
plot(density(sig))
lines(density(isig, adj=1.5), col="red")
```

ledge  

**Description**

This function performs a Leading-Edge analysis on an object of class msviper

**Usage**

```r
ledge(mobj)
```

**Arguments**

- **mobj**
  msviper class object
loadExpset

Value

ms viper object updated with a ledge slot

See Also

ms viper

Examples

data(bcellViper, package="bcellViper")
sig <- rowTtest(dset, "description", "CB", "N")$statistic
mra <- msviper(sig, regulon)
mra <- ledge(mra)
summary(mra)

Description

This function load an expression file into a matrix

Usage

loadExpset(filename)

Arguments

filename Character string indicating the name of the expression file

Value

List containing a numeric matrix of expression data with samples in columns and probes in rows; and a vector of gene mapping annotations
### msviper

#### Description

This function performs MAster Regulator INference Analysis

#### Usage

```r
msviper(ges, regulon, nullmodel = NULL, pleiotropy = FALSE,
        minsize = 25, adaptive.size = FALSE, ges.filter = TRUE,
        synergy = 0, level = 10, pleiotropyArgs = list(regulators = 0.05,
        shadow = 0.05, targets = 10, penalty = 20, method = "adaptive"),
        cores = 1, verbose = TRUE)
```

#### Arguments

- **ges**: Vector containing the gene expression signature to analyze, or matrix with columns containing bootstrapped signatures
- **regulon**: Object of class regulon
- **nullmodel**: Matrix of genes by permutations containing the NULL model signatures. A parametric approach equivalent to shuffle genes will be used if nullmodel is omitted.
- **pleiotropy**: Logical, whether correction for pleiotropic regulation should be performed
- **minsize**: Number indicating the minimum allowed size for the regulons
- **adaptive.size**: Logical, whether the weight (likelihood) should be used for computing the regulon size
- **ges.filter**: Logical, whether the gene expression signature should be limited to the genes represented in the interactome
- **synergy**: Number indicating the synergy computation mode: (0) for no synergy computation; (0-1) for establishing the p-value cutoff for individual TFs to be included in the synergy analysis; (>1) number of top TFs to be included in the synergy analysis
- **level**: Integer, maximum level of combinatorial regulation
- **pleiotropyArgs**: List of 5 numbers for the pleiotropy correction indicating: regulators p-value threshold, pleiotropic interaction p-value threshold, minimum number of targets in the overlap between pleiotropic regulators, penalty for the pleiotropic interactions and the pleiotropy analysis method, either absolute or adaptive
- **cores**: Integer indicating the number of cores to use (only 1 in Windows-based systems)
- **verbose**: Logical, whether progression messages should be printed in the terminal
Value
A msviper object containing the following components:

- **signature** The gene expression signature
- **regulon** The final regulon object used
- **es** Enrichment analysis results including regulon size, normalized enrichment score and p-value
- **param** msviper parameters, including minsize, adaptive.size

See Also
viper

Examples
```r
data(bcellViper, package="bcellViper")
sig <- rowTtest(dset, "description", c("CB", "CC"), "N")$statistic
dnull <- ttestNull(dset, "description", c("CB", "CC"), "N", per=100) # Only 100 permutations to reduce computation time
mra <- msviper(sig, regulon, dnull)
plot(mra, cex=.7)
```

Description
This class contains the results generated by the msviper function

Slots
- **signature**: Matrix containing the gene expression signature
- **regulon**: Object of class regulon
- **es**: List containing 6 objects:
  - **es$es**: Named vector of class numeric containing the enrichment scores
  - **es$nes**: Named vector of class numeric containing the normalized enrichment scores
  - **es$nes.se**: Named vector of class numeric containing the standard error for the normalized enrichment score
  - **es$size**: Named vector of class numeric containing the size -number of target genes- for each regulator
  - **es$p.value**: Named vector of class numeric containing the enrichment p-values
  - **es$nes.bt**: Matrix containing the normalized enrichment score if the msviper test is performed with bootstraps
- **param**: List containing 3 elements:
  - **param$minsize**: Integer indicating the minimum allowed size for the regulons
param$adaptive.size: Logical indicating whether the weight (likelihood) should be used for computing the regulon size
param$iterative: Logical indicating whether a two step analysis with adaptive redundancy estimation should be performed
nullmodel: Matrix of genes by permutations containing the NULL model signatures
ledge: List containing the leading edge genes for each regulator. This slot is added by the ledge function
shadow: Two columns matrix containing the gene names for the shadow pairs. The first column contain the most probable regulator and the second column the one that was identified because a shadow effect

msviperAnnot  msVIPER annotation change

Description
This function changes the annotation of genes in msviper objects

Usage
msviperAnnot(mobj, annot, complete = TRUE)

Arguments
mobj  msviper object generated by msviper function
annot Vector os character strings containing the gene names and gene identifiers as vector names attribute
complete Logical, whether the signature and target names should be also transformed

Value
msviper object with updated annotations

See Also
msviper

Examples

data(bcellViper, package="bcellViper")
sig <- rowTtest(dset, "description", "CB", "N")$statistic
mra <- msviper(sig, regulon)
tmp <- unique(c(names(mra$regulon), rownames(mra$signature)))
annot <- 1:length(tmp)
names(annot) <- tmp
plot(mra, cex=.7)
mra <- msviperAnnot(mra, annot)
plot(mra, cex=.7)
**msviperClass**

**msVPER class**

**Description**

This function generates an instance of the msviper class from a signature, NES signature and regulon object.

**Usage**

