

Package: bcaboot (via r-universe)

October 16, 2026

Title Bias Corrected Bootstrap Confidence Intervals

Version 1.0

VignetteBuilder knitr

Description Computation of bootstrap confidence intervals in an almost automatic fashion as described in Efron and Narasimhan (2020, <[doi:10.1080/10618600.2020.1714633](https://doi.org/10.1080/10618600.2020.1714633)>).

Depends R (>= 3.5.0)

URL <https://bnaras.github.io/bcaboot/>,
<https://github.com/bnaras/bcaboot>

BugReports <https://github.com/bnaras/bcaboot/issues>

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 7.3.3

Roxygen list(markdown = TRUE)

Suggests ggplot2, glmnet, rmarkdown, knitr, tinytest

Imports cli, graphics, generics, lifecycle, rlang, stats, tibble,
utils

Repository <https://bnaras.r-universe.dev>

Date/Publication 2026-04-08 20:33:22 UTC

RemoteUrl <https://github.com/bnaras/bcaboot>

RemoteRef HEAD

RemoteSha 78c283fb95b969b105c893ee83573cdcd65cb9fb

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bcaboot-package	<i>Automatic Construction of Bootstrap Confidence Intervals</i>
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Description

Bootstrap confidence intervals depend on three elements: (a) the cumulative distribution of the bootstrap replications, (b) the bias-correction, and (c) the acceleration number that measures the rate of change in the standard deviation of the estimate as the data changes. The first two of these depend only on the bootstrap distribution, and not how it is generated: parametrically or non-parametrically. Therefore, the only difference in a parametric bca analysis would lie in the nonparametric estimation of the acceleration, often a negligible error.

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See Also

Useful links:

- <https://bnaras.github.io/bcaboot/>
- <https://github.com/bnaras/bcaboot>
- Report bugs at <https://github.com/bnaras/bcaboot/issues>

autoplot.bcaboot	<i>Plot BCa bootstrap confidence intervals</i>
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Description

Creates a ggplot showing BCa and standard confidence intervals across coverage levels.

Usage

```
## S3 method for class 'bcaboot'  
autoplot(object, ...)
```

Arguments

object A bcaboot object from `bca_nonpar()` or `bca_par()`.
 ... Ignored.

Value

A ggplot object.

Examples

```
## Not run:
data(diabetes, package = "bcaboot")
Xy <- cbind(diabetes$x, diabetes$y)
rfun <- function(Xy) {
  y <- Xy[, 11]; X <- Xy[, 1:10]
  summary(lm(y ~ X))$adj.r.squared
}
set.seed(1234)
result <- bca_nonpar(Xy, 1000, rfun, n_groups = 34, verbose = FALSE)
autoplot(result)

## End(Not run)
```

bca_nonpar

Nonparametric BCa bootstrap confidence intervals

Description

Computes nonparametric bias-corrected and accelerated (BCa) bootstrap confidence intervals. Consolidates the functionality of the deprecated `bcajack`, `bcajack2`, and `bcanon` functions.

Usage

```
bca_nonpar(
  x,
  B,
  func,
  ...,
  accel = c("regression", "jackknife"),
  conf.level = c(0.95, 0.9, 0.8, 0.68),
  n_groups = nrow(x),
  group_reps = 5,
  kl_fraction = 0.333,
  n_jack = 2,
  jack_groups = 12,
  boot_data = NULL,
  verbose = TRUE
)
```

