

Package ‘chisquare’

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Title Chi-Square and G-Square Test of Independence, Power and Residual Analysis, Measures of Categorical Association

Version 1.1.1

Description Provides the facility to perform the chi-square and G-square test of independence, calculates the retrospective power of the traditional chi-square test, compute permutation and Monte Carlo p-value, and provides measures of association for tables of any size such as Phi, Phi corrected, odds ratio with 95 percent CI and p-value, Yule' Q and Y, adjusted contingency coefficient, Cramer's V, V corrected, V standardised, bias-corrected V, W, Cohen's w, Goodman-Kruskal's lambda, and tau. It also calculates standardised, moment-corrected standardised, and adjusted standardised residuals, and their significance, as well as the Quetelet Index, IJ association factor, and adjusted standardised counts. It also computes the chi-square-maximising version of the input table. Different outputs are returned in nicely formatted tables.

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chisquare	<i>R function for Chi-square, (N-1) Chi-square, and G-Square test of independence, power calculation, measures of association, and standardised/moment-corrected standardised/adjusted standardised residuals, visualisation of odds ratio in 2xk tables (where k >= 2)</i>
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Description

The function performs the chi-square test (both in its original format and in the N-1 version) and the G-square test of independence on the input contingency table. It also calculates the retrospective power of the traditional chi-square test and various measures of categorical association for tables of any size, returns standardised, moment-corrected standardised, adjusted standardised residuals (with indication of their significance), Quetelet Index, IJ association factor, adjusted standardised counts, and the chi-square-maximising version of the input table. It also calculates relative and absolute contributions to the chi-square statistic. The p value associated to the chi-square statistic is also computed via both a permutation- and a Monte Carlo-based method. The 95 percent confidence interval around those p values is also provided. Nicely-formatted output tables are rendered. Optionally, in 2xk tables (where k >= 2), a plot of the odds ratios can be rendered. Visit this [LINK](#) to access the package's vignette.

Usage

```
chisquare(  
  data,  
  B = 1000,  
  plot.or = FALSE,  
  reference.level = 1,  
  row.level = 1,  
  or.alpha = 0.05,  
  power.alpha = 0.05,  
  adj.alpha = FALSE,  
  marginal.type = "average",  
  custom.row.totals = NULL,  
  custom.col.totals = NULL,  
  format = "short",  
  graph = FALSE,  
  oneplot = TRUE,  
  tfs = 13  
)
```

Arguments

data	Dataframe containing the input contingency table.
B	Number of simulated tables to be used to calculate the permutation- and the Monte Carlo-based p value (1000 by default).

<code>plot.or</code>	Takes TRUE or FALSE (default) if the user wants a plot of the odds ratios to be rendered (only for 2xk tables, where $k \geq 2$).
<code>reference.level</code>	The index of the column reference level for odds ratio calculations (default: 1). The user must select the column level to serve as the reference level (only for 2xk tables, where $k \geq 2$).
<code>row.level</code>	The index of the row category to be used in odds ratio calculations (1 or 2; default: 1). The user must select the row level to which the calculation of the odds ratios make reference (only for 2xk tables, where $k \geq 2$).
<code>or.alpha</code>	The significance level used for the odds ratios' confidence intervals (default: 0.05).
<code>power.alpha</code>	The significance level used for the calculation of the power of the traditional chi-square test (default: 0.05).
<code>adj.alpha</code>	Takes TRUE or FALSE (default) if the user wants or does not want the significance level of the residuals (standardised, adjusted standardised, and moment-corrected) to be corrected using the Sidak's adjustment method (see Details).
<code>marginal.type</code>	Defines the target marginal sums used for table standardisation via Iterative Proportional Fitting. It takes <i>average</i> (default) to have target row and column marginals equal to the table's grand total divided by the number of rows and columns, respectively; it takes <i>percent</i> to have target marginals equal to fractions of a grand total set to 100.
<code>custom.row.totals</code>	A vector of numbers indicating the target row marginals to be used for table standardisation via Iterative Proportional Fitting (NULL by default).
<code>custom.col.totals</code>	A vector of numbers indicating the target column marginals to be used for table standardisation via Iterative Proportional Fitting (NULL by default).
<code>format</code>	Takes <i>short</i> (default) if the dataset is a dataframe storing a contingency table; if the input dataset is a dataframe storing two columns that list the levels of the two categorical variables, <i>long</i> will preliminarily cross-tabulate the levels of the categorical variable in the 1st column against the levels of the variable stored in the 2nd column.
<code>graph</code>	Takes TRUE or FALSE (default) if the user wants or does not want to plot the permutation and Monte Carlo distribution of the chi-square statistic across the number of simulated tables set by the B parameter.
<code>oneplot</code>	Takes TRUE (default) or FALSE if the user wants or does not want to render of the permutation and Monte Carlo distribution in the same plot.
<code>tfs</code>	Numerical value to set the size of the font used in the main body of the various output tables (13 by default).