```r
msviperClass(nes, signature, regulon, nullmodel = NULL)
```

**Arguments**

- `nes`: Numeric vector of NES values
- `signature`: Numeric vector of gene expression signature
- `regulon`: Instance of class regulon
- `nullmodel`: Optional matrix containing the signatures for the null model

**Value**

msviper class object

**Examples**

```r
data(bcellViper, package="bcellViper")
sig <- rowTtest(dset, "description", c("CB", "CC"), "N")$statistic
mra <- msviper(sig, regulon)
mra1 <- msviperClass(mra$es$nes, sig, regulon)
summary(mra1)
plot(mra1)
```

**msviperCombinatorial**

**msviper combinatorial analysis**

**Description**

This function performs combinatorial analysis for msviper objects.

**Usage**

```r
msviperCombinatorial(mobj, regulators = 100, nullmodel = NULL,
                      minsize = NULL, adaptive.size = NULL, level = 10, cores = 1,
                      processAll = FALSE, verbose = TRUE)
```
Arguments

mobj  msviper object generated by msviper function
regulators  Either a number between 0 and 1 indicating the p-value cutoff for individual TFs to be included in the combinations analysis; (>1) indicating the number of top TFs to be included in the combinations analysis; or a vector of character strings indicating the TF IDs to be included in the analysis
nullmodel  Matrix of genes by permutations containing the NULL model signatures. Taken from mobj by default
minsize  Number indicating the minimum allowed size for the regulons, taken from mobj by default
adaptive.size  Logical, whether the weight (likelihood) should be used for computing the size, taken from mobj by default
level  Integer, maximum level of combinatorial regulation
cores  Integer indicating the number of cores to use (only 1 in Windows-based systems)
processAll  Logical, whether all pairs, even if not significant, should be processed for synergy
verbose  Logical, whether progression messages should be printed in the terminal

Value

A msviper object

See Also

ms viper

Examples

data(bcellViper, package="bcellViper")
sig <- rowTtest(dset, "description", c("CB", "CC"), "N")$statistic
dnull <- ttestNull(dset, "description", c("CB", "CC"), "N", per=100) # Only 100 permutations to reduce computation time
mra <- msviper(sig, regulon, dnull)
mra <- msviperCombinatorial(mra, 20)
plot(mra, cex=.7)

msviperSynergy  msviper synergy analysis

Description

This function performs a synergy analysis for combinatorial regulation

Usage

msviperSynergy(mobj, per = 1000, seed = 1, cores = 1, verbose = TRUE)
Arguments

**mobj** ms viper object containing combinatorial regulation results generated by `msviperCombinatorial`

**per** Integer indicating the number of permutations

**seed** Integer indicating the seed for the permutations, 0 for disable it

**cores** Integer indicating the number of cores to use (only 1 in Windows-based systems)

**verbose** Logical, whether progression messages should be printed in the terminal

Value

Updated ms viper object containing the synergy p-value

See Also

`msviper`

Examples

data(bcellViper, package="bcellViper")
sig <- rowTtest(dset, "description", c("CB", "CC"), "N")$statistic
dnull <- ttestNull(dset, "description", c("CB", "CC"), "N", per=100) # Only 100 permutations to reduce computation time
mra <- msviper(sig, regulon, dnull)
mra <- msviperCombinatorial(mra, 20)
mra <- msviperSynergy(mra)
summary(mra)

plot.msviper  

Plot ms viper results

Description

This function generate a plot for ms viper results showing the enrichment of the target genes for each significant master regulator on the gene expression signature

Usage

