

Package ‘bayesboot’

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Type Package

Title An Implementation of Rubin's (1981) Bayesian Bootstrap

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Description Functions for performing the Bayesian bootstrap as introduced by Rubin (1981) <[doi:10.1214/aos/1176345338](https://doi.org/10.1214/aos/1176345338)> and for summarizing the result. The implementation can handle both summary statistics that works on a weighted version of the data and summary statistics that works on a resampled data set.

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URL <https://github.com/rasmusab/bayesboot>

BugReports <https://github.com/rasmusab/bayesboot/issues>

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as.bayesboot	<i>Coerce to a bayesboot object</i>
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Description

This converts an object into a data frame and adds the class bayesboot. Doing this is only useful in the case you would want to use the plot and summary methods for bayesboot objects.

Usage

```
as.bayesboot(object)
```

Arguments

object Any object that can be converted to a data frame.

Value

A data.frame with subclass bayesboot.

bayesboot	<i>The Bayesian bootstrap</i>
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Description

Performs a Bayesian bootstrap and returns a data.frame with a sample of size R representing the posterior distribution of the (possibly multivariate) summary statistic.

Usage

```
bayesboot(
  data,
  statistic,
  R = 4000,
  R2 = 4000,
  use.weights = FALSE,
  .progress = "none",
  .parallel = FALSE,
  ...
)
```

Arguments

<code>data</code>	Either a vector or a list, or a matrix or a <code>data.frame</code> with one datapoint per row. The format of data should be compatible with the first argument of <code>statistic</code>
<code>statistic</code>	A function implementing the summary statistic of interest where the first argument should take the data. If <code>use.weights = TRUE</code> then the second argument should take a vector of weights.
<code>R</code>	The size of the posterior sample from the Bayesian bootstrap.
<code>R2</code>	When <code>use.weights = FALSE</code> this is the size of the resample of the data used to approximate the weighted statistic.
<code>use.weights</code>	When <code>TRUE</code> the data will be reweighted, like in the original Bayesian bootstrap. When <code>FALSE</code> (the default) the reweighting will be approximated by resampling the data.
<code>.progress</code>	The type of progress bar ("none", "text", "tk", and "win"). See the <code>.progress</code> argument to adply in the <code>plyr</code> package.
<code>.parallel</code>	If <code>TRUE</code> enables parallel processing. See the <code>.parallel</code> argument to adply in the <code>plyr</code> package.
<code>...</code>	Other arguments passed on to <code>statistic</code>

Details

The summary statistic is a function of the data that represents a feature of interest, where a typical statistic is the mean. In `bayesboot` it is most efficient to define the statistic as a function taking the data as the first argument and a vector of weights as the second argument. An example of such a function is [weighted.mean](#). Indicate that you are using a statistic defined in this way by setting `use.weights = TRUE`.

It is also possible to define the statistic as a function only taking data (and no weights) by having `use.weights = FALSE` (the default). This will, for each of the R Bayesian bootstrap draws, give a resampled version of the data of size `R2` to `statistic`. This will be much slower than using `use.weights = TRUE` but will work with a larger range of statistics (the [median](#), for example)

For more information regarding this implementation of the Bayesian bootstrap see the blog post [Easy Bayesian Bootstrap in R](#). For more information about the model behind the Bayesian bootstrap see the blog post [The Non-parametric Bootstrap as a Bayesian Model](#) and, of course, [the original Bayesian bootstrap paper by Rubin \(1981\)](#).

Value

A `data.frame` with `R` rows, each row being a draw from the posterior distribution of the Bayesian bootstrap. The number of columns is decided by the length of the output from `statistic`. If `statistic` does not return a vector or data frame with named values then the columns will be given the names `V1`, `V2`, `V3`, etc. While the output is a `data.frame` it has subclass `bayesboot` which enables specialized [summary](#) and [plot](#) functions for the result of a `bayesboot` call.

Note

- While `R` and `R2` are set to 4000 by default, that should not be taken to indicate that a sample of size 4000 is sufficient nor recommended.

- When using `use.weights = FALSE` it is important to use a summary statistic that does not depend on the sample size. That is, doubling the size of a dataset by cloning data should result in the same statistic as when using the original dataset. An example of a statistic that depends on the sample size is the sample standard deviation (that is, `sd`), and when using bayesboot it would make more sense to use the population standard deviation (as in the example below).

References

Miller, R. G. (1974) The jackknife - a review. *Biometrika*, **61(1)**, 1–15.

Rubin, D. B. (1981). The Bayesian bootstrap. *The annals of statistics*, **9(1)**, 130–134.

