

Package ‘groupedstats’

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Type Package

Title Grouped Statistical Analyses in a Tidy Way

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Description Collection of functions to run statistical tests
across all combinations of multiple grouping variables.

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URL <https://indrajeetpatil.github.io/groupedstats/>,
<https://github.com/IndrajeetPatil/groupedstats/>

BugReports <https://github.com/IndrajeetPatil/groupedstats/issues/>

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grouped_aov	<i>Running analysis of variance (aov) across multiple grouping variables.</i>
-------------	---

Description

Running analysis of variance (aov) across multiple grouping variables.

Usage

```
grouped_aov(
  data,
  grouping.vars,
  formula,
  effsize = "eta",
  output = "tidy",
  ...
)
```

Arguments

data	A data frame in which the variables specified in the formula will be found. If missing, the variables are searched for in the standard way.
grouping.vars	Grouping variables.
formula	A formula specifying the model.
effsize	Character describing the effect size to be displayed: "eta" (default) or "omega".
output	A character describing what output is expected. Two possible options: "tidy" (default), which will return the results, or "tukey", which will return results from Tukey's Honest Significant Differences method for <i>post hoc</i> comparisons. The "glance" method to get model summary is currently not supported for this function.
...	Currently ignored.

Examples

```
# uses dataset included in the `groupedstats` package
set.seed(123)
library(groupedstats)

# effect size
groupedstats::grouped_aov(
  formula = wt ~ mpg,
  data = mtcars,
  grouping.vars = am,
  effsize = "eta"
)
```

grouped_glm	<i>Function to run generalized linear model (glm) across multiple grouping variables.</i>
-------------	---

Description

Function to run generalized linear model (glm) across multiple grouping variables.

Usage

```
grouped_glm(
  data,
  grouping.vars,
  ...,
  output = "tidy",
  tidy.args = list(conf.int = TRUE, conf.level = 0.95),
  augment.args = list()
)
```

Arguments

data	Dataframe (or tibble) from which variables are to be taken.
grouping.vars	Grouping variables.
...	Additional arguments to broom::tidy, broom::glance, or broom::augment S3 method.
output	A character describing what output is expected. Two possible options: "tidy" (default), which will return the results, or "glance", which will return model summaries.
tidy.args	A list of arguments to be used in the relevant S3 method.
augment.args	A list of arguments to be used in the relevant S3 method.

Value

A tibble dataframe with tidy results from linear model.

See Also

[grouped_lm](#), [grouped_lmer](#), [grouped_glm](#)

Examples

```
groupedstats::grouped_glm(
  data = mtcars,
  formula = am ~ wt,
  grouping.vars = cyl,
  family = stats::binomial(link = "logit")
)
```

grouped_glm	<i>Function to run generalized linear mixed-effects model (glmer) across multiple grouping variables.</i>
-------------	---

Description

Function to run generalized linear mixed-effects model (glmer) across multiple grouping variables.

Usage

```
grouped_glm(
  data,
  grouping.vars,
  ...,
  output = "tidy",
  tidy.args = list(conf.int = TRUE, conf.level = 0.95, effects = "fixed", conf.method =
    "Wald"),
  augment.args = list()
)
```

Arguments

data	Dataframe (or tibble) from which variables are to be taken.
grouping.vars	Grouping variables.
...	Arguments passed on to lme4::glmer
formula	a two-sided linear formula object describing both the fixed-effects and random-effects part of the model, with the response on the left of a ~ operator and the terms, separated by + operators, on the right. Random-effects terms are distinguished by vertical bars (" ") separating expressions for design matrices from grouping factors.