```r
## S3 method for class 'msviper'
plot(x, mrs = 10, color = c("cornflowerblue", "salmon"), pval = NULL, bins = 500, cex = 0, density = 0, smooth = 0, sep = 0.2, hybrid = TRUE, include = c("expression", "activity"), gama = 2, ...)```
Arguments

- **x**: msVIPER object produced by `msVIPER` function
- **mrs**: Either an integer indicating the number of master regulators to include in the plot, or a character vector containing the names of the master regulators to include in the plot
- **color**: Vector of two components indicating the colors for the negative and positive parts of the regulon
- **pval**: Optional matrix of p-values to include in the plot
- **bins**: Number of bins to split the vector of scores in order to compute the density color of the bars
- **cex**: Number indicating the text size scaling, 0 indicates automatic scaling
- **density**: Integer indicating the number of steps for the kernel density. Zero for not plotting it
- **smooth**: Number indicating the proportion of point for smoothing the density distribution. Zero for not using the smoother
- **sep**: Number indicating the separation from figure and text
- **hybrid**: Logical, whether the 3-tail approach used for computing the enrichment should be reflected in the plot
- **include**: Vector indicating the information to include as heatmap to the right of the msVIPER plot: expression and activity
- **gama**: Positive number indicating the exponential transformation for the activity and expression color scale
- **...**: Given for compatibility to the plot generic function

Value

Nothing, a plot is generated in the default output device

See Also

`msVIPER`

Examples

```r
data(bcellViper, package="bcellViper")
sig <- rowTtest(dset, "description", c("CB", "CC"), "N")$statistic
dnull <- ttestNull(dset, "description", c("CB", "CC"), "N", per=100) # Only 100 permutations to reduce computation time
mra <- msVIPER(sig, regulon, dnull)
plot(mra, cex=.7)
```
pruneRegulon

Prune Regulons

Description

This function limits the maximum size of the regulons

Usage

pruneRegulon(regulon, cutoff = 50, adaptive = TRUE, eliminate = FALSE, wm = NULL)

Arguments

regulon Object of class regulon
cutoff Number indicating the maximum size for the regulons (maximum number of target genes)
adaptive Logical, whether adaptive size should be used (i.e. sum(likelihood^2))
eliminate Logical whether regulons smaller than cutoff should be eliminated
wm Optional numeric vector of weights (0:1) for the genes

Value

Pruned regulon

See Also

viper, msviper

Examples

data(bcellViper, package="bcellViper")
hist(sapply(regulon, function(x) sum(x$likelihood)/max(x$likelihood)), nclass=20)
preg <- pruneRegulon(regulon, 400)
hist(sapply(preg, function(x) sum(x$likelihood)/max(x$likelihood)), nclass=20)
**pwea3NULLf**  
*Null model function*

**Description**
This function generates the NULL model function, which computes the normalized enrichment score and associated p-value.

