

Package ‘svrep’

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Type Package

Title Tools for Creating, Updating, and Analyzing Survey Replicate Weights

Version 0.5.0

Description Provides tools for creating and working with survey replicate weights, extending functionality of the 'survey' package from Lumley (2004) <[doi:10.18637/jss.v009.i08](https://doi.org/10.18637/jss.v009.i08)>. Implements bootstrap methods for complex surveys, including the generalized survey bootstrap as described by Beaumont and Patak (2012) <[doi:10.1111/j.1751-5823.2011.00166.x](https://doi.org/10.1111/j.1751-5823.2011.00166.x)>. Methods are provided for applying nonresponse adjustments to both full-sample and replicate weights as described by Rust and Rao (1996) <[doi:10.1177/096228029600500305](https://doi.org/10.1177/096228029600500305)>. Implements methods for sample-based calibration described by Opsomer and Erciulescu (2021) <<https://www150.statcan.gc.ca/n1/pub/12-001-x/2021002/article/00006-eng.htm>>. Diagnostic functions are included to compare weights and weighted estimates from different sets of replicate weights.

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URL <https://bschneider.github.io/svrep/>,
<https://github.com/bschneider/svrep>

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as_bootstrap_design *Convert a survey design object to a bootstrap replicate design*

Description

Converts a survey design object to a replicate design object with replicate weights formed using a bootstrap method. Supports stratified, cluster samples with one or more stages of sampling. At each stage of sampling, either simple random sampling (with or without replacement) or unequal probability sampling (with or without replacement) may be used.

Usage

```
as_bootstrap_design(
  design,
  type = "Rao-Wu-Yue-Beaumont",
  replicates = 500,
  compress = TRUE,
  mse = getOption("survey.replicates.mse"),
  samp_method_by_stage = NULL
)
```

Arguments

- | | |
|------------|--|
| design | A survey design object created using the 'survey' (or 'srvyr') package, with class 'survey.design' or 'svyimputationList'. |
| type | <p>The type of bootstrap to use, which should be chosen based on its applicability to the sampling method used for the survey. The available types are the following:</p> <ul style="list-style-type: none"> • "Rao-Wu-Yue-Beaumont" (the default): The bootstrap method of Beaumont and Émond (2022), which is a generalization of the Rao-Wu-Yue bootstrap, and is applicable to a wide variety of designs, including single-stage and multistage stratified designs. The design may have different sampling methods used at different stages. Each stage of sampling may potentially be PPS (i.e., use unequal probabilities), with or without replacement, and may potentially use Poisson sampling. <p>For a stratum with a fixed sample size of n sampling units, resampling in each replicate resamples $(n - 1)$ sampling units with replacement.</p> <ul style="list-style-type: none"> • "Rao-Wu": The basic Rao-Wu $(n - 1)$ bootstrap method, which is only applicable to single-stage designs or multistage designs where the first-stage sampling fractions are small (and can thus be ignored). Accommodates stratified designs. All sampling within a stratum must be simple random sampling with or without replacement, although the first-stage sampling is effectively treated as sampling without replacement. • "Preston": Preston's multistage rescaled bootstrap, which is applicable to single-stage designs or multistage designs with arbitrary sampling fractions. Accommodates stratified designs. All sampling within a stratum must be simple random sampling with or without replacement. • "Canty-Davison": The Canty-Davison bootstrap, which is only applicable to single-stage designs, with arbitrary sampling fractions. Accommodates stratified designs. All sampling with a stratum must be simple random sampling with or without replacement. |
| replicates | Number of bootstrap replicates (should be as large as possible, given computer memory/storage limitations). A commonly-recommended default is 500. |

| | |
|----------------------|--|
| compress | Use a compressed representation of the replicate weights matrix. This reduces the computer memory required to represent the replicate weights and has no impact on estimates. |
| mse | If TRUE, compute variances from sums of squares around the point estimate from the full-sample weights, If FALSE, compute variances from sums of squares around the mean estimate from the replicate weights. |
| samp_method_by_stage | (Optional). By default, this function will automatically determine the sampling method used at each stage. However, this argument can be used to ensure the correct sampling method is identified for each stage. Accepts a vector with length equal to the number of stages of sampling. Each element should be one of the following: <ul style="list-style-type: none"> • "SRSWOR" - Simple random sampling, without replacement • "SRSWR" - Simple random sampling, with replacement • "PPSWOR" - Unequal probabilities of selection, without replacement • "PPSWR" - Unequal probabilities of selection, with replacement • "Poisson" - Poisson sampling: each sampling unit is selected into the sample at most once, with potentially different probabilities of inclusion for each sampling unit. |

Value

A replicate design object, with class `svyrep.design`, which can be used with the usual functions, such as `svymean()` or `svyglm()`.

Use `weights(..., type = 'analysis')` to extract the matrix of replicate weights.

Use `as_data_frame_with_weights()` to convert the design object to a data frame with columns for the full-sample and replicate weights.

See Also

Use [estimate_boot_reps_for_target_cv](#) to help choose the number of bootstrap replicates.

For some complex designs, one can use [make_rwyb_bootstrap_weights](#) to create Rao-Wu-Yue-Beaumont bootstrap weights or adjustment factors given information for each stage of sampling (the type of sampling, strata IDs, cluster IDs, selection probabilities, etc.).

For systematic samples, one-PSU-per-stratum designs, or other especially complex sample designs, one can use the generalized survey bootstrap method. See [as_gen_boot_design](#) or [make_gen_boot_factors](#).

Examples

```
library(survey)
# Example 1: A multistage sample with two stages of SRSWOR

## Load an example dataset from a multistage sample, with two stages of SRSWOR
data("mu284", package = 'survey')
multistage_srswor_design <- svydesign(data = mu284,
```

```

                                ids = ~ id1 + id2,
                                fpc = ~ n1 + n2)

## Convert the survey design object to a bootstrap design
set.seed(2022)
bootstrap_rep_design <- as_bootstrap_design(multistage_srswor_design,
                                           replicates = 500)

## Compare std. error estimates from bootstrap versus linearization
data.frame(
  'Statistic' = c('total', 'mean', 'median'),
  'SE (bootstrap)' = c(SE(svytotal(x = ~ y1, design = bootstrap_rep_design)),
                      SE(svymean(x = ~ y1, design = bootstrap_rep_design)),
                      SE(svyquantile(x = ~ y1, quantile = 0.5,
                                      design = bootstrap_rep_design))),
  'SE (linearization)' = c(SE(svytotal(x = ~ y1, design = multistage_srswor_design)),
                          SE(svymean(x = ~ y1, design = multistage_srswor_design)),
                          SE(svyquantile(x = ~ y1, quantile = 0.5,
                                          design = multistage_srswor_design))),

  check.names = FALSE
)

# Example 2: A multistage-sample,
# first stage selected with unequal probabilities without replacement
# second stage selected with simple random sampling without replacement

data("library_multistage_sample", package = "svrep")

multistage_pps <- svydesign(data = library_multistage_sample,
                          ids = ~ PSU_ID + SSU_ID,
                          fpc = ~ PSU_SAMPLING_PROB + SSU_SAMPLING_PROB,
                          pps = "brewer")

bootstrap_rep_design <- as_bootstrap_design(
  multistage_pps, replicates = 500,
  samp_method_by_stage = c("PPSWOR", "SRSWOR")
)

## Compare std. error estimates from bootstrap versus linearization
data.frame(
  'Statistic' = c('total', 'mean'),
  'SE (bootstrap)' = c(
    SE(svytotal(x = ~ TOTCIR, na.rm = TRUE,
               design = bootstrap_rep_design)),
    SE(svymean(x = ~ TOTCIR, na.rm = TRUE,
              design = bootstrap_rep_design))),
  'SE (linearization)' = c(
    SE(svytotal(x = ~ TOTCIR, na.rm = TRUE,
               design = multistage_pps)),
    SE(svymean(x = ~ TOTCIR, na.rm = TRUE,
              design = multistage_pps))),

  check.names = FALSE
)

```

`as_data_frame_with_weights`

Convert a survey design object to a data frame with weights stored as columns

Description

Convert a survey design object to a data frame with weights stored as columns

Usage

```
as_data_frame_with_weights(  
  design,  
  full_wgt_name = "FULL_SAMPLE_WGT",  
  rep_wgt_prefix = "REP_WGT_"  
)
```

Arguments

`design` A survey design object, created with either the `survey` or `srvyr` packages.