Examples

```
### A Bayesian bootstrap analysis of a mean ###

# Heights of the last ten American presidents in cm (Kennedy to Obama).
heights <- c(183, 192, 182, 183, 177, 185, 188, 188, 182, 185);
b1 <- bayesboot(heights, mean)
# But it's more efficient to use the a weighted statistic.
b2 <- bayesboot(heights, weighted.mean, use.weights = TRUE)

# The result of bayesboot can be plotted and summarized
plot(b2)
summary(b2)

# It can also be easily post processed.
# Here the probability that the mean is > 182 cm.
mean( b2[,1] > 182)

### A Bayesian bootstrap analysis of a SD ###

# When use.weights = FALSE it is important that the summary statistics
# does not change as a function of sample size. This is the case with
# the sample standard deviation, so here we have to implement a
# function calculating the population standard deviation.
pop.sd <- function(x) {
  n <- length(x)
  sd(x) * sqrt( (n - 1) / n)
}

b3 <- bayesboot(heights, pop.sd)
summary(b3)

### A Bayesian bootstrap analysis of a correlation coefficient ###

# Data comparing two methods of measuring blood flow.
# From Table 1 in Miller (1974) and used in an example
# by Rubin (1981, p. 132).
blood.flow <- data.frame(
  dye = c(1.15, 1.7, 1.42, 1.38, 2.80, 4.7, 4.8, 1.41, 3.9),
  efp = c(1.38, 1.72, 1.59, 1.47, 1.66, 3.45, 3.87, 1.31, 3.75))
```

```

# Using the weighted correlation (corr) from the boot package.
library(boot)
b4 <- bayesboot(blood.flow, corr, R = 1000, use.weights = TRUE)
hist(b4[,1])

### A Bayesian bootstrap analysis of lm coefficients ###

# A custom function that returns the coefficients of
# a weighted linear regression on the blood.flow data
lm.coefs <- function(d, w) {
  coef( lm(efp ~ dye, data = d, weights = w) )
}

b5 <- bayesboot(blood.flow, lm.coefs, R = 1000, use.weights = TRUE)

# Plotting the marginal posteriors
plot(b5)

# Plotting a scatter of regression lines from the posterior
plot(blood.flow)
for(i in sample(nrow(b5), size = 20)) {
  abline(coef = b5[i, ], col = "grey")
}

```

plot.bayesboot	<i>Plot the result of bayesboot</i>
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Description

Produces histograms showing the marginal posterior distributions from a bayesboot call. Uses the [plotPost](#) function to produce the individual histograms.

Usage

```

## S3 method for class 'bayesboot'
plot(x, cred.mass = 0.95, plots.per.page = 3, cex = 1.2, cex.lab = 1.3, ...)

```

Arguments

x	The bayesboot object to plot.
cred.mass	the probability mass to include in credible intervals, or NULL to suppress plotting of credible intervals.
plots.per.page	The maximum numbers of plots per page.
cex, cex.lab, ...	Further parameters passed on to plotPost .

plotPost

Graphic display of a posterior probability distribution

Description

Plot the posterior probability distribution for a single parameter from a vector of samples, typically from an MCMC process, with appropriate summary statistics.

Usage

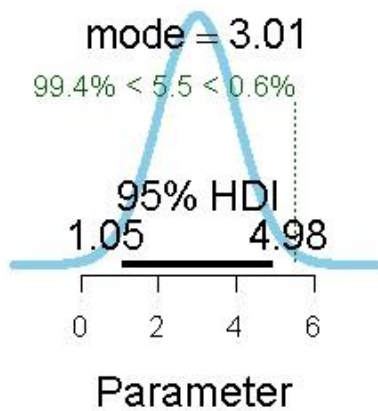
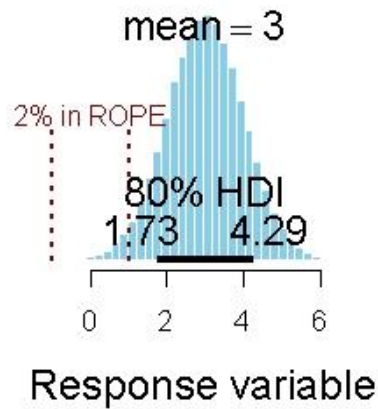
```
plotPost(
  paramSampleVec,
  credMass = 0.95,
  compVal = NULL,
  ROPE = NULL,
  HDItextPlace = 0.7,
  showMode = FALSE,
  showCurve = FALSE,
  ...
)
```

Arguments

paramSampleVec	A vector of samples drawn from the target distribution.
credMass	the probability mass to include in credible intervals, or NULL to suppress plotting of credible intervals.
compVal	a value for comparison with those plotted.
ROPE	a two element vector, such as $c(-1, 1)$, specifying the limits of the Region Of Practical Equivalence.
HDItextPlace	a value in $[0,1]$ that controls the horizontal position of the labels at the ends of the HDI bar.
showMode	logical: if TRUE, the mode is displayed instead of the mean.
showCurve	logical: if TRUE, the posterior density will be represented by a kernel density function instead of a histogram.
...	graphical parameters and the breaks parameter for the histogram.

