

Package ‘colleyRstats’

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Type Package

Title Functions to Streamline Statistical Analysis and Reporting

Version 0.1.1

Description Built upon popular R packages such as 'ggstatsplot' and 'ARTool', this collection offers a wide array of tools for simplifying reproducible analyses, generating high-quality visualizations, and producing 'APA'-compliant outputs. The primary goal of this package is to significantly reduce repetitive coding efforts, allowing you to focus on interpreting results. Whether you're dealing with ANOVA assumptions, reporting effect sizes, or creating publication-ready visualizations, this package makes these tasks easier.

URL <https://github.com/M-Colley/colleyRstats>

BugReports <https://github.com/M-Colley/colleyRstats/issues>

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add_pareto_emoa_column
Add PARETO_EMOA Column to a Data Frame

Description

This function calculates the Pareto front using emoa for a given set of objectives in a data frame and adds a new column, PARETO_EMOA, which indicates whether each row in the data frame belongs to the Pareto front.

Usage

```
add_pareto_emoa_column(data, objectives)
```

Arguments

<code>data</code>	A data frame containing the data, including the objective columns.
<code>objectives</code>	A character vector specifying the names of the objective columns in data. These columns should be numeric and will be used to calculate the Pareto front.

Value

A data frame with the same columns as data, along with an additional column, PARETO_EMOA, which is TRUE for rows that are on the Pareto front and FALSE otherwise.

Examples

```
# Define objective columns
objectives <- c("trust", "predictability", "perceivedSafety", "Comfort")

# Example data frame
main_df <- data.frame(
  trust = runif(10),
  predictability = runif(10),
  perceivedSafety = runif(10),
  Comfort = runif(10)
)
```

```
# Add the Pareto front column
main_df <- add_pareto_emoa_column(data = main_df, objectives)
head(main_df)
```

```
add_pareto_moocore_column
```

Add PARETO_MOOCORE Column to a Data Frame

Description

This function calculates the Pareto front using moocore for a given set of objectives in a data frame and adds a new column, PARETO_MOOCORE, which indicates whether each row in the data frame belongs to the Pareto front.

Usage

```
add_pareto_moocore_column(data, objectives)
```

Arguments

<code>data</code>	A data frame containing the data, including the objective columns.
<code>objectives</code>	A character vector specifying the names of the objective columns in data. These columns should be numeric and will be used to calculate the Pareto front.

Value

A data frame with the same columns as `data`, along with an additional column, PARETO_MOOCORE, which is TRUE for rows that are on the Pareto front and FALSE otherwise.

Examples

```
# Define objective columns
objectives <- c("trust", "predictability", "perceivedSafety", "Comfort")

# Example data frame
main_df <- data.frame(
  trust = runif(10),
  predictability = runif(10),
  perceivedSafety = runif(10),
  Comfort = runif(10)
)

# Add the Pareto front column
main_df <- add_pareto_moocore_column(data = main_df, objectives)
head(main_df)
```

analyze_and_report *Analyze one dependent variable and produce everything a paper needs*

Description

One-call pipeline for a single dependent variable: checks the assumptions (producing a ready-made methods sentence via [assumption_methods_text\(\)](#)), builds the matching **ggstatsplot** figure with automatic parametric/non-parametric selection, reports the omnibus test via [reportggstatsplot\(\)](#), and – for more than two groups – reports the significant post-hoc comparisons via [reportggstatsplotPostHoc\(\)](#).

Usage

```
analyze_and_report(
  data,
  dv,
  iv,
  design = c("between", "within"),
  ylab = dv,
  xlabel = NULL,
  plotType = "boxviolin",
  sink_to = NULL
)
```

Arguments

data	the data frame
dv	the dependent variable (column name as string)
iv	the independent variable (column name as string); coerced to a factor if it is not one already
design	"between" for between-subjects data (default) or "within" for repeated measures
ylab	label for the dependent variable; defaults to dv
xlabels	optional labels for the x-axis
plotType	either "box", "violin", or "boxviolin" (default)
sink_to	optional path of a .tex file; the methods sentence, omnibus result, and post-hoc sentences are written there so a manuscript can <code>\input{}</code> them

Value

Invisibly returns a list with components `plot` (the `ggplot`), `methods` (assumption-check sentence), `text` (omnibus result), `posthoc` (post-hoc sentences, or `NULL` for two groups), and `sentences` (all text combined, in manuscript order).

Examples

```
result <- analyze_and_report(mtcars, dv = "mpg", iv = "cyl")
result$plot
```

assumption_methods_text

Methods-section sentence justifying the test selection

Description

Runs the group-wise Shapiro-Wilk normality check (and optionally Levene's test for homogeneity of variances) and turns the outcome into a ready-made methods-section sentence, including the relevant statistics. This is the justification reviewers expect next to the choice of a parametric or non-parametric test.

Usage

```
assumption_methods_text(data, x, y, include_homogeneity = FALSE)
```

Arguments

data	the data frame
x	the grouping variable (column name as string)
y	the dependent variable (column name as string)
include_homogeneity	whether to also report Levene's test. Useful for between-subjects designs. Default FALSE.

Value

Invisibly returns the sentence(s) as a single string; the text is also emitted via `message()`.

Examples

```
set.seed(1)
d <- data.frame(g = rep(c("A", "B"), each = 20), v = rnorm(40))
assumption_methods_text(d, x = "g", y = "v")
```

`checkAssumptionsForAnova`

Check the assumptions for an ANOVA with a variable number of factors: Normality and Homogeneity of variance assumption.

Description

Check the assumptions for an ANOVA with a variable number of factors: Normality and Homogeneity of variance assumption.

Usage

```
checkAssumptionsForAnova(data, y, factors)
```

```
check_assumptions_anova(data, y, factors)
```

Arguments

<code>data</code>	the data frame
<code>y</code>	The dependent variable for which assumptions should be checked
<code>factors</code>	A character vector of factor names

Value

A message indicating whether to use parametric or non-parametric ANOVA

Examples

```
set.seed(123)

main_df <- data.frame(
  tlx_mental = rnorm(40),
  Video = factor(rep(c("A", "B"), each = 20)),
  DriverPosition = factor(rep(c("Left", "Right"), times = 20))
)

checkAssumptionsForAnova(
  data = main_df,
  y = "tlx_mental",
  factors = c("Video", "DriverPosition")
)
```

`check_homogeneity_by_group`*Check homogeneity of variances across groups*

Description

Check homogeneity of variances across groups

Usage

```
check_homogeneity_by_group(data, x, y)
```

Arguments

<code>data</code>	the data frame
<code>x</code>	the grouping variable (column name as string)
<code>y</code>	the dependent variable (column name as string)

Value

TRUE if Levene's test is non-significant ($p \geq .05$), FALSE otherwise. The Levene test result (columns `df1`, `df2`, `statistic`, `p`) is attached in the "test" attribute, e.g. for use in a methods section via [assumption_methods_text\(\)](#).

`check_normality_by_group`*Check normality for groups*

Description

Check normality for groups

Usage

```
check_normality_by_group(data, x, y)
```

Arguments

<code>data</code>	the data frame
<code>x</code>	the x column
<code>y</code>	the y column

Value

TRUE if all groups are normal, FALSE otherwise. The per-group Shapiro-Wilk statistics are attached as a data frame in the "tests" attribute (columns: group, W, p_value), e.g. for use in a methods section via `assumption_methods_text()`. For groups with more than 5000 non-missing values, Shapiro-Wilk is computed on a random sample of 5000 observations (a warning is emitted); the returned value still reflects that sampled test. Because the sample is drawn randomly, results for such large groups are not reproducible unless a seed is set beforehand.