- family** a GLM family, see [glm](#) and [family](#).
- control** a list (of correct class, resulting from [lmerControl\(\)](#) or [glmerControl\(\)](#) respectively) containing control parameters, including the nonlinear optimizer to be used and parameters to be passed through to the nonlinear optimizer, see the `*lmerControl` documentation for details.
- start** a named list of starting values for the parameters in the model, or a numeric vector. A numeric `start` argument will be used as the starting value of θ . If `start` is a list, the `theta` element (a numeric vector) is used as the starting value for the first optimization step (default=1 for diagonal elements and 0 for off-diagonal elements of the lower Cholesky factor); the fitted value of θ from the first step, plus `start[["fixef"]]`, are used as starting values for the second optimization step. If `start` has both `fixef` and `theta` elements, the first optimization step is skipped. For more details or finer control of optimization, see [modular](#).
- verbose** integer scalar. If > 0 verbose output is generated during the optimization of the parameter estimates. If > 1 verbose output is generated during the individual penalized iteratively reweighted least squares (PIRLS) steps.
- nAGQ** integer scalar - the number of points per axis for evaluating the adaptive Gauss-Hermite approximation to the log-likelihood. Defaults to 1, corresponding to the Laplace approximation. Values greater than 1 produce greater accuracy in the evaluation of the log-likelihood at the expense of speed. A value of zero uses a faster but less exact form of parameter estimation for GLMMs by optimizing the random effects and the fixed-effects coefficients in the penalized iteratively reweighted least squares step. (See Details.)
- subset** an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
- weights** an optional vector of ‘prior weights’ to be used in the fitting process. Should be NULL or a numeric vector.
- na.action** a function that indicates what should happen when the data contain NAs. The default action (`na.omit`, inherited from the ‘factory fresh’ value of `getOption("na.action")`) strips any observations with any missing values in any variables.
- offset** this can be used to specify an *a priori* known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more `offset` terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See [model.offset](#).
- contrasts** an optional list. See the `contrasts.arg` of [model.matrix.default](#).
- mustart** optional starting values on the scale of the conditional mean, as in [glm](#); see there for details.
- etastart** optional starting values on the scale of the unbounded predictor as in [glm](#); see there for details.

	devFunOnly	logical - return only the deviance evaluation function. Note that because the deviance function operates on variables stored in its environment, it may not return <i>exactly</i> the same values on subsequent calls (but the results should always be within machine tolerance).
output		A character describing what output is expected. Two possible options: "tidy" (default), which will return the results, or "glance", which will return model summaries.
tidy.args		A list of arguments to be used in the relevant S3 method.
augment.args		A list of arguments to be used in the relevant S3 method.

Value

A tibble dataframe with tidy results from linear model or model summaries.

grouped_lm	<i>Running linear model (lm) across multiple grouping variables.</i>
------------	--

Description

Running linear model (lm) across multiple grouping variables.

Usage

```
grouped_lm(
  data,
  grouping.vars,
  ...,
  output = "tidy",
  tidy.args = list(conf.int = TRUE, conf.level = 0.95),
  augment.args = list()
)
```

Arguments

data	Dataframe (or tibble) from which variables are to be taken.
grouping.vars	Grouping variables.
...	Additional arguments to broom::tidy, broom::glance, or broom::augment S3 method.
output	A character describing what output is expected. Two possible options: "tidy" (default), which will return the results, or "glance", which will return model summaries.
tidy.args	A list of arguments to be used in the relevant S3 method.
augment.args	A list of arguments to be used in the relevant S3 method.

Value

A tibble dataframe with tidy results from linear model.

See Also

[grouped_slr](#), [grouped_tidy](#)

Examples

```
# loading needed libraries
library(ggplot2)

# getting tidy output of results
grouped_lm(
  data = mtcars,
  grouping.vars = cyl,
  formula = mpg ~ am * wt,
  output = "tidy"
)

# getting model summaries
# diamonds dataset from ggplot2
grouped_lm(
  data = diamonds,
  grouping.vars = c(cut, color),
  formula = price ~ carat * clarity,
  output = "glance"
)
```

grouped_lmer

Linear mixed-effects model (lmer) across multiple grouping variables.

Description

Linear mixed-effects model (lmer) across multiple grouping variables.

Usage

```
grouped_lmer(
  data,
  grouping.vars,
  ...,
  output = "tidy",
  tidy.args = list(conf.int = TRUE, conf.level = 0.95, effects = "fixed", conf.method =
    "Wald"),
  augment.args = list()
)
```

