

# Package ‘samplingbook’

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samplingbook-package    *Survey Sampling Procedures*

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## Description

Sampling procedures from the book 'Stichproben. Methoden und praktische Umsetzung mit R' by Goeran Kauermann and Helmut Kuechenhoff (2010)

## Details

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Type:        Package  
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stratamean	Stratified Sample Mean Estimation
stratasamp	Sample Size Calculation for Stratified Sampling
tax	Hypothetical Tax Refund Data Frame

### Author(s)

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### References

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

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election

*German Parliament Election Data*

---

### Description

Data frame with number of citizens eligible to vote and results of the elections in 2002 and 2005 for the German Bundestag, the first chamber of the German parliament.

### Usage

```
data(election)
```

### Format

A data frame with 299 observations (corresponding to constituencies) on the following 13 variables.

state factor, the 16 German federal states

eligible\_02 number of citizens eligible to vote in 2002

SPD\_02 a numeric vector, percentage for the Social Democrats SPD in 2002

UNION\_02 a numeric vector, percentage for the conservative Christian Democrats CDU/CSU in 2002

GREEN\_02 a numeric vector, percentage for the Greens in 2002  
FDP\_02 a numeric vector, percentage for the Liberal Party FDP in 2002  
LEFT\_02 a numeric vector, percentage for the Left Party PDS in 2002  
eligible\_05 number of citizens eligible to vote in 2005  
SPD\_05 a numeric vector, percentage for the Social Democrats SPD in 2005  
UNION\_05 a numeric vector, percentage for the conservative Christian Democrats CDU/CSU in 2005  
GREEN\_05 a numeric vector, percentage for the Greens in 2005  
FDP\_05 a numeric vector, percentage for the Liberal Party FDP in 2005  
LEFT\_05 a numeric vector, percentage for the Left Party in 2005

## Details

### German Federal Elections

Half of the Members of the German Bundestag are elected directly from Germany's 299 constituencies, the other half one on the parties' land lists. Accordingly, each voter has two votes in the elections to the German Bundestag. The first vote, allowing voters to elect their local representatives to the Bundestag, decides which candidates are sent to Parliament from the constituencies. The second vote is cast for a party list. And it is this second vote that determines the relative strengths of the parties represented in the Bundestag. At least 598 Members of the German Bundestag are elected in this way. In addition to this, there are certain circumstances in which some candidates win what are known as 'overhang mandates' when the seats are being distributed.

The data set provides the percentage of second votes for each party, which determines the number of seats each party gets in parliament. These percentages are calculated by the number of votes for a party divided by number of valid votes.

## Source

The data is provided by the R package flexclust.

## References

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

Homepage of the Bundestag: <http://www.bundestag.de>.

Friedrich Leisch. A Toolbox for K-Centroids Cluster Analysis. Computational Statistics and Data Analysis, 51 (2), 526-544, 2006.

## Examples

```
data(election)
summary(election)

# 1) Draw a simple sample of size n=20
n <- 20
set.seed(67396)
```

```

index <- sample(1:nrow(election), size=n)
sample1 <- election[index,]
Smean(sample1$SPD_02, N=nrow(election))
# true mean
mean(election$SPD_02)

# 2) Estimate sample size to forecast proportion of SPD in election of 2005
sample.size.prop(e=0.01, P=mean(election$SPD_02), N=Inf)

# 3) Usage of previous knowledge by model based estimation
# draw sample of size n = 20
N <- nrow(election)
set.seed(67396)
sample <- election[sort(sample(1:N, size=20)),]
# secondary information SPD in 2002
X.mean <- mean(election$SPD_02)
# forecast proportion of SPD in election of 2005
mbes(SPD_05 ~ SPD_02, data=sample, aux=X.mean, N=N, method='all')
# true value
Y.mean <- mean(election$SPD_05)
Y.mean
# Use a second predictor variable
X.mean2 <- c(mean(election$SPD_02),mean(election$GREEN_02))
# forecast proportion of SPD in election of 2005 with two predictors
mbes(SPD_05 ~ SPD_02+GREEN_02, data=sample, aux=X.mean2, N=N, method='regr')

```

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htestimate

*Horvitz-Thompson Estimator*


---

## Description

Calculates Horvitz-Thompson estimate with different methods for variance estimation such as Yates and Grundy, Hansen-Hurwitz and Hajek.