`cite_methods`*Citations and methods boilerplate for the analyses used*

Description

Prints a ready-made methods phrase plus the BibTeX entries for the R packages behind the requested analysis methods, so a manuscript's methods section and bibliography can be filled in one step.

Usage

```
cite_methods(methods = c("ggstatsplot", "effectsize"), bibtex = TRUE)
```

Arguments

<code>methods</code>	Character vector of analysis methods to cite. Any of "art" (Aligned Rank Transform via ARTool), "dunn" (Dunn's test via FSA), "nparld" (nparLD), "ggstatsplot", "effectsize", and "colleyrstats" (this package).
<code>bibtex</code>	whether to include the BibTeX entries. Default TRUE.

Value

Invisibly returns the generated lines as a character vector; the text is also emitted via `message()`. Methods whose package is not installed are skipped with a message.

Examples

```
cite_methods("ggstatsplot", bibtex = FALSE)
```

colleyRstats_setup *Configure Global R Environment for colleyRstats*

Description

Sets ggplot2 themes and conflict preferences to match the standards used in the colleyRstats workflow.

Usage

```
colleyRstats_setup(  
  set_options = FALSE,  
  set_theme = TRUE,  
  set_conflicts = TRUE,  
  print_citation = TRUE,  
  verbose = TRUE  
)
```

Arguments

set_options	Logical. If TRUE, prints a notice that global options are no longer changed automatically. Default is FALSE.
set_theme	Logical. If TRUE, sets the default ggplot2 theme to <code>see::theme_lucid</code> with custom modifications. Default is TRUE.
set_conflicts	Logical. If TRUE, sets conflicted preferences to favor dplyr and other tidyverse packages. Default is TRUE.
print_citation	Logical. If TRUE, prints the citation information for this package. Default is TRUE.
verbose	Logical. If TRUE, emit informational messages. Default is TRUE.

Value

Invisibly returns NULL.

Examples

```
# Runs everywhere, no extra packages, no session side effects  
colleyRstats::colleyRstats_setup(  
  set_options = FALSE,  
  set_theme = FALSE,  
  set_conflicts = FALSE,  
  print_citation = FALSE,  
  verbose = FALSE  
)  
  
# Full setup (requires suggested packages; changes session defaults)
```

```
if (requireNamespace("ggplot2", quietly = TRUE) &&
    requireNamespace("see", quietly = TRUE)) {
  local({
    old_theme <- ggplot2::theme_get()
    on.exit(ggplot2::theme_set(old_theme), add = TRUE)

    colleyRstats::colleyRstats_setup(
      set_options = FALSE,
      set_conflicts = FALSE, # avoid persisting conflict prefs in checks
      print_citation = FALSE,
      verbose = TRUE
    )

    ggplot2::ggplot(mtcars, ggplot2::aes(mpg, wt)) +
      ggplot2::geom_point()
  })
}
```

data the data frame *Replace values across a data frame*

Description

Replace all occurrences of given values in all columns of a data frame.

The data data frame contains a collection of records, with attributes organized in columns. It may include various types of values, such as numerical, categorical, or textual data.

Usage

```
replace_values(data, to_replace, replace_with)
```

Arguments

<code>data</code>	The input data frame to be modified.
<code>to_replace</code>	A vector of values to be replaced within the data frame. This must be the same length as <code>replace_with</code> .
<code>replace_with</code>	A vector of corresponding replacement values. This must be the same length as <code>to_replace</code> .

Value

Modified data frame with specified values replaced.

Examples

```
data <- data.frame(
  q1 = c("neg2", "neg1", "0"),
  q2 = c("1", "neg2", "neg1")
)

replace_values(
  data,
  to_replace = c("neg2", "neg1"),
  replace_with = c("-2", "-1")
)
```

debug_contr_error *Debug contrast errors in ANOVA-like models*

Description

Debug contrast errors in ANOVA-like models

Usage

```
debug_contr_error(dat, subset_vec = NULL)
```

Arguments

dat A data frame of predictors.
subset_vec Optional logical or numeric index vector used to subset rows before checks.

Value

A list with two elements:

nlevels Integer vector giving the number of levels for each factor variable in `dat`.

levels List of factor level labels for each factor variable in `dat`.

Examples

```
dat <- data.frame(
  group = factor(rep(letters[1:3], each = 3)),
  score = rnorm(9)
)

debug_contr_error(dat = dat)
```

generateEffectPlot	<i>Function to define a plot, either showing the main or interaction effect in bold.</i>
--------------------	--

Description

Function to define a plot, either showing the main or interaction effect in bold.

Usage

```
generateEffectPlot(  
  data,  
  x,  
  y,  
  fillColourGroup,  
  ytext = "testylab",  
  xtext = "testxlab",  
  legendPos = c(0.1, 0.23),  
  legendHeading = NULL,  
  shownEffect = "main",  
  effectLegend = FALSE,  
  effectDescription = NULL,  
  xLabelsOverwrite = NULL,  
  useLatexMarkup = FALSE,  
  numberColors = 6  
)
```

```
plot_effect(  
  data,  
  x,  
  y,  
  fillColourGroup,  
  ytext = "testylab",  
  xtext = "testxlab",  
  legendPos = c(0.1, 0.23),  
  legendHeading = NULL,  
  shownEffect = "main",  
  effectLegend = FALSE,  
  effectDescription = NULL,  
  xLabelsOverwrite = NULL,  
  useLatexMarkup = FALSE,  
  numberColors = 6  
)
```

Arguments

data	the data frame
------	----------------

x	factor shown on the x-axis
y	dependent variable
fillColourGroup	group to color
ytext	label for y-axis
xtext	label for x-axis
legendPos	position for legend
legendHeading	custom heading for legend
shownEffect	either "main" or "interaction"
effectLegend	TRUE: show legend for effect (Default: FALSE)
effectDescription	custom label for effect
xLabelsOverwrite	custom labels for x-axis
useLatexMarkup	use latex font and markup
numberColors	number of colors

Value

a plot

Examples

```
set.seed(123)
main_df <- data.frame(
  strategy = factor(rep(c("A", "B"), each = 20)),
  Emotion   = factor(rep(c("Happy", "Sad"), times = 20)),
  trust_mean = rnorm(40, mean = 5, sd = 1)
)

generateEffectPlot(
  data = main_df,
  x = "strategy",
  y = "trust_mean",
  fillColourGroup = "Emotion",
  ytext = "Trust",
  xtext = "Strategy",
  legendPos = c(0.1, 0.23)
)
```

generateMoboPlot	<i>Generate a Multi-objective Optimization Plot</i>
------------------	---

Description

This function generates a multi-objective optimization plot using ggplot2. The plot visualizes the relationship between the x and y variables, grouping and coloring by a fill variable, with the option to customize legend position, labels, and annotation of sampling and optimization phases.