Details

The function produces the following **measures of categorical associations**:

- Phi (with indication of the magnitude of the effect size; only for 2x2 tables)

- Phi max (used to compute Phi corrected; only for 2x2 tables)
- Phi corrected (with indication of the magnitude of the effect size; only for 2x2 tables)
- Phi signed (with indication of the magnitude of the effect size; only for 2x2 tables)
- Yule's Q (only for 2x2 tables, includes 95perc confidence interval, p-value, and indication of the magnitude of the effect)
- Yule's Y (only for 2x2 tables, includes 95perc confidence interval, p-value and indication of the magnitude of the effect)
- Odds ratio (for 2x2 tables, includes 95perc confidence interval, p value, and indication of the magnitude of the effect)
- Independent odds ratios (for tables larger than 2x2)
- Adjusted contingency coefficient C (with indication of the magnitude of the effect)
- Cramer's V (with 95perc confidence interval; includes indication of the magnitude of the effect)
- Cramer's V max (used to compute V corrected; for tables of any size)
- Cramer's V corrected (with indication of the magnitude of the effect)
- Cramer's V standardised (with indication of the magnitude of the effect)
- Bias-corrected Cramer's V (with indication of the magnitude of the effect)
- Cohen's w (with indication of the magnitude of the effect)
- W coefficient (includes 95perc confidence interval and magnitude of the effect)
- Goodman-Kruskal's lambda (both asymmetric and symmetric)
- Corrected version of lambda (both asymmetric and symmetric)
- Goodman-Kruskal's tau (asymmetric)

Retrospective Power of the Traditional Chi-Square Test

The function calculates the retrospective power of the traditional chi-square test, which is the probability of correctly rejecting the null hypothesis when it is false. The power is determined by the observed chi-square statistic, the sample size, and the degrees of freedom, without explicitly calculating an effect size, following the method described by Oyeyemi et al. 2010.

The degrees of freedom are calculated as $(\text{number of rows} - 1) * (\text{number of columns} - 1)$. The alpha level is set by default at 0.05 and can be customized using the `power.alpha` parameter. The power is then estimated using the non-centrality parameter based on the observed chi-square statistic.

The calculation involves determining the critical chi-squared value based on the alpha level and degrees of freedom, and then computing the probability that the chi-squared distribution with the given degrees of freedom exceeds this critical value.

The resulting power value indicates how likely the test is to detect an effect if one exists. A power value close to 1 suggests a high probability of detecting a true effect, while a lower value indicates a higher risk of a Type II error. Typically, a power value of 0.8 or higher is considered robust in most research contexts.

Suggestion of a suitable chi-square testing method

The first rendered table includes a suggestion for the applicable chi-squared test method, derived from an internal analysis of the input contingency table. The decision logic used is as follows:

For 2x2 tables:

- if the grand total is equal to or larger than 5 times the number of cells, the traditional Chi-Square test is suggested. Permutation or Monte Carlo methods can also be considered.

- if the grand total is smaller than 5 times the number of cells, the minimum expected count is checked:

(A) if it is equal to or larger than 1, the $(N-1)/N$ adjusted Chi-Square test is suggested, with an option for Permutation or Monte Carlo methods.

(B) if it is less than 1, the Permutation or Monte Carlo method is recommended.

For tables larger than 2x2:

- the logic is similar to that for 2x2 tables, with the same criteria for suggesting the traditional Chi-Square test, the $(N-1)/N$ adjusted test, or the Permutation or Monte Carlo methods.

The rationale of a threshold for the applicability of the traditional chi-square test corresponding to 5 times the number of cells is based on the following.

Literature indicates that the traditional chi-squared test's validity is not as fragile as once thought, especially when considering the average expected frequency across all cells in the cross-tab, rather than the minimum expected value in any single cell. An average expected frequency of at least 5 across all cells of the input table should be sufficient for maintaining the chi-square test's reliability at the 0.05 significance level.

As a consequence, a table's grand total equal to or larger than 5 times the number of cells should ensure the applicability of the traditional chi-square test (at alpha 0.05).

See: Roscoe-Byars 1971; Greenwood-Nikulin 1996; Zar 2014; Alberti 2024.

For the rationale of the use of the $(N-1)/N$ adjusted version of the chi-square test, and for the permutation and Monte Carlo method, see below.

Chi-square statistics adjusted using the $(N-1)/N$ adjustment

The adjustment is done by multiplying the chi-square statistics by $(N-1)/N$, where N is the table grand total (sample size). The p-value of the corrected statistic is calculated the regular way (i.e., using the same degrees of freedom as in the traditional test). The correction seems particularly relevant for tables where N is smaller than 20 and where the expected frequencies are equal or larger than 1. The corrected chi-square test proves more conservative when the sample size is small. As N increases, the term $(N-1)/N$ approaches 1, making the adjusted chi-square value virtually equivalent to the unadjusted value.

