Package 'diggit'

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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

```
aecdf(dnull, symmetric = FALSE)
```

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

Value

function with two parameters, `x` and `alternative`

`aqtl` *Inference of aQTL*

Description

This function infers aQTLs from F-CNVs and VIPER activity

Usage

```
aqtl(x, ...)

## S4 method for signature 'diggit'
aqtl(x, mr = 0.01, mr.adjust = c("none", "fdr",
  "bonferroni"), fcnv = 0.01, fcnv.adjust = c("none", "fdr", "bonferroni"),
  method = c("spearman", "mi", "pearson", "kendall"), mindy = FALSE,
  cores = 1, verbose = TRUE)
```

Arguments

x	Object of class diggit
...	Additional parameters to pass to the function
mr	Either a numerical value between 0 and 1 indicating the p-value threshold for the Master Regulator (MR) selection, or a vector of character strings listing the MRs
mr.adjust	Character string indicating the multiple hypothesis test correction for the MRs
fcnv	Either a numerical value between 0 and 1 indicating the p-value threshold for the F-CNV, or a vector of character strings listing the F-CNVs
fcnv.adjust	Character string indicating the multiple hypothesis test correction for the F-CNVs
method	Character string indicating the method for computing the association between F-CNV and regulator activity (aQTL analysis)
mindy	Logical, whether only post-translational modulators of each evaluated TF should be considered as putative genetic driver
cores	Integer indicating the number of cores to use (1 for Windows-based systems)
verbose	Logical, whether progress should be reported

Value

Updated diggit object with viper and aqtl slots

Examples

```
data(gbm.expression, package="diggitdata")
data(gbm.cnv, package="diggitdata")
data(gbm.aracne, package="diggitdata")
dobj <- diggitClass(expset=gbmExprs, cnv=gbmCNV, regulon=gbmTFregulon)
dobj <- fCNV(dobj)
dobj <- aqtl(dobj, mr=c("CEBPD", "STAT3"), fcnv.adjust="fdr")
dobj
diggitAqtl(dobj)[, 1:4]
```

---

conditional *Conditional analysis of CNVs*

Description

This function performs the conditional analysis of fCNVs

Usage

```
conditional(x, ...)

## S4 method for signature 'diggit'
conditional(x, pheno = "cond", group1, group2 = NULL,
  cnv = 0.2, mr = 0.01, mr.adjust = c("none", "fdr", "bonferroni"),
  modul = 0.01, modul.adjust = c("none", "fdr", "bonferroni"),
  fet.pval = 0.05, cores = 1, verbose = TRUE)
```

Arguments

x	Object of class diggit
...	Additional parameters to pass to the function
pheno	Character string indicating the feature for sample groups
group1	Character string indicating the treatment group
group2	Optional character string indicating the reference group
cnv	Single number or vector of two numbers indicating the thresholds for CNVs
mr	Either vector of character strings indicating the MR genes, or number indicating the corrected p-value threshold for selecting the MRs
mr.adjust	Character string indicating the multiple-hypothesis correction to apply to the MR p-values
modul	Number indicating the p-value threshold for a modulator to be considered associated with the MR activity
modul.adjust	Character string indicating the multiple-hypothesis correction to apply to the aQTL results
fet.pval	Number indicating the FET p-value threshold for the association between CNVs and sample groups
cores	Integer indicating the number of cores to use (1 for Windows-based systems)
verbose	Logical, whether progress should be reported

Value

Object of class diggit with conditional analysis results

Examples

```
data(gbm.expression, package="diggitdata")
data(gbm.cnv, package="diggitdata")
data(gbm.aracne, package="diggitdata")
dobj <- diggitClass(expset=gbmExprs, cnv=gbmCNV, regulon=gbmTFregulon)
dobj <- fCNV(dobj)
dobj <- aqtl(dobj, mr=c("CEBPD", "STAT3"), fcnv.adjust="fdr", verbose=FALSE)
dobj <- conditional(dobj, pheno="subtype", group1="MES", group2="PN", mr="STAT3", verbose=FALSE)
dobj
```

