Package ‘correlation’

October 12, 2022

Type Package
Title Methods for Correlation Analysis
Version 0.8.3
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Description Lightweight package for computing different kinds of correlations, such as partial correlations, Bayesian correlations, multilevel correlations, polychoric correlations, biweight correlations, distance correlations and more. Part of the `easystats` ecosystem.
License GPL-3
URL https://easystats.github.io/correlation/
BugReports https://github.com/easystats/correlation/issues
Depends R (>= 3.6)
Imports bayestestR (>= 0.13.0), datasets, datawizard (>= 0.5.1), insight (>= 0.18.4), parameters (>= 0.18.2), stats
Suggests BayesFactor, poorman, energy, ggplot2, ggraph, gt, Hmisc, knitr, lme4, mbend, polycor, ppcor, psych, rmarkdown, rmcorr, rstanarm, see, testthat (>= 3.1.0), tidygraph, wdm, WRS2
VignetteBuilder knitr
Encoding UTF-8
Language en-US
RoxygenNote 7.2.1
Config/testthat/edition 3
Config/Needs/website rstudio/bshlib, r-lib/pkgdown, easystats/easystatstemplate
NeedsCompilation no
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Repository  CRAN
Date/Publication  2022-10-09 00:00:02 UTC

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correlation  Correlation Analysis

Description

Performs a correlation analysis. You can easily visualize the result using plot() (see examples here).

Usage

correlation(
  data,
  data2 = NULL,
  select = NULL,
)
correlation

select2 = NULL,
rename = NULL,
method = "pearson",
p_adjust = "holm",
cl = 0.95,
bayesian = FALSE,
bayesian_prior = "medium",
bayesian_ci_method = "hdi",
bayesian_test = c("pd", "rope", "bf"),
redundant = FALSE,
include_factors = FALSE,
partial = FALSE,
partial_bayesian = FALSE,
multilevel = FALSE,
ranktransform = FALSE,
winsorize = FALSE,
verbose = TRUE,
standardize_names = getOption("easystats.standardize_names", FALSE),
...)

Arguments

data A data frame.
data2 An optional data frame. If specified, all pair-wise correlations between the variables in data and data2 will be computed.

select, select2 (Ignored if data2 is specified.) Optional names of variables that should be selected for correlation. Instead of providing the data frames with those variables that should be correlated, data can be a data frame and select and select2 are (quoted) names of variables (columns) in data. correlation() will then compute the correlation between data[select] and data[select2]. If only select is specified, all pairwise correlations between the select variables will be computed. This is a "pipe-friendly" alternative way of using correlation() (see 'Examples').

rename In case you wish to change the names of the variables in the output, these arguments can be used to specify these alternative names. Note that the number of names should be equal to the number of columns selected. Ignored if data2 is specified.

method A character string indicating which correlation coefficient is to be used for the test. One of "pearson" (default), "kendall", "spearman" (but see also the robust argument), "biserial", "polychoric", "tetrachoric", "biweight", "distance", "percentage" (for percentage bend correlation), "blomqvist" (for Blomqvist's coefficient), "hoeffding" (for Hoeffding's D), "gamma", "gaussian" (for Gaussian Rank correlation) or "shepherd" (for Shepherd's Pi correlation). Setting "auto" will attempt at selecting the most relevant method (polychoric when ordinal factors involved, tetrachoric when dichotomous factors involved,
point-biserial if one dichotomous and one continuous and pearson otherwise). See below the details section for a description of these indices.

**p_adjust** Correction method for frequentist correlations. Can be one of "holm" (default), "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "somers" or "none". See `stats::p.adjust()` for further details.

**ci** Confidence/Credible Interval level. If "default", then it is set to 0.95 (95% CI).

**bayesian** If TRUE, will run the correlations under a Bayesian framework.

**bayesian_prior** For the prior argument, several named values are recognized: "medium.narrow", "medium", "wide", and "ultrawide". These correspond to scale values of 1/sqrt(27), 1/3, 1/sqrt(3) and 1, respectively. See the `BayesFactor::correlationBF` function.

**bayesian_ci_method, bayesian_test** See arguments in `model_parameters()` for BayesFactor tests.

**redundant** Should the data include redundant rows (where each given correlation is repeated two times).

**include_factors** If TRUE, the factors are kept and eventually converted to numeric or used as random effects (depending of multilevel). If FALSE, factors are removed upfront.

**partial** Can be TRUE or "semi" for partial and semi-partial correlations, respectively.

**partial_bayesian** If partial correlations under a Bayesian framework are needed, you will also need to set partial_bayesian to TRUE to obtain "full" Bayesian partial correlations. Otherwise, you will obtain pseudo-Bayesian partial correlations (i.e., Bayesian correlation based on frequentist partialization).

**multilevel** If TRUE, the factors are included as random factors. Else, if FALSE (default), they are included as fixed effects in the simple regression model.