`full_wgt_name` The column name to use for the full-sample weights

`rep_wgt_prefix` For replicate design objects, a prefix to use for the column names of the replicate weights. The column names will be created by appending the replicate number after the prefix.

Value

A data frame, with new columns containing the weights from the survey design object

Examples

```
data("lou_vax_survey", package = 'svrep')  
  
library(survey)  
# Create a survey design object  
survey_design <- svydesign(data = lou_vax_survey,  
  weights = ~ SAMPLING_WEIGHT,  
  ids = ~ 1)  
  
rep_survey_design <- as.svrepdesign(survey_design,  
  type = "boot",  
  replicates = 10)  
  
# Adjust the weights for nonresponse  
nr_adjusted_design <- redistribute_weights(  
  design = rep_survey_design,  
  reduce_if = RESPONSE_STATUS == "Nonrespondent",
```

```

    increase_if = RESPONSE_STATUS == "Respondent",
    by = c("RACE_ETHNICITY", "EDUC_ATTAINMENT")
  )

  # Save the survey design object as a data frame
  nr_adjusted_data <- as_data_frame_with_weights(
    nr_adjusted_design,
    full_wgt_name = "NR_ADJUSTED_WGT",
    rep_wgt_prefix = "NR_ADJUSTED_REP_WGT_"
  )
  head(nr_adjusted_data)

  # Check the column names of the result
  colnames(nr_adjusted_data)

```

| | |
|--------------------|---|
| as_gen_boot_design | <i>Convert a survey design object to a generalized bootstrap replicate design</i> |
|--------------------|---|

Description

Converts a survey design object to a replicate design object with replicate weights formed using the generalized bootstrap method. The generalized survey bootstrap is a method for forming bootstrap replicate weights from a textbook variance estimator, provided that the variance estimator can be represented as a quadratic form whose matrix is positive semidefinite (this covers a large class of variance estimators).

Usage

```

as_gen_boot_design(
  design,
  variance_estimator = NULL,
  replicates = 500,
  tau = "auto",
  psd_option = "warn",
  mse = getOption("survey.replicates.mse"),
  compress = TRUE
)

```

Arguments

| | |
|--------------------|---|
| design | A survey design object created using the 'survey' (or 'srvyr') package, with class 'survey.design' or 'svyimputationList'. |
| variance_estimator | The name of the variance estimator whose quadratic form matrix should be created. See the section "Variance Estimators" below. Options include: |

| | |
|------------|---|
| | <ul style="list-style-type: none"> • "Yates-Grundy": The Yates-Grundy variance estimator based on first-order and second-order inclusion probabilities. • "Horvitz-Thompson": The Horvitz-Thompson variance estimator based on first-order and second-order inclusion probabilities. • "Poisson Horvitz-Thompson": The Horvitz-Thompson variance estimator based on assuming Poisson sampling, with first-order inclusion probabilities inferred from the sampling probabilities of the survey design object. • "Stratified Multistage SRS": The usual stratified multistage variance estimator based on estimating the variance of cluster totals within strata at each stage. • "Ultimate Cluster": The usual variance estimator based on estimating the variance of first-stage cluster totals within first-stage strata. • "SD1": The non-circular successive-differences variance estimator described by Ash (2014), sometimes used for variance estimation for systematic sampling. • "SD2": The circular successive-differences variance estimator described by Ash (2014). This estimator is the basis of the "successive-differences replication" estimator commonly used for variance estimation for systematic sampling. |
| replicates | Number of bootstrap replicates (should be as large as possible, given computer memory/storage limitations). A commonly-recommended default is 500. |
| tau | <p>Either "auto", or a single number. This is the rescaling constant used to avoid negative weights through the transformation $\frac{w+\tau-1}{\tau}$, where w is the original weight and τ is the rescaling constant tau.</p> <p>If tau="auto", the rescaling factor is determined automatically as follows: if all of the adjustment factors are nonnegative, then tau is set equal to 1; otherwise, tau is set to the smallest value needed to rescale the adjustment factors such that they are all at least 0.01.</p> |
| psd_option | <p>Either "warn" (the default) or "error". This option specifies what will happen if the target variance estimator has a quadratic form matrix which is not positive semidefinite. This can occasionally happen, particularly for two-phase designs. If psd_option="error", then an error message will be displayed.</p> <p>If psd_option="warn", then a warning message will be displayed, and the quadratic form matrix will be approximated by the most similar positive semidefinite matrix. This approximation was suggested by Beaumont and Patak (2012), who note that this is conservative in the sense of producing overestimates of variance. Beaumont and Patak (2012) argue that this overestimation is expected to be small in magnitude. See get_nearest_psd_matrix for details of the approximation.</p> |
| mse | If TRUE, compute variances from sums of squares around the point estimate from the full-sample weights, If FALSE, compute variances from sums of squares around the mean estimate from the replicate weights. |
| compress | This reduces the computer memory required to represent the replicate weights and has no impact on estimates. |

Value

A replicate design object, with class `svyrep.design`, which can be used with the usual functions, such as `svymean()` or `svyglm()`.

Use `weights(..., type = 'analysis')` to extract the matrix of replicate weights.

Use `as_data_frame_with_weights()` to convert the design object to a data frame with columns for the full-sample and replicate weights.

Statistical Details

Let $v(\hat{T}_y)$ be the textbook variance estimator for an estimated population total \hat{T}_y of some variable y . The base weight for case i in our sample is w_i , and we let \check{y}_i denote the weighted value $w_i y_i$. Suppose we can represent our textbook variance estimator as a quadratic form: $v(\hat{T}_y) = \check{y}'\Sigma\check{y}^T$, for some $n \times n$ matrix Σ . The only constraint on Σ is that, for our sample, it must be symmetric and positive semidefinite.

The bootstrapping process creates B sets of replicate weights, where the b -th set of replicate weights is a vector of length n denoted $\mathbf{a}^{(b)}$, whose k -th value is denoted $a_k^{(b)}$. This yields B replicate estimates of the population total, $\hat{T}_y^{*(b)} = \sum_{k \in S} a_k^{(b)} \check{y}_k$, for $b = 1, \dots, B$, which can be used to estimate sampling variance.

$$v_B(\hat{T}_y) = \frac{\sum_{b=1}^B (\hat{T}_y^{*(b)} - \hat{T}_y)^2}{B}$$

This bootstrap variance estimator can be written as a quadratic form:

$$v_B(\hat{T}_y) = \check{y}'\Sigma_B\check{y}$$

where

$$\Sigma_B = \frac{\sum_{b=1}^B (\mathbf{a}^{(b)} - \mathbf{1}_n) (\mathbf{a}^{(b)} - \mathbf{1}_n)'}{B}$$

Note that if the vector of adjustment factors $\mathbf{a}^{(b)}$ has expectation $\mathbf{1}_n$ and variance-covariance matrix Σ , then we have the bootstrap expectation $E_*(\Sigma_B) = \Sigma$. Since the bootstrap process takes the sample values \check{y} as fixed, the bootstrap expectation of the variance estimator is $E_*(\check{y}'\Sigma_B\check{y}) = \check{y}'\Sigma\check{y}$. Thus, we can produce a bootstrap variance estimator with the same expectation as the textbook variance estimator simply by randomly generating $\mathbf{a}^{(b)}$ from a distribution with the following two conditions:

Condition 1: $E_*(\mathbf{a}) = \mathbf{1}_n$

Condition 2: $E_*(\mathbf{a} - \mathbf{1}_n) (\mathbf{a} - \mathbf{1}_n)' = \Sigma$

While there are multiple ways to generate adjustment factors satisfying these conditions, the simplest general method is to simulate from a multivariate normal distribution: $\mathbf{a} \sim MVN(\mathbf{1}_n, \Sigma)$. This is the method used by this function.