`correlation` *Correlation test*

Description

This function computes the correlation between x and y given both are numeric vectors, between the columns of x if it is a numeric matrix, or between the columns of x and y if both are numeric matrixes

Usage

```
correlation(x, y = NULL, method = c("pearson", "spearman", "kendall"),
  pairwise = FALSE)
```

Arguments

`x`	Numeric vector or matrix
`y`	Optional numeric vector or matrix
`method`	Character string indicating the correlation method
`pairwise`	Logical, wether columns of x and y should be compared in a pairwise manner. x and y must have the same number of columns

Details

This function computes correlation and associated p-values

Value

Numeric value, vector or matrix of results

Examples

```
x <- seq(0, 10, length=50)
y <- x+rnorm(length(x), sd=2)
correlation(x, y)
```

diggit-class *The diggit class*

Description

This class stores parameters and results of the diggit algorithm

This function generates diggit class objects

Usage

```
diggitClass(expset = NULL, cnv = NULL, regulon = NULL, mindy = NULL,
  fcnv = NULL, mr = NULL, viper = NULL, aqtl = NULL,
  conditional = NULL)
```

Arguments

expset	ExpressionSet object or numeric matrix of expression data, with features in rows and samples in columns
cnv	Numeric matrix of CNV data
regulon	Regulon class object containing the transcriptional interactome
mindy	Regulon class object containing the post-translational interactome
fcnv	Vector of F-CNV p-values
mr	Vector of master regulator Z-score (NES)
viper	Numeric matrix of VIPER results
aqtl	Numeric matrix of aQTL p-values
conditional	List containing the conditional analysis results

Details

see diggit-methods for related methods

Value

Object of class diggit

Slots

expset: ExpressionSet object containing the gene expression data

cnv: Matrrix containing the CNV data

regulon: Regulon object containing the transcriptional interactome

mindy: Regulon object containing the post-translational interactome

fcnv: Numeric vector containing the p-values for functional CNVs

mr: Numeric vector of normalized enrichment scores for the MARINa analysis

`viper`: Numeric matrix of normalized enrichment scores for the VIPER analysis

`aqtl`: Numeric matrix of association p-values for the aQTL analysis

`conditional`: List containing the conditional analysis results

Examples

```
data(gbm.expression, package="diggitdata")
data(gbm.aracne, package="diggitdata")
dobj <- diggitClass(expset=gbmExprs, regulon=gbmTFregulon)
print(dobj)
```

`fCNV` *Inference of functional CNVs*

Description

This function infers functional CNVs by computing their association with gene expression

Usage

```
fCNV(x, ...)

## S4 method for signature 'diggit'
fCNV(x, expset = NULL, cnv = NULL,
  method = c("spearman", "mi", "pearson", "kendall"), cores = 1,
  verbose = TRUE)

## S4 method for signature 'ExpressionSet'
fCNV(x, cnv, method = c("spearman", "mi", "pearson",
  "kendall"), cores = 1, verbose = TRUE)

## S4 method for signature 'matrix'
fCNV(x, cnv, method = c("spearman", "mi", "pearson",
  "kendall"), cores = 1, verbose = TRUE)

## S4 method for signature 'data.frame'
fCNV(x, cnv, method = c("spearman", "mi", "pearson",
  "kendall"), cores = 1, verbose = TRUE)
```

Arguments

`x`	Object of class diggit, expressionSet object or numeric matrix of expression data, with features in rows and samples in columns
`...`	Additional arguments
`expset`	Optional numeric matrix of expression data
`cnv`	Optional numeric matrix of CNVs

method	Character string indicating the method for computing the association between CNVs and expression
cores	Integer indicating the number of cores to use (1 for Windows-based systems)
verbose	Logical, whether to report analysis progress