Usage

```
generateMoboPlot(  
  data,  
  x,  
  y,  
  fillColourGroup = "ConditionID",  
  ytext,  
  legendPos = c(0.65, 0.85),  
  numberSamplingSteps = 5,  
  labelPosFormulaY = "top",  
  verticalLinePosY = 0.75  
)  
  
plot_mobo(  
  data,  
  x,  
  y,  
  fillColourGroup = "ConditionID",  
  ytext,  
  legendPos = c(0.65, 0.85),  
  numberSamplingSteps = 5,  
  labelPosFormulaY = "top",  
  verticalLinePosY = 0.75  
)
```

Arguments

data	A data frame containing the data to be plotted.
x	A string representing the column name in data to be used for the x-axis. Can be either numeric or factor.
y	A string representing the column name in data to be used for the y-axis. This should be a numeric variable.
fillColourGroup	A string representing the column name in data that defines the fill color grouping for the plot. Default is "ConditionID".

ytext	A custom label for the y-axis. If not provided, the y-axis label will be the title-cased version of y.
legendPos	A numeric vector of length 2 specifying the position of the legend inside the plot. Default is <code>c(0.65, 0.85)</code> .
numberSamplingSteps	An integer specifying the number of initial sampling steps before the optimization phase begins. Default is 5.
labelPosFormulaY	A string specifying the vertical position of the polynomial equation label in the plot. Acceptable values are "top", "center", or "bottom". Default is "top".
verticalLinePosY	A numeric value of the y-coordinate where the "sampling" and "optimization" line should be drawn.

Value

A ggplot object representing the multi-objective optimization plot, ready to be rendered.

Examples

```
library(ggplot2)
library(ggpmisc)

# Example with numeric x-axis
df <- data.frame(
  x = 1:20,
  y = rnorm(20),
  ConditionID = rep(c("A", "B"), 10)
)
generateMoboPlot(df, x = "x", y = "y")

# Example with factor x-axis
df <- data.frame(
  x = factor(rep(1:5, each = 4)),
  y = rnorm(20),
  ConditionID = rep(c("A", "B"), 10)
)
generateMoboPlot(df, x = "x", y = "y", numberSamplingSteps = 3)
```

generateMoboPlot2 *Generate a Multi-objective Optimization Plot*

Description

This function generates a multi-objective optimization plot using ggplot2. The plot visualizes the relationship between the x and y variables, grouping and coloring by a fill variable, with the option to customize legend position, labels, and annotation of sampling and optimization phases. Appropriate if you use <https://github.com/Pascal-Jansen/Bayesian-Optimization-for-Unity> in version 1.1.0 or higher.

Usage

```
generateMoboPlot2(
  data,
  x = "Iteration",
  y,
  phaseCol = "Phase",
  fillColourGroup = "ConditionID",
  ytext,
  legendPos = c(0.65, 0.85),
  labelPosFormulaY = "top",
  labelPosFormulaX = "left",
  horizontalLinePosY = 0.75,
  horizontalLineDistToText = 0.3,
  fillLabels = NULL,
  annotationTextSize = 5
)
```

```
plot_mobo2(
  data,
  x = "Iteration",
  y,
  phaseCol = "Phase",
  fillColourGroup = "ConditionID",
  ytext,
  legendPos = c(0.65, 0.85),
  labelPosFormulaY = "top",
  labelPosFormulaX = "left",
  horizontalLinePosY = 0.75,
  horizontalLineDistToText = 0.3,
  fillLabels = NULL,
  annotationTextSize = 5
)
```

Arguments

<code>data</code>	A data frame containing the data to be plotted.
<code>x</code>	A string representing the column name in data to be used for the x-axis. Can be either numeric or factor. Default is "Iteration".
<code>y</code>	A string representing the column name in data to be used for the y-axis. This should be a numeric variable.
<code>phaseCol</code>	the name of the column for the color of the phase (sampling or optimization)
<code>fillColourGroup</code>	A string representing the column name in data that defines the fill color grouping for the plot. Default is "ConditionID".
<code>ytext</code>	A custom label for the y-axis. If not provided, the y-axis label will be the title-cased version of y.

legendPos	A numeric vector of length 2 specifying the position of the legend inside the plot. Default is <code>c(0.65, 0.85)</code> .
labelPosFormulaY	A string specifying the vertical position of the polynomial equation label in the plot. Acceptable values are "top", "center", or "bottom". Default is "top".
labelPosFormulaX	A string specifying the position of the polynomial equation label in the plot. Acceptable values are "left", "center", or "right". Default is "left".
horizontalLinePosY	A numeric value of the y-coordinate where the "sampling" and "optimization" line should be drawn. Default is 0.75
horizontalLineDistToText	A numeric value of the y-coordinate where the "sampling" and "optimization" text should be drawn below the line. Default is 0.3
fillLabels	An optional named character vector mapping raw factor levels to display labels for the fill/colour legend (e.g. <code>c("value_only" = "Value Only", "llm_only" = "LLM Only")</code>). If NULL (default), the original factor levels are used as-is.
annotationTextSize	numeric. The font size for embedded text annotations inside the plot (e.g., "Sampling", "Optimization" labels, and the regression equations). Default is 5.0.

Value

A ggplot object representing the multi-objective optimization plot, ready to be rendered.

Examples

```
library(ggplot2)
library(ggpmisc)

# Example with numeric x-axis
df <- data.frame(
  x = 1:20,
  y = rnorm(20),
  ConditionID = rep(c("A", "B"), 10),
  Phase = rep(c("Sampling", "Optimization"), 10)
)
generateMoboPlot2(data = df, x = "x", y = "y")
```

ggbetweenstatsWithPriorNormalityCheck

Check the data's distribution. If non-normal, take the non-parametric variant of ggbetweenstats. x and y have to be in parentheses, e.g., "ConditionID".

Description

Check the data's distribution. If non-normal, take the non-parametric variant of *ggbetweenstats*. *x* and *y* have to be in parentheses, e.g., "ConditionID".

Usage

```
ggbetweenstatsWithPriorNormalityCheck(  
  data,  
  x,  
  y,  
  ylab,  
  xlabel = NULL,  
  showPairwiseComp = TRUE,  
  plotType = "boxviolin"  
)
```

```
plot_between_stats(  
  data,  
  x,  
  y,  
  ylab,  
  xlabel = NULL,  
  showPairwiseComp = TRUE,  
  plotType = "boxviolin"  
)
```

Arguments

<code>data</code>	the data frame
<code>x</code>	the independent variable, most likely "ConditionID"
<code>y</code>	the dependent variable under investigation
<code>ylab</code>	label to be shown for the dependent variable
<code>xlabel</code>	labels to be used for the x-axis
<code>showPairwiseComp</code>	whether to show pairwise comparisons, TRUE as default
<code>plotType</code>	either "box", "violin", or "boxviolin" (default)

Value

A ggplot object produced by `ggstatsplot::ggbetweenstats`, which can be printed or further modified with `+`.

Examples

```
set.seed(123)  
  
# Toy within-subject style data
```

```

main_df <- data.frame(
  Participant = factor(rep(1:20, each = 3)),
  CondID      = factor(rep(c("A", "B", "C"), times = 20)),
  tlx_mental  = rnorm(60, mean = 50, sd = 10)
)

# Custom x-axis labels
labels_xlab <- c("Condition A", "Condition B", "Condition C")

ggbetweenstatsWithPriorNormalityCheck(
  data = main_df,
  x = "CondID",
  y = "tlx_mental", ylab = "Mental Demand",
  xlabel = labels_xlab,
  showPairwiseComp = TRUE
)

```

```
ggbetweenstatsWithPriorNormalityCheckAsterisk
```

Check the data's distribution. If non-normal, take the non-parametric variant of ggbetweenstats. x and y have to be in parentheses, e.g., "ConditionID".

Description

Check the data's distribution. If non-normal, take the non-parametric variant of *ggbetweenstats*. x and y have to be in parentheses, e.g., "ConditionID".

Usage

```

ggbetweenstatsWithPriorNormalityCheckAsterisk(
  data,
  x,
  y,
  ylab,
  xlabel,
  plotType = "boxviolin"
)

plot_between_stats_asterisk(data, x, y, ylab, xlabel, plotType = "boxviolin")

```

Arguments

data	the data frame
x	the independent variable, most likely "ConditionID"
y	the dependent variable under investigation

ylab	label to be shown for the dependent variable
xlabels	labels to be used for the x-axis
plotType	either "box", "violin", or "boxviolin" (default)

Value

A ggplot object produced by `ggstatsplot::ggbetweenstats` with additional significance annotations, which can be printed or modified.