See: Upton 1982; Rhoades-Overall 1982; Campbel 2007; Richardson 2011; Alberti 2024.

Permutation-based and Monte Carlo p-value for the chi-square statistic

The p-value of the observed chi-square statistic is also calculated on the basis of both a permutation-based and a Monte Carlo approach. In the first case, the dataset is permuted B times (1000 by default), whereas in the second method B establishes the number of random tables generated under the null hypothesis of independence (1000 by default).

As for the permutation method, the function does the following internally:

(1) Converts the input dataset to long format and expands to individual observations;

- (2) Calculates the observed chi-squared statistic;
- (3) Randomly shuffles (B times) the labels of the levels of one variable, and recalculates chi-squared statistic for each shuffled dataset;
- (4) Computes the p-value based on the distribution of permuted statistics (see below).

For the rationale of the permutation-based approach, see for instance Agresti et al 2022.

For the rationale of the Monte Carlo approach, see for instance the description in Beh-Lombardo 2014: 62-64.

Both simulated p-values are calculated as follows:

$sum(chistat.simulated \geq chisq.stat) / B$, where

chistat.simulated is a vector storing the B chi-squared statistics generated under the Null Hypothesis, and *chisq.stat* is the observed chi-squared statistic.

Both distributions can be optionally plotted setting the graph parameter to TRUE.

Confidence interval around the permutation-based and Monte Carlo p-value

The function calculates the 95 percent Confidence Interval around the simulated p-values. The Wald CI quantifies the uncertainty around the simulated p-value estimate. For a 95 percent CI, the standard z-value of 1.96 is used. The standard error for the estimated p-value is computed as the square root of (estimated p-value * (1 - estimated p-value) / number of simulations-1).

The lower and upper bounds of the CI are then calculated as follows:

Lower Confidence Interval = estimated p-value - (z-value * standard error)

Upper Confidence Interval = estimated p-value + (z-value * standard error)

Finally, the lower and upper CIs are clipped to lie within 0 and 1.

The implemented procedure aligns with the one described at this link: <https://blogs.sas.com/content/iml/2015/10/28/simulation-exact-tables.html>

For the Wald confidence interval see Fagerland et al 2017.

Cells' relative contribution (in percent) to the chi-square statistic

The cells' relative contribution (in percent) to the chi-square statistic is calculated as:

$chisq.values / chisq.stat * 100$, where

chisq.values and *chisq.stat* are the chi-square value in each individual cell of the table and the value of the chi-square statistic, respectively. The *average contribution* is calculated as $100 / (nr * nc)$, where *nr* and *nc* are the number of rows and columns in the table respectively.

Cells' absolute contribution (in percent) to the chi-square statistic

The cells' absolute contribution (in percent) to the chi-square statistic is calculated as:

$chisq.values/n * 100$, where

$chisq.values$ and n are the chi-square value in each individual cell of the table and the table's grand total, respectively. The *average contribution* is calculated as sum of all the absolute contributions divided by the number of cells in the table.

For both the relative and absolute contributions to the chi-square, see: Beasley-Schumacker 1995: 90.

Chi-square-maximising table

The chi-square-maximising table is the version of the input cross-tab that, while preserving the marginal configuration, produces the largest divergence between the observed and the expected counts and, therefore, the maximum chi-squared value achievable given the observed marginals.

The table is worked out using the routine described by Berry and colleagues. This allocation routine effectively maximises the chi-square statistic by concentrating (to the maximum extent possible given the marginals) the levels of one variable into specific levels of the other.

As Berry and colleagues have noted, there can be alternative positions for the zeros in the chi-square-maximising table, but the obtained non-zero counts are the only ones that allow the maximisation of the chi-squared statistic.

The chi-square-maximising table is used to compute Cramer's V max, which is in turn used to compute Cramer's V corrected (equal to phi-corrected for 2x2 tables; see below).

On the chi-square-maximising table, see Berry et al. 2018.

Moment-corrected standardised residuals

The moment-corrected standardised residuals are calculated as follows:

$stand.res / (\sqrt{((nr - 1) * (nc - 1) / (nr * nc))})$, where

$stand.res$ is each cell's standardised residual, nr and nc are the number of rows and columns respectively.

See Garcia-Perez-Nunez-Anton 2003: 827.

Adjusted standardised residuals

The adjusted standardised residuals are calculated as follows:

$stand.res[i, j] / \sqrt{((1 - sr[i]/n) * (1 - sc[j]/n))}$, where

$stand.res$ is the standardised residual for cell ij , sr is the row sum for row i , sc is the column sum for column j , and n is the table grand total. The *adjusted standardised residuals* should be used in place of the standardised residuals since the latter are not truly standardised because they have a nonunit variance. The standardised residuals therefore underestimate the divergence between the observed and the expected counts. The adjusted standardised residuals (and the moment-corrected ones) correct that deficiency.