## Usage

```
htestimate(y, N, PI, pk, pik, method = 'yg')
```

## Arguments

y	vector of observations
N	integer for population size
PI	square matrix of second order inclusion probabilities with n rows and cols. It is necessary to be specified for variance estimation by methods 'ht' and 'yg'.
pk	vector of first order inclusion probabilities of length n for the sample elements. It is necessary to be specified for variance estimation by methods 'hh' and 'ha'.
pik	an optional vector of first order inclusion probabilities of length N for the population elements . It can be used for variance estimation by method 'ha'.

method method to be used for variance estimation. Options are 'yg' (Yates and Grundy) and 'ht' (Horvitz-Thompson), approximate options are 'hh' (Hansen-Hurwitz) and 'ha' (Hajek).

### Details

For using methods 'yg' or 'ht' has to be provided matrix PI, and for 'hh' and 'ha' has to be specified vector pk of inclusion probabilities. Additionally, for Hajek method 'ha' can be specified pik. Unless, an approximate Hajek method is used.

### Value

The function `htestimate` returns a value, which is a list consisting of the components

`call` is a list of call components: y observations, N population size, PI inclusion probabilities, pk inclusion probabilities of sample, pik full inclusion probabilities and method method for variance estimation

`mean` mean estimate

`se` standard error of the mean estimate

### Author(s)

Juliane Manitz

### References

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

### See Also

[pps.sampling](#)

### Examples

```
data(influenza)
summary(influenza)

# pps.sampling()
set.seed(108506)
pps <- pps.sampling(z=influenza$population,n=20,method='midzuno')
sample <- influenza[pps$sample,]
# htestimate()
N <- nrow(influenza)
# exact variance estimate
PI <- pps$PI
htestimate(sample$cases, N=N, PI=PI, method='yg')
htestimate(sample$cases, N=N, PI=PI, method='ht')
# approximate variance estimate
pk <- pps$pik[pps$sample]
htestimate(sample$cases, N=N, pk=pk, method='hh')
```

```

pik <- pps$pik
htestimate(sample$cases, N=N, pk=pk, pik=pik, method='ha')
# without pik just approximate calculation of Hajek method
htestimate(sample$cases, N=N, pk=pk, method='ha')
# calculate confidence interval based on normal distribution for number of cases
est.ht <- htestimate(sample$cases, N=N, PI=PI, method='ht')
est.ht$mean*N
lower <- est.ht$mean*N - qnorm(0.975)*N*est.ht$se
upper <- est.ht$mean*N + qnorm(0.975)*N*est.ht$se
c(lower,upper)
# true number of influenza cases
sum(influenza$cases)

```

---

influenza	<i>Population and Cases of Influenza for Administrative Districts of Germany</i>
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---

### Description

The data frame `influenza` provides cases of influenza and inhabitants for administrative districts of Germany in 2007.

### Usage

```
data(influenza)
```

### Format

A data frame with 424 observations on the following 4 variables.

`id` a numeric vector

`district` a factor with levels LK Aachen, LK Ahrweiler, ..., SK Zweibruecken, names of administrative districts in Germany

`population` a numeric vector specifying the number of inhabitants in the specific administrative district

`cases` a numeric vector specifying the number of influenza cases in the specific administrative district

### Details

Data of 2007. If you want to use the population numbers in the future, be aware of local governmental reorganizations, e.g. district unions.

### Source

Database SurvStat of Robert Koch-Institute. Many thanks to Hermann Claus.

## References

Database of Robert Koch-Institute <http://www3.rki.de/SurvStat/>

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

## Examples

```
data(influenza)
summary(influenza)

# 1) Usage of pps.sampling
set.seed(108506)
pps <- pps.sampling(z=influenza$population,n=20,method='midzuno')
pps
sample <- influenza[pps$sample,]
sample

# 2) Usage of htestimate
set.seed(108506)
pps <- pps.sampling(z=influenza$population,n=20,method='midzuno')
sample <- influenza[pps$sample,]
# htestimate()
N <- nrow(influenza)
# exact variance estimate
PI <- pps$PI
htestimate(sample$cases, N=N, PI=PI, method='ht')
htestimate(sample$cases, N=N, PI=PI, method='yg')
# approximate variance estimate
pk <- pps$pik[pps$sample]
htestimate(sample$cases, N=N, pk=pk, method='hh')
pik <- pps$pik
htestimate(sample$cases, N=N, pk=pk, pik=pik, method='ha')
# without pik just approximative calculation of Hajek method
htestimate(sample$cases, N=N, pk=pk, method='ha')
# calculate confidence interval based on normal distribution for number of cases
est.ht <- htestimate(sample$cases, N=N, PI=PI, method='ht')
est.ht$mean*N
lower <- est.ht$mean*N - qnorm(0.975)*N*est.ht$se
upper <- est.ht$mean*N + qnorm(0.975)*N*est.ht$se
c(lower,upper)
# true number of influenza cases
sum(influenza$cases)
```

## Description

mbes is used for model based estimation of population means using auxiliary variables. Difference, ratio and regression estimates are available.