Examples

```
set.seed(123)

# Toy within-subject style data
main_df <- data.frame(
  Participant = factor(rep(1:20, each = 3)),
  CondID      = factor(rep(c("A", "B", "C"), times = 20)),
  tlx_mental  = rnorm(60, mean = 50, sd = 10)
)

# Custom x-axis labels
labels_xlab <- c("Condition A", "Condition B", "Condition C")

ggbetweenstatsWithPriorNormalityCheckAsterisk(
  data = main_df,
  x = "CondID", y = "tlx_mental", ylab = "Mental Demand", xlabels = labels_xlab
)
```

ggwithinstatsWithPriorNormalityCheck

Check the data's distribution. If non-normal, take the non-parametric variant of `ggwithinstats`. `x` and `y` have to be in parentheses, e.g., "ConditionID".

Description

Check the data's distribution. If non-normal, take the non-parametric variant of `ggwithinstats`. `x` and `y` have to be in parentheses, e.g., "ConditionID".

Usage

```
ggwithinstatsWithPriorNormalityCheck(
  data,
  x,
  y,
```

```

  ylab,
  xlabels = NULL,
  showPairwiseComp = TRUE,
  plotType = "boxviolin"
)

plot_within_stats(
  data,
  x,
  y,
  ylab,
  xlabels = NULL,
  showPairwiseComp = TRUE,
  plotType = "boxviolin"
)

```

Arguments

<code>data</code>	the data frame
<code>x</code>	the independent variable, most likely "ConditionID"
<code>y</code>	the dependent variable under investigation
<code>ylab</code>	label to be shown for the dependent variable
<code>xlabels</code>	labels to be used for the x-axis
<code>showPairwiseComp</code>	whether to show pairwise comparisons, TRUE as default
<code>plotType</code>	either "box", "violin", or "boxviolin" (default)

Value

A ggplot object produced by `ggstatsplot::ggwithinstats` with additional significance annotations, which can be printed or modified.

Examples

```

#' set.seed(123)

# Toy within-subject style data
main_df <- data.frame(
  Participant = factor(rep(1:20, each = 3)),
  CondID      = factor(rep(c("A", "B", "C"), times = 20)),
  tlx_mental  = rnorm(60, mean = 50, sd = 10)
)

# Custom x-axis labels
labels_xlab <- c("Condition A", "Condition B", "Condition C")

ggwithinstatsWithPriorNormalityCheck(

```

```

data = main_df,
x = "CondID", y = "tlx_mental",
ylab = "Mental Demand",
xlabels = labels_xlab,
showPairwiseComp = TRUE
)

```

```
ggwithinstatsWithPriorNormalityCheckAsterisk
```

Check the data's distribution. If non-normal, take the non-parametric variant of ggwithinstats. x and y have to be in parentheses, e.g., "ConditionID". Add Asterisks instead of p-values.

Description

Check the data's distribution. If non-normal, take the non-parametric variant of *ggwithinstats*. x and y have to be in parentheses, e.g., "ConditionID". Add Asterisks instead of p-values.

Usage

```

ggwithinstatsWithPriorNormalityCheckAsterisk(
  data,
  x,
  y,
  ylab,
  xlabels,
  plotType = "boxviolin"
)

plot_within_stats_asterisk(data, x, y, ylab, xlabels, plotType = "boxviolin")

```

Arguments

data	the data frame
x	the independent variable, most likely "ConditionID"
y	the dependent variable under investigation
ylab	label to be shown for the dependent variable
xlabels	labels to be used for the x-axis
plotType	either "box", "violin", or "boxviolin" (default)

Value

A ggplot object produced by `ggstatsplot::ggwithinstats` with additional significance annotations, which can be printed or modified.

Examples

```

set.seed(123)

# Toy within-subject style data
main_df <- data.frame(
  Participant = factor(rep(1:20, each = 3)),
  CondID      = factor(rep(c("A", "B", "C"), times = 20)),
  tlx_mental  = rnorm(60, mean = 50, sd = 10)
)

# Custom x-axis labels
labels_xlab <- c("Condition A", "Condition B", "Condition C")

ggwithinstatsWithPriorNormalityCheckAsterisk(
  data = main_df,
  x = "CondID", y = "tlx_mental",
  ylab = "Mental Demand", xlabels = labels_xlab
)

```

latexify_report

Transform text from report::report() into LaTeX-friendly output.

Description

This function transforms the text output from `report::report()` by performing several substitutions to prepare the text for LaTeX typesetting. In particular, it replaces instances of R2, %, and ~ with the corresponding LaTeX code. Additionally, it provides options to:

- Omit bullet items marked as "non-significant" (when `only_sig = TRUE`).
- Remove a concluding note about standardized parameters (when `remove_std = TRUE`).
- Wrap bullet items in a LaTeX `itemize` environment or leave them as plain text (controlled by `itemize`).

Usage

```

latexify_report(
  x,
  print_result = TRUE,
  only_sig = FALSE,
  remove_std = FALSE,
  itemize = TRUE
)

```

Arguments

<code>x</code>	Character vector or a single string containing the report text.
<code>print_result</code>	Logical. If TRUE (default), the formatted text is printed to the console.
<code>only_sig</code>	Logical. If TRUE, bullet items containing "non-significant" are omitted. Default is FALSE.
<code>remove_std</code>	Logical. If TRUE, the final standardized parameters note is removed. Default is FALSE.
<code>itemize</code>	Logical. If TRUE (default), bullet items are wrapped in a LaTeX <code>itemize</code> environment; otherwise the bullet markers are simply removed.

Value

A single string with the LaTeX-friendly formatted report text.

Examples

```
if (requireNamespace("report", quietly = TRUE)) {
  # Simple linear model on the iris dataset
  model <- stats::lm(
    Sepal.Length ~ Sepal.Width + Petal.Length,
    data = datasets::iris
  )

  # Format the report output, showing only significant items, removing the
  # standard note, and wrapping bullet items in an itemize environment.
  report_text <- try(report::report(model), silent = TRUE)
  if (!inherits(report_text, "try-error")) {
    latexify_report(
      report_text,
      only_sig = TRUE,
      remove_std = TRUE,
      itemize = TRUE
    )
  }
}
```

latex_preamble

LaTeX preamble required by the report functions

Description

All report functions emit LaTeX text that relies on a small set of custom commands. This helper prints the complete set, ready to paste into a manuscript preamble, or writes it to a file that can be included with `\input{}` (or renamed to `.sty` and loaded via `\usepackage`).

Usage

```
latex_preamble(path = NULL)
```

Arguments

path Optional path of a .tex file to write the definitions to.

Value

Invisibly returns the macro definitions as a character vector; the text is also emitted via `message()`.

Examples

```
latex_preamble()
```

na.zero	<i>Replace NA values with zero</i>
---------	------------------------------------

Description

Replace NA values with zero

Usage

```
na.zero(x)
```

Arguments

x A vector.

Value

A vector with NAs replaced by zeros.

Examples

```
na.zero(c(NA, 1, NA, 2))
```

normalize	<i>This function normalizes the values in a vector to the range [new_min, new_max] based on their original range [old_min, old_max].</i>
-----------	--

Description

This function normalizes the values in a vector to the range [new_min, new_max] based on their original range [old_min, old_max].