**Usage**
```
pwea3 NULLf(pwnull, cores = 1, verbose = TRUE)
```

**Arguments**
- `pwnull`: Object generated by `pwea3NULLgroups` function
- `cores`: Integer indicating the number of cores to use (only 1 in Windows-based systems)
- `verbose`: Logical, whether progression messages should be printed in the terminal

**Value**
List of function to compute NES and p-value

---

**pwea3NULLgroups**  
*Regulon-specific NULL model*

**Description**
This function generates the regulon-specific NULL models.

**Usage**
```
pwea3NULLgroups(pwnull, groups, cores = 1, verbose = TRUE)
```

**Arguments**
- `pwnull`: Numerical matrix representing the null model, with genes as rows (geneID as rownames) and permutations as columns
- `groups`: List containing the regulons
- `cores`: Integer indicating the number of cores to use (only 1 in Windows-based systems)
- `verbose`: Logical, whether progression messages should be printed in the terminal

**Value**
A list containing two elements:
- `groups` Regulon-specific NULL model containing the enrichment scores
- `ss` Direction of the regulon-specific NULL model
The regulon class

Description

This class contains interactome data

Slots

List of regulators with the following slots:

- `tfmode`: Named vector of class numeric containing the regulator mode of action scores, with target genes as name attribute
- `likelihood`: Vector of class numeric containing the relative likelihood for each target gene

rowTtest

Student's t-test for rows

Description

This function performs a Student's t-test on each row of a matrix

Usage

```r
rowTtest(x, ...)  
## S4 method for signature 'matrix'
rowTtest(x, y = NULL, mu = 0, alternative = "two.sided")  
## S4 method for signature 'ExpressionSet'
rowTtest(x, pheno, group1, group2 = NULL, mu = 0, alternative = "two.sided")
```

Arguments

- `x`: ExpressionSet object or Numerical matrix containing the test samples
- `...`: Additional parameters added to keep compatibility
- `y`: Optional numerical matrix containing the reference samples. If omitted x will be tested against mean = mu
- `mu`: Number indicating the alternative hypothesis when y is omitted
- `alternative`: Character string indicating the tail for the test, either two.sided, greater or lower
- `pheno`: Character string indicating the phenotype data to use
- `group1`: Vector of character strings indicating the category from phenotype pheno to use as test group
- `group2`: Vector of character strings indicating the category from phenotype pheno to use as control group
Value

List of Student-t-statistic (statistic) and p-values (p.value)

Examples

data(bcellViper, package="bcellViper")
d1 <- exprs(dset)
res <- rowTtest(d1[, 1:10], d1[, 11:20])
res$statistic[1:5, ]
res$p.value[1:5, ]
data(bcellViper, package="bcellViper")
res <- rowTtest(dset, "description", "CB", "N")
res$statistic[1:5, ]
res$p.value[1:5, ]

scale.signatureDistance

Scaling of signatureDistance objects

Description

This function scales the signatureDistance so its range is (-1, 1)

Usage

## S3 method for class 'signatureDistance'
scale(x, center = TRUE, scale = TRUE)

Arguments

x signatureDistance object
center Not used, given for compatibility with the generic function scale
scale Not used, given for compatibility with the generic function scale

Value

Scaled signatureDistance object
scaleGroups

Signatures with grouping variable

Description

scaleGroups compares each group vs. the remaining groups using a Student’s t-test

Usage

scaleGroups(x, groups)

Arguments

x Numerical matrix with genes in rows and samples in columns

groups Vector of same length as columns has the dset containing the labels for grouping the samples