For more info see: Haberman 1973.

Significance of the residuals

The significance of the residuals (standardised, moment-corrected standardised, and adjusted standardised) is assessed using alpha 0.05 or, optionally (by setting the parameter `adj.alpha` to TRUE), using an adjusted alpha calculated using the Sidak's method:

$$\mathit{alpha.adj} = 1 - (1 - 0.05)^{1/(nr * nc)}, \text{ where}$$

nr and nc are the number of rows and columns in the table respectively. The adjusted alpha is then converted into a critical two-tailed z value.

See: Beasley-Schumacker 1995: 86, 89.

Quetelet Index and IJ association factor

The Quetelet Index expresses the relative change in probability in one variable when considering the association with the other. The sign indicates the direction of the change, that is, whether the probability increases or decreases, compared to the probability expected under the hypothesis of independence. The IJ association factor is centred around 1.0 and represents the factor by which the probability in one variable changes when considering the association with the other. A decrease in probability is indicated by a factor smaller than 1.

The Quetelet index is computed as:

$$(\mathit{observedfreq}/\mathit{expectedfreq}) - 1$$

The IJ association factor is computed as:

$$\mathit{observedfreq}/\mathit{expectedfreq}$$

The thresholds for an IJ factor indicating a noteworthy change in probability, based on Agresti 2013, are: "larger than 2.0" and "smaller than 0.5". The thresholds for the Quetelet Index are based on those, and translate into "larger than 1.0" and "smaller than -0.50". For example, a Quetelet index greater than 1.0 indicates that the observed probability is more than double the expected probability under independence, corresponding to an increase of over 100 percent. Similarly, a Quetelet index less than -0.5 indicates that the observed probability is less than half the expected probability, corresponding to a substantial decrease of over 50 percent.

For the Quetelet Index, see: Mirkin 2023.

For the IJ association factor, see: Agresti 2013; Fagerland et al 2017. Note that the IJ association factor is called 'Pearson ratio' by Goodman 1996.

Adjusted standardised counts

The function computes adjusted standardised counts for the input contingency table. It first standardises the counts via Iterative Proportional Fitting (see below) so that all row and column totals equal unity; then adjusts these standardised counts by subtracting the table's grand mean (that is, the grand total divided by the number of cells).

The resulting adjusted standardised counts isolate the core association structure of the contingency table by removing the confounding effects of marginal distributions. This allows for meaningful comparisons across different tables, even when the original tables have different marginal totals.

In the adjusted standardised counts, a value of 0 indicates independence between the row and column variables for that cell. Positive values indicate a higher association than expected under independence, while negative values indicate a lower association than expected.

Unlike standardised residuals, these adjusted standardised counts can be directly compared across tables of the same size, making them particularly useful for comparative analyses across different samples, time periods, or contexts.

It goes without saying that, in the process of table standardisation, any target marginals can be chosen. The choice of target values affects the scale of the standardised counts but not their relative relationships. By setting all the row and columns sums to unity, the function follows Rosenthal-Rosnow 2008.

See: Fienberg 1971; Rosenthal-Rosnow 2008.

Phi corrected

To refine the phi coefficient, scholars have introduced a corrected version. It accounts for the fact that the original coefficient (1) does not always have a maximum achievable value of unity since it depends on the marginal configuration, and therefore (2) it is not directly comparable across tables with different marginals. To calculate phi-corrected, one first computes phi-max, which represents the maximum possible value of phi under the given marginal totals. Phi-corrected is equal to phi/phi-max.

For more details see: Cureton 1959; Liu 1980; Davenport et al. 1991; Rash et al. 2011; Alberti 2024.

See also *Chi-square-maximising table* above.

95perc confidence interval around Cramer's V

The calculation of the 95perc confidence interval around Cramer's V is based on Smithson 2003: 39-41, and builds on the R code made available by the author on the web (<http://www.michaelsmithson.online/stats/CIstuff/CI.htm>).

Table standardisation via Iterative Proportional Fitting and Cramer's V standardised

This version of the coefficient is computed on the standardised table, which is returned and rendered by the function. The *standardised table* is internally obtained via the *Iterative Proportional Fitting* routine described, for instance, in Reynold 1977: 32-33. Since a number of association measures, among which Cramer's V, are affected by the skewness in the marginal distributions, the original table is first standardised and then Cramer's V is computed.

The rationale of the use of standardised tables as basis to compute Cramer's V is that coefficients calculated on standardised tables are comparable across tables because the impact of different marginal distributions is controlled for.

The value obtained by subtracting the ratio Cramer's V to Cramer's V standardised from 1 gives an idea of the reduction of the magnitude of V due to the skewness of the marginal sums (multiplied by 100 can be interpreted as percentage reduction).