**ranktransform** If TRUE, will rank-transform the variables prior to estimating the correlation, which is one way of making the analysis more resistant to extreme values (outliers). Note that, for instance, a Pearson’s correlation on rank-transformed data is equivalent to a Spearman’s rank correlation. Thus, using robust=TRUE and method="spearman" is redundant. Nonetheless, it is an easy option to increase the robustness of the correlation as well as flexible way to obtain Bayesian or multilevel Spearman-like rank correlations.

**winsorize** Another way of making the correlation more "robust" (i.e., limiting the impact of extreme values). Can be either FALSE or a number between 0 and 1 (e.g., 0.2) that corresponds to the desired threshold. See the `winsorize()` function for more details.

**verbose** Toggle warnings.

**standardize_names** This option can be set to TRUE to run `insight::standardize_names()` on the output to get standardized column names. This option can also be set globally by running options(easystats.standardize_names = TRUE).

**...** Additional arguments (e.g., alternative) to be passed to other methods. See `stats::cor.test` for further details.
Correlation

Details

Correlation Types:

- **Pearson’s correlation**: This is the most common correlation method. It corresponds to the covariance of the two variables normalized (i.e., divided) by the product of their standard deviations.

- **Spearman’s rank correlation**: A non-parametric measure of rank correlation (statistical dependence between the rankings of two variables). The Spearman correlation between two variables is equal to the Pearson correlation between the rank values of those two variables; while Pearson’s correlation assesses linear relationships, Spearman’s correlation assesses monotonic relationships (whether linear or not). Confidence Intervals (CI) for Spearman’s correlations are computed using the Fieller et al. (1957) correction (see Bishara and Hittner, 2017).

- **Kendall’s rank correlation**: In the normal case, the Kendall correlation is preferred than the Spearman correlation because of a smaller gross error sensitivity (GES) and a smaller asymptotic variance (AV), making it more robust and more efficient. However, the interpretation of Kendall’s tau is less direct than that of Spearman’s rho, in the sense that it quantifies the difference between the percentage of concordant and discordant pairs among all possible pairwise events. Confidence Intervals (CI) for Kendall’s correlations are computed using the Fieller et al. (1957) correction (see Bishara and Hittner, 2017).

- **Biweight midcorrelation**: A measure of similarity that is median-based, instead of the traditional mean-based, thus being less sensitive to outliers. It can be used as a robust alternative to other similarity metrics, such as Pearson correlation (Langfelder & Horvath, 2012).

- **Distance correlation**: Distance correlation measures both linear and non-linear association between two random variables or random vectors. This is in contrast to Pearson’s correlation, which can only detect linear association between two random variables.

- **Percentage bend correlation**: Introduced by Wilcox (1994), it is based on a down-weight of a specified percentage of marginal observations deviating from the median (by default, 20%).

- **Shepherd’s Pi correlation**: Equivalent to a Spearman’s rank correlation after outliers removal (by means of bootstrapped Mahalanobis distance).

- **Blomqvist’s coefficient**: The Blomqvist’s coefficient (also referred to as Blomqvist’s Beta or medial correlation; Blomqvist, 1950) is a median-based non-parametric correlation that has some advantages over measures such as Spearman’s or Kendall’s estimates (see Shmid & Schimdt, 2006).

- **Hoeffding’s D**: The Hoeffding’s D statistics is a non-parametric rank based measure of association that detects more general departures from independence (Hoeffding 1948), including non-linear associations. Hoeffding’s D varies between -0.5 and 1 (if there are no tied ranks, otherwise it can have lower values), with larger values indicating a stronger relationship between the variables.

- **Somers’ D**: The Somers’ D statistics is a non-parametric rank based measure of association between a binary variable and a continuous variable, for instance, in the context of logistic regression the binary outcome and the predicted probabilities for each outcome. Usually, Somers’ D is a measure of ordinal association, however, this implementation it is limited to the case of a binary outcome.

- **Point-Biserial and biserial correlation**: Correlation coefficient used when one variable is continuous and the other is dichotomous (binary). Point-Biserial is equivalent to a Pearson’s correlation, while Biserial should be used when the binary variable is assumed to have an
underlying continuity. For example, anxiety level can be measured on a continuous scale, but can be classified dichotomously as high/low.

- **Gamma correlation**: The Goodman-Kruskal gamma statistic is similar to Kendall’s Tau coefficient. It is relatively robust to outliers and deals well with data that have many ties.

- **Winsorized correlation**: Correlation of variables that have been formerly Winsorized, i.e., transformed by limiting extreme values to reduce the effect of possibly spurious outliers.

- **Gaussian rank Correlation**: The Gaussian rank correlation estimator is a simple and well-performing alternative for robust rank correlations (Boudt et al., 2012). It is based on the Gaussian quantiles of the ranks.

- **Polychoric correlation**: Correlation between two theorized normally distributed continuous latent variables, from two observed ordinal variables.

