Package 'omics'

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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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R topics documented:

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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.

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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 `as.data.frame` 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 (`coef`), standard errors (`coef.se`), and corresponding p-values (`pval`).
residuals	if `save.residuals` 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](#)

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na.count	*Count Missing Values*

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.

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pqq   *Quantile-Quantile Plot for p-values*

Description

Computes value to produce a quantile-quantile plot in $-log_1 0$ 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 $-log_1 0$ 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.

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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

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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

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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 as.character to a character vector.
...	further arguments to be passed to regexec.

Details

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

Value

A matrix of matched substrings.

See Also

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

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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](#)

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var.components   *Extract Variance Components*

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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