Package 'ci'

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Description An educational package providing intuitive functions for calculating confidence intervals (CI) for various statistical parameters. Designed primarily for teaching and learning about statistical inference (particularly confidence intervals). Offers user-friendly wrappers around established methods for proportions, means, and bootstrap-based intervals. Integrates seamlessly with Tidyverse workflows, making it ideal for classroom demonstrations and student exercises. **License** GPL (>= 3) URL https://github.com/GegznaV/ci BugReports https://github.com/GegznaV/ci/issues **Encoding UTF-8** RoxygenNote 7.3.3 **Depends** R (>= 4.1.0) Imports DescTools, dplyr, tidyr, purrr, forcats, tibble, checkmate **Suggests** testthat (>= 3.0.0), knitr, rmarkdown Config/testthat/edition 3 VignetteBuilder knitr NeedsCompilation no Author Vilmantas Gegzna [aut, cre] (ORCID: <https://orcid.org/0000-0002-9500-5167>) Maintainer Vilmantas Gegzna < Gegzna V@gmail.com> Repository CRAN **Date/Publication** 2025-10-22 19:30:02 UTC

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ci_binom

Proportion CI: Binary Variable (2 groups)

Description

Calculates confidence intervals (CI) for proportions in binary variables. This enhanced version of DescTools::BinomCI() returns a data frame.

Usage

```
ci_binom(x, n, method = "modified wilson", conf.level = 0.95, ...)
```

Arguments

X	Number of events of interest or favorable outcomes.
n	Total number of events.
method	Calculation method: "modified wilson", "wilson", "agresti-coull", and others. See DescTools::BinomCI() documentation.
conf.level	Confidence level. Default: 0.95.
•••	Additional parameters for ${\tt DescTools::BinomCI()}$. See the documentation for that function.

Details

Similar to DescTools::BinomCI(), but uses the modified Wilson method by default and returns a data frame instead of a vector, enabling plotting with **ggplot2**.

Value

A data frame with columns:

- est (<dbl>) proportion estimate;
- lwr.ci, upr.ci (<dbl>) lower and upper CI bounds;
- x (<int>) number of events of interest;
- n (<int>) total number of events.

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Examples

```
# Example 1: Survey responses
# 54 out of 80 people agree with a statement
# What is the true proportion of agreement in the population?
ci_binom(x = 54, n = 80)
# Interpretation: We're 95% confident the true proportion
# is between lwr.ci and upr.ci (roughly 0.57 to 0.78)
# Example 2: Medical treatment success
# 23 out of 30 patients recovered
ci_binom(x = 23, n = 30)
# Example 3: Coin flips
# Testing if a coin is fair: 58 heads in 100 flips
ci_binom(x = 58, n = 100)
# If 0.5 is in the CI, we can't rule out the coin being fair
# Example 4: Effect of sample size
# Same proportion (54/80 is approximately 0.675) but different sample sizes
ci_binom(x = 54, n = c(80, 100, 200, 500))
# Notice: Larger samples give narrower (more precise) CIs
# Example 5: Two separate groups
# Group A: 23 successes, Group B: 45 successes
successes <- c(23, 45)
ci_binom(successes, n = sum(successes))
# Example 6: Student exam pass rates
# 67 out of 85 students passed
ci_binom(x = 67, n = 85)
# Example 7: Different confidence levels
# 90% confidence (narrower interval, less confident)
ci_binom(x = 54, n = 80, conf.level = 0.90)
# 99% confidence (wider interval, more confident)
ci_binom(x = 54, n = 80, conf.level = 0.99)
# Example 8: Comparing different methods
ci_binom(x = 15, n = 25, method = "wilson")
ci_binom(x = 15, n = 25, method = "agresti-coull")
# Different methods can give slightly different results
```

ci_boot

Confidence Intervals via Bootstrap

Description

Calculates confidence intervals (CI) using bootstrap methods. This enhanced version of DescTools::BootCI() returns a data frame.