- **Tetrachoric correlation**: Special case of the polychoric correlation applicable when both observed variables are dichotomous.

**Partial Correlation**: Partial correlations are estimated as the correlation between two variables after adjusting for the (linear) effect of one or more other variable. The correlation test is then run after having partialized the dataset, independently from it. In other words, it considers partialization as an independent step generating a different dataset, rather than belonging to the same model. This is why some discrepancies are to be expected for the t- and p-values, CIs, BFs etc (but not the correlation coefficient) compared to other implementations (e.g., ppcor). (The size of these discrepancies depends on the number of covariates partialled-out and the strength of the linear association between all variables.) Such partial correlations can be represented as Gaussian Graphical Models (GGM), an increasingly popular tool in psychology. A GGM traditionally include a set of variables depicted as circles (“nodes”), and a set of lines that visualize relationships between them, which thickness represents the strength of association (see Bhushan et al., 2019).

**Multilevel correlations** are a special case of partial correlations where the variable to be adjusted for is a factor and is included as a random effect in a mixed model (note that the remaining continuous variables of the dataset will still be included as fixed effects, similarly to regular partial correlations). The model is a random intercept model, i.e. the multilevel correlation is adjusted for (1 | groupfactor). That said, there is an important difference between using cor_test() and correlation(): If you set multilevel=TRUE in correlation() but partial is set to FALSE (as per default), then a back-transformation from partial to non-partial correlation will be attempted (through pcor_to_cor()). However, this is not possible when using cor_test() so that if you set multilevel=TRUE in it, the resulting correlations are partial one. Note that for Bayesian multilevel correlations, if partial = FALSE, the back transformation will also recompute p-values based on the new r scores, and will drop the Bayes factors (as they are not relevant anymore). To keep Bayesian scores, set partial = TRUE.

**Notes**: Kendall and Spearman correlations when bayesian=TRUE: These are technically Pearson Bayesian correlations of rank transformed data, rather than pure Bayesian rank correlations (which have different priors).

**Value**

A correlation object that can be displayed using the print, summary or table methods.

**Multiple tests correction**: The p_adjust argument can be used to adjust p-values for multiple comparisons. All adjustment methods available in p.adjust function stats package are supported.
References


Examples

```r
library(correlation)
results <- correlation(iris)
results
summary(results)
summary(results, redundant = TRUE)

# pipe-friendly usage with grouped dataframes from {dplyr} package
if (require("poorman")) {
  iris %>%
    correlation(select = "Petal.Width", select2 = "Sepal.Length")
}

# Grouped dataframe
# grouped correlations
iris %>%
  group_by(Species) %>%
  correlation()

# selecting specific variables for correlation
mtcars %>%
  group_by(am) %>%
  correlation(
    select = c("cyl", "wt"),
    select2 = c("hp")
  )
}

# supplying custom variable names
correlation(anscombe, select = c("x1", "x2"), rename = c("var1", "var2"))
```
# automatic selection of correlation method
correlation(mtcars[-2], method = "auto")

---

correlation-deprecated

**Deprecated functions**

**Description**

 Deprecated functions

**Usage**

distance_mahalanobis(...)

**Arguments**

...  Args.

---

cor_lower  Return the upper or lower triangular part

**Description**

 Return the upper or lower triangular part of the correlation matrix.

**Usage**

cor_lower(x, diag = FALSE, ...)

**Arguments**

x  A correlation object.

diag  Should the diagonal be included?

...  Other arguments to be passed to or from other functions.
**Examples**

```r
x <- correlation(mtcars, redundant = TRUE) # Generate full matrix
x <- cor_lower(x)

if (require("ggplot2")) {
  ggplot(x, aes(x = Parameter2, y = Parameter1, fill = r)) +
  geom_tile()
}

# Sorted
x <- correlation(mtcars, redundant = TRUE) # Generate full matrix
x <- cor_sort(x)
x <- cor_lower(x)

if (require("ggplot2")) {
  ggplot(x, aes(x = Parameter2, y = Parameter1, fill = r)) +
  geom_tile()
}
```

---

**cor_smooth**

Smooth a non-positive definite correlation matrix to make it positive definite.

---

**Description**

Make correlations positive definite using psych::cor.smooth. If smoothing is done, inferential statistics ($p$-values, confidence intervals, etc.) are removed, as they are no longer valid.