The standardisation is performed so that the rows feature the same sums, and the columns features the same sum, while keeping the table's grand total unchanged. This removes the effect of skewed marginal distributions, while preserving the association structure of the original table.

The target row and column marginals used in the standardisation process are set using the `marginal.type`, `custom.row.totals`, and `custom.col.totals` parameters.

In the iterative procedure, the convergence to the established marginals is reached when the counts obtained in a given iteration do not differ from the ones obtained in the previous iteration by more than a threshold internally set to 0.001. The maximum number of iterations is internally set to 10,000 to prevent infinite loop; after that, the convergence is deemed as failed.

For table standardisation as a preliminary step towards coefficients comparison across tables, see for example Smith 1976; Reynolds 1977; Liu 1980.

Bias-corrected Cramer's V

The bias-corrected Cramer's V is based on Bergsma 2013: 323–328.

W coefficient

It addresses some limitations of Cramer's V. When the marginal probabilities are unevenly distributed, V may overstate the strength of the association, proving pretty high even when the overall association is weak. W is based on the distance between observed and expected frequencies. It uses the squared distance to adjust for the unevenness of the marginal distributions in the table. The indication of the magnitude of the association is based on Cohen 1988 (see above). Unlike Kvalseth 2018a, the calculation of the 95 percent confidence interval is based on a bootstrap approach (employing 10k resampled tables, and the 2.5th and 97.5th percentiles of the bootstrap distribution).

For more details see: Kvalseth 2018a.

Indication of the magnitude of the association as indicated by the chi-squared-based coefficients

The function provides indication of the magnitude of the association (effect size) for the phi, phi signed, phi corrected, Cadj, Cramer's V, V corrected, V standardised, V bias-corrected, Cohen's w, and W.

The verbal articulation of the effect size is based on Cohen 1988.

Phi, phi signed, phi corrected and w are assessed against the well-known Cohen's classification scheme's thresholds (small 0.1, medium 0.3, large 0.5). For input cross-tabs larger than 2x2, the Cadj, Cramer's V, V corrected, V standardised, V bias-corrected, and W coefficients are assessed against thresholds that depend on the table's df, which (as per Cohen 1988) correspond to the smaller between the rows and columns number, minus 1. On the basis of the table's df, the three thresholds are calculated as follows:

small effect: $0.100 / \sqrt{\min(nr,nc)-1}$

medium effect: $0.300 / \sqrt{\min(nr,nc)-1}$

large effect: $0.500 / \sqrt{\min(nr,nc)-1}$

where nr and nc are the number of rows and number of columns respectively, and $\min(nr,nc)-1$ corresponds to the table's df. Essentially, the thresholds for a small, medium, and large effect are computed by dividing the Cohen's thresholds for a 2x2 table (df=1) by the square root of the input table's df.

Consider a V value of (say) 0.350; its effect size interpretation changes based on the table's dimension:

for a 2x2 table, 0.350 corresponds to a "medium" effect;

for a 3x3 table, 0.350 still corresponds to a "medium" effect;

for a 4x4 table, 0.350 corresponds to a "large" effect.

The examples illustrate that for the same (say) V value, the interpreted effect size can shift from "medium" in a smaller table to "large" in a larger table. In simpler terms, the threshold for determining a "large" effect, for instance, becomes more accessible to reach as the table's size increases.

It is crucial to be aware of this as it highlights that the same coefficient value can imply different magnitudes of effect depending on the table's size.

See: Cohen 1988; Sheskin 2011; Alberti 2024.

Corrected Goodman-Kruskal's lambda

The corrected Goodman-Kruskal's lambda adeptly addresses skewed or unbalanced marginal probabilities which create problems to the traditional lambda. By emphasizing categories with higher probabilities through a process of squaring maximum probabilities and normalizing with marginal probabilities, this refined coefficient addresses inherent limitations of lambda.

For more details see: Kvalseth 2018b.

Magnitude of the association as indicated by Yule's Q and Yule's Y

Given the relationship between Q and Y and the odds ratio, the magnitude of the association indicated by Q and Y is based on the thresholds proposed by Ferguson 2009 for the odds ratio (see below). Specifically, the thresholds for Q (in terms of absolute value) are:

- $|Q| < 0.330$ - Negligible
- $0.330 \leq |Q| < 0.500$ - Small
- $0.500 \leq |Q| < 0.600$ - Medium
- $|Q| \geq 0.600$ - Large

For Yule's Y (absolute value):

- $|Y| < 0.171$ - Negligible
- $0.171 \leq |Y| < 0.268$ - Small
- $0.268 \leq |Y| < 0.333$ - Medium
- $|Y| \geq 0.333$ - Large

Yule's Q has a probabilistic interpretation. It tells us how much more likely is to draw pairs of individuals who share the same characteristics (concordant pairs) as opposed to drawing pairs who do not (discordant pairs).