**Usage**

```
mbes(formula, data, aux, N = Inf, method = 'all', level = 0.95, ...)
```

**Arguments**

formula	object of class formula (or one that can be coerced to that class): symbolic description for connection between primary and secondary information
data	data frame containing variables in the model
aux	known mean of auxiliary variable, which provides secondary information
N	positive integer for population size. Default is N=Inf, which means that calculations are carried out without finite population correction.
method	estimation method. Options are 'simple', 'diff', 'ratio', 'regr', 'all'. Default is method='all'.
level	coverage probability for confidence intervals. Default is level=0.95.
...	further options for linear regression model

**Details**

The option method='simple' calculates the simple sample estimation without using the auxiliary variable. The option method='diff' calculates the difference estimate, method='ratio' the ratio estimate, and method='regr' the regression estimate which is based on the selected model. The option method='all' calculates the simple and all model based estimates. For methods 'diff', 'ratio' and 'all' the formula has to be  $y \sim x$  with  $y$  primary and  $x$  secondary information. For method 'regr', it is the symbolic description of the linear regression model. In this case, it can be used more than one auxiliary variable. Thus, aux has to be a vector of the same length as the number of auxiliary variables in order as specified in the formula.

**Value**

The function mbes returns an object, which is a list consisting of the components

call	is a list of call components: formula formula, data data frame, aux given value for mean of auxiliary variable, N population size, type type of model based estimation and level coverage probability for confidence intervals
info	is a list of further information components: N population size, n sample size, p number of auxiliary variables, aux true mean of auxiliary variables in population and x.mean sample means of auxiliary variables
simple	is a list of result components, if method='simple' or method='all' is selected: mean mean estimate of population mean for primary information, se standard error of the mean estimate, and ci vector of confidence interval boundaries
diff	is a list of result components, if method='diff' or method='all' is selected: mean mean estimate of population mean for primary information, se standard error of the mean estimate, and ci vector of confidence interval boundaries
ratio	is a list of result components, if method='ratio' or method='all' is selected: mean mean estimate of population mean for primary information, se standard error of the mean estimate, and ci vector of confidence interval boundaries

`regr` is a list of result components, if `type='regr'` or `type='all'` is selected: mean estimate of population mean for primary information, se standard error of mean estimate, `ci` vector of confidence interval boundaries, and `model` underlying linear regression model

### Author(s)

Juliane Manitz

### References

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

### See Also

[Smean](#), [Sprop](#)

### Examples

```
## 1) simple suppositious example
data(pop)
# Draw a random sample of size=3
set.seed(802016)
data <- pop[sample(1:5, size=3),]
names(data) <- c('id','x','y')
# difference estimator
mbes(formula=y~x, data=data, aux=15, N=5, method='diff', level=0.95)
# ratio estimator
mbes(formula=y~x, data=data, aux=15, N=5, method='ratio', level=0.95)
# regression estimator
mbes(formula=y~x, data=data, aux=15, N=5, method='regr', level=0.95)

## 2) Bundestag election
data(election)
# draw sample of size n = 20
N <- nrow(election)
set.seed(67396)
sample <- election[sort(sample(1:N, size=20)),]
# secondary information SPD in 2002
X.mean <- mean(election$SPD_02)
# forecast proportion of SPD in election of 2005
mbes(SPD_05 ~ SPD_02, data=sample, aux=X.mean, N=N, method='all')
# true value
Y.mean <- mean(election$SPD_05)
Y.mean
# Use a second predictor variable
X.mean2 <- c(mean(election$SPD_02),mean(election$GREEN_02))
# forecast proportion of SPD in election of 2005 with two predictors
mbes(SPD_05 ~ SPD_02+GREEN_02, data=sample, aux=X.mean2, N=N, method='regr')

## 3) money sample
```

```

data(money)
mu.X <- mean(money$X)
x <- money$X[which(!is.na(money$y))]
y <- na.omit(money$y)
# estimation
mbes(y~x, aux=mu.X, N=13, method='all')

## 4) model based two-phase sampling with mbes()
id <- 1:1000
x <- rep(c(1,0,1,0),times=c(10,90,70,830))
y <- rep(c(1,0,NA),times=c(15,85,900))
phase <- rep(c(2,1), times=c(100,900))
data <- data.frame(id,x,y,phase)
# mean of x out of first phase
mean.x <- mean(data$x)
mean.x
N1 <- length(data$x)
# calculation of estimation for y
est.y <- mbes(y~x, data=data, aux=mean.x, N=N1, method='ratio')
est.y
# correction of standard error with uncertainty in first phase
v.y <- var(data$y, na.rm=TRUE)
se.y <- sqrt(est.y$ratio$se^2 + v.y/N1)
se.y
# corrected confidence interval
lower <- est.y$ratio$mean - qnorm(0.975)*se.y
upper <- est.y$ratio$mean + qnorm(0.975)*se.y
c(lower, upper)

```

---

money

*Money Data Frame*

---

### Description

Data provides guesses and true values for students wallet money.