Arguments

<code>x</code>	An $n \times p$ data matrix. Rows are observed p -vectors, assumed independently sampled. If $p = 1$ then <code>x</code> can be a vector.
<code>B</code>	Number of bootstrap replications (integer).
<code>func</code>	Function computing the parameter of interest. <code>func(x, ...)</code> should return a scalar for any data matrix.
<code>...</code>	Additional arguments passed to <code>func</code> .
<code>accel</code>	Method for estimating acceleration: "regression" (default) uses local regression on bootstrap count vectors nearest to uniform; "jackknife" uses classical delete-one (or delete-group) jackknife influence values.
<code>conf.level</code>	Confidence levels for the intervals (e.g., <code>c(0.95, 0.90, 0.80, 0.68)</code>). Only values in $(0, 1)$ are used.
<code>n_groups</code>	Number of groups for jackknife. Default <code>nrow(x)</code> gives delete-one jackknife. Set smaller (e.g., 20-40) to speed up computation on large datasets.
<code>group_reps</code>	When <code>n_groups < nrow(x)</code> , number of random grouping repetitions to average over. Only used with <code>accel = "jackknife"</code> .
<code>kl_fraction</code>	Fraction of bootstrap count vectors nearest to uniform used in the local regression. Only used with <code>accel = "regression"</code> . Default 1/3.
<code>n_jack</code>	Number of delete-d jackknife repetitions for estimating internal (Monte Carlo) standard error. Set to 0 to skip.
<code>jack_groups</code>	Number of groups per jackknife fold.
<code>boot_data</code>	Optional pre-computed bootstrap data: a list with components <code>Y</code> ($B \times n$ count matrix), <code>tt</code> (bootstrap replicates), <code>t0</code> (original estimate). When provided, <code>B</code> is ignored and no resampling is performed.
<code>verbose</code>	Logical; show progress bar during bootstrap.

Value

An object of class "bcaboot" with components:

limits 9-row matrix of confidence limits (columns: `bca`, `jacksd`, `std`, `pct`)

stats 2-row matrix of estimates and jackknife SEs (columns: `theta`, `sdboot`, `z0`, `a`, `sdjack`)

B_mean Bootstrap sample size and mean of replicates

ustats Bias-corrected estimator and its SE

diagnostic gbca diagnostic (when `accel = "regression"`)

References

Efron B (1987). Better bootstrap confidence intervals. *JASA* 82, 171-200.

Efron B and Narasimhan B (2020). The Automatic Construction of Bootstrap Confidence Intervals. *Journal of Computational and Graphical Statistics*, 29(3), 608-619. doi:10.1080/10618600.2020.1714633

Examples

```

data(diabetes, package = "bcaboot")
Xy <- cbind(diabetes$x, diabetes$y)
rfun <- function(Xy) {
  y <- Xy[, 11]
  X <- Xy[, 1:10]
  summary(lm(y ~ X))$adj.r.squared
}
set.seed(1234)
result <- bca_nonpar(x = Xy, B = 1000, func = rfun, n_groups = 34,
                    verbose = FALSE)
print(result)

```

bca_par

*Parametric BCa bootstrap confidence intervals***Description**

Computes parametric bootstrap confidence intervals for a real-valued parameter θ in a p -parameter exponential family.

Usage

```

bca_par(
  t0,
  tt,
  bb,
  conf.level = c(0.95, 0.9, 0.8, 0.68),
  n_jack = 6,
  jack_groups = 10,
  truncation = 0.001,
  kl_fraction = 0.333,
  conf_density = FALSE,
  func
)

```

Arguments

t0	Observed estimate of θ , usually by maximum likelihood.
tt	A vector of B parametric bootstrap replications of θ .
bb	A B by p matrix of natural sufficient vectors, where p is the dimension of the exponential family.
conf.level	Confidence levels for the intervals.
n_jack	Number of jackknife repetitions for internal SE. Set to 0 to skip.
jack_groups	Number of groups per jackknife fold.

truncation	Truncation parameter for acceleration calculation. Can be a vector to compute acceleration at multiple levels.
kl_fraction	Proportion of "nearby" b vectors used in gradient estimation.
conf_density	Logical; if TRUE, return BCa confidence density weights.
func	Optional function for ABC (analytical bootstrap) limits.

Value

An object of class "bcaboot" with components:

limits 9-row matrix of confidence limits

stats 2-row matrix of estimates and jackknife SEs

B_mean Bootstrap sample size and mean of replicates

ustats Bias-corrected estimator and its SE

abc ABC limits and stats (when func provided)

conf_density Confidence density weights (when requested)

accel_matrix Acceleration at multiple truncation levels

References

Efron B (1987). Better bootstrap confidence intervals. JASA 82, 171-200.