Yule's Y represents the difference between the probabilities in the diagonal and off-diagonal cells, in the equivalent symmetric tables with equal marginals. In other words, Y measures the extent to which the probability of falling in the diagonal cells exceeds the probability of falling in the off-diagonal cells, in the standardised version of the table.

Note that, if either cross-tab's diagonal features 0, the *Haldane-Anscombe correction* is applied to both Q and Y. This results in a coefficient approaching, but not reaching, 1 in such circumstances, with the exact value depending on the table's frequencies. For more info on the correction, see the *Odds Ratio* section below.

On Yule's Q and Y, see Yule 1912.

On Yule's Y, see also Reynolds 1977.

On the probabilistic interpretation of Q, see: Davis 1971; Goodman-Kruskal 1979.

On the sensitivity of Yule's Q and Pearson's phi to different types of associations, see Alberti 2024.

Odds Ratio

For 2x2 tables, a single odds ratio is computed.

For tables larger than 2x2, independent odds ratios are computed for adjacent rows and columns, so representing the minimal set of ORs needed to describe all pairwise relationships in the contingency table.

For tables of size $2 \times k$ (where $k \geq 2$), pairwise odds ratios can be plotted (along with their confidence interval) by setting the `plot.or` parameter to TRUE (see the *Odd Ratios plot* section further down).

In all three scenarios, the *Haldane-Anscombe correction* is applied when zeros are present along any of the table's diagonals. This correction consists of adding 0.5 to every cell of the relevant 2×2 subtable before calculating the odds ratio. This ensures:

- For 2×2 tables: The correction is applied to the entire table if either diagonal contains a zero.
- For larger tables: The correction is applied to each 2×2 subtable used to calculate an independent odds ratio, if that subtable has a zero in either diagonal.
- For $2 \times k$ tables: The correction is applied to each pairwise comparison that involves a zero in either diagonal.

Note that, the *Haldane-Anscombe correction* results in a finite (rather than infinite) odds ratio, with the exact value depending on the table's frequencies.

On the Haldane-Anscombe correction, see: Fleiss et al 2003.

Odds Ratio effect size magnitude

The magnitude of the association indicated by the odds ratio is based on the thresholds (and corresponding reciprocals) suggested by Ferguson 2009 (for other thresholds, see for instance Chen et al 2010):

- $OR < 2.0$ - Negligible
- $2.0 \leq OR < 3.0$ - Small
- $3.0 \leq OR < 4.0$ - Medium
- $OR \geq 4.0$ - Large

As noted earlier, the effect size magnitude for Yule's Q and Yule's Y is based on the above odds ratio's thresholds.

Odd Ratios plot

For $2 \times k$ table, where $k \geq 2$:

by setting the `plot.or` parameter to TRUE, a plot showing the odds ratios and their 95percent confidence interval will be rendered. The confidence level can be modified via the `or.alpha` parameter.

The odds ratios are calculated for the column levels, and one of them is to be selected by the user as a reference for comparison via the `reference.level` parameter (set to 1 by default). Also, the user may want to select the row category to which the calculation of the odds ratios makes reference (using the `row.level` parameter, which is set to 1 by default).

As mentioned earlier, if any of the 2×2 subtables on which the odds ratio is calculated features zeros along any of the diagonal, the *Haldane-Anscombe* correction is applied.

To better understand the rationale of plotting the odds ratios, consider the following example, which uses on the famous Titanic data:

Create a 2×3 contingency table:

```
mytable <- matrix(c(123, 158, 528, 200, 119, 181), nrow = 2, byrow = TRUE)
colnames(mytable) <- c("1st", "2nd", "3rd")
rownames(mytable) <- c("Died", "Survived")
```

Now, we perform the test and visualise the odds ratios:

```
chisquare(mytable, plot.or=TRUE, reference.level=1, row.level=1)
```

In the rendered plot, we can see the odds ratios and confidence intervals for the second and third column level (i.e., 2nd class and 3rd class) because the first column level has been selected as reference level. The odds ratios are calculated making reference to the first row category (i.e., *Died*). From the plot, we can see that, compared to the 1st class, passengers on the 2nd class have 2.16 times larger odds of dying; passengers on the 3rd class have 4.74 times larger odds of dying compared to the 1st class.

Note that if we set the `row.level` parameter to 2, we make reference to the second row category, i.e. *Survived*:

```
chisquare(mytable, plot.or=TRUE, reference.level=1, row.level=2)
```

In the plot, we can see that passengers in the 2nd class have 0.46 times the odds of surviving of passengers in the 1st class, while passengers from the 3rd class have 0.21 times the odds of surviving of those travelling in the 1st class.

Other measures of categorical association

For the other measures of categorical association provided by the function, see for example Sheskin 2011: 1415-1427.