### Usage

```
data(money)
```

### Format

A data frame with 13 observations (corresponding to the students) on the following 3 variables.

`id` a numeric vector of identification number

`X` a numeric vector of secondary information, guesses of money in the wallet

`y` a numeric vector of primary information, counted money in the wallet. NA means subject was not included into the sample.

### Details

In a lesson an experiment was made, in which the students were asked to guess the current amount of money in their wallet. A simple sample of these students was drawn, who counted the money in their wallet exactly. Using this secondary information, model based estimation of the population mean is possible.

### References

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

### Examples

```
data(money)
print(money)

# Usage of mbes()
mu.X <- mean(money$X)
x <- money$X[which(!is.na(money$y))]
y <- na.omit(money$y)
# estimation
mbes(y~x, aux=mu.X, N=13, method='all')
```

---

pop

*Small Suppositious Sampling Example*

---

### Description

pop is a suppositious data frame for a small population with 5 elements. It is used for simple illustration of survey sampling estimators.

### Usage

```
data(pop)
```

### Format

A data frame with 5 observations on the following 3 variables.

id a numeric vector of individual identification values

X a numeric vector of first characteristic

Y a numeric vector of second characteristic

### References

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

**Examples**

```

data(pop)
print(pop)

## 1) Usage of Smean()
data(pop)
Y <- pop$Y
Y
# Draw a random sample pop size=3
set.seed(93456)
y <- sample(x = Y, size = 3)
sort(y)
# Estimation with infiniteness correction
est <- Smean(y = y, N = length(pop$Y))
est

## 2) Usage of mbes()
data(pop)
# Draw a random sample of size=3
set.seed(802016)
data <- pop[sample(1:5, size=3),]
names(data) <- c('id', 'x', 'y')
# difference estimator
mbes(formula=y~x, data=data, aux=15, N=5, method='diff', level=0.95)
# ratio estimator
mbes(formula=y~x, data=data, aux=15, N=5, method='ratio', level=0.95)
# regression estimator
mbes(formula=y~x, data=data, aux=15, N=5, method='regr', level=0.95)

```

pps.sampling

*Sampling with Probabilities Proportional to Size***Description**

The function provides sample techniques with sampling probabilities which are proportional to the size of a quantity  $z$ .

**Usage**

```
pps.sampling(z, n, id = 1:N, method = 'sampford', return.PI = FALSE)
```

**Arguments**

<code>z</code>	vector of quantities which determine the sampling probabilities in the population
<code>n</code>	positive integer for sample size
<code>id</code>	an optional vector with identification values for population elements. Default is 'id = 1:N', where 'N' is length of 'z'.

method	the sampling method to be used. Options are 'sampford', 'tille', 'midzuno' or 'madow'.
return.PI	logical. If TRUE the pairwise inclusion probabilities for all individuals in the population are returned.

### Details

The different methods vary in their run time. Therefore, method='sampford' is stopped if  $N > 200$  or if  $n/N < 0.3$ . method='tille' is stopped if  $N > 500$ . In case of large populations use method='midzuno' or method='madow'.

### Value

The function `pps.sampling` returns a value, which is a list consisting of the components

call	is a list of call components: z vector of quantity data, n sample size, id identification values, and method sampling method
sample	resulted sample
pik	inclusion probabilities
PI	sample second order inclusion probabilities
PI.full	full second order inclusion probabilities

### Author(s)

Juliane Manitz

### References

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

### See Also

[htestimate](#)