Value

Objet of class diggit with updated fCNV slot

Examples

```
data(gbm.expression, package="diggitdata")
data(gbm.cnv, package="diggitdata")
genes <- intersect(rownames(gbmExprs), rownames(gbmCNV))[1:100]
gbmCNV <- gbmCNV[match(genes, rownames(gbmCNV)), ]
dgo <- diggitClass(expset=gbmExprs, cnv=gbmCNV)

dgo <- fCNV(dgo)
dgo
diggitFcnv(dgo)[1:5]
dgo <- fCNV(gbmExprs, gbmCNV)
print(dgo)
diggitFcnv(dgo)[1:5]
dgo <- fCNV(exprs(gbmExprs), gbmCNV)
dgo
diggitFcnv(dgo)[1:5]
dgo <- fCNV(as.data.frame(exprs(gbmExprs)), gbmCNV)
dgo
diggitFcnv(dgo)[1:5]
```

---

marina *Inference of Master Regulators*

Description

This function infers the master regulators for the transition between two phenotypes

Usage

```
marina(x, ...)

## S4 method for signature 'matrix'
marina(x, y = NULL, mu = 0, regulon, per = 1000,
  cores = 1, verbose = TRUE)

## S4 method for signature 'ExpressionSet'
marina(x, pheno = "cond", group1, group2 = NULL,
  mu = 0, regulon, per = 1000, cores = 1, verbose = TRUE)
```

```
## S4 method for signature 'diggit'
marina(x, pheno, group1, group2 = NULL, mu = 0,
  regulon = NULL, per = 1000, cores = 1, verbose = TRUE)
```

Arguments

x	Object of class diggit, expressionSet object or numerical matrix containing the test samples
...	Additional arguments
y	Numerical matrix containing the control samples
mu	Number indicating the control mean when y is ommited
regulon	Transcriptional interactome
per	Interger indicating the number of permutations to compute the marina null model
cores	Integer indicating the number of cores to use (1 for 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

Updated diggit object with Master Regulator results

Examples

```
cores <- 3*(Sys.info()[1] != "Windows")+1
data(gbm.expression, package="diggitdata")
data(gbm.aracne, package="diggitdata")

eset <- exprs(gbmExprs)
samples <- pData(gbmExprs)[["subtype"]]
x <- eset[, samples=="MES"]
y <- eset[, samples=="PN"]
dgo <- marina(x, y, regulon=gbmTFregulon, per=100, cores=cores)
dgo
diggitMR(dgo)[1:5]
dgo <- marina(gbmExprs, pheno="subtype", group1="MES", group2="PN", regulon=gbmTFregulon, per=100, cores=cores)
dgo
diggitMR(dgo)[1:5]
x <- diggitClass(expset=gbmExprs, regulon=gbmTFregulon)
dgo <- marina(x, pheno="subtype", group1="MES", group2="PN", per=100, cores=cores)
dgo
diggitMR(dgo)[1:5]
```

`mutualInfo` *Mutual information*

Description

This function estimates the mutual information between x and y given both are numeric vectors, between the columns of x if it is a numeric matrix, or between the columns of x and y if both are numeric matrixes

Usage

```
mutualInfo(x, y = NULL, per = 0, pairwise = FALSE, bw = 100,
  cores = 1, verbose = TRUE)
```

Arguments

`x`	Numeric vector or matrix
`y`	Optional numeric vector or matrix
`per`	Integer indicating the number of permutations to compute p-values
`pairwise`	Logical, wether columns of x and y should be compared in a pairwise maner. x and y must have the same number of columns
`bw`	Integer indicating the grid size for integrating the joint probability density
`cores`	Integer indicating the number of cores to use (1 for Windows-based systems)
`verbose`	Logical, whether progression bars should be shown

Details

This function estimates the mutual information between continuous variables using a fix bandwidth implementation

Value

Numeric value, vector or matrix of results

Examples

```
x <- seq(0, pi, length=100)
y <- 5*sin(x)+rnorm(100)
cor.test(x, y)
mutualInfo(x, y, per=100)
```

plot,diggit-method *Diggit plot*

Description

This function generate plots for the diggit conditional analysis

Usage

```
## S4 method for signature 'diggit'
plot(x, mr = NULL, cluster = NULL, sub = NULL, ...)
```

Arguments

x	Diggit class object
mr	Optional vector of character strings indicating the MR names
cluster	Optional vector of cluster names
sub	Optional sub-title for the plot
...	Additional parameters to pass to the plot function