Details on Rescaling to Avoid Negative Adjustment Factors

Let $\mathbf{A} = [\mathbf{a}^{(1)} \cdots \mathbf{a}^{(b)} \cdots \mathbf{a}^{(B)}]$ denote the $(n \times B)$ matrix of bootstrap adjustment factors. To eliminate negative adjustment factors, Beaumont and Patak (2012) propose forming a rescaled matrix of nonnegative replicate factors \mathbf{A}^S by rescaling each adjustment factor $a_k^{(b)}$ as follows:

$$a_k^{S,(b)} = \frac{a_k^{(b)} + \tau - 1}{\tau}$$

where $\tau \geq 1 - a_k^{(b)} \geq 1$ for all k in $\{1, \dots, n\}$ and all b in $\{1, \dots, B\}$.

The value of τ can be set based on the realized adjustment factor matrix \mathbf{A} or by choosing τ prior to generating the adjustment factor matrix \mathbf{A} so that τ is likely to be large enough to prevent negative bootstrap weights.

If the adjustment factors are rescaled in this manner, it is important to adjust the scale factor used in estimating the variance with the bootstrap replicates, which becomes $\frac{\tau^2}{B}$ instead of $\frac{1}{B}$.

$$\text{Prior to rescaling: } v_B(\hat{T}_y) = \frac{1}{B} \sum_{b=1}^B (\hat{T}_y^{*(b)} - \hat{T}_y)^2$$

$$\text{After rescaling: } v_B(\hat{T}_y) = \frac{\tau^2}{B} \sum_{b=1}^B (\hat{T}_y^{S*(b)} - \hat{T}_y)^2$$

When sharing a dataset that uses rescaled weights from a generalized survey bootstrap, the documentation for the dataset should instruct the user to use replication scale factor $\frac{\tau^2}{B}$ rather than $\frac{1}{B}$ when estimating sampling variances.

Variance Estimators

The **Horvitz-Thompson** variance estimator:

$$v(\hat{Y}) = \sum_{i \in s} \sum_{j \in s} \left(1 - \frac{\pi_i \pi_j}{\pi_{ij}}\right) \frac{y_i}{\pi_i} \frac{y_j}{\pi_j}$$

The **Poisson Horvitz-Thompson** variance estimator is simply the Horvitz-Thompson variance estimator, but where $\pi_{ij} = \pi_i \times \pi_j$, which is the case for Poisson sampling.

The **Yates-Grundy** variance estimator:

$$v(\hat{Y}) = -\frac{1}{2} \sum_{i \in s} \sum_{j \in s} \left(1 - \frac{\pi_i \pi_j}{\pi_{ij}}\right) \left(\frac{y_i}{\pi_i} - \frac{y_j}{\pi_j}\right)^2$$

The **Stratified Multistage SRS** variance estimator is the recursive variance estimator proposed by Bellhouse (1985) and used in the 'survey' package's function `svyrecvar`. The estimator can be used for any number of sampling stages. For illustration, we describe its use for two sampling stages.

$$v(\hat{Y}) = \hat{V}_1 + \hat{V}_2$$

where

$$\hat{V}_1 = \sum_{h=1}^H \left(1 - \frac{n_h}{N_h}\right) \frac{n_h}{n_h - 1} \sum_{i=1}^{n_h} (y_{hi} - \bar{y}_{hi})^2$$

and

$$\hat{V}_2 = \sum_{h=1}^H \frac{n_h}{N_h} \sum_{i=1}^{n_h} v_{hi}(y_{hi.})$$

where n_h is the number of sampled clusters in stratum h , N_h is the number of population clusters in stratum h , $y_{hi.}$ is the weighted cluster total in cluster i of stratum h , $\bar{y}_{hi.}$ is the mean weighted cluster total of stratum h , ($\bar{y}_{hi.} = \frac{1}{n_h} \sum_{i=1}^{n_h} y_{hi.}$), and $v_{hi}(y_{hi.})$ is the estimated sampling variance of $y_{hi.}$.

The **Ultimate Cluster** variance estimator is simply the stratified multistage SRS variance estimator, but ignoring variances from later stages of sampling.

$$v(\hat{Y}) = \hat{V}_1$$

This is the variance estimator used in the 'survey' package when the user specifies `option(survey.ultimate.cluster = TRUE)` or uses `svyrecvar(..., one.stage = TRUE)`. When the first-stage sampling fractions are small, analysts often omit the finite population corrections ($1 - \frac{n_h}{N_h}$) when using the ultimate cluster estimator.

The **SD1** and **SD2** variance estimators are "successive difference" estimators sometimes used for systematic sampling designs. Ash (2014) describes each estimator as follows:

$$\hat{v}_{SD1}(\hat{Y}) = \left(1 - \frac{n}{N}\right) \frac{n}{2(n-1)} \sum_{k=2}^n (\check{y}_k - \check{y}_{k-1})^2$$

$$\hat{v}_{SD2}(\hat{Y}) = \left(1 - \frac{n}{N}\right) \frac{1}{2} \left[\sum_{k=2}^n (\check{y}_k - \check{y}_{k-1})^2 + (\check{y}_n - \check{y}_1)^2 \right]$$

where $\check{y}_k = y_k/\pi_k$ is the weighted value of unit k with selection probability π_k . The SD1 estimator is recommended by Wolter (1984). The SD2 estimator is the basis of the successive difference replication estimator commonly used for systematic sampling designs. See Ash (2014) for details.

For multistage samples, SD1 and SD2 are applied to the clusters at each stage, separately by stratum. For later stages of sampling, the variance estimate from a stratum is multiplied by the product of sampling fractions from earlier stages of sampling. For example, at a third stage of sampling, the variance estimate from a third-stage stratum is multiplied by $\frac{n_1}{N_1} \frac{n_2}{N_2}$, which is the product of sampling fractions from the first-stage stratum and second-stage stratum.

Two-Phase Designs

For a two-phase design, `variance_estimator` should be a list of variance estimators' names, with two elements, such as `list('Ultimate Cluster', 'Poisson Horvitz-Thompson')`. In two-phase designs, only the following estimators may be used for the second phase:

- "Ultimate Cluster"
- "Stratified Multistage SRS"
- "Poisson Horvitz-Thompson"

For statistical details on the handling of two-phase designs, see the documentation for [make_twophase_quad_form](#).

References

The generalized survey bootstrap was first proposed by Bertail and Combris (1997). See Beaumont and Patak (2012) for a clear overview of the generalized survey bootstrap. The generalized survey bootstrap represents one strategy for forming replication variance estimators in the general framework proposed by Fay (1984) and Dippo, Fay, and Morganstein (1984).

- Ash, S. (2014). "Using successive difference replication for estimating variances." **Survey Methodology**, Statistics Canada, 40(1), 47–59.

- Bellhouse, D.R. (1985). "Computing Methods for Variance Estimation in Complex Surveys." **Journal of Official Statistics**, Vol.1, No.3.

- Beaumont, Jean-François, and Zdenek Patak. 2012. "On the Generalized Bootstrap for Sample Surveys with Special Attention to Poisson Sampling: Generalized Bootstrap for Sample Surveys." *International Statistical Review* 80 (1): 127–48. <https://doi.org/10.1111/j.1751-5823.2011.00166.x>.