### Examples

```
## 1) simple suppositious example
data <- data.frame(id = 1:7, z = c(1.8, 2 ,3.2 ,2.9 ,1.5 ,2.0 ,2.2))
# Usage of pps.sampling for Sampford method
set.seed(178209)
pps.sample_sampford <- pps.sampling(z=data$z, n=2, method='sampford', return.PI=FALSE)
pps.sample_sampford
# sampling elements
id.sample <- pps.sample_sampford$sample
id.sample
# other methods
set.seed(178209)
pps.sample_tille <- pps.sampling(z=data$z, n=2, method='tille')
pps.sample_tille
```

```

set.seed(178209)
pps.sample_midzuno <- pps.sampling(z=data$z, n=2, method='midzuno')
pps.sample_midzuno
set.seed(178209)
pps.sample_madow <- pps.sampling(z=data$z, n=2, method='madow')
pps.sample_madow

## 2) influenza
data(influenza)
summary(influenza)

set.seed(108506)
pps <- pps.sampling(z=influenza$population,n=20,method='midzuno')
pps
sample <- influenza[pps$sample,]
sample

```

---

sample.size.mean

*Sample Size Calculation for Mean Estimation*


---

### Description

The function `sample.size.mean` returns the sample size needed for mean estimations either with or without consideration of finite population correction.

### Usage

```
sample.size.mean(e, S, N = Inf, level = 0.95)
```

### Arguments

e	positive number specifying the precision which is half width of confidence interval
S	standard deviation in population
N	positive integer for population size. Default is N=Inf, which means that calculations are carried out without finite population correction.
level	coverage probability for confidence intervals. Default is level=0.95.

### Value

The function `sample.size.mean` returns a value, which is a list consisting of the components

call	is a list of call components: e precision, S standard deviation in population, and N integer for population size
n	estimate of sample size

### Author(s)

Juliane Manitz

## References

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

## See Also

[Smean](#), [sample.size.prop](#)

## Examples

```
# sample size for precision e=4
sample.size.mean(e=4,S=10,N=300)
# sample size for precision e=1
sample.size.mean(e=1,S=10,N=300)
```

---

sample.size.prop

*Sample Size Calculation for Proportion Estimation*

---

## Description

The function `sample.size.prop` returns the sample size needed for proportion estimation either with or without consideration of finite population correction.

## Usage

```
sample.size.prop(e, P = 0.5, N = Inf, level = 0.95)
```

## Arguments

e	positive number specifying the precision which is half width of confidence interval
P	expected proportion of events with domain between values 0 and 1. Default is $P=0.5$ .
N	positive integer for population size. Default is $N=Inf$ , which means that calculations are carried out without finite population correction.
level	coverage probability for confidence intervals. Default is $level=0.95$ .

## Details

For meaningful calculation, precision  $e$  should be chosen smaller than 0.5, because the domain of  $P$  is between values 0 and 1. Furthermore, precision  $e$  should be smaller than proportion  $P$ , respectively  $(1-P)$ .



**Value**

The function `sample.size.prop` returns a value, which is a list consisting of the components

<code>call</code>	is a list of call components <code>e</code> precision, <code>P</code> expected proportion, <code>N</code> population size, and level coverage probability for confidence intervals
<code>n</code>	estimate of sample size

**Author(s)**

Juliane Manitz

**References**

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

**See Also**

[Sprop](#), [sample.size.mean](#)

**Examples**

```
## 1) examples with different precisions
# precision 1% for election forecast of SPD in 2005
sample.size.prop(e=0.01, P=0.5, N=Inf)
data(election)
sample.size.prop(e=0.01, P=mean(election$SPD_02), N=Inf)
# precision 5% for questionnaire
sample.size.prop(e=0.05, P=0.5, N=300)
sample.size.prop(e=0.05, P=0.5, N=Inf)
# precision 10%
sample.size.prop(e=0.1, P=0.5, N=300)
sample.size.prop(e=0.1, P=0.5, N=1000)

## 2) tables in the book
# table 2.2
P_vector <- c(0.2, 0.3, 0.4, 0.5)
N_vector <- c(10, 100, 1000, 10000)
results <- matrix(NA, ncol=4, nrow=4)
for (i in 1:length(P_vector)){
  for (j in 1:length(N_vector)){
    x <- try(sample.size.prop(e=0.1, P=P_vector[i], N=N_vector[j]))
    if (class(x)=='try-error') {results[i,j] <- NA}
    else {results[i,j] <- x$n}
  }
}
dimnames(results) <- list(paste('P=',P_vector, sep=''), paste('N=',N_vector, sep=''))
results
# table 2.3
P_vector <- c(0.5, 0.1)
e_vector <- c(0.1, 0.05, 0.03, 0.02, 0.01)
```

```

results <- matrix(NA, ncol=2, nrow=5)
for (i in 1:length(e_vector)){
  for (j in 1:length(P_vector)){
    x <- try(sample.size.prop(e=e_vector[i], P=P_vector[j], N=Inf))
    if (class(x)=='try-error') {results[i,j] <- NA}
    else {results[i,j] <- x$n}
  }
}
dimnames(results) <- list(paste('e=',e_vector, sep=' '), paste('P=',P_vector, sep=' '))
results

```

---

Smean

*Sampling Mean Estimation*


---

### Description

The function `Smean` estimates the population mean out of simple samples either with or without consideration of finite population correction.