**Usage**

```r
cor_smooth(x, method = "psych", verbose = TRUE, ...)
is.positive_definite(x, tol = 10^-12, ...)
is_positive_definite(x, tol = 10^-12, ...)
```

**Arguments**

- **x** A correlation matrix.
- **method** Smoothing method. Can be psych (will use psych::cor.smooth()), hj (Jorjani et al., 2003) or lrs (Schaeffer, 2014). For the two last, will use mbend::bend() (check its documentation for details).
- **verbose** Set to FALSE to silence the function.
- **...** Other arguments to be passed to or from other functions.
- **tol** The minimum eigenvalue to be considered as acceptable.
Examples

```r
set.seed(123)
data <- as.matrix(mtcars)
# Make missing data so pairwise correlation matrix is non-positive definite
data[sample(seq_len(352), size = 60)] <- NA
data <- as.data.frame(data)
x <- correlation(data)
is.positive_definite(x)

smoothed <- cor_smooth(x)
```

---

cor_sort  
**Sort a correlation matrix to improve readability of groups and clusters**

Description

Sort a correlation matrix based on hclust.

Usage

```r
cor_sort(x, distance = "correlation", ...)
```

Arguments

- `x`: A correlation matrix.
- `distance`: How the distance between each variable should be calculated. If correlation (default; suited for correlation matrices), the matrix will be rescaled to 0-1 (distance = 0 indicating correlation of 1; distance = 1 indicating correlation of -1). If raw, then the matrix will be used as a distance matrix as-is. Can be others (euclidean, manhattan, ...), in which case it will be passed to `dist()` (see the arguments for it).

... Other arguments to be passed to or from other functions.

Examples

```r
x <- correlation(mtcars)
cor_sort(as.matrix(x))
cor_sort(x, hclust_method = "ward.D2")  # It can also reorder the long form output
cor_sort(summary(x, redundant = TRUE))  # As well as from the summary
```
Description

This function performs a correlation test between two variables. You can easily visualize the result using \texttt{plot()} (see examples here).

Usage

\begin{verbatim}
cor_test(
  data,
  x, y,
  method = "pearson",
  ci = 0.95,
  bayesian = FALSE,
  bayesian_prior = "medium",
  bayesian_ci_method = "hdi",
  bayesian_test = c("pd", "rope", "bf"),
  include_factors = FALSE,
  partial = FALSE,
  partial_bayesian = FALSE,
  multilevel = FALSE,
  ranktransform = FALSE,
  winsorize = FALSE,
  verbose = TRUE,
  ...
)
\end{verbatim}

Arguments

- \texttt{data}: A data frame.
- \texttt{x, y}: Names of two variables present in the data.
- \texttt{method}: A character string indicating which correlation coefficient is to be used for the test. One of "pearson" (default), "kendall", "spearman" (but see also the \texttt{robust} argument), "biserial", "polychoric", "tetrachoric", "biweight", "distance", "percentage" (for percentage bend correlation), "blomqvist" (for Blomqvist's coefficient), "hoeffding" (for Hoeffding's D), "gamma", "gaussian" (for Gaussian Rank correlation) or "shepherd" (for Shepherd's Pi correlation). Setting "auto" will attempt at selecting the most relevant method (polychoric when ordinal factors involved, tetrachoric when dichotomous factors involved, point-biserial if one dichotomous and one continuous and pearson otherwise). See below the \texttt{details} section for a description of these indices.
- \texttt{ci}: Confidence/Credible Interval level. If "default", then it is set to 0.95 (95% CI).
- \texttt{bayesian}: If TRUE, will run the correlations under a Bayesian framework.
cor_test

bayesian_prior For the prior argument, several named values are recognized: "medium.narrow", "medium", "wide", and "ultrawide". These correspond to scale values of $1/\sqrt{27}, 1/3, 1/\sqrt{3}$ and 1, respectively. See the BayesFactor::correlationBF function.

bayesian_ci_method, bayesian_test See arguments in model_parameters() for BayesFactor tests.

include_factors If TRUE, the factors are kept and eventually converted to numeric or used as random effects (depending of multilevel). If FALSE, factors are removed upfront.

partial Can be TRUE or "semi" for partial and semi-partial correlations, respectively.

partial_bayesian If partial correlations under a Bayesian framework are needed, you will also need to set partial_bayesian to TRUE to obtain "full" Bayesian partial correlations. Otherwise, you will obtain pseudo-Bayesian partial correlations (i.e., Bayesian correlation based on frequentist partialization).

multilevel If TRUE, the factors are included as random factors. Else, if FALSE (default), they are included as fixed effects in the simple regression model.

ranktransform If TRUE, will rank-transform the variables prior to estimating the correlation, which is one way of making the analysis more resistant to extreme values (outliers). Note that, for instance, a Pearson’s correlation on rank-transformed data is equivalent to a Spearman’s rank correlation. Thus, using robust=TRUE and method="spearman" is redundant. Nonetheless, it is an easy option to increase the robustness of the correlation as well as flexible way to obtain Bayesian or multilevel Spearman-like rank correlations.

winsorize Another way of making the correlation more "robust" (i.e., limiting the impact of extreme values). Can be either FALSE or a number between 0 and 1 (e.g., 0.2) that corresponds to the desired threshold. See the winsorize() function for more details.

verbose Toggle warnings.

... Additional arguments (e.g., alternative) to be passed to other methods. See stats::cor.test for further details.