Arguments

<code>data</code>	Dataframe (or tibble) from which variables are to be taken.
<code>grouping.vars</code>	Grouping variables.
<code>...</code>	Arguments passed on to <code>lme4::lmer</code>
<code>formula</code>	a two-sided linear formula object describing both the fixed-effects and random-effects part of the model, with the response on the left of a <code>~</code> operator and the terms, separated by <code>+</code> operators, on the right. Random-effects terms are distinguished by vertical bars (<code> </code>) separating expressions for design matrices from grouping factors. Two vertical bars (<code> </code>) can be used to specify multiple uncorrelated random effects for the same grouping variable. (Because of the way it is implemented, the <code> </code> -syntax <i>works only for design matrices containing numeric (continuous) predictors</i> ; to fit models with independent categorical effects, see <code>dummy</code> or the <code>lmer_alt</code> function from the afex package.)
<code>REML</code>	logical scalar - Should the estimates be chosen to optimize the REML criterion (as opposed to the log-likelihood)?
<code>control</code>	a list (of correct class, resulting from <code>lmerControl()</code> or <code>glmerControl()</code> respectively) containing control parameters, including the nonlinear optimizer to be used and parameters to be passed through to the nonlinear optimizer, see the <code>*lmerControl</code> documentation for details.
<code>start</code>	a named <code>list</code> of starting values for the parameters in the model. For <code>lmer</code> this can be a numeric vector or a list with one component named <code>"theta"</code> .
<code>verbose</code>	integer scalar. If <code>> 0</code> verbose output is generated during the optimization of the parameter estimates. If <code>> 1</code> verbose output is generated during the individual penalized iteratively reweighted least squares (PIRLS) steps.
<code>subset</code>	an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
<code>weights</code>	an optional vector of ‘prior weights’ to be used in the fitting process. Should be <code>NULL</code> or a numeric vector. Prior weights are <i>not</i> normalized or standardized in any way. In particular, the diagonal of the residual covariance matrix is the squared residual standard deviation parameter <code>sigma</code> times the vector of inverse weights. Therefore, if the weights have relatively large magnitudes, then in order to compensate, the <code>sigma</code> parameter will also need to have a relatively large magnitude.
<code>na.action</code>	a function that indicates what should happen when the data contain NAs. The default action (<code>na.omit</code> , inherited from the ‘factory fresh’ value of <code>getOption("na.action")</code>) strips any observations with any missing values in any variables.
<code>offset</code>	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be <code>NULL</code> or a numeric vector of length equal to the number of cases. One or more <code>offset</code> terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See <code>model.offset</code> .

	contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
	devFunOnly	logical - return only the deviance evaluation function. Note that because the deviance function operates on variables stored in its environment, it may not return <i>exactly</i> the same values on subsequent calls (but the results should always be within machine tolerance).
output		A character describing what output is expected. Two possible options: "tidy" (default), which will return the results, or "glance", which will return model summaries.
tidy.args		A list of arguments to be used in the relevant S3 method.
augment.args		A list of arguments to be used in the relevant S3 method.

Value

A tibble dataframe with tidy results from a linear mixed-effects model. Note that p -value is computed using `parameters::p_value`.

Examples

```
# for reproducibility
set.seed(123)

# loading libraries containing data
library(gapminder)

# getting tidy output of results
# let's use only subset of the data
groupedstats::grouped_lmer(
  data = gapminder,
  formula = scale(lifeExp) ~ scale(gdpPercap) + (gdpPercap | continent),
  grouping.vars = year,
  REML = FALSE,
  tidy.args = list(effects = "fixed", conf.int = TRUE, conf.level = 0.95),
  output = "tidy"
)
```

grouped_proptest	<i>Function to run proportion test on grouped data.</i>
------------------	---

Description

Function to run proportion test on grouped data.

Usage

```
grouped_proptest(data, grouping.vars, measure, ...)
```

Arguments

data	Dataframe (or tibble) from which variables are to be taken.
grouping.vars	Grouping variables.
measure	A variable for which proportion test needs to be carried out for each combination of levels of factors entered in grouping.vars.
...	Currently ignored.

Value

Dataframe with percentages and statistical details from a proportion test.

Examples

```
# for reproducibility
set.seed(123)

groupedstats::grouped_proptest(
  data = mtcars,
  grouping.vars = cyl,
  measure = am
)
```

grouped_slr	<i>Running simple linear regression (slr) on multiple variables across multiple grouping variables.</i>
-------------	---

Description

Running simple linear regression (slr) on multiple variables across multiple grouping variables.

Usage

```
grouped_slr(data, dep.vars, indep.vars, grouping.vars)
```

Arguments

data	Dataframe from which variables are to be taken.
dep.vars	List criterion or dependent variables for simple linear model (y in $y \sim x$).
indep.vars	List predictor or independent variables for simple linear model (x in $y \sim x$).
grouping.vars	List of grouping variables.

Value

A tibble dataframe with tidy results from simple linear regression analyses. The estimates are standardized, i.e. the lm model used is $\text{scale}(y) \sim \text{scale}(x)$, and not $y \sim x$.