Additional notes on calculations:

- the **Phi** coefficient is based on the chi-square statistic as per Sheskin 2011's equation 16.21, whereas the **Phi signed** is after Sheskin's equation 16.20;
- the **2-sided p value of Yule's Q** is calculated following Sheskin 2011's equation 16.24;
- **Cohen's w** is calculated as $V * \sqrt{\min(nr, nc) - 1}$, where V is Cramer's V , and nr and nc are the number of rows and columns respectively; see Sheskin 2011: 679;
- the **symmetric** version of **Goodman-Kruskal's lambda** is calculated as per Reynolds 1984: 55-57;
- **Goodman-Kruskal's tau** is calculated as per Reynolds 1984: 57-60.

Value

The function produces **optional charts** (distribution of the permuted chi-square statistic and a plot of the odds ratios between a reference column level and the other ones, the latter only for 2xk tables where $k \geq 2$), and a number of **output tables** that are nicely formatted with the help of the *gt* package. The output tables are listed below:

- Input contingency table (with some essential analytical results annotated at the bottom)
- Expected frequencies
- Cells' chi-square value
- Cells' relative contribution (in percent) to the chi-square statistic (cells in RED feature a larger-than-average contribution)
- Cells' absolute contribution (in percent) to the chi-square statistic (colour same as above)
- Chi-square-maximising table (with indication of the associated chi-square value, that is, the maximum value of the chi-square statistic achievable given the table margins)

- Standardised residuals (RED for large significant residuals, BLUE for small significant residuals)
- Moment-corrected standardised residuals (colour same as above)
- Adjusted standardised residuals (colour same as above)
- Table of independent odds ratios (for tables larger than 2x2)
- Quetelet Indices
- IJ association factors
- Adjusted standardised counts
- Input contingency table standardised via Iterative Proportional Fitting
- Table of output statistics, p values, and association measures

Also, the function returns a **list containing the following elements**:

- **input.table**:
 - *crosstab*: input contingency table.
- **chi.sq.maxim.table**:
 - *chi.sq.maximising.table*: chi-square-maximising table.
- **standardised.table**:
 - *standard.table*: standardised table on which Cramer's V standardised is computed.
- **chi.sq.related.results**:
 - *exp.freq*: table of expected frequencies.
 - *smallest.exp.freq*: smallest expected frequency.
 - *avrg.exp.freq*: average expected frequency.
 - *chisq.values*: cells' chi-square value.
 - *chisq.relat.contrib*: cells' relative contribution (in percent) to the chi-square statistic.
 - *chisq.abs.contrib*: cells' absolute contribution (in percent) to the chi-square statistic.
 - *chisq.statistic*: observed chi-square value.
 - *chisq.p.value*: p value of the chi-square statistic.
 - *chisq.max*: chi-square value computed on the chi-square-maximising table.
 - *chi.sq.power*: retrospective power of the traditional chi-square test.
 - *chisq.adj*: chi-square statistic adjusted using the (N-1)/N correction.
 - *chisq.adj.p.value*: p value of the adjusted chi-square statistic.
 - *chisq.p.value.perm*: permutation-based p value, based on B permuted tables.
 - *chisq.p.value.perm CI lower boundary*: lower boundary of the 95 percent CI around the permutation-based p value.
 - *chisq.p.value.perm CI upper boundary*: upper boundary of the 95 percent CI around the permutation-based p value.
 - *chisq.p.value.MC*: Monte Carlo p value, based on B random tables.
 - *chisq.p.value.MC CI lower boundary*: lower boundary of the 95 percent CI around the Monte Carlo p value.
 - *chisq.p.value.MC CI upper boundary*: upper boundary of the 95 percent CI around the Monte Carlo p value.