Usage

```
normalize(x_vector, old_min, old_max, new_min, new_max)
```

Arguments

x_vector	A numeric vector that you want to normalize.
old_min	The minimum value in the original scale of the data.
old_max	The maximum value in the original scale of the data.
new_min	The minimum value in the new scale to which you want to normalize the data.
new_max	The maximum value in the new scale to which you want to normalize the data.

Value

A numeric vector with the normalized values.

Examples

```
normalize(c(1, 2, 3, 4, 5), 1, 5, 0, 1)
```

not_empty	<i>Ensure input is not empty</i>
-----------	----------------------------------

Description

Stops execution if x is NULL, empty, or contains only NAs.

Usage

```
not_empty(x, msg = "Input must not be empty.")
```

Arguments

x	The object to check
msg	The error message to display

Value

Invisible TRUE if valid.

not_in	<i>Negate %in% membership</i>
--------	-------------------------------

Description

Negate %in% membership

Usage

```
not_in(x, y)
```

```
x %!in% y
```

Arguments

x	Vector of values to test.
y	Vector of values to match against.

Value

Logical vector indicating non-membership.

n_fun	<i>Build a median/size label for plot annotations</i>
-------	---

Description

Build a median/size label for plot annotations

Usage

```
n_fun(x)
```

Arguments

x	A numeric vector.
---	-------------------

Value

A data frame with the median and label.

pathPrep	<i>Convert Windows paths to R-friendly format</i>
----------	---

Description

Convert Windows paths to R-friendly format

Usage

```
pathPrep(path = "clipboard", read_fn = NULL, write_fn = NULL)
```

Arguments

path	Path to convert or the string "clipboard" to read from the clipboard.
read_fn	Optional custom function to read from the clipboard.
write_fn	Optional custom function to write to the clipboard.

Value

A normalized path string.

remove_outliers_REI	<i>Flag suspicious survey responses via the Response Entropy Index (REI)</i>
---------------------	--

Description

This function takes a data frame, optional header information, variables to consider, and a range for a Likert scale. It then calculates the Response Entropy Index (REI) and flags suspicious entries based on percentiles. Note that no rows are removed; entries are only flagged via the Suspicious column.

Usage

```
remove_outliers_REI(df, header = FALSE, variables = "", range = c(1, 5))
```

Arguments

df	Data frame containing the data.
header	Logical indicating if the data frame has a header. Defaults to FALSE.
variables	Character string specifying which variables to consider, separated by commas.
range	Numeric vector of length 2 specifying the range of the Likert scale (used to sanity-check the responses). Defaults to c(1, 5).

Details

Missing responses are ignored when tallying answers. Responses outside the declared Likert range trigger a warning (they often indicate mis-coded data) but are still included in the REI computation.

For more information on the REI method, refer to: [Response Entropy Index Method](#)

Value

A data frame with calculated REI, percentile, and a 'Suspicious' flag.

Examples

```
df <- data.frame(var1 = c(1, 2, 3), var2 = c(2, 3, 4))
result <- remove_outliers_REI(df, TRUE, "var1,var2", c(1, 5))
```

reportART

Generate the Latex-text based on the ARTool (see <https://github.com/mjskay/ARTool>). The ART result must be piped into an anova(). Only significant main and interaction effects are reported. P-values are rounded for the third digit. Attention: Effect sizes are not calculated! Attention: the independent variables of the formula and the term specifying the participant must be factors (i.e., use as.factor()).

Description

To easily copy and paste the results to your manuscript, the following commands must be defined in

Latex: `\newcommand{\F}[3]{\F({#1},{#2})={#3}} \newcommand{\p}{\textit{p=}} \newcommand{\pminor}{\textit{p=}}`

Usage

```
reportART(
  model,
  dv = "Testdependentvariable",
  write_to_clipboard = FALSE,
  sink_to = NULL
)
```

```
report_art(
  model,
  dv = "Testdependentvariable",
  write_to_clipboard = FALSE,
  sink_to = NULL
)
```

Arguments

model	the model of the art
dv	the name of the dependent variable that should be reported
write_to_clipboard	whether to write to the clipboard
sink_to	optional path of a .tex file to write the sentences to, so a manuscript can <code>\input{}</code> them

Value

Invisibly returns the reported sentence(s) as a character vector; the text is also emitted via `message()`.

Examples

```
if (requireNamespace("ARTool", quietly = TRUE)) {
  set.seed(123)

  main_df <- data.frame(
    tlx_mental = stats::rnorm(80),
    Video      = factor(rep(c("A", "B"), each = 40)),
    gesture    = factor(rep(c("G1", "G2"), times = 40)),
    eHMI       = factor(rep(c("On", "Off"), times = 40)),
    UserID     = factor(rep(1:20, each = 4))
  )

  art_model <- ARTool::art(
    tlx_mental ~ Video * gesture * eHMI +
      Error(UserID / (gesture * eHMI)),
    data = main_df
  )

  model_anova <- stats::anova(art_model)
  reportART(model_anova, dv = "mental demand")
}
```

 reportArtCon

Report significant ART contrasts (art.con) as LaTeX text

Description

Companion to `reportDunnTest()` for aligned-rank-transform (ART) models. It extracts the significant pairwise comparisons produced by `ARTool::art.con()` (an **emmeans** contrast grid), computes the mean and standard deviation of the groups involved from the raw data, and prints LaTeX-formatted sentences.

Usage

```

reportArtCon(
  ac,
  data,
  iv = "testiv",
  dv = "testdv",
  paired = FALSE,
  id = NULL,
  sink_to = NULL
)

report_art_con(
  ac,
  data,
  iv = "testiv",
  dv = "testdv",
  paired = FALSE,
  id = NULL,
  sink_to = NULL
)

```

Arguments

ac	the contrast object returned by <code>ARTool::art.con()</code> (or its <code>summary()</code>)
data	the raw data frame used to fit the model
iv	independent variable (the contrasted factor)
dv	dependent variable
paired	whether to compute the rank-biserial effect size for paired (within-subjects) data. Defaults to FALSE. When TRUE, <code>id</code> is required.
id	the subject/pairing column, used only when <code>paired = TRUE</code> . Replicate trials per subject and condition are averaged before pairing.
sink_to	optional path of a <code>.tex</code> file to write the sentences to, so a manuscript can <code>\input{}</code> them

Details

The p-values are taken as-is from the contrast object, i.e. they are already adjusted by whatever `adjust` was passed to `art.con()` (e.g. "holm"). The effect size is the rank-biserial correlation computed from the raw data. ART is most often used for within-subjects designs; pass `paired = TRUE` together with `id` (the subject column) to obtain the paired rank-biserial effect size.

Attention: `ac` must be a pairwise contrast over a single factor `iv` (e.g. `art.con(model, ~ interaction_mode, adjust = "holm")`).

Required commands in LaTeX: `\newcommand{\padjminor}{\textit{p}_{adj}<$}} \newcommand{\padj}{\textit{p}_{adj}}`
`\newcommand{\rankbiserial}[1]{r_{rb} = #1$}`

Value

Invisibly returns the reported sentence(s) as a character vector; the text is also emitted via `message()`.