See Also

[grouped_lm](#), [grouped_tidy](#)

Examples

```
# for reproducibility
set.seed(123)

# in case of just one grouping variable
groupedstats::grouped_slr(
  data = iris,
  dep.vars = c(Sepal.Length, Petal.Length),
  indep.vars = c(Sepal.Width, Petal.Width),
  grouping.vars = Species
)
```

grouped_summary	<i>Descriptive statistics for multiple variables for all grouping variable levels</i>
-----------------	---

Description

Descriptive statistics for multiple variables for all grouping variable levels

Usage

```
grouped_summary(
  data,
  grouping.vars,
  measures = NULL,
  measures.type = "numeric",
  topcount.long = FALSE,
  k = 2L,
  ...
)
```

Arguments

data	Dataframe from which variables need to be taken.
grouping.vars	A list of grouping variables. Please use unquoted arguments (i.e., use <code>x</code> and not <code>"x"</code>).
measures	List variables for which summary needs to be computed. If not specified, all variables of type specified in the argument <code>measures.type</code> will be used to calculate summaries. Don't explicitly set <code>measures.type = NULL</code> in function call, which will produce an error because the function will try to find a column in a dataframe named "NULL".

<code>measures.type</code>	A character indicating whether summary for <i>numeric</i> ("numeric") or <i>factor/character</i> ("factor") variables is expected (Default: <code>measures.type = "numeric"</code>). This function can't be used for both numeric and variables simultaneously.
<code>topcount.long</code>	If <code>measures.type = factor</code> , you can get the top counts in long format for plotting purposes. (Default: <code>topcount.long = FALSE</code>).
<code>k</code>	Number of digits after decimal point (should be an integer) (Default: <code>k = 3</code>).
<code>...</code>	Currently ignored.

Value

Dataframe with descriptive statistics for numeric variables (n, mean, sd, median, min, max).

Examples

```
# for reproducibility
set.seed(123)

# another possibility
groupedstats::grouped_summary(
  data = iris,
  grouping.vars = Species,
  measures = Sepal.Length:Petal.Width,
  measures.type = "numeric"
)

# if no measures are chosen, all relevant columns will be summarized
groupedstats::grouped_summary(
  data = ggplot2::msleep,
  grouping.vars = vore,
  measures.type = "factor"
)

# for factors, you can also convert the dataframe to a long format with counts
groupedstats::grouped_summary(
  data = ggplot2::msleep,
  grouping.vars = c(vore),
  measures = c(genus:order),
  measures.type = "factor",
  topcount.long = TRUE
)
```

<code>grouped_ttest</code>	<i>Function to run t-test on multiple variables across multiple grouping variables.</i>
----------------------------	---

Description

Function to run *t*-test on multiple variables across multiple grouping variables.

Usage

```
grouped_ttest(  
  data,  
  dep.vars,  
  indep.vars,  
  grouping.vars,  
  paired = FALSE,  
  var.equal = FALSE  
)
```

Arguments

<code>data</code>	Dataframe from which variables are to be taken.
<code>dep.vars</code>	List dependent variables for a t -test (y in $y \sim x$).
<code>indep.vars</code>	List independent variables for a t -test (x in $y \sim x$).
<code>grouping.vars</code>	List of grouping variables.
<code>paired</code>	A logical indicating whether you want a paired t -test (Default: <code>paired = FALSE</code> ; independent t -test, i.e.).
<code>var.equal</code>	A logical variable indicating whether to treat the two variances as being equal. If <code>TRUE</code> , then the pooled variance is used to estimate the variance otherwise the Welch (or Satterthwaite) approximation to the degrees of freedom is used (Default: <code>var.equal = FALSE</code> ; Welch's t -test, i.e.).

Value

A tibble dataframe with tidy results from t -test analyses.

Examples

```
# for reproducibility  
set.seed(123)  
  
groupedstats::grouped_ttest(  
  data = dplyr::filter(.data = ggplot2::diamonds, color == "E" | color == "J"),  
  dep.vars = c(carat, price, depth),  
  indep.vars = color,  
  grouping.vars = clarity,  
  paired = FALSE,  
  var.equal = FALSE  
)
```

grouped_wilcox	<i>Function to run two-sample Wilcoxon tests on multiple variables across multiple grouping variables.</i>
----------------	--

Description

Function to run two-sample Wilcoxon tests on multiple variables across multiple grouping variables.
Running Wilcox test across multiple grouping variables.