- **G.square:**
 - *Gsq.statistic*: observed G-square value.
 - *Gsq.p.value*: p value of the G-square statistic.
- **post.hoc:**
 - *stand.resid*: table of chi-square standardised residuals.
 - *mom.corr.stand.resid*: table of moment-corrected standardised residuals.
 - *adj.stand.resid*: table of adjusted standardised residuals.
 - *Quetelet.Index*: table of Quetelet indices.
 - *IJ.assoc.fact.*: table of IJ association factors.
 - *adj.stand.counts*: table of adjusted standardised counts.
- **margin.free.assoc.measures:**
 - *Yule's Q*: Q coefficient (only for 2x2 tables).
 - *Yule's Q CI lower boundary*: lower boundary of the 95perc CI.
 - *Yule's Q CI upper boundary*: upper boundary of the 95perc CI.
 - *Yule's Q p.value*: 2-tailed p value of Yule's Q.
 - *Yule's Y*: Y coefficient (only for 2x2 tables).
 - *Yule's Y CI lower boundary*: lower boundary of the 95perc CI.
 - *Yule's Y CI upper boundary*: upper boundary of the 95perc CI.
 - *Yule's Y p.value*: 2-tailed p value of Yule's Y.
 - *Odds ratio*: odds ratio (for 2x2 tables).
 - *Odds ratio CI lower boundary*: lower boundary of the 95perc CI.
 - *Odds ratio CI upper boundary*: upper boundary of the 95perc CI.
 - *Odds ratio p.value*: p value of the odds ratio.
 - *ORs*: table of independent odds ratios (for tables larger than 2x2).
- **chi.sq.based.assoc.measures:**
 - *Phi.signed*: signed Phi coefficient (only for 2x2 tables).
 - *Phi*: Phi coefficient (only for 2x2 tables).
 - *Phi.max*: Maximum value of Phi given the marginals (only for 2x2 tables).
 - *Phi.corr*: corrected Phi coefficient (equal to Phi/Phi max; only for 2x2 tables).
 - *Cadj*: adjusted contingency coefficient C.
 - *Cramer's V*: Cramer's V coefficient.
 - *Cramer's V CI lower boundary*: lower boundary of the 95perc CI.
 - *Cramer's V CI upper boundary*: upper boundary of the 95perc CI.
 - *Cramer's V max*: Maximum value of Cramer's V given the marginals.
 - *Cramer's V corr*: corrected V coefficient (equal to V/Vmax; for tables of any size).
 - *Cramer's V standard.*: Cramer's V computed on the standardised table.
 - *1-(Cramer's V/V standard.)*: value indicating the reduction of the magnitude of V due to the skewness of the marginal sums.
 - *Cramer's Vbc*: bias-corrected Cramer's V coefficient.
 - *w*: Cohen's w.
 - *W*: W coefficient.

- *W CI lower boundary*: lower boundary of the 95perc CI.
- *W CI upper boundary*: upper boundary of the 95perc CI.

- **PRE.assoc.measures:**

- *lambda (rows dep.)*: Goodman-Kruskal's lambda coefficient (considering the rows being the dependent variable).
- *lambda (cols dep.)*: Goodman-Kruskal's lambda coefficient (considering the columns being the dependent variable).
- *lambda (symmetric)*: Goodman-Kruskal's symmetric lambda coefficient.
- *lambda corrected (rows dep.)*: corrected version of the lambda coefficient (considering the rows being the dependent variable).
- *lambda corrected (cols dep.)*: corrected version of the lambda coefficient (considering the columns being the dependent variable).
- *lambda corrected (symmetric)*: corrected version of the symmetric lambda coefficient.
- *tau (rows dep.)*: Goodman-Kruskal's tau coefficient (considering the rows being the dependent variable).
- *tau (cols dep.)*: Goodman-Kruskal's tau coefficient (considering the columns being the dependent variable).

Note that the *p-values* returned in the above list are expressed in scientific notation, whereas the ones reported in the output table featuring the tests' result and measures of association are reported as broken down into classes (e.g., <0.05, or <0.01, etc), with the exception of the Monte Carlo p-value and its CI.

The **following examples**, which use in-built datasets, can be run to familiarise with the function:

```
-perform the test on the in-built 'social_class' dataset:
result <- chisquare(social_class)
```

```
-perform the test on a 2x2 subset of the 'diseases' dataset:
mytable <- diseases[3:4,1:2]
result <- chisquare(mytable)
```

```
-perform the test on a 2x2 subset of the 'safety' dataset:
mytable <- safety[c(4,1),c(1,6)]
result <- chisquare(mytable)
```

```
-build a toy dataset in 'long' format (gender vs. opinion about death sentence):
mytable <- data.frame(GENDER=c(rep("F", 360), rep("M", 340)), OPINION=c(rep("oppose",
235), rep("favour", 125), rep("oppose", 160), rep("favour", 180)))
```

```
-perform the test specifying that the input table is in 'long' format:
result <- chisquare(mytable, format="long")
```


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Examples

```
# Perform the analysis on a 2x2 subset of the in-built 'social_class' dataset
result <- chisquare(social_class[c(1:2), c(1:2)], B=9)
```

diseases	<i>Dataset: Cross-tabulation of quantity of tobacco smoked daily vs. cause of death</i>
----------	---

Description

Cross-tabulation (15x4) of the amount of tobacco smoked on a daily basis (in grams) against cause of death.

After: Velleman P F, Hoaglin D C, Applications, Basics, and Computing of Exploratory Data Analysis, Wadsworth Pub Co 1984 (Exhibit 8-1)

Usage

```
data(diseases)
```

Format

```
dataframe
```

safety	<i>Dataset: Cross-tabulation of people's feeling of safety vs. town size</i>
--------	--

Description

Cross-tabulation (4x6).

Usage

```
data(safety)
```

Format

```
dataframe
```

social_class

Dataset: Cross-tabulation of social class vs. diagnostic category for a sample of psychiatric patients

Description

Cross-tabulation (3x4) after: Everitt B.S (1992), The Analysis of Contingency Tables, Chapman&Hall/CRC, second edition, table 3.13.

Usage

```
data(social_class)
```

Format

```
dataframe
```

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