Examples

```
if (requireNamespace("ARTool", quietly = TRUE) &&
    requireNamespace("emmeans", quietly = TRUE)) {
  set.seed(123)
  n <- 20
  df <- data.frame(
    UserID = factor(rep(seq_len(n), times = 3)),
    mode   = factor(rep(c("Hand", "Eye", "Both"), each = n)),
    prime  = factor(rep(rep(c("A", "B"), each = n / 2), times = 3))
  )
  df$score <- as.numeric(df$mode) * 2 + stats::rnorm(nrow(df))

  m <- ARTool::art(score ~ mode * prime + Error(UserID / mode), data = df)
  ac <- ARTool::art.con(m, ~ mode, adjust = "holm")
  reportArtCon(ac, data = df, iv = "mode", dv = "score", paired = TRUE, id = "UserID")
}
```

reportArtConTable	<i>Report ART contrasts (art.con) as a LaTeX table. Customizable with sensible defaults. Companion to reportDunnTestTable().</i>
-------------------	--

Description

Required commands in LaTeX: `\newcommand{\padjminor}{\textit{p}_{adj}<$}` `\newcommand{\padj}{\textit{p}_{adj}}` `\newcommand{\rankbiseria1}[1]{r_{rb} = #1$}`

Usage

```
reportArtConTable(
  ac,
  data,
  iv = "testiv",
  dv = "testdv",
  paired = FALSE,
  id = NULL,
  orderByP = FALSE,
  numberDigitsForPValue = 4,
  latexSize = "small",
  orderText = TRUE,
  sink_to = NULL
)

report_art_con_table(
```

```

ac,
data,
iv = "testiv",
dv = "testdv",
paired = FALSE,
id = NULL,
orderByP = FALSE,
numberDigitsForPValue = 4,
latexSize = "small",
orderText = TRUE,
sink_to = NULL
)

```

Arguments

ac	the contrast object returned by <code>ARTool::art.con()</code> (or its <code>summary()</code>)
data	the raw data frame used to fit the model
iv	independent variable (the contrasted factor)
dv	dependent variable
paired	whether to compute the rank-biserial effect size for paired (within-subjects) data. Defaults to FALSE. When TRUE, <code>id</code> is required.
id	the subject/pairing column, used only when <code>paired = TRUE</code> . Replicate trials per subject and condition are averaged before pairing.
orderByP	whether to order by the p value
numberDigitsForPValue	the number of digits to show
latexSize	which size for the text
orderText	whether to order the comparisons alphabetically; ignored when <code>orderByP = TRUE</code>
sink_to	optional path of a <code>.tex</code> file to write the table to, so a manuscript can <code>\input{}</code> it

Value

Invisibly returns the rendered LaTeX table as a string (or NULL when xtable is unavailable); the table is also printed.

Examples

```

if (requireNamespace("ARTool", quietly = TRUE) &&
    requireNamespace("emmeans", quietly = TRUE)) {
  set.seed(123)
  n <- 20
  df <- data.frame(
    UserID = factor(rep(seq_len(n), times = 3)),
    mode = factor(rep(c("Hand", "Eye", "Both"), each = n)),
    prime = factor(rep(rep(c("A", "B"), each = n / 2), times = 3))
  )
}

```

```

)
df$score <- as.numeric(df$mode) * 2 + stats::rnorm(nrow(df))

m <- ARTool::art(score ~ mode * prime + Error(UserID / mode), data = df)
ac <- ARTool::art.con(m, ~ mode, adjust = "holm")
reportArtConTable(ac, data = df, iv = "mode", dv = "score", paired = TRUE, id = "UserID")
}

```

reportDunnTest	<i>Report dunnTest as text. Required commands in LaTeX:</i>
	<code>\newcommand{\padminor}{\textit{p\$_{adj}<\$}}</code>
	<code>\newcommand{\padj}{\textit{p\$_{adj}\$=}}</code>
	<code>\newcommand{\rankbiserial}[1]{r_{rb} = #1\$}</code>

Description

Report dunnTest as text. Required commands in LaTeX: `\newcommand{\padminor}{\textit{p$_{adj}<$}}`
`\newcommand{\padj}{\textit{p$_{adj}$=}}` `\newcommand{\rankbiserial}[1]{r_{rb} = #1$}`

Usage

```

reportDunnTest(d, data, iv = "testiv", dv = "testdv", sink_to = NULL)

report_dunn_test(d, data, iv = "testiv", dv = "testdv", sink_to = NULL)

```

Arguments

d	the dunn test object
data	the data frame
iv	independent variable
dv	dependent variable
sink_to	optional path of a .tex file to write the sentences to, so a manuscript can <code>\input{}</code> them

Value

Invisibly returns the reported sentence(s) as a character vector; the text is also emitted via `message()`.

Examples

```

if (requireNamespace("FSA", quietly = TRUE)) {
  # Use built-in iris data
  data(iris)

  # Dunn test on Sepal.Length by Species
  d <- FSA::dunnTest(Sepal.Length ~ Species,
    data = iris,

```

```

    method = "holm"
  )

  # Report the Dunn test
  reportDunnTest(d,
    data = iris,
    iv   = "Species",
    dv   = "Sepal.Length"
  )
}

```

reportDunnTestTable	<i>report Dunn test as a table. Customizable with sensible defaults. Required commands in LaTeX:</i> $\newcommand{\padjminor}{\textit{p}_{\textit{adj}}<\$}$ $\newcommand{\padj}{\textit{p}_{\textit{adj}}\$}$ $\newcommand{\rankbiserial}[1]{r_{\textit{rb}} = \#1\$}$
---------------------	--

Description

report Dunn test as a table. Customizable with sensible defaults. Required commands in LaTeX:
 $\newcommand{\padjminor}{\textit{p}_{\textit{adj}}<\$}$ $\newcommand{\padj}{\textit{p}_{\textit{adj}}\$}$
 $\newcommand{\rankbiserial}[1]{r_{\textit{rb}} = \#1\$}$

Usage

```

reportDunnTestTable(
  d = NULL,
  data,
  iv = "testiv",
  dv = "testdv",
  orderByP = FALSE,
  numberDigitsForPValue = 4,
  latexSize = "small",
  orderText = TRUE,
  sink_to = NULL
)

report_dunn_test_table(
  d = NULL,
  data,
  iv = "testiv",
  dv = "testdv",
  orderByP = FALSE,
  numberDigitsForPValue = 4,
  latexSize = "small",
  orderText = TRUE,

```

```

    sink_to = NULL
  )

```

Arguments

d	the dunn test object
data	the data frame
iv	independent variable
dv	dependent variable
orderByP	whether to order by the p value
numberDigitsForPValue	the number of digits to show
latexSize	which size for the text
orderText	whether to order the comparisons alphabetically; ignored when orderByP = TRUE
sink_to	optional path of a .tex file to write the table to, so a manuscript can \input{} it

Value

Invisibly returns the rendered LaTeX table as a string (or NULL when xtable is unavailable); the table is also printed.

Examples

```

if (requireNamespace("FSA", quietly = TRUE)) {
  # Use built-in iris data
  data(iris)

  # Dunn test on Sepal.Length by Species
  d <- FSA::dunnTest(Sepal.Length ~ Species,
    data = iris,
    method = "holm"
  )

  # Report the Dunn test
  reportDunnTestTable(d,
    data = iris,
    iv = "Species",
    dv = "Sepal.Length"
  )
}

```

reportggstatsplot *Report statistical details for ggstatsplot.*

Description

Report statistical details for ggstatsplot.

Usage

```
reportggstatsplot(  
  p,  
  iv = "independent",  
  dv = "Testdependentvariable",  
  write_to_clipboard = FALSE,  
  sink_to = NULL  
)  
  
report_ggstatsplot(  
  p,  
  iv = "independent",  
  dv = "Testdependentvariable",  
  write_to_clipboard = FALSE,  
  sink_to = NULL  
)
```

Arguments

p	the object returned by ggwithinstats or ggbetweenstats
iv	the independent variable
dv	the dependent variable
write_to_clipboard	whether to write to the clipboard
sink_to	optional path of a .tex file to write the sentence to, so a manuscript can <code>\input{}</code> it

Value

Invisibly returns the reported sentence(s) as a character vector; the text is also emitted via `message()`.