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Usage

```
ci_boot(.data, x, y = NULL, conf.level = 0.95, ...)
```

Arguments

.data Data frame.
x, y Column names (unquoted).
conf.level Confidence level. Default: 0.95.
... Additional parameters for DescTools::BootCI(), including:

FUN – function for which CI is calculated;
bci.method – interval method:

"perc" – percentile method,
"bca" – bias-corrected and accelerated (BCa) method (see note below),
others;
R – number of replications, typically 1,000 to 10,000.

Details

Similar to DescTools::BootCI(), but:

- First argument is a data frame;
- Arguments x and y are unquoted column names;
- Responds to dplyr::group_by() for subgroup calculations;
- Returns a data frame for convenient plotting with **ggplot2**.

Value

A data frame with confidence intervals. Columns depend on arguments and grouping:

- (if grouped) grouping variable names;
- Column matching the statistic name (from FUN) containing the estimate;
- lwr.ci, upr.ci lower and upper CI bounds.

Note

Notes:

- 1. Each group should have at least 20 observations for bootstrap methods.
- 2. Use set.seed() for reproducible results.
- 3. If using bci.method = "bca" produces the warning "extreme order statistics used as endpoints", the BCa method is unsuitable; use "perc" instead (https://rcompanion.org/handbook/E_ 04.html).

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```
# Bootstrap is useful when:
# - Data is skewed (not normal)
# - You want CI for statistics other than the mean (e.g., median, SD)
# - You don't want to assume a specific distribution
data(iris, package = "datasets")
head(iris)
set.seed(123) # For reproducible results
# Example 1: CI for the median (resistant to outliers)
iris |>
  ci_boot(Petal.Length, FUN = median, R = 1000, bci.method = "perc")
# Compare to mean CI - median is often more robust
# Example 2: CI for the median by group
iris |>
  dplyr::group_by(Species) |>
  ci_boot(Petal.Length, FUN = median, R = 1000, bci.method = "perc")
# Useful when groups have different distributions
# Example 3: CI for standard deviation
# How variable is petal length?
set.seed(456)
iris |>
  ci_boot(Petal.Length, FUN = sd, R = 1000, bci.method = "perc")
# Example 4: CI for interquartile range (IQR)
# IQR = 75th percentile - 25th percentile
set.seed(789)
iris |>
  ci_boot(Petal.Length, FUN = IQR, R = 1000, bci.method = "perc")
# Example 5: CI for correlation coefficient (Pearson's r)
# How related are petal length and width?
set.seed(101)
iris |>
  dplyr::group_by(Species) |>
  ci_boot(
    Petal.Length, Petal.Width,
   FUN = cor, method = "pearson",
   R = 1000, bci.method = "perc"
  )
# Look for CIs that don't include 0 (suggests real correlation)
# Example 6: Comparing BCa and percentile methods
set.seed(111)
# BCa method (often more accurate but requires more assumptions)
iris |> ci_boot(Petal.Length, FUN = median, R = 1000, bci.method = "bca")
# Percentile method (simpler, more robust)
```

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```
iris |> ci_boot(Petal.Length, FUN = median, R = 1000, bci.method = "perc")
# Example 7: Effect of number of bootstrap replications
set.seed(222)
# Fewer replications (faster but less stable)
iris |> ci_boot(Petal.Length, FUN = median, R = 500, bci.method = "perc")
# More replications (slower but more stable)
iris |> ci_boot(Petal.Length, FUN = median, R = 5000, bci.method = "perc")
# For teaching: 1000 is usually enough; for research: 5000-10000
# Example 8: Handling missing values
set.seed(333)
iris |>
 ci_boot(
   Petal.Length,
   FUN = median, na.rm = TRUE,
   R = 1000, bci.method = "bca"
 )
# Example 9: With mtcars dataset
set.seed(444)
data(mtcars, package = "datasets")
mtcars |>
 dplyr::group_by(cyl) |>
 ci_boot(mpg, FUN = median, R = 1000, bci.method = "perc")
# Compare median MPG for different cylinder counts
# Example 10: Spearman correlation (rank-based, robust to outliers)
set.seed(555)
iris |>
 dplyr::group_by(Species) |>
 ci_boot(
   Petal.Length, Petal.Width,
   FUN = cor, method = "spearman",
   R = 1000, bci.method = "perc"
 )
```

ci_mean_t

Mean CI from Data

Description

ci_mean_t() calculates the mean's confidence interval (CI) using the *classic* formula with Student's t coefficient for data in data frame format. This enhanced version of DescTools::MeanCI() responds to dplyr::group_by(), enabling subgroup calculations. Result is a data frame.