- Bertail, and Combris. 1997. "Bootstrap Généralisé d'un Sondage." *Annales d'Économie Et de Statistique*, no. 46: 49. <https://doi.org/10.2307/20076068>.

- Dippo, Cathryn, Robert Fay, and David Morganstein. 1984. "Computing Variances from Complex Samples with Replicate Weights." In, 489–94. Alexandria, VA: American Statistical Association. http://www.asasrms.org/Proceedings/papers/1984_094.pdf.

- Fay, Robert. 1984. "Some Properties of Estimates of Variance Based on Replication Methods." In, 495–500. Alexandria, VA: American Statistical Association. http://www.asasrms.org/Proceedings/papers/1984_095.pdf.

See Also

Use [estimate_boot_reps_for_target_cv](#) to help choose the number of bootstrap replicates. For greater customization of the method, [make_quad_form_matrix](#) can be used to represent several common variance estimators as a quadratic form's matrix, which can then be used as an input to [make_gen_boot_factors](#). The function [rescale_reps](#) is used to implement the rescaling of the bootstrap adjustment factors.

Examples

```
## Not run:
library(survey)

# Example 1: Bootstrap based on the Yates-Grundy estimator ----
set.seed(2014)

data('election', package = 'survey')

## Create survey design object
pps_design_yg <- svydesign(
  data = election_pps,
  id = ~1, fpc = ~p,
```

```

    pps = ppsmat(election_jointprob),
    variance = "YG"
  )

  ## Convert to generalized bootstrap replicate design
  gen_boot_design_yg <- pps_design_yg |>
    as_gen_boot_design(variance_estimator = "Yates-Grundy",
                      replicates = 1000, tau = "auto")

  svytotal(x = ~ Bush + Kerry, design = pps_design_yg)
  svytotal(x = ~ Bush + Kerry, design = gen_boot_design_yg)

# Example 2: Bootstrap based on the successive-difference estimator ----

data('library_stsys_sample', package = 'svrep')

## First, ensure data are sorted in same order as was used in sampling
library_stsys_sample <- library_stsys_sample[
  order(library_stsys_sample$SAMPLING_SORT_ORDER),
]

## Create a survey design object
design_obj <- svydesign(
  data = library_stsys_sample,
  strata = ~ SAMPLING_STRATUM,
  ids = ~ 1,
  fpc = ~ STRATUM_POP_SIZE
)

## Convert to generalized bootstrap replicate design
gen_boot_design_sd2 <- as_gen_boot_design(
  design = design_obj,
  variance_estimator = "SD2",
  replicates = 2000
)

## Estimate sampling variances
svytotal(x = ~ TOTSTAFF, na.rm = TRUE, design = gen_boot_design_sd2)
svytotal(x = ~ TOTSTAFF, na.rm = TRUE, design = design_obj)

# Example 3: Two-phase sample ----
# -- First stage is stratified systematic sampling,
# -- second stage is response/nonresponse modeled as Poisson sampling

nonresponse_model <- glm(
  data = library_stsys_sample,
  family = quasibinomial('logit'),
  formula = I(RESPONSE_STATUS == "Survey Respondent") ~ 1,
  weights = 1/library_stsys_sample$SAMPLING_PROB
)

library_stsys_sample[['RESPONSE_PROBENSITY']] <- predict(
  nonresponse_model,

```

```

newdata = library_stsys_sample,
type = "response"
)

twophase_design <- twophase(
  data = library_stsys_sample,
  # Identify cases included in second phase sample
  subset = ~ I(RESPONSE_STATUS == "Survey Respondent"),
  strata = list(~ SAMPLING_STRATUM, NULL),
  id = list(~ 1, ~ 1),
  probs = list(NULL, ~ RESPONSE_PROBENSITY),
  fpc = list(~ STRATUM_POP_SIZE, NULL),
)

twophase_boot_design <- as_gen_boot_design(
  design = twophase_design,
  variance_estimator = list(
    "SD2", "Poisson Horvitz-Thompson"
  )
)

svytotal(x = ~ LIBRARIA, design = twophase_boot_design)

## End(Not run)

```

calibrate_to_estimate *Calibrate weights from a primary survey to estimated totals from a control survey, with replicate-weight adjustments that account for variance of the control totals*

Description

Calibrate the weights of a primary survey to match estimated totals from a control survey, using adjustments to the replicate weights to account for the variance of the estimated control totals. The adjustments to replicate weights are conducted using the method proposed by Fuller (1998). This method can be used to implement general calibration as well as post-stratification or raking specifically (see the details for the `calfun` parameter).

Usage

```

calibrate_to_estimate(
  rep_design,
  estimate,
  vcov_estimate,
  cal_formula,
  calfun = survey::cal.linear,
  bounds = list(lower = -Inf, upper = Inf),
  verbose = FALSE,

```

```

    maxit = 50,
    epsilon = 1e-07,
    variance = NULL,
    col_selection = NULL
  )

```

Arguments

| | |
|---------------|---|
| rep_design | A replicate design object for the primary survey, created with either the <code>survey</code> or <code>srvyr</code> packages. |
| estimate | A vector of estimated control totals. The names of entries must match the names from calling <code>svytotal(x = cal_formula, design = rep_design)</code> . |
| vcov_estimate | A variance-covariance matrix for the estimated control totals. The column names and row names must match the names of <code>estimate</code> . |
| cal_formula | A formula listing the variables to use for calibration. All of these variables must be included in <code>rep_design</code> . |
| calfun | A calibration function from the <code>survey</code> package, such as <code>cal.linear</code> , <code>cal.raking</code> , or <code>cal.logit</code> . Use <code>cal.linear</code> for ordinary post-stratification, and <code>cal.raking</code> for raking. See <code>calibrate</code> for additional details. |
| bounds | Parameter passed to <code>grake</code> for calibration. See <code>calibrate</code> for details. |
| verbose | Parameter passed to <code>grake</code> for calibration. See <code>calibrate</code> for details. |
| maxit | Parameter passed to <code>grake</code> for calibration. See <code>calibrate</code> for details. |
| epsilon | Parameter passed to <code>grake</code> for calibration. After calibration, the absolute difference between each calibration target and the calibrated estimate will be no larger than <code>epsilon</code> times (1 plus the absolute value of the target). See <code>calibrate</code> for details. |
| variance | Parameter passed to <code>grake</code> for calibration. See <code>calibrate</code> for details. |
| col_selection | Optional parameter to determine which replicate columns will have their control totals perturbed. If supplied, <code>col_selection</code> must be an integer vector with length equal to the length of <code>estimate</code> . |

Details

With the Fuller method, each of k randomly-selected replicate columns from the primary survey are calibrated to control totals formed by perturbing the k -dimensional vector of estimated control totals using a spectral decomposition of the variance-covariance matrix of the estimated control totals. Other replicate columns are simply calibrated to the unperturbed control totals.

Because the set of replicate columns whose control totals are perturbed should be random, there are multiple ways to ensure that this matching is reproducible. The user can either call `set.seed` before using the function, or supply a vector of randomly-selected column indices to the argument `col_selection`.

Value

A replicate design object, with full-sample weights calibrated to totals from estimate, and replicate weights adjusted to account for variance of the control totals. The element `col_selection` indicates, for each replicate column of the calibrated primary survey, which column of replicate weights it was matched to from the control survey.

References

Fuller, W.A. (1998). "Replication variance estimation for two-phase samples." *Statistica Sinica*, 8: 1153-1164.

Opsomer, J.D. and A. Erciulescu (2021). "Replication variance estimation after sample-based calibration." *Survey Methodology*, 47: 265-277.