Details

This function compute signatures using groups information

Value

Numeric matrix of signatures (z-scores) with genes in rows and groups in columns

Examples

data(bcellViper, package="bcellViper")
res <- scaleGroups(exprs(dset)[, 1:20], rep(1:4, rep(5, 4)))
res[1:5, ]

shadow

Shadow analysis for msviper objects

Description

This function performs shadow analysis on msviper objects

Usage

shadow(mobj, regulators = 0.01, targets = 10, shadow = 0.01, per = 1000, nullmodel = NULL, minsize = NULL, adaptive.size = NULL, iterative = NULL, seed = 1, cores = 1, verbose = TRUE)
Arguments

- `mobj` msviper object generated by `msviper`
- `regulators` This parameter represents different ways to select a subset of regulators for performing the shadow analysis, it can be either a p-value cutoff, the total number of regulons to be used for computing the shadow effect, or a vector of regulator ids to be considered
- `targets` Integer indicating the minimum number of common targets to compute shadow analysis
- `shadow` Number indicating the p-value threshold for the shadow effect
- `per` Integer indicating the number of permutations
- `nullmodel` Null model in marix format
- `minsize` Integer indicating the minimum size allowed for the regulons
- `adaptive.size` Logical, whether the target weight should be considered when computing the regulon size
- `iterative` Logical, whether a two step analysis with adaptive redundancy estimation should be performed
- `seed` Integer indicating the seed for the permutations, 0 for disable it
- `cores` Integer indicating the number of cores to use (only 1 in Windows-based systems)
- `verbose` Logical, whether progression messages should be printed in the terminal

Value

An updated msviper object with an additional slot (shadow) containing the shadow pairs

See Also

`msviper`

Examples

data(bcellViper, package="bcellViper")
sig <- rowTtest(dset, "description", c("CB", "CC"), "N")$statistic
dnull <- ttestNull(dset, "description", c("CB", "CC"), "N", per=100) # Only 100 permutations to reduce computation
mra <- msviper(sig, regulon, dnull)
mra <- shadow(mra, regulators=10)
summary(mra)
**shadowRegulon**  

*Correction for pleiotropy*

**Description**

This function penalize the regulatory interactions based on pleiotropy analysis.

**Usage**

```r
shadowRegulon(ss, nes, regul, regulators = 0.05, shadow = 0.05, targets = 10, penalty = 2, method = c("absolute", "adaptive"))
```

**Arguments**

- `ss`: Named vector containing the gene expression signature
- `nes`: Named vector containing the normalized enrichment scores
- `regul`: Regulon object
- `regulators`: Number indicating the number of top regulators to consider for the analysis or the p-value threshold for considering significant regulators
- `shadow`: Number indicating the p-value threshold for considering a significant shadow effect
- `targets`: Integer indicating the minimal number of overlapping targets to consider a pair of regulators for pleiotropy analysis
- `penalty`: Number higher than 1 indicating the penalty for the pleiotropic interactions. 1 = no penalty
- `method`: Character string indicating the method to use for computing the pleiotropy, either absolute or adaptive

**Value**

Corrected regulon object

---

**signatureDistance**  

*Signature Distance*

**Description**

This function computes the similarity between columns of a data matrix.

**Usage**

```r
signatureDistance(dset1, dset2 = NULL, nn = NULL, groups = NULL, scale = TRUE, two.tails = TRUE, ws = 2)
```
signatureDistance-class

Description

This class contains the results generated by `signatureDistance` function.

Slots

Matrix of class `numeric` containing the similarity scores
**sigT**  
*Sigoid transformation*

**Description**  
This function transforms a numeric vector using a sigmoid function.

**Usage**  
`sigT(x, slope = 20, inflection = 0.5)`

**Arguments**  
- `x`: Numeric vector
- `slope`: Number indicating the slope at the inflection point
- `inflection`: Number indicating the inflection point

**Value**  
Numeric vector

---

**summary.msviper**  
*List msviper results*

**Description**  
This function generates a table of msviper results.

**Usage**  
```r
## S3 method for class 'msviper'
summary(object, mrs = 10, ...)  
```

**Arguments**  
- `object`: msviper object
- `mrs`: Either number of top MRs to report or vector containing the genes to display
- `...`: Given for compatibility with the summary generic function

**Value**  
Data.frame with results
ttestNull  Null model by sample permutation testing

Description

This function performs sample permutation and t-test to generate a null model.