### Usage

```
Smean(y, N = Inf, level = 0.95)
```

### Arguments

<code>y</code>	vector of sample data
<code>N</code>	positive integer specifying population size. Default is <code>N=Inf</code> , which means that calculations are carried out without finite population correction.
<code>level</code>	coverage probability for confidence intervals. Default is <code>level=0.95</code> .

### Value

The function `Smean` returns a value, which is a list consisting of the components

<code>call</code>	is a list of call components: <code>y</code> vector with sample data, <code>n</code> sample size, <code>N</code> population size, <code>level</code> coverage probability for confidence intervals
<code>mean</code>	mean estimate
<code>se</code>	standard error of the mean estimate
<code>ci</code>	vector of confidence interval boundaries

### Author(s)

Juliane Manitz

**References**

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

**See Also**

[Sprop](#), [sample.size.mean](#)

**Examples**

```
data(pop)
Y <- pop$Y
Y
# Draw a random sample of size=3
set.seed(93456)
y <- sample(x = Y, size = 3)
sort(y)
# Estimation with infiniteness correction
est <- Smean(y = y, N = length(pop$Y))
est
```

---

Sprop

*Sampling Proportion Estimation*

---

**Description**

The function Sprop estimates the proportion out of samples either with or without consideration of finite population correction. Different methods for calculating confidence intervals for example based on binomial distribution (Agresti and Coull or Clopper-Pearson) or based on hypergeometric distribution are used.

**Usage**

```
Sprop(y, m, n = length(y), N = Inf, level = 0.95)
```

**Arguments**

y	vector of sample data containing values 0 and 1
m	an optional non-negative integer for number of positive events
n	an optional positive integer for sample size. Default is $n = \text{length}(y)$ .
N	positive integer for population size. Default is $N = \text{Inf}$ , which means calculations are carried out without finite population correction.
level	coverage probability for confidence intervals. Default is $\text{level} = 0.95$ .

**Details**

Sprop can be called by usage of a data vector y with the observations 1 for event and 0 for failure. Moreover, it can be called by specifying the number of events m and trials n.

**Value**

The function `Sprop` returns a value, which is a list consisting of the components

<code>call</code>	is a list of call components: <code>y</code> sample data, <code>m</code> number of positive events in the sample, <code>n</code> sample size, <code>N</code> population size, <code>level</code> coverage probability for confidence intervals
<code>p</code>	proportion estimate
<code>se</code>	standard error of the proportion estimate
<code>ci</code>	is a list of confidence interval boundaries for proportion. In case of a finite population of size <code>N</code> , it is given <code>approx</code> , the hypergeometric confidence interval with normal distribution approximation, and <code>exact</code> , the exact hypergeometric confidence interval. If the population is very large <code>N=Inf</code> , it is calculated <code>bin</code> , the binomial confidence interval, which is asymptotic, <code>cp</code> the exact confidence interval based on binomial distribution (Clopper-Pearson), and <code>ac</code> , the asymptotic confidence interval based on binomial distribution by Wilson (Agresti and Coull (1998)).
<code>nr</code>	In case of finite population of size <code>N</code> , it is given a list of confidence interval boundaries for number in population with <code>approx</code> , the hypergeometric confidence interval with normal distribution approximation, and <code>exact</code> , the exact hypergeometric confidence interval.

**Author(s)**

Juliane Manitz

**References**

Kauermann, Goeran/Kuechenhoff, Helmut (2010): *Stichproben. Methoden und praktische Umsetzung mit R*. Springer.

Agresti, Alan/Coull, Brent A. (1998): Approximate Is Better than 'Exact' for Interval Estimation of Binomial Proportions. *The American Statistician*, Vol. 52, No. 2, pp. 119-126.