Details

Correlation Types:

- **Pearson’s correlation**: This is the most common correlation method. It corresponds to the covariance of the two variables normalized (i.e., divided) by the product of their standard deviations.

- **Spearman’s rank correlation**: A non-parametric measure of rank correlation (statistical dependence between the rankings of two variables). The Spearman correlation between two variables is equal to the Pearson correlation between the rank values of those two variables; while Pearson’s correlation assesses linear relationships, Spearman’s correlation assesses monotonic relationships (whether linear or not). Confidence Intervals (CI) for Spearman’s correlations are computed using the Fieller et al. (1957) correction (see Bishara and Hittner, 2017).
• **Kendall’s rank correlation**: In the normal case, the Kendall correlation is preferred than the Spearman correlation because of a smaller gross error sensitivity (GES) and a smaller asymptotic variance (AV), making it more robust and more efficient. However, the interpretation of Kendall’s tau is less direct than that of Spearman’s rho, in the sense that it quantifies the difference between the percentage of concordant and discordant pairs among all possible pairwise events. Confidence Intervals (CI) for Kendall’s correlations are computed using the Fieller et al. (1957) correction (see Bishara and Hittner, 2017).

• **Biweight midcorrelation**: A measure of similarity that is median-based, instead of the traditional mean-based, thus being less sensitive to outliers. It can be used as a robust alternative to other similarity metrics, such as Pearson correlation (Langfelder & Horvath, 2012).

• **Distance correlation**: Distance correlation measures both linear and non-linear association between two random variables or random vectors. This is in contrast to Pearson’s correlation, which can only detect linear association between two random variables.

• **Percentage bend correlation**: Introduced by Wilcox (1994), it is based on a down-weight of a specified percentage of marginal observations deviating from the median (by default, 20%).

• **Shepherd’s Pi correlation**: Equivalent to a Spearman’s rank correlation after outliers removal (by means of bootstrapped Mahalanobis distance).

• **Blomqvist’s coefficient**: The Blomqvist’s coefficient (also referred to as Blomqvist’s Beta or medial correlation; Blomqvist, 1950) is a median-based non-parametric correlation that has some advantages over measures such as Spearman’s or Kendall’s estimates (see Shmid & Schimdt, 2006).

• **Hoeffding’s D**: The Hoeffding’s D statistics is a non-parametric rank based measure of association that detects more general departures from independence (Hoeffding 1948), including non-linear associations. Hoeffding’s D varies between -0.5 and 1 (if there are no tied ranks, otherwise it can have lower values), with larger values indicating a stronger relationship between the variables.

• **Somers’ D**: The Somers’ D statistics is a non-parametric rank based measure of association between a binary variable and a continuous variable, for instance, in the context of logistic regression the binary outcome and the predicted probabilities for each outcome. Usually, Somers’ D is a measure of ordinal association, however, this implementation it is limited to the case of a binary outcome.

• **Point-Biserial and biserial correlation**: Correlation coefficient used when one variable is continuous and the other is dichotomous (binary). Point-Biserial is equivalent to a Pearson’s correlation, while Biserial should be used when the binary variable is assumed to have an underlying continuity. For example, anxiety level can be measured on a continuous scale, but can be classified dichotomously as high/low.

• **Gamma correlation**: The Goodman-Kruskal gamma statistic is similar to Kendall’s Tau coefficient. It is relatively robust to outliers and deals well with data that have many ties.

• **Winsorized correlation**: Correlation of variables that have been formerly Winsorized, i.e., transformed by limiting extreme values to reduce the effect of possibly spurious outliers.

• **Gaussian rank Correlation**: The Gaussian rank correlation estimator is a simple and well-performing alternative for robust rank correlations (Boudt et al., 2012). It is based on the Gaussian quantiles of the ranks.

• **Polychoric correlation**: Correlation between two theorized normally distributed continuous latent variables, from two observed ordinal variables.

• **Tetrachoric correlation**: Special case of the polychoric correlation applicable when both observed variables are dichotomous.
Partial Correlation: Partial correlations are estimated as the correlation between two variables after adjusting for the (linear) effect of one or more other variable. The correlation test is then run after having partialized the dataset, independently from it. In other words, it considers partialization as an independent step generating a different dataset, rather than belonging to the same model. This is why some discrepancies are to be expected for the t- and p-values, CIs, BFs etc (but not the correlation coefficient) compared to other implementations (e.g., ppcor). (The size of these discrepancies depends on the number of covariates partialled-out and the strength of the linear association between all variables.) Such partial correlations can be represented as Gaussian Graphical Models (GGM), an increasingly popular tool in psychology. A GGM traditionally include a set of variables depicted as circles ("nodes"), and a set of lines that visualize relationships between them, which thickness represents the strength of association (see Bhushan et al., 2019).