Examples

```
library(ggstatsplot)  
library(dplyr)  
  
# Generate a plot  
plt <- ggbetweenstats(mtcars, am, mpg)
```

```
reportggstatsplot(plt, iv = "am", dv = "mpg")
```

```
reportggstatsplotPostHoc
```

Report significant post-hoc pairwise comparisons

Description

This function extracts significant pairwise comparisons from a `ggstatsplot` object, calculates the mean and standard deviation for the groups involved using the raw data, and prints LaTeX-formatted sentences reporting the results.

Usage

```
reportggstatsplotPostHoc(
  data,
  p,
  iv = "testiv",
  dv = "testdv",
  label_mappings = NULL,
  sink_to = NULL
)

report_ggstatsplot_posthoc(
  data,
  p,
  iv = "testiv",
  dv = "testdv",
  label_mappings = NULL,
  sink_to = NULL
)
```

Arguments

<code>data</code>	A data frame containing the raw data used to generate the plot.
<code>p</code>	A <code>ggstatsplot</code> object (e.g., returned by <code>ggbetweenstats</code>) containing the pairwise comparison statistics.
<code>iv</code>	Character string. The column name of the independent variable (grouping variable).
<code>dv</code>	Character string. The column name of the dependent variable.
<code>label_mappings</code>	Optional named list or vector. Used to rename factor levels in the output text (e.g., <code>list("old_name" = "New Label")</code>).
<code>sink_to</code>	optional path of a <code>.tex</code> file to write the sentences to, so a manuscript can <code>\input{}</code> them

Value

Invisibly returns the reported sentence(s) as a character vector; the text is also emitted via `message()`.

LaTeX Requirements

To easily copy and paste the results to your manuscript, the following commands (or similar) must be defined in your LaTeX preamble, as the function outputs commands taking arguments (e.g., `\m{value}`):

```
\newcommand{\m}[1]{\textit{M}=#1}
\newcommand{\sd}[1]{\textit{SD}=#1}
\newcommand{\padj}[1]{\p_{adj}=#1$}
\newcommand{\padjminor}[1]{\p_{adj}<#1$}
```

Examples

```
library(ggstatsplot)
library(dplyr)

# Generate a plot
plt <- ggbetweenstats(mtcars, am, mpg)

# Report stats
reportggstatsplotPostHoc(
  data = mtcars,
  p = plt,
  iv = "am",
  dv = "mpg",
  label_mappings = list("0" = "Automatic", "1" = "Manual")
)
```

reportMeanAndSD	<i>Report the mean and standard deviation of a dependent variable for all levels of an independent variable rounded to the 2nd digit.</i>
-----------------	---

Description

#' To easily copy and paste the results to your manuscript, the following commands must be defined in Latex: `\newcommand{\m}{\textit{M=}}` `\newcommand{\sd}{\textit{SD=}}`

Usage

```
reportMeanAndSD(data, iv = "testiv", dv = "testdv", sink_to = NULL)

report_mean_sd(data, iv = "testiv", dv = "testdv", sink_to = NULL)
```

Arguments

data	the data frame
iv	the independent variable
dv	the dependent variable
sink_to	optional path of a .tex file to write the lines to, so a manuscript can <code>\input{}</code> them

Value

Invisibly returns the formatted lines as a character vector; the text is also emitted via `message()`.

Examples

```
example_data <- data.frame(Condition = rep(c("A", "B", "C"),
each = 10), TLX1 = stats::rnorm(30))

reportMeanAndSD(example_data, iv = "Condition", dv = "TLX1")
```

reportNparLD	<i>Report the model produced by nparLD. The model provided must be the model generated by the command 'nparLD' nparLD (see https://CRAN.R-project.org/package=nparLD).</i>
--------------	--

Description

#' Only significant main and interaction effects are reported. P-values are rounded for the third digit and relative treatment effects (RTE) are included when available. Attention: the independent variables of the formula and the term specifying the participant must be factors (i.e., use `as.factor()`).

Usage

```
reportNparLD(
  model,
  dv = "Testdependentvariable",
  write_to_clipboard = FALSE,
  sink_to = NULL
)

report_nparld(
  model,
  dv = "Testdependentvariable",
  write_to_clipboard = FALSE,
  sink_to = NULL
)
```

Arguments

`model` the model
`dv` the dependent variable
`write_to_clipboard`
 whether to write to the clipboard
`sink_to` optional path of a .tex file to write the sentences to, so a manuscript can
 \input{} them

Details

#' To easily copy and paste the results to your manuscript, the following commands must be defined in Latex: `\newcommand{\F}{\textit{F=}}` `\newcommand{\df}{\textit{df=}}` `\newcommand{\p}{\textit{p=}}` `\newcommand{\pminor}{\textit{p$<$}}`

Value

Invisibly returns the reported sentence(s) as a character vector; the text is also emitted via `message()`.

Examples

```

if (requireNamespace("nparLD", quietly = TRUE)) {
  # Small toy data set for nparLD
  set.seed(123)
  example_data <- data.frame(
    Subject = factor(rep(1:10, each = 3)),
    Time    = factor(rep(c("T1", "T2", "T3"), times = 10)),
    TLX1    = stats::rnorm(30, mean = 50, sd = 10)
  )

  # Fit nparLD model
  model <- nparLD::nparLD(
    TLX1 ~ Time,
    data      = example_data,
    subject   = "Subject",
    description = FALSE
  )

  # Report the nparLD result
  reportNparLD(model, dv = "TLX1")
}

```

reportNPAV

Generate the Latex-text based on the NPAV by Lüpsen (see <https://www.uni-koeln.de/~{}luepsen/R/>). Only significant main and interaction effects are reported. P-values are rounded for the third digit and partial eta squared values are provided when possible. Attention: the independent variables of the formula and the term specifying the participant must be factors (i.e., use `as.factor()`).

Description

Deprecated: reportNPAV() will be removed in a future release. Use reportART() with ARTool instead.

Usage

```
reportNPAV(
  model,
  dv = "Testdependentvariable",
  write_to_clipboard = FALSE,
  sink_to = NULL
)
```

Arguments

model	the model of the np.anova
dv	the name of the dependent variable that should be reported
write_to_clipboard	whether to write to the clipboard
sink_to	optional path of a .tex file to write the sentences to, so a manuscript can <code>\input{}</code> them

Details

To easily copy and paste the results to your manuscript, the following commands must be defined in Latex: `\newcommand{\F}[3]{\mathcal{F}(\{#1\},\{#2\})=\{#3\}}` `\newcommand{\p}{\textit{p=}}` `\newcommand{\pminor}{\textit{p=}}`

Value

Invisibly returns the reported sentence(s) as a character vector; the text is also emitted via `message()`.

Examples

```
model <- data.frame(
  Df = c(1, 1, 10),
  `F value` = c(6.12, 5.01, NA),
  `Pr(>F)` = c(0.033, 0.045, NA),
  check.names = FALSE
)
rownames(model) <- c("Video", "gesture:eHMI", "Residuals")
reportNPAV(model, dv = "mental workload")
```

 report_all

 Analyze and report several dependent variables at once

Description

Runs `analyze_and_report()` for each dependent variable (e.g., all questionnaire scales of a study) and additionally returns a summary table of the omnibus tests with Holm-adjusted p-values across the dependent variables, plus – when **patchwork** is installed – a combined figure.