Usage

ttestNull(x, ...)

## S4 method for signature 'matrix'
ttestNull(x, y, per = 1000, repos = TRUE,
          seed = 1, cores = 1, verbose = TRUE)

## S4 method for signature 'ExpressionSet'
ttestNull(x, pheno, group1, group2, per = 1000,
          repos = TRUE, seed = 1, verbose = TRUE)

Arguments

x  ExpressionSet object or Matrix containing the test dataset
...
  Additional parameters added to keep compatibility
y  Matrix containing the reference dataset
per  Integer indicating the number of permutations
repos  Logical, whether the permutations should be performed with reposition
seed  Integer indicating the seed for the permutations, 0 for disable it
cores  Integer indicating the number of cores to use (set to 1 in windows systems)
verbose  Logical, whether progression messages should be printed in the terminal
pheno  Character string indicating the phenotype data to use
group1  Vector of character strings indicating the category from phenotype pheno to use
         as test group
group2  Vector of character strings indicating the category from phenotype pheno to use
         as control group

Value

Matrix of z-scores with genes in rows and permutations in columns

See Also

msVIPER, VIPER
Examples

```r
data(bcellViper, package="bcellViper")
d1 <- exprs(dset)
dnull <- ttestNull(d1[, 1:10], d1[, 11:20], per=100)
dim(dnull)
plot(density(dnull))
data(bcellViper, package="bcellViper")
dnull <- ttestNull(dset, "description", "CB", "CC", per=100)
dim(dnull)
plot(density(dnull))
```

Description

This function performs Virtual Inference of Protein-activity by Enriched Regulon analysis.

Usage

```r
viper(eset, regulon, dnull = NULL, pleiotropy = FALSE, nes = TRUE,
method = c("none", "scale", "rank", "mad", "ttest"), bootstraps = 0,
minsize = 25, adaptive.size = FALSE, eset.filter = TRUE,
mvws = 1, pleiotropyArgs = list(regulators = 0.05, shadow = 0.05,
targets = 10, penalty = 20, method = "adaptive"), cores = 1,
verbose = TRUE)
```

Arguments

- `eset` ExpressionSet object or Numeric matrix containing the expression data or gene expression signatures, with samples in columns and genes in rows.
- `regulon` Object of class regulon or list of objects of class regulon for metaVIPER analysis.
- `dnull` Numeric matrix for the null model, usually generated by `nullTtest`.
- `pleiotropy` Logical, whether correction for pleiotropic regulation should be performed.
- `nes` Logical, whether the enrichment score reported should be normalized.
- `method` Character string indicating the method for computing the single samples signature, either scale, rank, mad, ttest or none.
- `bootstraps` Integer indicating the number of bootstraps iterations to perform. Only the scale method is implemented with bootstraps.
- `minsize` Integer indicating the minimum number of targets allowed per regulon.
- `adaptive.size` Logical, whether the weighting scores should be taken into account for computing the regulon size.
- `eset.filter` Logical, whether the dataset should be limited only to the genes represented in the interactome.
- `mvws` Number or vector indicating either the exponent score for the metaViper weights, or the inflection point and trend for the sigmoid function describing the weights in metaViper.
pleiotropyArgs  list of 5 numbers for the pleotropy correction indicating: regulators p-value threshold, pleiotropic interaction p-value threshold, minimum number of targets in the overlap between pleiotropic regulators, penalty for the pleiotropic interactions and the method for computing the pleiotropy, either absolute or adaptive
cores  Integer indicating the number of cores to use (only 1 in Windows-based systems)
verbose  Logical, whether progression messages should be printed in the terminal

