

# Package: bbw (via r-universe)

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**Type** Package

**Title** Blocked Weighted Bootstrap

**Version** 0.2.0

**Description** The blocked weighted bootstrap (BBW) is an estimation technique for use with data from two-stage cluster sampled surveys in which either prior weighting (e.g. population-proportional sampling or PPS as used in Standardized Monitoring and Assessment of Relief and Transitions or SMART surveys) or posterior weighting (e.g. as used in rapid assessment method or RAM and simple spatial sampling method or S3M surveys) is implemented. See Cameron et al (2008)  [<doi:10.1162/rest.90.3.414>](https://doi.org/10.1162/rest.90.3.414) for application of bootstrap to cluster samples. See Aaron et al (2016)  [<doi:10.1371/journal.pone.0163176>](https://doi.org/10.1371/journal.pone.0163176) and Aaron et al (2016)  [<doi:10.1371/journal.pone.0162462>](https://doi.org/10.1371/journal.pone.0162462) for application of the blocked weighted bootstrap to estimate indicators from two-stage cluster sampled surveys.

**Imports** car, withr

**Depends** R (>= 3.0.1)

**Suggests** knitr, rmarkdown, testthat, spelling, covr

**License** GPL-3

**Encoding** UTF-8

**Language** en-GB

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.2

**URL** <https://github.com/rapidsurveys/bbw>, <https://rapidsurveys.io/bbw/>

**BugReports** <https://github.com/rapidsurveys/bbw/issues>

**VignetteBuilder** knitr

**Repository** <https://rapidsurveys.r-universe.dev>

**RemoteUrl** <https://github.com/rapidsurveys/bbw>

**RemoteRef** HEAD

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bootBW	<i>Blocked Weighted Bootstrap</i>
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### Description

The **blocked weighted bootstrap (BBW)** is an estimation technique for use with data from two-stage cluster sampled surveys in which either prior weighting (e.g. **population proportional sampling** or **PPS** as used in **SMART** surveys) or posterior weighting (e.g. as used in **RAM** and **S3M** surveys).

### Usage

```
bootBW(x, w, statistic, params, outputColumns, replicates = 400)
```

### Arguments

x	A data frame with primary sampling unit (PSU) in column named psu
w	A data frame with primary sampling unit (PSU) in column named psu and survey weight (i.e. PSU population) in column named pop
statistic	A function operating on data in x (see example)
params	Parameters (named columns in x) passed to the function specified in statistic
outputColumns	Names of columns in output data frame
replicates	Number of bootstrap replicates

**Value**

A data frame with:

- ncol = length(outputColumns)
- nrow = replicates
- names = outputColumns

**Examples**

```
# Example function - estimate a proportion for a binary (0/1) variable):
```

```
oneP <- function(x, params) {
  v1 <- params[1]
  v1Data <- x[[v1]]
  oneP <- mean(v1Data, na.rm = TRUE)
  return(oneP)
}
```

```
# Example call to bootBW function using RAM-OP test data:
```

```
bootP <- bootBW(x = indicatorsHH,
               w = villageData,
               statistic = oneP,
               params = "anc1",
               outputColumns = "anc1",
               replicates = 9)
```

```
# Example estimate with 95% CI:
```

```
quantile(bootP, probs = c(0.500, 0.025, 0.975), na.rm = TRUE)
```

---

bootClassic

*Simple proportion statistics function for bootstrap estimation*

---

**Description**

Simple proportion statistics function for bootstrap estimation

**Usage**

```
bootClassic(x, params)
```

**Arguments**

x	A data frame with <b>primary sampling unit (PSU)</b> in column named psu and with data column/s containing the binary variable/s (0/1) of interest with column names corresponding to params values
params	A vector of column names corresponding to the binary variables of interest contained in x

**Value**

A numeric vector of the mean of each binary variable of interest with length equal to length(params)

**Examples**

```
# Example call to bootClassic function

meanResults <- bootClassic(x = indicatorsHH,
                           params = "anc1")
```