Usage

```
report_all(
  data,
  dvs,
  iv,
  design = c("between", "within"),
  labels = NULL,
  xlabel = NULL,
  plotType = "boxviolin",
  sink_dir = NULL
)
```

Arguments

data	the data frame
dvs	character vector of dependent variable column names
iv	the independent variable (column name as string)
design	"between" (default) or "within"
labels	optional named character vector mapping a dv name to its axis label, e.g. <code>c(tlx_mental = "Mental Demand")</code>
xlabels	optional labels for the x-axis, passed to every plot
plotType	either "box", "violin", or "boxviolin" (default)
sink_dir	optional directory; each dv's sentences are written to <code><sink_dir>/<dv>.tex</code> so a manuscript can <code>\input{}</code> them

Value

Invisibly returns a list with components `results` (named list of `analyze_and_report()` results), `summary` (data frame with one row per dv: method, statistic, p.value, and Holm-adjusted p.holm), and `combined_plot` (a patchwork figure, or NULL when patchwork is not installed).

Examples

```
out <- report_all(mtcars, dvs = c("mpg", "disp"), iv = "cyl")
out$summary
```

reshape_data	<i>Reshape Excel Data Based on Custom Markers and Include Custom ID Column</i>
--------------	--

Description

This function takes an Excel file with data in a wide format and transforms it to a long format. It includes a customizable "ID" column in the first position and repeats it for each slice. The function identifies sections of columns between markers that start with a user-defined string (default is "videoinfo") and appends those sections under the first section, aligning by column index.

Usage

```
reshape_data(
  input_filepath,
  sheetName = "Results",
  marker = "videoinfo",
  id_col = "ID",
  output_filepath
)
```

Arguments

`input_filepath` String, the file path of the input Excel file.

`sheetName` String, the name of the sheet to read from the Excel file. Default is "Results".

`marker` String, the string that identifies the start of a new section of columns. Default is "videoinfo".

`id_col` String, the name of the column to use as the ID column. Default is "ID".

`output_filepath` String, the file path for the output Excel file.

Details

Relevant if you receive data in wide-format but cannot use built-in functionality due to naming (e.g., in LimeSurvey)

Value

None, writes the reshaped data to an Excel file specified by `output_filepath`.

Examples

```
if (requireNamespace(c("write_xlsx", "readxl"), quietly = TRUE)) {
  tmp_in <- tempfile(fileext = ".xlsx")
  tmp_out <- tempfile(fileext = ".xlsx")

  # Minimal toy input that includes your required pieces:
```

```

# an ID column and something that contains the marker value.
toy <- data.frame(
  ID = c(1, 1, 2, 2),
  section = c("videoinfo", "videoinfo", "videoinfo", "videoinfo"),
  key = c("fps", "duration_s", "fps", "duration_s"),
  value = c(30, 12.3, 25, 9.8),
  stringsAsFactors = FALSE
)

writexl::write_xlsx(toy, tmp_in)

reshape_data(
  input_filepath = tmp_in,
  marker = "videoinfo",
  id_col = "ID",
  output_filepath = tmp_out
)

out <- readxl::read_excel(tmp_out)
print(out)
}

```

rFromNPAV

Calculation based on Rosenthal's formula (1994). N stands for the number of measurements. Necessary command:

Description

Calculation based on Rosenthal's formula (1994). N stands for the *number of measurements*. Necessary command:

Usage

```
rFromNPAV(pvalue, N)
```

Arguments

pvalue	p value
N	number of measurements in the experiment

Value

Invisibly returns a list with components:

- r: effect size as a numeric scalar.
- z: corresponding z-statistic.
- text: LaTeX-formatted character string that is also sent to the console.

Examples

```
rFromNPAV(0.02, N = 180)
```

rFromWilcox	<i>Calculation based on Rosenthal's formula (1994). N stands for the number of measurements.</i>
-------------	--

Description

Calculation based on Rosenthal's formula (1994). N stands for the *number of measurements*.

Usage

```
rFromWilcox(wilcoxModel, N)
```

Arguments

wilcoxModel	the Wilcox model
N	number of measurements in the experiment

Value

Invisibly returns a list with components:

- r: effect size as a numeric scalar.
- z: corresponding z-statistic.
- text: character string that is also sent to the console.

Examples

```
set.seed(1)
d <- data.frame(
  group = rep(c("A", "B"), each = 10),
  value = rnorm(20)
)
w <- stats::wilcox.test(value ~ group, data = d, exact = FALSE)
rFromWilcox(w, N = nrow(d))
```

rFromWilcoxAdjusted	<i>rFromWilcoxAdjusted</i>
---------------------	----------------------------

Description

rFromWilcoxAdjusted

Usage

```
rFromWilcoxAdjusted(wilcoxModel, N, adjustFactor)
```

Arguments

wilcoxModel	the Wilcox model
N	number of measurements in the experiment
adjustFactor	an adjustment factor

Value

Invisibly returns a list with components:

- r: adjusted effect size as a numeric scalar.
- z: adjusted z-statistic.
- text: character string that is also sent to the console.

Examples

```
set.seed(1)
d <- data.frame(
  group = rep(c("A", "B"), each = 10),
  value = rnorm(20)
)
w <- stats::wilcox.test(value ~ group, data = d, exact = FALSE)
rFromWilcoxAdjusted(w, N = nrow(d), adjustFactor = 2)
```

save_paper_figure	<i>Save a plot with publication-ready defaults</i>
-------------------	--

Description

Saves a ggplot with sizes matching common two-column conference/journal layouts (e.g., ACM): a single-column figure is 3.33 in wide, a full-width figure 7 in. On Windows and Linux, PDFs are rendered with `grDevices::cairo_pdf` so that fonts are embedded and unicode glyphs survive; on macOS the default pdf device is used instead, because R's cairo on macOS is known to crash some setups (e.g., GitHub Actions runners) and the macOS device handles fonts well on its own.

Usage

```
save_paper_figure(
  plot = ggplot2::last_plot(),
  filename,
  columns = 1,
  width = NULL,
  height = NULL,
  dpi = 300,
  device = NULL
)
```

Arguments

plot	The plot to save (defaults to the last plot displayed).
filename	Output path; the extension selects the device (.pdf is recommended for LaTeX).
columns	1 for a single-column figure, 2 for a full-width figure. Ignored when width is given.
width	Figure width in inches; overrides columns.
height	Figure height in inches. Defaults to 2/3 of the width.
dpi	Resolution for raster output. Default 300.
device	Graphics device passed to <code>ggplot2::ggsave()</code> . The default NULL selects it automatically as described above; pass e.g. <code>grDevices::cairo_pdf</code> explicitly to override.

Value

Invisibly returns filename.

Examples

```
p <- ggplot2::ggplot(mtcars, ggplot2::aes(factor(cyl), mpg)) +
  ggplot2::geom_boxplot()
save_paper_figure(p, file.path(tempdir(), "cyl-mpg.pdf"), columns = 1)
```

stat_sum_df

Generating the sum and adding a crossbar.

Description

Generating the sum and adding a crossbar.

Usage

```
stat_sum_df(fun, geom = "crossbar", ...)
```

Arguments

fun	function
geom	geom to be shown
...	Additional arguments passed to stat_summary

Value

A ggplot2 layer that can be added to a ggplot object.

Examples

```
# Simple summary function: use the mean as y, ymin, and ymax
mean_fun <- function(x) {
  m <- mean(x, na.rm = TRUE)
  data.frame(y = m, ymin = m, ymax = m)
}

ggplot2::ggplot(mtcars, ggplot2::aes(x = factor(cyl), y = mpg)) +
  stat_sum_df(mean_fun)
```

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