Examples

```
## Not run:

# Load example data for primary survey ----

suppressPackageStartupMessages(library(survey))
data(api)

primary_survey <- svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc) |>
  as.svrepdesign(type = "JK1")

# Load example data for control survey ----

control_survey <- svydesign(id = ~ 1, fpc = ~fpc, data = apisrs) |>
  as.svrepdesign(type = "JK1")

# Estimate control totals ----

estimated_controls <- svytotal(x = ~ stype + enroll,
                              design = control_survey)
control_point_estimates <- coef(estimated_controls)
control_vcov_estimate <- vcov(estimated_controls)

# Calibrate totals for one categorical variable and one numeric ----

calibrated_rep_design <- calibrate_to_estimate(
  rep_design = primary_survey,
  estimate = control_point_estimates,
  vcov_estimate = control_vcov_estimate,
  cal_formula = ~ stype + enroll
)

# Inspect estimates before and after calibration ----

##_ For the calibration variables, estimates and standard errors
##_ from calibrated design will match those of the control survey
```



```

svytotal(x = ~ stype + enroll, design = primary_survey)
svytotal(x = ~ stype + enroll, design = control_survey)
svytotal(x = ~ stype + enroll, design = calibrated_rep_design)

##_ Estimates from other variables will be changed as well

svymean(x = ~ api00 + api99, design = primary_survey)
svymean(x = ~ api00 + api99, design = control_survey)
svymean(x = ~ api00 + api99, design = calibrated_rep_design)

# Inspect weights before and after calibration ----

summarize_rep_weights(primary_survey, type = 'overall')
summarize_rep_weights(calibrated_rep_design, type = 'overall')

# For reproducibility, specify which columns are randomly selected for Fuller method ----

column_selection <- calibrated_rep_design$col_selection
print(column_selection)

calibrated_rep_design <- calibrate_to_estimate(
  rep_design = primary_survey,
  estimate = control_point_estimates,
  vcov_estimate = control_vcov_estimate,
  cal_formula = ~ stype + enroll,
  col_selection = column_selection
)

## End(Not run)

```

| | |
|---------------------|---|
| calibrate_to_sample | <i>Calibrate weights from a primary survey to estimated totals from a control survey, with replicate-weight adjustments that account for variance of the control totals</i> |
|---------------------|---|

Description

Calibrate the weights of a primary survey to match estimated totals from a control survey, using adjustments to the replicate weights to account for the variance of the estimated control totals. The adjustments to replicate weights are conducted using the method proposed by Opsomer and Erciulescu (2021). This method can be used to implement general calibration as well as post-stratification or raking specifically (see the details for the `cal_fun` parameter).

Usage

```

calibrate_to_sample(
  primary_rep_design,
  control_rep_design,
  cal_formula,

```

```

  calfun = survey::cal.linear,
  bounds = list(lower = -Inf, upper = Inf),
  verbose = FALSE,
  maxit = 50,
  epsilon = 1e-07,
  variance = NULL,
  control_col_matches = NULL
)

```

Arguments

primary_rep_design A replicate design object for the primary survey, created with either the `survey` or `srvyr` packages.

control_rep_design A replicate design object for the control survey.

cal_formula A formula listing the variables to use for calibration. All of these variables must be included in both `primary_rep_design` and `control_rep_design`.

calfun A calibration function from the `survey` package, such as `cal.linear`, `cal.raking`, or `cal.logit`. Use `cal.linear` for ordinary post-stratification, and `cal.raking` for raking. See `calibrate` for additional details.

bounds Parameter passed to `grake` for calibration. See `calibrate` for details.

verbose Parameter passed to `grake` for calibration. See `calibrate` for details.

maxit Parameter passed to `grake` for calibration. See `calibrate` for details.

epsilon Parameter passed to `grake` for calibration. After calibration, the absolute difference between each calibration target and the calibrated estimate will be no larger than `epsilon` times (1 plus the absolute value of the target). See `calibrate` for details.

variance Parameter passed to `grake` for calibration. See `calibrate` for details.

control_col_matches Optional parameter to control which control survey replicate is matched to each primary survey replicate. Entries of `NA` denote a primary survey replicate not matched to any control survey replicate. If this parameter is not used, matching is done at random.

Details

With the Opsomer-Erciulescu method, each column of replicate weights from the control survey is randomly matched to a column of replicate weights from the primary survey, and then the column from the primary survey is calibrated to control totals estimated by perturbing the control sample's full-sample estimates using the estimates from the matched column of replicate weights from the control survey.

If there are fewer columns of replicate weights in the control survey than in the primary survey, then not all primary replicate columns will be matched to a replicate column from the control survey.

If there are more columns of replicate weights in the control survey than in the primary survey, then the columns of replicate weights in the primary survey will be duplicated k times, where k is the smallest positive integer such that the resulting number of columns of replicate weights for the primary survey is greater than or equal to the number of columns of replicate weights in the control survey.

Because replicate columns of the control survey are matched *at random* to primary survey replicate columns, there are multiple ways to ensure that this matching is reproducible. The user can either call [set.seed](#) before using the function, or supply a mapping to the argument `control_col_matches`.

Value

A replicate design object, with full-sample weights calibrated to totals from `control_rep_design`, and replicate weights adjusted to account for variance of the control totals. If `primary_rep_design` had fewer columns of replicate weights than `control_rep_design`, then the number of replicate columns and the length of `rscales` will be increased by a multiple k , and the scale will be updated by dividing by k .

The element `control_column_matches` indicates, for each replicate column of the calibrated primary survey, which column of replicate weights it was matched to from the control survey. Columns which were not matched to control survey replicate column are indicated by NA.

The element `degf` will be set to match that of the primary survey to ensure that the degrees of freedom are not erroneously inflated by potential increases in the number of columns of replicate weights.

References

Opsomer, J.D. and A. Erciulescu (2021). "Replication variance estimation after sample-based calibration." *Survey Methodology*, 47: 265-277.

Examples

```
## Not run:

# Load example data for primary survey ----

suppressPackageStartupMessages(library(survey))
data(api)

primary_survey <- svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc) |>
  as.svrepdesign(type = "JK1")

# Load example data for control survey ----

control_survey <- svydesign(id = ~ 1, fpc = ~fpc, data = apisrs) |>
  as.svrepdesign(type = "JK1")

# Calibrate totals for one categorical variable and one numeric ----
```

```

calibrated_rep_design <- calibrate_to_sample(
  primary_rep_design = primary_survey,
  control_rep_design = control_survey,
  cal_formula = ~ stype + enroll,
)

# Inspect estimates before and after calibration ----

##_ For the calibration variables, estimates and standard errors
##_ from calibrated design will match those of the control survey

svytotal(x = ~ stype + enroll, design = primary_survey)
svytotal(x = ~ stype + enroll, design = control_survey)
svytotal(x = ~ stype + enroll, design = calibrated_rep_design)

##_ Estimates from other variables will be changed as well

svymean(x = ~ api00 + api99, design = primary_survey)
svymean(x = ~ api00 + api99, design = control_survey)
svymean(x = ~ api00 + api99, design = calibrated_rep_design)

# Inspect weights before and after calibration ----

summarize_rep_weights(primary_survey, type = 'overall')
summarize_rep_weights(calibrated_rep_design, type = 'overall')

# For reproducibility, specify how to match replicates between surveys ----

column_matching <- calibrated_rep_design$control_col_matches
print(column_matching)

calibrated_rep_design <- calibrate_to_sample(
  primary_rep_design = primary_survey,
  control_rep_design = control_survey,
  cal_formula = ~ stype + enroll,
  control_col_matches = column_matching
)

## End(Not run)

```

```
estimate_boot_reps_for_target_cv
```

Estimate the number of bootstrap replicates needed to reduce the bootstrap simulation error to a target level

Description

This function estimates the number of bootstrap replicates needed to reduce the simulation error of a bootstrap variance estimator to a target level, where "simulation error" is defined as error caused by using only a finite number of bootstrap replicates and this simulation error is measured as a simulation coefficient of variation ("simulation CV").

