

Package: omics (via r-universe)

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Title '--omics' Data Analysis Toolbox

Description A collection of functions to analyse '--omics' datasets such as DNA methylation and gene expression profiles.

Depends R (>= 3.0.0), methods

Imports lme4, pheatmap

Suggests testthat

NeedsCompilation no

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cpma *Cross Phenotype Meta-Analysis*

Description

Performs (signed) cross phenotype meta-analysis.

Usage

```
cpma(ps)
```

Arguments

ps a (non-empty) numeric vector of p -values.

Value

A list with class `htest` containing the following components:

statistic	the value of the χ^2 test statistic.
parameter	the estimated rate λ .
p.value	the p -value for the test.
method	a character string indicating the type of test performed.
data.name	a character string giving the name of the data.

References

Cotsapas, C., et al. 2011 Pervasive Sharing of Genetic Effects in Autoimmune Disease. *PLOS Genetics* 7(8):e1002254.

mlm *Multiple Linear Models*

Description

Fits multiple linear models.

Usage

```
mlm(formula, data, vars, save.residuals=FALSE)
```

Arguments

formula	an object of class formula (or one that can be coerced to that class): a symbolic description of the models to be fitted.
data	an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model.
vars	a character vector of variables of interest.
save.residuals	whether model residuals should be stored and returned.

Value

A list with elements:

coefficients	if 'vars' is missing or non-empty, an array (or data frame, if vars contains a single element) of regression coefficient estimates (<code>coef</code>), standard errors (<code>coef.se</code>), and corresponding <i>p</i> -values (<code>pval</code>).
residuals	if <code>save.residuals</code> is TRUE, a matrix of model residuals.

See Also

[lm](#)

Examples

```
coefs <- matrix(runif(6*10), 6, 10)
X <- matrix(rnorm(100*5), 100, 5)
Y <- cbind(1, X)

models <- mlm(Y ~ X)
str(models)
```

mlmer

Multiple Linear Mixed-Effects Models

Description

Fits multiple linear mixed-effects models.

Usage

```
mlmer(formula, data, vars, lrt=TRUE, save.residuals=FALSE, save.ranks=TRUE)
```

Arguments

formula	an object of class formula (or one that can be coerced to that class): a symbolic description of the models to be fitted.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
vars	a character vector of variables of interest.
lrt	whether p -values should be computed using likelihood-ratio tests.
save.residuals	whether model residuals should be stored and returned.
save.ranks	whether random effect ranks should be stored and returned.

Value

A list with elements:

coefficients	if 'vars' is missing or non-empty, an array (or data frame, if vars contains a single element) of regression coefficient estimates (coef), standard errors (coef.se), and corresponding p -values (pval).
residuals	if save.residuals is TRUE, a matrix of model residuals.
ranef.ranks	if save.ranks is TRUE (default), a list of rank matrices (one per random effect) that can be visualized using ranks.heatmap .

See Also

[lmer](#) and [mlm](#)

na.count	<i>Count Missing Values</i>
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Description

Counts the number of missing values.

Usage

```
na.count(X, margin, fraction=TRUE)
```

Arguments

X	an array, including a matrix.
margin	a vector giving the subscripts to count over.
fraction	whether to return the fraction of missing values.

Value

The number (or fraction) of missing values.

pqq *Quantile-Quantile Plot for p-values*

Description

Computes value to produce a quantile-quantile plot in $-\log_{10}$ scale of the given p -values.

Usage

```
pqq(ps)
pqq.ci(n, level=0.95)
```

Arguments

`ps` a (non-empty) numeric vector of p -values.
`n` number of p -values.
`level` significance level.

Value

For `pqq`, a list containing the following components (all in $-\log_{10}$ scale):

`x` a vector of (sorted) expected p -values.
`y` a vector of (sorted) observed p -values.

For `pqq.ci`, a matrix with the lower and upper bounds for the confidence interval at the given significance level.

ranef.ranks *Extract Random Effect Rank Distributions*

Description

Extracts random effect rank distributions from a linear mixed-effects model.

Usage

```
## S3 method for class 'merMod'
ranef.ranks(model, groups)
```

Arguments

`model` a linear mixed-effects model estimated using [lmer](#).
`groups` a character vector of random effects of interest.

Value

If `which` is missing, a list of rank distribution vectors for all random intercepts in the model. Otherwise, a list of rank distribution vectors for random intercepts specified by `which`.

See Also

[mlmer](#)

ranks.heatmap

Plot Random Effect Rank Distributions

Description

Plots the rank distribution matrix for a random effect generated by [mlmer](#).

Usage

```
ranks.heatmap(x, col="red")
```

Arguments

`x` a matrix with the rank distribution for a random effect generated by [mlmer](#).
`col` the color corresponding to "higher-than-expected" counts.

Side Effects

Generates a new plot.

See Also

[mlmer](#)

re.match

Pattern Matching and Extraction

Description

Matches and extracts substrings using regular expressions.

Usage

```
re.match(pattern, x, ...)
```

Arguments

pattern	character string containing a regular expression.
x	a character vector where matches are sought, or an object which can be coerced by <code>as.character</code> to a character vector.
...	further arguments to be passed to <code>regexec</code> .

Details

This function is a wrapper for consecutive calls to `regexec` and `regmatches`.

Value

A matrix of matched substrings.

See Also

[regexec](#) and [regmatches](#)

setutils

Set Operations on Multiple Vectors

Description

Performs set operations on multiple vectors.

Usage

```
mintersect(..., sorted=FALSE)
```

```
munion(..., sorted=FALSE)
```

Arguments

...	input vectors
sorted	whether the result should be sorted

Value

Set intersection or union of the given vectors

See Also

[intersect](#) and [union](#)

var.components	<i>Extract Variance Components</i>
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Description

Extracts variance components from a linear mixed-effects model.

Usage

```
## S3 method for class 'merMod'  
var.components(model)
```

Arguments

model a linear mixed-effects model estimated using [lmer](#).

Value

A data frame with elements:

group	the name of the random effect.
var.name	the name of the variable.
var	the estimated variance.
var.prop	the estimated proportion of variance.

See Also

[mlmer](#)

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