Value
A matrix of inferred activity for each regulator gene in the network across all samples

See Also
msviper

Examples
```r
data(bcellViper, package="bcellViper")
d1 <- exprs(dset)
res <- viper(d1, regulon)
dim(d1)
d1[1:5, 1:5]
regulon
dim(res)
res[1:5, 1:5]
```

viperRPT  

viperRPT

Description
This function computes residual post-translational activity

Usage
```r
viperRPT(vipermat, expmat, weights = matrix(1, nrow(vipermat),
  ncol(vipermat), dimnames = list(rownames(vipermat), colnames(vipermat)) ),
  method = c("spline", "lineal", "rank"), robust = FALSE, cores = 1)
```

Arguments
- `vipermat`  Numeric matrix containing the viper protein activity inferences
- `expmat`  Numeric matrix or expressionSet containing the expression data
- `weights`  List of numeric matrix of sample weights
- `method`  Character string indicating the method to use, either rank, lineal or spline
- `robust`  Logical, whether the contribution of outliers is down-weighted by using a gaussian kernel estimate for the join probability density
- `cores`  Integer indicating the number of cores to use
viperSignature

Value

Matrix of RPT-activity values

See Also

viper

Examples

```r
data(bcellViper, package="bcellViper")
vipermat <- viper(dset, regulon)
rpt <- viperRPT(vipermat, dset)
rpt[1:5, 1:5]
```

viperSignature

Generic S4 method for signature and sample-permutation null model for VIPER

Description

This function generates a viperSignature object from a test dataset based on a set of samples to use as reference

Usage

viperSignature(eset, ...)

## S4 method for signature 'ExpressionSet'
viperSignature(eset, pheno, refgroup,  
method = c("zscore", "ttest", "mean"), per = 100, bootstrap = TRUE,  
seed = 1, cores = 1, verbose = TRUE)

## S4 method for signature 'matrix'
viperSignature(eset, ref, method = c("zscore",  
"ttest", "mean"), per = 100, bootstrap = TRUE, seed = 1,  
cores = 1, verbose = TRUE)

Arguments

eset

ExpressionSet object or numeric matrix containing the test dataset, with genes in rows and samples in columns

...  

Additional parameters added to keep compatibility

pheno

Character string indicating the phenotype data to use

refgroup

Vector of character string indicating the category of pheno to use as reference group
viperSignature-class

This class contains the results produced by the `viperSignature` function.

**Slots**

- `signature`: Matrix of class `numeric` with genes in rows and samples in columns containing the gene expression signatures.
- `nullmodel`: Matrix of class `numeric` with genes in rows and permutations in columns containing the sample-permutation based signatures to be used as NULL model.
viperSimilarity

viperSimilarity  VIPER similarity

Description
If ws is a single number, weighting is performed using an exponential function. If ws is a 2 numbers vector, weighting is performed with a symmetric sigmoid function using the first element as inflection point and the second as trend.

Usage
viperSimilarity(x, nn = NULL, ws = c(4, 2), method = c("two.sided", "greater", "less"))

Arguments
x  Numeric matrix containing the VIPER results with samples in columns and regulators in rows
nn  Optional number of top regulators to consider for computing the similarity
ws  Number indicating the weighting exponent for the signature, or vector of 2 numbers indicating the inflection point and the value corresponding to a weighting score of .1 for a sigmoid transformation, only used if nn is omitted
method  Character string indicating whether the most active (greater), less active (less) or both tails (two.sided) of the signature should be used for computing the similarity

Details
This function computes the similarity between VIPER signatures

Value
signatureDistance object

Examples
data(bcellViper, package="bcellViper")
dd <- viperSimilarity(exprs(dset))
dd[1:5, 1:5]
scale(dd)[1:5, 1:5]
as.matrix(as.dist(dd))[1:5, 1:5]
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