Value

Nothing, plots are generated in the default output device

Examples

```
data(gbm.expression, package="diggitdata")
data(gbm.cnv, package="diggitdata")
data(gbm.aracne, package="diggitdata")
dobj <- diggitClass(expset=gbmExprs, cnv=gbmCNV, regulon=gbmTFregulon)
dobj <- fCNV(dobj)
dobj <- aqtl(dobj, mr=c("CEBPD", "STAT3"), fcnv.adjust="fdr", verbose=FALSE)
dobj <- conditional(dobj, pheno="subtype", group1="MES", group2="PN", mr="STAT3", verbose=FALSE)
plot(dobj, cluster="3")
```

print,diggit-method *Basic methods for class diggit*

Description

This document lists a series of basic methods for the class diggit

Usage

```
## S4 method for signature 'diggit'
print(x, pval = 0.05)

## S4 method for signature 'diggit'
show(object)

## S4 method for signature 'diggit'
exprs(object)

## S4 method for signature 'diggit'
diggitCNV(x)

## S4 method for signature 'diggit'
diggitRegulon(x)

## S4 method for signature 'diggit'
diggitMindy(x)

## S4 method for signature 'diggit'
diggitFcnv(x)

## S4 method for signature 'diggit'
diggitMR(x)

## S4 method for signature 'diggit'
diggitViper(x)

## S4 method for signature 'diggit'
diggitAqtl(x)

## S4 method for signature 'diggit'
diggitConditional(x)

## S4 method for signature 'diggit'
summary(object)

## S4 method for signature 'diggit'
head(x, rows = 4, cols = 4)

## S4 method for signature 'diggit'
mindyFiltering(x, mr = 0.01, mr.adjust = c("none", "fdr",
  "bonferroni"))
```

Arguments

x	Object of class diggit
pval	P-value threshold for the conditional analysis

object	Object of class diggit
rows	Integer indicating the maximum number of rows to show
cols	Integer indicating the maximum number of columns to show
mr	Either a numerical value between 0 and 1 indicating the p-value threshold for the Master Regulator (MR) selection, or a vector of character strings listing the MRs
mr.adjust	Character string indicating the multiple hypothesis test correction for the MRs

Value

print returns summary information about the diggit object

show returns summary information about the object of class diggit

exprs returns the ExpressionSet object containing the expression profile data

diggitCNV returns a matrix containing the CNV data

diggitRegulon returns a regulon object containing the transcriptional interactome

diggitMindy returns a regulon object containing the post-translational interactome

diggitFcnv returns a vector of p-values for the F-CNVs

diggitMR returns a vector of master regulators NES

diggitViper returns a matrix of VIPER results

diggitAqtl returns a matrix of aQTLs (p-value)

diggitConditional returns a list containing the conditional analysis results

summary returns the integrated results from the conditional analysis

head returns a list containing a reduced view for an object of class diggit

mindyFiltering returns a diggit class object with CNV and aQTL slots filtered to contain only MINDy post-translational modulators of the MRs

Examples

```
data(gbm.expression, package="diggitdata")
data(gbm.cnv, package="diggitdata")
data(gbm.aracne, package="diggitdata")
dobj <- diggitClass(expset=gbmExprs, cnv=gbmCNV, regulon=gbmTFregulon)
print(dobj)
show(dobj)
exprs(dobj)
diggitCNV(dobj)[1:3, 1:3]
diggitRegulon(dobj)
diggitMindy(dobj)
diggitFcnv(dobj)
diggitMR(dobj)
diggitViper(dobj)
diggitAqtl(dobj)
diggitConditional(dobj)
head(dobj)
data(gbm.expression, package="diggitdata")
```

```
data(gbm.cnv, package="diggitdata")
data(gbm.mindy, package="diggitdata")
dobj <- diggitClass(expset=gbmExprs, cnv=gbmCNV, mindy=gbmMindy)
dobj <- fCNV(dobj)
dobj
dobj <- mindyFiltering(dobj, mr=c("STAT3", "CEBPD"))
dobj
```

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