Multilevel correlations are a special case of partial correlations where the variable to be adjusted for is a factor and is included as a random effect in a mixed model (note that the remaining continuous variables of the dataset will still be included as fixed effects, similarly to regular partial correlations). The model is a random intercept model, i.e. the multilevel correlation is adjusted for $(1 | groupfactor)$. That said, there is an important difference between using cor_test() and correlation(): If you set multilevel=TRUE in correlation() but partial is set to FALSE (as per default), then a back-transformation from partial to non-partial correlation will be attempted (through pcor_to_cor()). However, this is not possible when using cor_test() so that if you set multilevel=TRUE in it, the resulting correlations are partial one. Note that for Bayesian multilevel correlations, if partial = FALSE, the back transformation will also recompute p-values based on the new r scores, and will drop the Bayes factors (as they are not relevant anymore). To keep Bayesian scores, set partial = TRUE.

Notes: Kendall and Spearman correlations when bayesian=TRUE: These are technically Pearson Bayesian correlations of rank transformed data, rather than pure Bayesian rank correlations (which have different priors).

Examples

```
library(correlation)

cor_test(iris, "Sepal.Length", "Sepal.Width")
cor_test(iris, "Sepal.Length", "Sepal.Width", method = "spearman")
## Not run:
cor_test(iris, "Sepal.Length", "Sepal.Width", method = "percentage")
if (require("w fm", quietly = TRUE)) {
  cor_test(iris, "Sepal.Length", "Sepal.Width", method = "blomqvist")
}
if (require("Hmisc", quietly = TRUE)) {
}
cor_test(iris, "Sepal.Length", "Sepal.Width", method = "gamma")
cor_test(iris, "Sepal.Length", "Sepal.Width", method = "shepherd")
if (require("BayesFactor", quietly = TRUE)) {
}
```
# Robust (these two are equivalent)
cor_test(iris, "Sepal.Length", "Sepal.Width", method = "spearman")

# Winsorized
cor_test(iris, "Sepal.Length", "Sepal.Width", winsorize = 0.2)

# Tetrachoric
if (require("psych", quietly = TRUE)) {
  data <- iris
  data$Sepal.Width_binary <- ifelse(data$Sepal.Width > 3, 1, 0)
  data$Petal.Width_binary <- ifelse(data$Petal.Width > 1.2, 1, 0)
  cor_test(data, "Sepal.Width_binary", "Petal.Width_binary", method = "tetrachoric")
}

# Biserial
cor_test(data, "Sepal.Width", "Petal.Width_binary", method = "biserial")

# Polychoric
data$Petal.Width_ordinal <- as.factor(round(data$Petal.Width))
data$Sepal.Length_ordinal <- as.factor(round(data$Sepal.Length))
cor_test(data, "Petal.Width_ordinal", "Sepal.Length_ordinal", method = "polychoric")

# When one variable is continuous, will run 'polyserial' correlation
}

# Partial

# End(Not run)

---

**cor_text**  

*Correlation text*

**Description**

This function returns a formatted character of correlation statistics.

**Usage**

```r
cor_text(x, show_ci = TRUE, show_statistic = TRUE, show_sig = TRUE, ...)
```

**Arguments**

- **x**  
  A dataframe with correlation statistics.
- **show_ci**, **show_statistic**, **show_sig**
  Toggle on/off different parts of the text.
- **...**  
  Other arguments to be passed to or from other functions.
Examples
rez <- cor_test(mtcars, "mpg", "wt")
cor_text(rez)
cor_text(rez, show_statistic = FALSE, show_ci = FALSE, stars = TRUE)
rez <- correlation(mtcars)
cor_text(rez)

---
cor_to_ci

Convert correlation to p-values and CIs

Description
Get statistics, p-values and confidence intervals (CI) from correlation coefficients.

Usage
cor_to_ci(cor, n, ci = 0.95, method = "pearson", correction = "fieller", ...)
cor_to_p(cor, n, method = "pearson")

Arguments
cor A correlation matrix or coefficient.
n The sample size (number of observations).
ci Confidence/Credible Interval level. If "default", then it is set to $0.95$ ($95\%$ CI).
method A character string indicating which correlation coefficient is to be used for the test. One of "pearson" (default), "kendall", "spearman" (but see also the robust argument), "biserial", "polychoric", "tetrachoric", "biweight", "distance", "percentage" (for percentage bend correlation), "blomqvist" (for Blomqvist's coefficient), "hoeffding" (for Hoeffding's D), "gamma", "gaussian" (for Gaussian Rank correlation) or "shepherd" (for Shepherd's Pi correlation). Setting "auto" will attempt at selecting the most relevant method (polychoric when ordinal factors involved, tetrachoric when dichotomous factors involved, point-biserial if one dichotomous and one continuous and pearson otherwise). See below the details section for a description of these indices.
correction Only used if method is 'spearman' or 'kendall'. Can be 'fieller' (default; Fieller et al., 1957), 'bw' (only for Spearman) or 'none'. Bonett and Wright (2000) claim their correction ('bw') performs better, though the Bishara and Hittner (2017) paper favours the Fieller correction. Both are generally very similar.
...