---

bootPROBIT

*PROBIT statistics function for bootstrap estimation*


---

**Description**

PROBIT statistics function for bootstrap estimation

**Usage**

```
bootPROBIT(x, params, threshold = THRESHOLD)
```

**Arguments**

x	A data frame with <b>primary sampling unit (PSU)</b> in column named psu and with data column/s containing the continuous variable/s of interest with column names corresponding to params values
params	A vector of column names corresponding to the continuous variables of interest contained in x
threshold	cut-off value for continuous variable to differentiate case and non-case

**Value**

A numeric vector of the PROBIT estimate of each continuous variable of interest with length equal to length(params)

**Examples**

```
# Example call to bootBW function:

bootPROBIT(x = indicatorsCH1,
            params = "muac1",
            threshold = 115)
```

---

indicatorsCH1 *Child Morbidity, Health Service Coverage, Anthropometry*

---

### Description

Child indicators on morbidity, health service coverage and anthropometry calculated from survey data collected in survey conducted in 4 districts from 3 regions in Somalia.

### Usage

indicatorsCH1

### Format

A data frame with 14 columns and 3090 rows.

<b>Variable</b>	<b>Description</b>
psu	The PSU identifier. This must use the same coding system used to identify the PSUs that is used in the indicators d
mID	The mother identifier
cID	The child identifier
ch1	Diarrhoea in the past 2 weeks (0/1)
ch2	Fever in the past 2 weeks (0/1)
ch3	Cough in the past 2 weeks (0/1)
ch4	Immunisation card (0/1)
ch5	BCG immunisation (0/1)
ch6	Vitamin A coverage in the past month (0/1)
ch7	Anti-helminth coverage in the past month (0/1)
sex	Sex of child
muac1	Mid-upper arm circumference in mm
muac2	Mid-upper arm circumference in mm
oedema	Oedema (0/1)

### Source

Mother and child health and nutrition survey in 3 regions of Somalia

### Examples

indicatorsCH1

indicatorsCH2

*Infant and Child Feeding Index***Description**

Infant and young child feeding indicators using the infant and child feeding index (ICFI) by Arimond and Ruel. Calculated from survey data collected in survey conducted in 4 districts from 3 regions in Somalia.

**Usage**

indicatorsCH2

**Format**

A data frame with 13 columns and 2083 rows.

**Variable**      **Description**

psu	The PSU identifier. This must use the same coding system used to identify the PSUs that is used in the indicators
mID	The mother identifier
cID	The child identifier
ebf	Exclusive breastfeeding (0/1)
cbf	Continued breastfeeding (0/1)
ddd	Dietary diversity (0/1)
mfd	Meal frequency (0/1)
icfi	Infant and child feeding index (from 0 to 6)
iycf	Good IYCF
icfiProp	Good ICFI
age	Child's age
bf	Child is breastfeeding (0/1)
bfStop	Age in months child stopped breastfeeding

**Source**

Mother and child health and nutrition survey in 3 regions of Somalia

**Examples**

indicatorsCH2

indicatorsHH

*Mother Indicators Dataset***Description**

Mother indicators for health and nutrition calculated from survey data collected in survey conducted in 4 districts from 3 regions in Somalia.

**Usage**

indicatorsHH

**Format**

A data frame with 24 columns and 2136 rows:

<b>Variable</b>	<b>Description</b>
psu	The PSU identifier. This must use the same coding system used to identify the PSUs that is used in the indicators d
mID	The mother identifier
mMUAC	Mothers with mid-upper arm circumference < 230 mm (0/1)
anc1	At least 1 antenatal care visit with a trained health professional (0/1)
anc2	At least 4 antenatal care visits with any service provider (0/1)
anc3	FeFol coverage (0/1)
anc4	Vitamin A coverage (0/1)
wash1	Improved sources of drinking water (0/1)
wash2	Improved sources of other water (0/1)
wash3	Probable safe drinking water (0/1)
wash4	Number of litres of water collected in a day
wash5	Improved toilet facilities (0/1)
wash6	Human waste disposal practices / behaviour (0/1)
wash7a	Handwashing score (from 0 to 5)
wash7b	Handwashing score of 5 (0/1)
hhs1	Household hunger score (from 0 to 6)
hhs2	Little or no hunger (0/1)
hhs3	Moderate hunger (0/1)
hhs4	Severe hunger (0/1)
mfg	Mother's dietary diversity score
pVitA	Plant-based vitamin A-rich foods (0/1)
aVitA	Animal-based vitamin A-rich foods (0/1)
xVitA	Any vitamin A-rich foods (0/1)
iron	Iron-rich foods (0/1)