DiCiccio T and Efron B (1992). More accurate confidence intervals in exponential families. Biometrika, 231-245.

Efron B and Narasimhan B (2020). The Automatic Construction of Bootstrap Confidence Intervals. Journal of Computational and Graphical Statistics, 29(3), 608-619. doi:[10.1080/10618600.2020.1714633](https://doi.org/10.1080/10618600.2020.1714633)

Examples

```
data(diabetes, package = "bcaboot")
X <- diabetes$x
y <- scale(diabetes$y, center = TRUE, scale = FALSE)
lm.model <- lm(y ~ X - 1)
mu.hat <- lm.model$fitted.values
sigma.hat <- stats::sd(lm.model$residuals)
t0 <- summary(lm.model)$adj.r.squared
y.star <- sapply(mu.hat, rnorm, n = 500, sd = sigma.hat)
tt <- apply(y.star, 1, function(y) summary(lm(y ~ X - 1))$adj.r.squared)
b.star <- y.star %*% X
set.seed(1234)
bca_par(t0 = t0, tt = tt, bb = b.star)
```

diabetes	<i>Blood and other measurements in diabetics</i>
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Description

The diabetes data frame has 442 rows and 3 columns. These are the data used in the Efron et al "Least Angle Regression" paper.

Format

This data frame contains the following columns:

- **x** a matrix with 10 columns
- **y** a numeric vector
- **x2** a matrix with 64 columns

Details

The x matrix has been standardized to have unit L2 norm in each column and zero mean. The matrix x2 consists of x plus certain interactions.

Source

https://web.stanford.edu/~hastie/Papers/LARS/LeastAngle_2002.pdf

References

Efron, Hastie, Johnstone and Tibshirani (2003) "Least Angle Regression" (with discussion) *Annals of Statistics*

glance.bcaboot	<i>Glance at a bcaboot result</i>
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Description

Returns a one-row tibble summarizing the bootstrap run.

Usage

```
## S3 method for class 'bcaboot'  
glance(x, ...)
```

Arguments

x	A bcaboot object from <code>bca_nonpar()</code> or <code>bca_par()</code> .
...	Ignored.

Value

A tibble with columns:

method "nonpar" or "par"

accel Acceleration method ("regression", "jackknife", or NA)

theta Point estimate

sdboot Bootstrap standard error

z0 Bias-correction constant

a Acceleration constant

sdjack Jackknife standard error (if available)

B Number of bootstrap replicates

boot_mean Mean of bootstrap replicates

Examples

```
data(diabetes, package = "bcaboot")
Xy <- cbind(diabetes$x, diabetes$y)
rfun <- function(Xy) {
  y <- Xy[, 11]; X <- Xy[, 1:10]
  summary(lm(y ~ X))$adj.r.squared
}
set.seed(1234)
result <- bca_nonpar(Xy, 1000, rfun, n_groups = 34, verbose = FALSE)
glance(result)
```

tidy.bcaboot

Tidy a bcaboot result

Description

Returns a tibble with one row per (confidence level, method) combination, following broom conventions.

Usage

```
## S3 method for class 'bcaboot'
tidy(x, ...)
```

Arguments

x A bcaboot object from [bca_nonpar\(\)](#) or [bca_par\(\)](#).

... Ignored.

Value

A tibble with columns:

conf.level Confidence level (e.g. 0.95)

method "bca" or "standard" (or "abc" when available)

estimate Point estimate (theta)

conf.low Lower confidence limit

conf.high Upper confidence limit

jacksd.low Jackknife SE of lower limit (BCa only; NA otherwise)

jacksd.high Jackknife SE of upper limit (BCa only; NA otherwise)

Examples

```
data(diabetes, package = "bcaboot")
Xy <- cbind(diabetes$x, diabetes$y)
rfun <- function(Xy) {
  y <- Xy[, 11]; X <- Xy[, 1:10]
  summary(lm(y ~ X))$adj.r.squared
}
set.seed(1234)
result <- bca_nonpar(Xy, 1000, rfun, n_groups = 34, verbose = FALSE)
tidy(result)
```

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