Usage

```
ci_mean_t(.data, x, conf.level = 0.95, ...)
```

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Arguments

.data Data frame.
 x Column name (unquoted).
 conf.level Confidence level. Default: 0.95.
 ... Additional parameters for DescTools::MeanCI(). See that function's documentation.

Value

A data frame with columns:

- (if present) grouping variable names;
- mean (<dbl>) mean estimate;
- lwr.ci, upr.ci (<dbl>) lower and upper CI bounds.

```
# Example with built-in dataset
data(npk, package = "datasets")
head(npk)
# Basic CI calculation for crop yield
ci_mean_t(npk, yield)
# Interpretation: We're 95% confident the true mean yield
# falls between lwr.ci and upr.ci
# Using pipe operator (tidyverse style)
npk |> ci_mean_t(yield)
# Compare yields with nitrogen (N) treatment vs. without
npk |>
 dplyr::group_by(N) |>
 ci_mean_t(yield)
# Look at the CIs: Do they overlap? Non-overlapping CIs suggest
# a potential difference between groups
# More complex grouping: Three factors at once
npk |>
 dplyr::group_by(N, P, K) |>
 ci_mean_t(yield)
# Example with iris dataset: Petal length by species
data(iris, package = "datasets")
iris |>
 dplyr::group_by(Species) |>
 ci_mean_t(Petal.Length)
# Notice how the three species have clearly different intervals
# Example with mtcars: MPG by number of cylinders
data(mtcars, package = "datasets")
```

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```
mtcars |>
  dplyr::group_by(cyl) |>
  ci_mean_t(mpg)

# 90% confidence interval (less confident, narrower interval)
npk |> ci_mean_t(yield, conf.level = 0.90)

# 99% confidence interval (more confident, wider interval)
npk |> ci_mean_t(yield, conf.level = 0.99)
```

ci_mean_t_stat

Mean CI from Descriptive Statistics

Description

ci_mean_t_stat() calculates the mean's confidence interval (CI) using the *classic* formula with Student's t coefficient when descriptive statistics (mean, standard deviation, sample size) are provided. Useful when these values are reported in scientific literature.

Usage

```
ci_mean_t_stat(mean_, sd_, n, group = "", conf.level = 0.95)
```

Arguments

mean_ Vector of group means.

sd_ Vector of group standard deviations.

n Vector of group sizes.

group Group name. Default: empty string ("").

conf.level Confidence level. Default: 0.95.

Value

A data frame with columns:

- group (<fct>) group name;
- mean (<dbl>) mean estimate;
- lwr.ci (<dbl>) lower CI bound (lwr. = lower);
- upr.ci (<dbl>) upper CI bound (upr. = upper);
- sd (<dbl>) standard deviation;
- n (<int>) sample/group size.

Calculations can be performed for multiple groups simultaneously.

ci_mean_t_stat

Note

Each of mean_, sd_, n, group must have length (a) of one value, or (b) matching the longest vector in this argument group.

See examples for clarification.