**Source**

Mother and child health and nutrition survey in 3 regions of Somalia

**Examples**

```
indicatorsHH
```

---

```
recode
```

```
Recode
```

---

**Description**

Utility function that recodes variables based on user recode specifications. Handles both numeric or factor variables.

**Usage**

```
recode(var, recodes, afr, anr = TRUE, levels)
```

**Arguments**

var Variable to recode

recodes Character string of recode specifications:

- Recode specifications in a character string separated by semicolons of the form input=output as in: "1=1;2=1;3:6=2;else=NA"

\item If an input value satisfies more than one specification, then the first (reading from left to right) is applied

\item If no specification is satisfied, then the input value is carried over to the result unchanged

\item `\code{NA}` is allowed on both input and output

\item The following recode specifications are supported:

```
\tabular{lll}{
\strong{Specification} \tab \strong{Example}          \tab \strong{Notes}
Single values          \tab \code{9=NA}              \tab
Set of values          \tab \code{c(1,2,5)=1}         \tab The left-hand-side is any
                        \tab \code{seq(1,9,2)='odd'}   \tab
                        \tab \code{1:10=1}            \tab
Range of values        \tab \code{7:9=3}             \tab Special values \code{lo} ar
                        \tab \code{lo:115=1}          \tab
Other values           \tab \code{else=NA}           \tab
}
```

\item Character values are quoted as in :

```
\code{recodes = "c(1,2,5)='sanitary' else='unsanitary'"}}
```



\item The output may be the (scalar) result of a function call as in:

```
\code{recodes = "999=median(var, na.rm = TRUE)"}
```

\item Users are advised to carefully check the results of `recode()` calls with any outputs that are the results of a function call.

\item The output may be the (scalar) value of a variable as in:

```
\code{recodes = "999=scalarVariable"}
```

\item If all of the output values are numeric, and if `'afr'` is `FALSE`, then a numeric result is returned; if `var` is a factor then (by default) so is the result.

afr	Return a factor. Default is TRUE if var is a factor and is FALSE otherwise
anr	Coerce result to numeric (default is TRUE)
levels	Order of the levels in the returned factor; the default is to use the sort order of the level names.

## Value

Recoded variable

## Examples

```
# Recode values from 1 to 9 to various specifications
var <- sample(x = 1:9, size = 100, replace = TRUE)

# Recode single values
recode(var = var, recodes = "9=NA")

# Recode set of values
recode(var = var, recodes = "c(1,2,5)=1")

# Recode range of values
recode(var = var, recodes = "1:3=1;4:6=2;7:9=3")

# Recode other values
recode(var = var, recodes = "c(1,2,5)=1;else=NA")
```

**Description**

Dataset containing cluster population weights for use in performing posterior weighting with the blocked weighted bootstrap approach. This dataset is from a mother and child health and nutrition survey conducted in 4 districts from 3 regions in Somalia.

**Usage**

```
villageData
```

**Format**

A data frame with 6 columns and 117 rows:

<b>Variable</b>	<b>Description</b>
region	Region in Somalia from which the cluster belongs to
district	District in Somalia from which the cluster belongs to
psu	The PSU identifier. This must use the same coding system used to identify the PSUs that is used in the indicators
lon	Longitude coordinate of the cluster
lat	Latitude coordinate of the cluster
pop	Population size of the cluster

**Source**

Mother and child health and nutrition survey in 3 regions of Somalia

**Examples**

```
villageData
```

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