Additional arguments (e.g., alternative) to be passed to other methods. See stats::cor.test for further details.
**cor_to_cov**

**Value**

A list containing a p-value and the statistic or the CI bounds.

**References**


**Examples**

```r
cor.test(iris$Sepal.Length, iris$Sepal.Width)
cor_to_p(-0.1175698, n = 150)
cor_to_p(cor(iris[1:4]), n = 150)
cor_to_ci(-0.1175698, n = 150)
cor_to_ci(cor(iris[1:4]), n = 150)

cor.test(iris$Sepal.Length, iris$Sepal.Width, method = "spearman")
cor_to_p(-0.1667777, n = 150, method = "spearman")
cor_to_ci(-0.1667777, ci = 0.95, n = 150)

cor.test(iris$Sepal.Length, iris$Sepal.Width, method = "kendall")
cor_to_p(-0.07699679, n = 150, method = "kendall")
```

**cor_to_cov**

*Convert a correlation to covariance*

**Description**

Convert a correlation to covariance

**Usage**

```r
cor_to_cov(cor, sd = NULL, variance = NULL, tol = .Machine$double.eps^((2/3))
```

**Arguments**

- `cor`: A correlation matrix, or a partial or a semipartial correlation matrix.
- `sd, variance`: A vector that contains the standard deviations, or the variance, of the variables in the correlation matrix.
- `tol`: Relative tolerance to detect zero singular values.

**Value**

A covariance matrix.
Examples

```r
cor <- cor(iris[1:4])
cov(iris[1:4])

cor_to_cov(cor, sd = sapply(iris[1:4], sd))
cor_to_cov(cor, variance = sapply(iris[1:4], var))
```

---

### Correlation Matrix to (Semi) Partial Correlations

**Description**

Convert a correlation matrix to a (semi)partial correlation matrix. Partial correlations are a measure of the correlation between two variables that remains after controlling for (i.e., "partialling" out) all the other relationships. They can be used for graphical Gaussian models, as they represent the direct interactions between two variables, conditioned on all remaining variables. This means that the squared partial correlation between a predictor X1 and a response variable Y can be interpreted as the proportion of (unique) variance accounted for by X1 relative to the residual or unexplained variance of Y that cannot be accounted by the other variables.

**Usage**

```r
cor_to_pcor(cor, tol = .Machine$double.eps^(2/3))
pcor_to_cor(pcor, tol = .Machine$double.eps^(2/3))
cor_to_spcor(cor = NULL, cov = NULL, tol = .Machine$double.eps^(2/3))
```

**Arguments**

- `cor`: A correlation matrix, or a partial or a semipartial correlation matrix.
- `tol`: Relative tolerance to detect zero singular values.
- `pcor`: A correlation matrix, or a partial or a semipartial correlation matrix.
- `cov`: A covariance matrix (or a vector of the SD of the variables). Required for semi-partial correlations.

**Details**

The semi-partial correlation is similar to the partial correlation statistic. However, it represents (when squared) the proportion of (unique) variance accounted for by the predictor X1, relative to the total variance of Y. Thus, it might be seen as a better indicator of the "practical relevance" of a predictor, because it is scaled to (i.e., relative to) the total variability in the response variable.

**Value**

The (semi) partial correlation matrix.
Examples

cor <- cor(iris[1:4])

# Partialize
cor_to_pcor(cor)
cor_to_spcor(cor, cov = sapply(iris[1:4], sd))

# Inverse
round(pcor_to_cor(cor_to_pcor(cor)) - cor, 2) # Should be 0

display.easycormatrix  Export tables into different output formats

Description

Export tables (i.e. data frame) into different output formats. print_md() is a alias for display(format = "markdown").

Usage

## S3 method for class 'easycormatrix'
display(
  object, 
  format = "markdown", 
  digits = 2, 
  p_digits = 3, 
  stars = TRUE, 
  include_significance = NULL, 
  ...
)

## S3 method for class 'easycorrelation'
print_md(x, digits = NULL, p_digits = NULL, stars = NULL, ...)

## S3 method for class 'easycorrelation'
print_html(x, digits = NULL, p_digits = NULL, stars = NULL, ...)

## S3 method for class 'easycormatrix'
print_md(
  x, 
  digits = NULL, 
  p_digits = NULL, 
  stars = NULL, 
  include_significance = NULL, 
  ...
)
## S3 method for class 'easyormatrix'
print_html(
    x,
    digits = NULL,
    p_digits = NULL,
    stars = NULL,
    include_significance = NULL,
    ...
)

### Arguments

- **object, x**: An object returned by `correlation()` or its summary.
- **format**: String, indicating the output format. Currently, only "markdown" is supported.
- **digits, p_digits**: To do...
- **stars**: To do...
- **include_significance**: To do...
- **...**: Currently not used.

