

# Package ‘diggit’

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**Description** Inference of Genetic Variants Driving Cellular Phenotypes  
by the DIGGIT algorithm

**License** file LICENSE

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|       |                                                                |
|-------|----------------------------------------------------------------|
| aecdf | <i>Approximate empirical commulative distribution function</i> |
|-------|----------------------------------------------------------------|

---

### 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 | <i>Inference of aQTL</i> |
|------|--------------------------|

---

### 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 | <i>Conditional analysis of CNVs</i> |
|-------------|-------------------------------------|

---

### 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 |

|                           |                                                                                                                                        |
|---------------------------|----------------------------------------------------------------------------------------------------------------------------------------|
| <code>mr</code>           | Either vector of character strings indicating the MR genes, or number indicating the corrected p-value threshold for selecting the MRs |
| <code>mr.adjust</code>    | Character string indicating the multiple-hypothesis correction to apply to the MR p-values                                             |
| <code>modul</code>        | Number indicating the p-value threshold for a modulator to be considered associated with the MR activity                               |
| <code>modul.adjust</code> | Character string indicating the multiple-hypothesis correction to apply to the aQTL results                                            |
| <code>fet.pval</code>     | Number indicating the FET p-value threshold for the association between CNVs and sample groups                                         |
| <code>cores</code>        | Integer indicating the number of cores to use (1 for Windows-based systems)                                                            |
| <code>verbose</code>      | 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
```

---

|                          |                         |
|--------------------------|-------------------------|
| <code>correlation</code> | <i>Correlation test</i> |
|--------------------------|-------------------------|

---

### 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

|                       |                                                                                                                                                                               |
|-----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>x</code>        | Numeric vector or matrix                                                                                                                                                      |
| <code>y</code>        | Optional numeric vector or matrix                                                                                                                                             |
| <code>method</code>   | Character string indicating the correlation method                                                                                                                            |
| <code>pairwise</code> | Logical, whether columns of <code>x</code> and <code>y</code> should be compared in a pairwise manner. <code>x</code> and <code>y</code> 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 | <i>The diggit class</i> |
|--------------|-------------------------|

---

**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: Matrix 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 <code>diggit</code> , <code>expressionSet</code> 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]
```

**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 omitted                                             |
| regulon | Transcriptional interactome                                                                      |
| per     | Integer 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 | <i>Mutual information</i> |
|------------|---------------------------|

---

## 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

|                       |                                                                                                                                   |
|-----------------------|-----------------------------------------------------------------------------------------------------------------------------------|
| <code>x</code>        | Numeric vector or matrix                                                                                                          |
| <code>y</code>        | Optional numeric vector or matrix                                                                                                 |
| <code>per</code>      | Integer indicating the number of permutations to compute p-values                                                                 |
| <code>pairwise</code> | Logical, whether columns of $x$ and $y$ should be compared in a pairwise manner. $x$ and $y$ must have the same number of columns |
| <code>bw</code>       | Integer indicating the grid size for integrating the joint probability density                                                    |
| <code>cores</code>    | Integer indicating the number of cores to use (1 for Windows-based systems)                                                       |
| <code>verbose</code>  | 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 | <i>Diggit plot</i> |
|--------------------|--------------------|

---

## 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 | <i>Basic methods for class diggit</i> |
|---------------------|---------------------------------------|

---

## 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 |

|                        |                                                                                                                                                                     |
|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>mr</code>        | 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 |
| <code>mr.adjust</code> | 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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