**See Also**

[Smean, sample.size.prop](#)

**Examples**

```
# 1) Survey in company to upgrade office climate
Sprop(m=45, n=100, N=300)
Sprop(m=2, n=100, N=300)

# 2) German opinion poll for 03/07/09 with
# (http://www.wahlrecht.de/umfragen/politbarometer.htm)
# a) 302 of 1206 respondents who would elect SPD.
# b) 133 of 1206 respondents who would elect the Greens.
Sprop(m=302, n=1206, N=Inf)
Sprop(m=133, n=1206, N=Inf)
```

```
# 3) Rare disease of animals (sample size n=500 of N=10.000 animals, one infection)
# for 95% one sided confidence level use level=0.9
Sprop(m=1, n=500, N=10000, level=0.9)

# 4) call with data vector y
y <- c(0,0,1,0,1,0,0,0,1,1,0,0,1)
Sprop(y=y, N=200)
# is the same as
Sprop(m=5, n=13, N=200)
```

---

stratamean

*Stratified Sample Mean Estimation*


---

### Description

The function `stratamean` estimates the population mean out of stratified samples either with or without consideration of finite population correction.

### Usage

```
stratamean(y, h, Nh, wh, level = 0.95, eae = FALSE)
```

### Arguments

<code>y</code>	vector of target variable.
<code>h</code>	vector of stratifying variable.
<code>Nh</code>	vector of sizes of every stratum, which has to be supplied in alphabetical or numerical order of the categories of <code>h</code> .
<code>wh</code>	vector of weights of every stratum, which has to be supplied in alphabetical or numerical order of the categories of <code>h</code> .
<code>level</code>	coverage probability for confidence intervals. Default is <code>level=0.95</code> .
<code>eae</code>	TRUE for extensive output with the result in each and every stratum. Default is <code>eae=FALSE</code> .

### Details

If the absolute stratum sizes `Nh` are given, the variances are calculated with finite population correction. Otherwise, if the stratum weights `wh` are given, the variances are calculated without finite population correction.

### Value

The function `stratamean` returns a value, which is a list consisting of the components

<code>call</code>	is a list of call components: <code>y</code> target variable in sample data, <code>h</code> stratifying variable in sample data, <code>Nh</code> sizes of every stratum, <code>wh</code> weights of every stratum, <code>fpc</code> finite population correction, <code>level</code> coverage probability for confidence intervals
-------------------	--

mean	mean estimate for population
se	standard error of the mean estimate for population
ci	vector of confidence interval boundaries for population

**Author(s)**

Shuai Shao and Juliane Manitz

**References**

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

**See Also**

[Smean](#), [Sprop](#)

**Examples**

```
# random data
testy <- rnorm(100)
testh <- c(rep("male",40), rep("female",60))
stratamean(testy, testh, wh=c(0.5, 0.5))
stratamean(testy, testh, wh=c(0.5, 0.5), eae=TRUE)

# tax data
data(tax)
summary(tax)

nh <- as.vector(table(tax$class))
wh <- nh/sum(nh)
stratamean(y=tax$diff, h=as.vector(tax$class), wh=wh, eae=TRUE)
```

---

stratasamp

*Sample Size Calculation for Stratified Sampling*

---

**Description**

The function `stratasamp` calculates the sample size for each stratum depending on type of allocation.

**Usage**

```
stratasamp(n, Nh, Sh = NULL, Ch = NULL, type = 'prop')
```

**Arguments**

n	positive integer specifying sampling size.
Nh	vector of population sizes of each stratum.
Sh	vector of standard deviation in each stratum.
Ch	vector of cost for a sample in each stratum.
type	type of allocation. Default is type='prop' for proportional, alternatives are type='opt' for optimal and type='costopt' for cost-optimal.

**Value**

The function `stratasamp` returns a matrix, which lists the strata and the sizes of observation depending on type of allocation.

**Author(s)**

Shuai Shao and Juliane Manitz

**References**

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

**See Also**

[stratamean](#), [stratasize](#), [sample.size.mean](#)

**Examples**

```
#random proportional stratified sample
stratasamp(n=500, Nh=c(5234,2586,649,157))
stratasamp(n=500, Nh=c(5234,2586,649,157), Sh=c(251,1165,8035,24725), type='opt')
```

---

stratasize

*Sample Size Determination for Stratified Sampling*

---

**Description**

The function `stratasize` determinates the total size of stratified samples depending on type of allocation and determinated by specified precision.

**Usage**

```
stratasize(e, Nh, Sh, level = 0.95, type = 'prop')
```

**Arguments**

e	positive number specifying sampling precision.
Nh	vector of population sizes in each stratum.
Sh	vector of standard deviation in each stratum.
level	coverage probability for confidence intervals. Default is level=0.95.
type	type of allocation. Default is type='prop' for proportional, alternative is type='opt' for optimal.

**Value**

The function `stratasize` returns a value, which is a list consisting of the components

call	is a list of call components: e specified precision, Nh population sizes of every stratum, Sh standard deviation of every stratum, method type of allocation, level coverage probability for confidence intervals.
n	determined total sample size.