Usage

```
estimate_boot_reps_for_target_cv(svrepstat, target_cv = 0.05)
```

Arguments

`svrepstat` An estimate obtained from a bootstrap replicate survey design object, with a function such as `svymean(..., return.replicates = TRUE)` or `withReplicates(..., return.replicates = TRUE)`.

`target_cv` A numeric value (or vector of numeric values) between 0 and 1. This is the target simulation CV for the bootstrap variance estimator.

Value

A data frame with one row for each value of `target_cv`. The column `TARGET_CV` gives the target coefficient of variation. The column `MAX_REPS` gives the maximum number of replicates needed for all of the statistics included in `svrepstat`. The remaining columns give the number of replicates needed for each statistic.

Suggested Usage

- **Step 1:** Determine the largest acceptable level of simulation error for key survey estimates, where the level of simulation error is measured in terms of the simulation CV. We refer to this as the "target CV." A conventional value for the target CV is 5%.
- **Step 2:** Estimate key statistics of interest using a large number of bootstrap replicates (such as 5,000) and save the estimates from each bootstrap replicate. This can be conveniently done using a function from the survey package such as `svymean(..., return.replicates = TRUE)` or `withReplicates(..., return.replicates = TRUE)`.
- **Step 3:** Use the function `estimate_boot_reps_for_target_cv()` to estimate the minimum number of bootstrap replicates needed to attain the target CV.

Statistical Details

Unlike other replication methods such as the jackknife or balanced repeated replication, the bootstrap variance estimator's precision can always be improved by using a larger number of replicates, as the use of only a finite number of bootstrap replicates introduces simulation error to the variance estimation process. Simulation error can be measured as a "simulation coefficient of variation" (CV), which is the ratio of the standard error of a bootstrap estimator to the expectation of that bootstrap estimator, where the expectation and standard error are evaluated with respect to the bootstrapping process given the selected sample.

For a statistic $\hat{\theta}$, the simulation CV of the bootstrap variance estimator $v_B(\hat{\theta})$ based on B replicate estimates $\hat{\theta}_1^*, \dots, \hat{\theta}_B^*$ is defined as follows:

$$CV_{\star}(v_B(\hat{\theta})) = \frac{\sqrt{\text{var}_{\star}(v_B(\hat{\theta}))}}{E_{\star}(v_B(\hat{\theta}))} = \frac{CV_{\star}(E_2)}{\sqrt{B}}$$

where

$$E_2 = (\hat{\theta}^* - \hat{\theta})^2$$

$$CV_*(E_2) = \frac{\sqrt{\text{var}_*(E_2)}}{E_*(E_2)}$$

and var_* and E_* are evaluated with respect to the bootstrapping process, given the selected sample.

The simulation CV, denoted $CV_*(v_B(\hat{\theta}))$, is estimated for a given number of replicates B by estimating $CV_*(E_2)$ using observed values and dividing this by \sqrt{B} . If the bootstrap errors are assumed to be normally distributed, then $CV_*(E_2) = \sqrt{2}$ and so $CV_*(v_B(\hat{\theta}))$ would not need to be estimated. Using observed replicate estimates to estimate the simulation CV instead of assuming normality allows simulation CV to be used for a wide array of bootstrap methods.

References

See Section 3.3 and Section 8 of Beaumont and Patak (2012) for details and an example where the simulation CV is used to determine the number of bootstrap replicates needed for various alternative bootstrap methods in an empirical illustration.

Beaumont, J.-F. and Z. Patak. (2012), "On the Generalized Bootstrap for Sample Surveys with Special Attention to Poisson Sampling." **International Statistical Review**, 80: 127-148. doi:10.1111/j.17515823.2011.00166.x.

See Also

Use [estimate_boot_sim_cv](#) to estimate the simulation CV for the number of bootstrap replicates actually used.

Examples

```
## Not run:
set.seed(2022)

# Create an example bootstrap survey design object ----
library(survey)
data('api', package = 'survey')

boot_design <- svydesign(id=~1, strata=~stype, weights=~pw,
                       data=apistrat, fpc=~fpc) |>
  svrep::as_bootstrap_design(replicates = 5000)

# Calculate estimates of interest and retain estimates from each replicate ----

estimated_means_and_proportions <- svymean(x = ~ api00 + api99 + stype, design = boot_design,
                                           return.replicates = TRUE)
custom_statistic <- withReplicates(design = boot_design,
                                   return.replicates = TRUE,
                                   theta = function(wts, data) {
                                     numerator <- sum(data$api00 * wts)
                                     denominator <- sum(data$api99 * wts)
                                     statistic <- numerator/denominator
                                     return(statistic)
                                   })

# Determine minimum number of bootstrap replicates needed to obtain given simulation CVs ----
```

```

estimate_boot_reps_for_target_cv(
  svrepstat = estimated_means_and_proportions,
  target_cv = c(0.01, 0.05, 0.10)
)

estimate_boot_reps_for_target_cv(
  svrepstat = custom_statistic,
  target_cv = c(0.01, 0.05, 0.10)
)

## End(Not run)

```

estimate_boot_sim_cv *Estimate the bootstrap simulation error*

Description

Estimates the bootstrap simulation error, expressed as a "simulation coefficient of variation" (CV).

Usage

```
estimate_boot_sim_cv(svrepstat)
```

Arguments

| | |
|-----------|--|
| svrepstat | An estimate obtained from a bootstrap replicate survey design object, with a function such as svymean(..., return.replicates = TRUE) or withReplicates(..., return.replicates = TRUE). |
|-----------|--|

Value

A data frame with one row for each statistic. The column STATISTIC gives the name of the statistic. The column SIMULATION_CV gives the estimated simulation CV of the statistic. The column N_REPLICATES gives the number of bootstrap replicates.

Statistical Details

Unlike other replication methods such as the jackknife or balanced repeated replication, the bootstrap variance estimator's precision can always be improved by using a larger number of replicates, as the use of only a finite number of bootstrap replicates introduces simulation error to the variance estimation process. Simulation error can be measured as a "simulation coefficient of variation" (CV), which is the ratio of the standard error of a bootstrap estimator to the expectation of that bootstrap estimator, where the expectation and standard error are evaluated with respect to the bootstrapping process given the selected sample.

For a statistic $\hat{\theta}$, the simulation CV of the bootstrap variance estimator $v_B(\hat{\theta})$ based on B replicate estimates $\hat{\theta}_1^*, \dots, \hat{\theta}_B^*$ is defined as follows:

$$CV_*(v_B(\hat{\theta})) = \frac{\sqrt{\text{var}_*(v_B(\hat{\theta}))}}{E_*(v_B(\hat{\theta}))} = \frac{CV_*(E_2)}{\sqrt{B}}$$

where

$$E_2 = (\hat{\theta}^* - \hat{\theta})^2$$

$$CV_*(E_2) = \frac{\sqrt{\text{var}_*(E_2)}}{E_*(E_2)}$$

and var_* and E_* are evaluated with respect to the bootstrapping process, given the selected sample.

The simulation CV, denoted $CV_*(v_B(\hat{\theta}))$, is estimated for a given number of replicates B by estimating $CV_*(E_2)$ using observed values and dividing this by \sqrt{B} . If the bootstrap errors are assumed to be normally distributed, then $CV_*(E_2) = \sqrt{2}$ and so $CV_*(v_B(\hat{\theta}))$ would not need to be estimated. Using observed replicate estimates to estimate the simulation CV instead of assuming normality allows simulation CV to be used for a wide array of bootstrap methods.

References

See Section 3.3 and Section 8 of Beaumont and Patak (2012) for details and an example where the simulation CV is used to determine the number of bootstrap replicates needed for various alternative bootstrap methods in an empirical illustration.