```
# Basic example: Test scores
# Suppose a class of 25 students has a mean score of 75 with SD of 10
ci_mean_t_stat(mean_ = 75, sd_ = 10, n = 25)
# The result tells us we can be 95% confident that the true mean score
# lies between the lower and upper CI bounds
# Example from literature: A study reports mean = 362, SD = 35, n = 100
ci_mean_t_stat(mean_ = 362, sd_ = 35, n = 100)
# Without argument names (order matters: mean, sd, n):
ci_mean_t_stat(362, 35, 100)
# Comparing multiple groups (e.g., teaching methods):
# Method A: mean = 78, SD = 8, n = 30 students
# Method B: mean = 82, SD = 7, n = 28 students
# Method C: mean = 75, SD = 9, n = 32 students
mean_val <- c(78, 82, 75)
std_{dev} <- c(8, 7, 9)
        <- c(30, 28, 32)
group <- c("Method A", "Method B", "Method C")</pre>
ci_mean_t_stat(mean_val, std_dev, n, group)
# Educational example: Effect of sample size on CI width
# Same mean and SD, but different sample sizes
ci_mean_t_stat(mean_ = 75, sd_ = 10, n = c(10, 25, 50, 100))
# Notice: Larger samples give narrower (more precise) confidence intervals
# Educational example: Changing confidence level (default is 95%)
ci_mean_t_stat(mean_ = 75, sd_ = 10, n = 25, conf.level = 0.99)
# 99% CI is wider than 95% CI (more confident = less precise)
# NOTE: Changing conf.level just to get narrower CI is a BAD PRACTICE!
# Please choose confidence level based on study design, not desired CI width.
# To display more decimal places, convert tibble to data frame:
result_ci <- ci_mean_t_stat(75, 10, 25)</pre>
as.data.frame(result_ci)
# Or use:
```

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```
# View(result_ci)
```

ci multinom

Proportion CI: Multinomial Variable (3 or more groups)

Description

Calculates simultaneous confidence intervals (CI) for proportions in multinomial variables (k >= 3). This enhanced version of DescTools::MultinomCI() returns a data frame.

Usage

```
ci_multinom(
   x,
   method = "goodman",
   conf.level = 0.95,
   gr_colname = "group",
   ...
)
```

Arguments

```
v Vector of group sizes. Best if elements have meaningful names (see examples).

method Calculation method: "goodman", "sisonglaz", "cplus1", and others. See
    DescTools::MultinomCI() documentation.

conf.level Confidence level. Default: 0.95.

gr_colname Column name (quoted) for group names. Default: "group".

Additional parameters for DescTools::MultinomCI().
```

Details

Similar to DescTools::MultinomCI(), but uses the Goodman method by default and returns a data frame, enabling convenient plotting with **ggplot2**.

Value

A data frame with columns:

- group or user-specified name (<fct>) group names;
- est (<dbl>) proportion estimate;
- lwr.ci, upr.ci (<dbl>) lower and upper CI bounds;
- x (<int>) group size;
- n (<int>) total number of events.

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```
# Example 1: Student grade distribution
# A: 20 students, B: 35 students, C: 25 students, D/F: 15 students
grades <- c("A" = 20, "B" = 35, "C" = 25, "D/F" = 15)
ci_multinom(grades)
# Each row shows the CI for that grade's proportion
# Example 2: Transportation preferences
transport <- c("Car" = 45, "Bus" = 30, "Bike" = 15, "Walk" = 20)
ci_multinom(transport)
# Example 3: Blood type distribution
blood_types <- c("0" = 156, "A" = 134, "B" = 38, "AB" = 22)
ci_multinom(blood_types)
# Example 4: Political party preference
parties <- c("Party A" = 380, "Party B" = 420, "Party C" = 200)
ci_multinom(parties)
# Unnamed frequencies (groups will be numbered)
ci_multinom(c(20, 35, 54))
# Using pipe operator
c("Small" = 20, "Medium" = 35, "Large" = 54) |>
  ci_multinom()
# Different method for simultaneous intervals
c("Small" = 33, "Medium" = 35, "Large" = 30) |>
  ci_multinom(method = "sisonglaz")
# Custom column name for groups
c("Dog" = 65, "Cat" = 48, "Bird" = 22, "Other" = 15) |>
  ci_multinom(gr_colname = "pet_type")
# Example 5: Teaching method effectiveness
# Outcome categories: Poor, Fair, Good, Excellent
outcomes <- c("Poor" = 8, "Fair" = 22, "Good" = 45, "Excellent" = 35)
ci_multinom(outcomes)
# Look for non-overlapping CIs to identify categories that differ significantly
```

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