Usage

```
grouped_wilcox(  
  data,  
  dep.vars,  
  indep.vars,  
  grouping.vars,  
  paired = FALSE,  
  correct = TRUE  
)
```

Arguments

data	Dataframe from which variables are to be taken.
dep.vars	List dependent variables for a two-sample Wilcoxon tests (y in $y \sim x$).
indep.vars	List independent variables for a two-sample Wilcoxon tests (x in $y \sim x$).
grouping.vars	List of grouping variables (if NULL, the entire dataframe will be used).
paired	A logical indicating whether you want a paired two-sample Wilcoxon tests (Default: paired = FALSE).
correct	A logical indicating whether to apply continuity correction in the normal approximation for the p-value (Default: correct = TRUE).

Value

A tibble dataframe with tidy results from two-sample Wilcoxon tests analyses.

See Also

[grouped_tidy](#)

Examples

```
# for reproducibility  
set.seed(123)  
  
# only with one grouping variable  
groupedstats::grouped_wilcox(  
  data = iris,  
  dep.vars = "sepal.length",  
  indep.vars = "sepal.width",  
  grouping.vars = "species",  
  paired = FALSE,  
  correct = TRUE  
)
```

```

data = dplyr::filter(.data = ggplot2::diamonds, color == "E" | color == "J"),
dep.vars = depth:table,
indep.vars = color,
grouping.vars = clarity,
paired = FALSE
)

```

lm_effsize_ci	<i>Confidence intervals for (partial) eta-squared and omega-squared for linear models.</i>
---------------	--

Description

This function will convert a linear model object to a dataframe containing statistical details for all effects along with effect size measure and its confidence interval. For more details, see `effectsize::eta_squared` and `effectsize::omega_squared`.

Usage

```
lm_effsize_ci(object, effsize = "eta", partial = TRUE, conf.level = 0.95, ...)
```

Arguments

object	The linear model object (can be of class <code>lm</code> , <code>aov</code> , <code>anova</code> , or <code>aovlist</code>).
effsize	Character describing the effect size to be displayed: "eta" (default) or "omega".
partial	Logical that decides if partial eta-squared or omega-squared are returned (Default: TRUE). If FALSE, eta-squared or omega-squared will be returned. Valid only for objects of class <code>lm</code> , <code>aov</code> , <code>anova</code> , or <code>aovlist</code> .
conf.level	Numeric specifying Level of confidence for the confidence interval (Default: 0.95).
...	Ignored.

Value

A dataframe with results from `stats::lm()` with partial eta-squared, omega-squared, and bootstrapped confidence interval for the same.

Author(s)

Indrajeet Patil

Examples

```
# for reproducibility
set.seed(123)

# model
mod <-
  stats::aov(
    formula = mpg ~ wt + qsec + Error(displ / am),
    data = mtcars
  )

# dataframe with effect size and confidence intervals
groupedstats::lm_effsize_ci(mod)
```

lm_effsize_standardizer

Standardize a dataframe with effect sizes for aov, lm, aovlist, etc. objects.

Description

The difference between `lm_effsize_ci` and `lm_effsize_standardizer` is that the former has more opinionated column naming, while the latter doesn't. The latter can thus be more helpful in writing a wrapper around this function.

Usage

```
lm_effsize_standardizer(
  object,
  effsize = "eta",
  partial = TRUE,
  conf.level = 0.95,
  ...
)
```

Arguments

<code>object</code>	The linear model object (can be of class <code>lm</code> , <code>aov</code> , <code>anova</code> , or <code>aovlist</code>).
<code>effsize</code>	Character describing the effect size to be displayed: "eta" (default) or "omega".
<code>partial</code>	Logical that decides if partial eta-squared or omega-squared are returned (Default: TRUE). If FALSE, eta-squared or omega-squared will be returned. Valid only for objects of class <code>lm</code> , <code>aov</code> , <code>anova</code> , or <code>aovlist</code> .
<code>conf.level</code>	Numeric specifying Level of confidence for the confidence interval (Default: 0.95).
<code>...</code>	Ignored.

Examples

```
set.seed(123)
groupedstats::lm_effsize_standardizer(
  object = stats::lm(formula = brainwt ~ vore, data = ggplot2::msleep),
  effsize = "eta",
  partial = FALSE,
  conf.level = 0.99
)
```

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