### Details

display() is useful when the table-output from functions, which is usually printed as formatted text-table to console, should be formatted for pretty table-rendering in markdown documents, or if knitted from rmarkdown to PDF or Word files.

### Value

A character vector. If `format = "markdown"`, the return value will be a character vector in markdown-table format.

### Examples

data(iris)
corr <- correlation(iris)
display(corr)

s <- summary(corr)
display(s)
is.cor  

**is.cor**  
Check if matrix resembles a correlation matrix

---

**Description**

Check if matrix resembles a correlation matrix

**Usage**

```r
is.cor(x)
```

**Arguments**

- `x` A matrix.

**Value**

TRUE if the matrix is a correlation matrix or FALSE otherwise.

---

isSquare  

**isSquare**  
Check if Square Matrix

---

**Description**

Check if Square Matrix

**Usage**

```r
isSquare(m)
```

**Arguments**

- `m` A matrix.

**Value**

TRUE if the matrix is square or FALSE otherwise.
matrix_inverse  Matrix Inversion

Description
Performs a Moore-Penrose generalized inverse (also called the Pseudoinverse).

Usage
matrix_inverse(m, tol = .Machine$double.eps^(2/3))

Arguments
m  Matrix for which the inverse is required.
tol  Relative tolerance to detect zero singular values.

Value
An inversed matrix.

See Also
pinv from the pracma package

Examples
m <- cor(iris[1:4])
matrix_inverse(m)

visualisation_recipe.easycor_test
Visualisation Recipe for 'correlation' Objects

Description
Objects from the correlation package can be easily visualized. You can simply run plot() on them, which will internally call the visualisation_recipe() method to produce a basic ggplot. You can customize this plot ad-hoc or via the arguments described below. See examples here.
Usage

```r
## S3 method for class 'easycor_test'
visualisation_recipe(
  x,
  show_data = "point",
  show_text = "subtitle",
  smooth = NULL,
  point = NULL,
  text = NULL,
  labs = NULL,
  ...
)
```

```r
## S3 method for class 'easycormatrix'
visualisation_recipe(
  x,
  show_data = "tile",
  show_text = "text",
  show_legend = TRUE,
  tile = NULL,
  point = NULL,
  text = NULL,
  scale = NULL,
  scale_fill = NULL,
  labs = NULL,
  type = show_data,
  ...
)
```

```r
## S3 method for class 'easycorrelation'
visualisation_recipe(x, ...)
```

Arguments

- **x**: A correlation object.
- **show_data**: Show data. For correlation matrices, can be "tile" (default) or "point".
- **show_text**: Show labels with matrix values.
- **...**: Other arguments passed to other functions.
- **show_legend**: Show legend. Can be set to FALSE to remove the legend.
- **tile, point, text, scale, scale_fill, smooth, labs**: Additional aesthetics and parameters for the geoms (see customization example).
- **type**: Alias for show_data, for backwards compatibility.

Examples
# Correlation Test
if (require("see")) {
  rez <- cor_test(mtcars, "mpg", "wt")

  layers <- visualisation_recipe(rez, labs = list(x = "Miles per Gallon (mpg)"))
  layers
  plot(layers)

  plot(rez,
       show_text = "label",
       point = list(color = "#f44336"),
       text = list(fontface = "bold"),
       show_statistic = FALSE, show_ci = FALSE, stars = TRUE
  )
}

# Correlation Matrix
if (require("see")) {
  rez <- correlation(mtcars)

  x <- cor_sort(as.matrix(rez))
  layers <- visualisation_recipe(x)
  layers
  plot(layers)

  x <- summary(rez, redundant = TRUE, digits = 3)
  plot(visualisation_recipe(x))

  x <- summary(rez)
  layers <- visualisation_recipe(x,
                                 show_data = "points",
                                 scale = list(range = c(10, 20)),
                                 scale_fill = list(
                                     high = "#FF5722",
                                     low = "#673AB7",
                                     name = "r"
                                 ),
                                 text = list(color = "white"),
                                 labs = list(title = "My Plot")
  )
  plot(layers) + theme_modern()
}

# Correlation Results (easycorrelation)
if (require("see") && require("tidygraph") && require("ggraph")) {

rez <- correlation(iris)

layers <- visualisation_recipe(rez)
layers
plot(layers)
}

---

**z_fisher**

*Fisher z-transformation*

**Description**

The Fisher z-transformation converts the standard Pearson’s *r* to a normally distributed variable *z’*. It is used to compute confidence intervals to correlations. The *z’* variable is different from the *z*-statistic.

**Usage**

```r
z_fisher(r = NULL, z = NULL)
```

**Arguments**

- *r, z*
  
The *r* or the *z’* value to be converted.

**Value**

The transformed value.

**References**


**Examples**

```r
z_fisher(r = 0.7)
z_fisher(z = 0.867)
```
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