Beaumont, J.-F. and Z. Patak. (2012), "On the Generalized Bootstrap for Sample Surveys with Special Attention to Poisson Sampling." **International Statistical Review**, 80: 127-148. doi:10.1111/j.17515823.2011.00166.x.

See Also

Use [estimate_boot_reps_for_target_cv](#) to help choose the number of bootstrap replicates.

Examples

```
## Not run:
set.seed(2022)

# Create an example bootstrap survey design ----
library(survey)
data('api', package = 'survey')

boot_design <- svydesign(id=~1, strata=~stype, weights=~pw,
                      data=apistrat, fpc=~fpc) |>
  svrep::as_bootstrap_design(replicates = 5000)

# Calculate estimates of interest and retain estimates from each replicate ----
estimated_means_and_proportions <- svymean(x = ~ api00 + api99 + stype, design = boot_design,
                                           return.replicates = TRUE)
custom_statistic <- withReplicates(design = boot_design,
```



```

        return.replicates = TRUE,
        theta = function(wts, data) {
          numerator <- sum(data$api00 * wts)
          denominator <- sum(data$api99 * wts)
          statistic <- numerator/denominator
          return(statistic)
        })
# Estimate simulation CV of bootstrap estimates ----

estimate_boot_sim_cv(
  svrepstat = estimated_means_and_proportions
)

estimate_boot_sim_cv(
  svrepstat = custom_statistic
)

## End(Not run)

```

get_design_quad_form *Determine the quadratic form matrix of a variance estimator for a survey design object*

Description

Determines the quadratic form matrix of a specified variance estimator, by parsing the information stored in a survey design object created using the 'survey' package.

Usage

```
get_design_quad_form(design, variance_estimator, ensure_psd = FALSE)
```

Arguments

design A survey design object created using the 'survey' (or 'srvyr') package, with class 'survey.design' or 'svyimputationList'. Also accepts two-phase design objects with class 'twophase2'; see the section below titled "Two-Phase Designs" for more information about handling of two-phase designs.

variance_estimator

The name of the variance estimator whose quadratic form matrix should be created.

See the section "Variance Estimators" below. Options include:

- **"Yates-Grundy"**: The Yates-Grundy variance estimator based on first-order and second-order inclusion probabilities.
- **"Horvitz-Thompson"**: The Horvitz-Thompson variance estimator based on first-order and second-order inclusion probabilities.

- **"Poisson Horvitz-Thompson"**: The Horvitz-Thompson variance estimator based on assuming Poisson sampling with specified first-order inclusion probabilities.
- **"Stratified Multistage SRS"**: The usual stratified multistage variance estimator based on estimating the variance of cluster totals within strata at each stage.
- **"Ultimate Cluster"**: The usual variance estimator based on estimating the variance of first-stage cluster totals within first-stage strata.
- **"SD1"**: The non-circular successive-differences variance estimator described by Ash (2014), sometimes used for variance estimation for systematic sampling.
- **"SD2"**: The circular successive-differences variance estimator described by Ash (2014). This estimator is the basis of the "successive-differences replication" estimator commonly used for variance estimation for systematic sampling.

ensure_psd A logical value, defaulting to FALSE. If ensure_psd = TRUE and the quadratic form is not already positive semidefinite, then the function `get_nearest_psd_matrix()` is used to approximate the quadratic form matrix by the nearest positive semidefinite matrix. This is necessary if the quadratic form is used as an input for replication methods such as the generalized bootstrap and is also useful if the quadratic form is to be used directly for estimating covariance matrices.

Value

A matrix representing the quadratic form of a specified variance estimator, based on extracting information about clustering, stratification, and selection probabilities from the survey design object.

Variance Estimators

The **Horvitz-Thompson** variance estimator:

$$v(\hat{Y}) = \sum_{i \in s} \sum_{j \in s} \left(1 - \frac{\pi_i \pi_j}{\pi_{ij}}\right) \frac{y_i}{\pi_i} \frac{y_j}{\pi_j}$$

The **Yates-Grundy** variance estimator:

$$v(\hat{Y}) = -\frac{1}{2} \sum_{i \in s} \sum_{j \in s} \left(1 - \frac{\pi_i \pi_j}{\pi_{ij}}\right) \left(\frac{y_i}{\pi_i} - \frac{y_j}{\pi_j}\right)^2$$

The **Stratified Multistage SRS** variance estimator is the recursive variance estimator proposed by Bellhouse (1985) and used in the 'survey' package's function `svyrecvar`. The estimator can be used for any number of sampling stages. For illustration, we describe its use for two sampling stages.

$$v(\hat{Y}) = \hat{V}_1 + \hat{V}_2$$

where

$$\hat{V}_1 = \sum_{h=1}^H \left(1 - \frac{n_h}{N_h}\right) \frac{n_h}{n_h - 1} \sum_{i=1}^{n_h} (y_{hi.} - \bar{y}_{hi.})^2$$

and

$$\hat{V}_2 = \sum_{h=1}^H \frac{n_h}{N_h} \sum_{i=1}^{n_h} v_{hi}(y_{hi.})$$

where n_h is the number of sampled clusters in stratum h , N_h is the number of population clusters in stratum h , $y_{hi.}$ is the weighted cluster total in cluster i of stratum h , $\bar{y}_{hi.}$ is the mean weighted cluster total of stratum h , ($\bar{y}_{hi.} = \frac{1}{n_h} \sum_{i=1}^{n_h} y_{hi.}$), and $v_{hi}(y_{hi.})$ is the estimated sampling variance of $y_{hi.}$.

The **Ultimate Cluster** variance estimator is simply the stratified multistage SRS variance estimator, but ignoring variances from later stages of sampling.

$$v(\hat{Y}) = \hat{V}_1$$

This is the variance estimator used in the 'survey' package when the user specifies `option(survey.ultimate.cluster = TRUE)` or uses `svyrecvar(..., one.stage = TRUE)`. When the first-stage sampling fractions are small, analysts often omit the finite population corrections ($1 - \frac{n_h}{N_h}$) when using the ultimate cluster estimator.

The **SD1** and **SD2** variance estimators are "successive difference" estimators sometimes used for systematic sampling designs. Ash (2014) describes each estimator as follows:

$$\hat{v}_{SD1}(\hat{Y}) = \left(1 - \frac{n}{N}\right) \frac{n}{2(n-1)} \sum_{k=2}^n (\check{y}_k - \check{y}_{k-1})^2$$

$$\hat{v}_{SD2}(\hat{Y}) = \left(1 - \frac{n}{N}\right) \frac{1}{2} \left[\sum_{k=2}^n (\check{y}_k - \check{y}_{k-1})^2 + (\check{y}_n - \check{y}_1)^2 \right]$$

where $\check{y}_k = y_k/\pi_k$ is the weighted value of unit k with selection probability π_k . The SD1 estimator is recommended by Wolter (1984). The SD2 estimator is the basis of the successive difference replication estimator commonly used for systematic sampling designs. See Ash (2014) for details.

For multistage samples, SD1 and SD2 are applied to the clusters at each stage, separately by stratum. For later stages of sampling, the variance estimate from a stratum is multiplied by the product of sampling fractions from earlier stages of sampling. For example, at a third stage of sampling, the variance estimate from a third-stage stratum is multiplied by $\frac{n_1}{N_1} \frac{n_2}{N_2}$, which is the product of sampling fractions from the first-stage stratum and second-stage stratum.

Two-Phase Designs

For a two-phase design, `variance_estimator` should be a list of variance estimators, with two elements, such as `list('Ultimate Cluster', 'Poisson Horvitz-Thompson')`. In two-phase designs, only the following estimators may be used for the second phase:

- "Ultimate Cluster"
- "Stratified Multistage SRS"
- "Poisson Horvitz-Thompson"

References

- Ash, S. (2014). "Using successive difference replication for estimating variances." **Survey Methodology**, Statistics Canada, 40(1), 47–59.
- Bellhouse, D.R. (1985). "Computing Methods for Variance Estimation in Complex Surveys." **Journal of Official Statistics**, Vol.1, No.3.
- Särndal, C.-E., Swensson, B., & Wretman, J. (1992). "Model Assisted Survey Sampling." Springer New York.