Details

The data are plotted either as a histogram (above) or, if `showCurve = TRUE`, as a fitted kernel density curve (below). Either the mean or the mode of the distribution is displayed, depending on the parameter `showMode`. The Highest Density Interval (HDI) is shown as a horizontal bar, with labels for the ends of the interval.



If values for a ROPE are supplied, these are shown as dark red vertical dashed lines, together with the percentage of probability mass within the ROPE. If a comparison value (`compVal`) is supplied, this is shown as a vertical green dotted line, together with the probability mass below and above this value.

Value

Returns an object of class `histogram` invisibly. Used for its plotting side-effect.

Note

The origin of this function is [the BEST package](#) which is based on Kruschke(2015, 2013).

Author(s)

John Kruschke, modified by Mike Meredith

References

Kruschke, J. K. (2015) *Doing Bayesian data analysis, second edition: A tutorial with R, JAGS, and Stan*. Waltham, MA: Academic Press / Elsevier.

Kruschke, J. K. (2013) Bayesian estimation supersedes the t test. *Journal of Experimental Psychology: General*, **142**(2), 573.

See Also

For details of the HDI calculation, see [hdi](#).

Examples

```
# Generate some data
tst <- rnorm(1e5, 3, 1)
plotPost(tst)
plotPost(tst, col='wheat', border='magenta')
plotPost(tst, credMass=0.8, ROPE=c(-1,1), xlab="Response variable")
plotPost(tst, showMode=TRUE, showCurve=TRUE, compVal=5.5)

# For integers:
tst <- rpois(1e5, 12)
plotPost(tst)

# A severely bimodal distribution:
tst2 <- c(rnorm(1e5), rnorm(5e4, 7))
plotPost(tst2) # A valid 95% CrI, but not HDI
plotPost(tst2, showCurve=TRUE) # Correct 95% HDI
```

print.bayesboot	<i>Print the first number of draws from the Bayesian bootstrap</i>
-----------------	--

Description

Print the first number of draws from the Bayesian bootstrap

Usage

```
## S3 method for class 'bayesboot'
print(x, n = 10, ...)
```

Arguments

x	The bayesboot object to print.
n	The number of draws to print.
...	Not used.

rudirichlet	<i>Produce random draws from a uniform Dirichlet distribution</i>
-------------	---

Description

`rudirichlet` produces n draws from a d -dimensional uniform Dirichlet distribution. Here "uniform" implies that any combination of values on the support of the distribution is equally likely, that is, the α parameters to the Dirichlet distribution are all set to 1.0.

Usage

```
rudirichlet(n, d)
```

Arguments

<code>n</code>	the number of draws.
<code>d</code>	the dimension of the Dirichlet distribution.

Details

In the context of the Bayesian bootstrap `rudirichlet` is used to produce the bootstrap weights. Therefore, `rudirichlet` can be used if you directly want to generate Bayesian bootstrap weights.

Value

An n by d matrix.

Examples

```
set.seed(123)
rudirichlet(2, 3)
# Should produce the following matrix:
#      [,1] [,2] [,3]
# [1,] 0.30681 0.2097 0.4834
# [2,] 0.07811 0.1390 0.7829

# The above could be seen as a sample of two Bayesian bootstrap weights for a
# dataset of size three.
```

summary.bayesboot	<i>Summarize the result of bayesboot</i>
-------------------	--

Description

Summarizes the result of a call to bayesboot by calculating means, SDs, highest density intervals and quantiles of the posterior marginals.

Usage

```
## S3 method for class 'bayesboot'  
summary(object, cred.mass = 0.95, ...)
```

Arguments

object	The bayesboot object to summarize.
cred.mass	The probability mass to include in the highest density intervals.
...	Not used.

Value

A data frame with three columns: (1) **statistic** the name of the statistic, (2) **measure** the name of the summarizing measure, and (3) **value** the value of the summarizing measure.

See Also

[hdi](#) in the HDInterval package for directly calculating highest density intervals from bayesboot objects.

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