**Author(s)**

Shuai Shao

**References**

Kauermann, Goeran/Kuechenhoff, Helmut (2011): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

**See Also**

[stratasamp](#), [stratamean](#)

**Examples**

```
#random proportional stratified sample
stratasize(e=0.1, Nh=c(100000,300000,600000), Sh=c(1,2,3))

#random optimal stratified sample
stratasize(e=0.1, Nh=c(100000,300000,600000), Sh=c(1,2,3), type="opt")
```



---

submean                      *Sub-sample Mean Estimation*

---

### Description

The function submean estimates the population mean out of sub-samples (two-stage samples) either with or without consideration of finite population correction in both stages.

### Usage

```
submean(y, PSU, N, M, N1, m.weight, n.weight, method = 'simple', level = 0.95)
```

### Arguments

y	vector of target variable.
PSU	vector of grouping variable which indicates the primary unit for each sample element.
N	positive integer specifying population size
M	positive integer specifying the number of primary units in the population.
N1	vector of sample sizes in each primary unit, which has to be specified in alphabetical or numerical order of the categories of l.
m.weight	vector of primary sample unit weights, which has to be specified in alphabetical or numerical order of the categories of l.
n.weight	vector of secondary sample unit weights in each primary sample unit, which has to be specified in alphabetical or numerical order of the categories of l.
method	estimation method. Default is "simple", alternative is "ratio".
level	coverage probability for confidence intervals. Default is level=0.95.

### Details

If the absolute sizes M and N1 are given, the variances are calculated with finite population correction. Otherwise, if the weights m.weight and n.weight are given, the variances are calculated without finite population correction.

### Value

The function submean returns a value, which is a list consisting of the components

call	is a list of call components: y target variable in sample data, PSU grouping variable in sample data, N population size, M number of primary population units, fpc finite population correction, method estimation method, level coverage probability for confidence intervals
mean	mean estimate for population
se	standard error of the mean estimate for population
ci	vector of confidence interval boundaries for population

**Author(s)**

Shuai Shao and Juliane Manitz

**References**

Kauermann, Goeran/Kuechenhoff, Helmut (2011): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

**See Also**

[Smean](#), [stratamean](#)

**Examples**

```
y <- c(23,33,24,25,72,74,71,37,42)
psu <- as.factor(c(1,1,1,1,2,2,2,3,3))
# with finite population correction
submean(y, PSU=psu, N=700, M=23, Nl=c(100,50,75), method='ratio')
# without finite population correction
submean(y, PSU=psu, N=700, m.weight=3/23, n.weight=c(4/100,3/50,2/75), method='ratio')

# Chinese wage data
data(wage)
summary(wage)
submean(wage$Wage, PSU=wage$Region, N=990, M=33, Nl=rep(30,14))
```

---

tax

*Hypothetical Tax Refund Data Frame*

---

**Description**

Simulated tax refund data frame including the estimated and actual refund value

**Usage**

```
data(tax)
```

**Format**

A data frame with 9083 observations on the following 5 variables.

`id` a numeric vector indicating the tax payer

`estRefund` a numeric vector representing the estimated value of tax refund by the tax payer

`actRefund` a numeric vector representing the actual tax refund calculated by the financial authority

`diff` difference between estimated and actual tax refund

`Class` a factor with levels 1, 2, 3, and 4 indicating the strata

**Source**

Due to data protection this is a simulated data set reflecting the real data.

**References**

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

**Examples**

```
data(tax)
summary(tax)

# illustration of stratamean
nh <- as.vector(table(tax$Class))
wh <- nh/sum(nh)
stratamean(y=tax$diff, h=as.vector(tax$Class), wh=wh, eae=TRUE)
```

---

wage

*Chinese wage data*

---

**Description**

A data frame with hypothetical Chinese wages differentiated by region and industrial sector.

**Usage**

```
data(wage)
```

**Format**

A data frame with 231 observations on the following 3 variables.

Region factor, Chinese regions with 14 levels.

Sector factor, industrial sector with 30 levels.

Wage a numeric vector, average wage in the region and sector measured in Chinese yuan.

**Details**

The dataset is hypothetical. Its structure imitates the data in the Chinese Statistical Yearbook. The values are simulated corresponding to the distribution of the real data which are not publicly accessible.

**References**

Kauermann, Goeran/Kuechenhoff, Helmut (2010): Stichproben. Methoden und praktische Umsetzung mit R. Springer.

**Examples**

```
# Chinese wage data
data(wage)
summary(wage)
submean(wage$Wage, PSU=wage$Region, N=990, M=33, NI=rep(30,14))
```

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