Examples

```
## Not run:
# Example 1: Quadratic form for successive-difference variance estimator ----

data('library_stsys_sample', package = 'svrep')

## First, ensure data are sorted in same order as was used in sampling
library_stsys_sample <- library_stsys_sample[
  order(library_stsys_sample$SAMPLING_SORT_ORDER),
]

## Create a survey design object
design_obj <- svydesign(
  data = library_stsys_sample,
  strata = ~ SAMPLING_STRATUM,
  ids = ~ 1,
  fpc = ~ STRATUM_POP_SIZE
)

## Obtain quadratic form
quad_form_matrix <- get_design_quad_form(
  design = design_obj,
  variance_estimator = "SD2"
)

## Estimate variance of estimated population total
y <- design_obj$variables$LIBRARIA
wts <- weights(design_obj, type = 'sampling')
y_wtd <- as.matrix(y) * wts
y_wtd[is.na(y_wtd)] <- 0

pop_total <- sum(y_wtd)

var_est <- t(y_wtd) %*% quad_form_matrix %*% y_wtd
std_error <- sqrt(var_est)

print(pop_total); print(std_error)

# Compare to estimate from assuming SRS
svytotal(x = ~ LIBRARIA, na.rm = TRUE,
```

```

        design = design_obj)

# Example 2: Two-phase design (second phase is nonresponse) ----

## Estimate response propensities, separately by stratum
library_stsys_sample[['RESPONSE_PROB']] <- svyglm(
  design = design_obj,
  formula = I(RESPONSE_STATUS == "Survey Respondent") ~ SAMPLING_STRATUM,
  family = quasibinomial('logistic')
) |> predict(type = 'response')

## Create a survey design object,
## where nonresponse is treated as a second phase of sampling
twophase_design <- twophase(
  data = library_stsys_sample,
  strata = list(~ SAMPLING_STRATUM, NULL),
  id = list(~ 1, ~ 1),
  fpc = list(~ STRATUM_POP_SIZE, NULL),
  probs = list(NULL, ~ RESPONSE_PROB),
  subset = ~ I(RESPONSE_STATUS == "Survey Respondent")
)

## Obtain quadratic form for the two-phase variance estimator,
## where first phase variance contribution estimated
## using the successive differences estimator
## and second phase variance contribution estimated
## using the Horvitz-Thompson estimator
## (with joint probabilities based on assumption of Poisson sampling)
get_design_quad_form(
  design = twophase_design,
  variance_estimator = list(
    "SD2",
    "Poisson Horvitz-Thompson"
  )
)

## End(Not run)

```

```
get_nearest_psd_matrix
```

Approximates a symmetric, real matrix by the nearest positive semidefinite matrix.

Description

Approximates a symmetric, real matrix by the nearest positive semidefinite matrix in the Frobenius norm, using the method of Higham (1988). For a real, symmetric matrix, this is equivalent to "zeroing out" negative eigenvalues. See the "Details" section for more information.

Usage

```
get_nearest_psd_matrix(X)
```

Arguments

`X` A symmetric, real matrix with no missing values.

Details

Let A denote a symmetric, real matrix which is not positive semidefinite. Then we can form the spectral decomposition $A = \Gamma\Lambda\Gamma'$, where Λ is the diagonal matrix whose entries are eigenvalues of A . The method of Higham (1988) is to approximate A with $\tilde{A} = \Gamma\Lambda_+\Gamma'$, where the ii -th entry of Λ_+ is $\max(\Lambda_{ii}, 0)$.

Value

The nearest positive semidefinite matrix of the same dimension as X .

References

- Higham, N. J. (1988). "Computing a nearest symmetric positive semidefinite matrix." *Linear Algebra and Its Applications*, 103, 103–118.

Examples

```
X <- matrix(
  c(2, 5, 5,
    5, 2, 5,
    5, 5, 2),
  nrow = 3, byrow = TRUE
)
get_nearest_psd_matrix(X)
```

| | |
|----------------------------|--|
| <code>is_psd_matrix</code> | <i>Check whether a matrix is positive semidefinite</i> |
|----------------------------|--|

Description

Check whether a matrix is positive semidefinite, based on checking for symmetric and negative eigenvalues.

Usage

```
is_psd_matrix(X, tolerance = sqrt(.Machine$double.eps))
```

Arguments

| | |
|------------------------|--|
| <code>X</code> | A matrix with no missing or infinite values. |
| <code>tolerance</code> | Tolerance for controlling whether a tiny computed eigenvalue will actually be considered negative. Computed negative eigenvalues will be considered negative if they are less than which are less than $-\text{abs}(\text{tolerance} * \text{max}(\text{eigen}(X)\$values))$. A small nonzero tolerance is recommended since eigenvalues are nearly always computed with some floating-point error. |

Value

A logical value. TRUE if the matrix is deemed positive semidefinite. Negative otherwise (including if `X` is not symmetric).

See Also

The function `get_nearest_psd_matrix()` can be used to approximate a symmetric matrix which is not positive semidefinite, by a similar positive semidefinite matrix.

Examples

```
X <- matrix(
  c(2, 5, 5,
    5, 2, 5,
    5, 5, 2),
  nrow = 3, byrow = TRUE
)

is_psd_matrix(X)

eigen(X)$values
```

| | |
|-----------|---|
| libraries | <i>Public Libraries Survey (PLS): A Census of U.S. Public Libraries in FY2020</i> |
|-----------|---|

Description

Data taken from a complete census of public libraries in the United States in FY2020 (April 2020 to March 2021). The Public Libraries Survey (PLS) is an annual census of public libraries in the U.S., including all public libraries identified by state library administrative agencies in the 50 states, the District of Columbia, and the outlying territories of American Samoa, Guam, the Northern Mariana Islands, and the U.S. Virgin Islands (Puerto Rico did not participate in FY2020).

The primary dataset, `library_census`, represents the full microdata from the census. The datasets `library_multistage_sample` and `library_stsys_sample` are samples drawn from `library_census` using different sampling methods.

Usage

```
data(library_census)
```

```
data(library_multistage_sample)
```

```
data(library_stsys_sample)
```

Format

Library Census (library_census):

The dataset includes 9,245 records (one per library) and 23 variables. Each column has a variable label, accessible using the function `var_label()` from the 'labelled' package or simply by calling `attr(x, 'label')` to a given column. These data include a subset of the variables included in the public-use data published by PLS, specifically from the Public Library System Data File. Particularly relevant variables include:

Identifier variables and survey response status:

- **FSCSKEY**: A unique identifier for libraries.
- **LIBNAME**: The name of the library
- **RESPONSE_STATUS**: Response status for the Public Library Survey: indicates whether the library was a respondent, nonrespondent, or was closed.

Numeric summaries:

- **TOTCIR**: Total circulation
- **VISITS**: Total visitors
- **REGBOR**: Total number of registered users
- **TOTSTAFF**: Total staff (measured in full-time equivalent staff)
- **LIBRARIA**: Total librarians (measured in full-time equivalent staff)
- **TOTOPEXP**: Total operating expenses
- **TOTINCM**: Total income
- **BRANLIB**: Number of library branches
- **CENTLIB**: Number of central library locations

Location:

- **LONGITUD**: Geocoded longitude (in WGS84 CRS)
- **LATITUD**: Geocoded latitude (in WGS84 CRS)
- **STABR**: Two-letter state abbreviation
- **CBSA**: Five-digit identifier for a core-based statistical area (CBSA)
- **MICROF**: Flag for a metropolitan or micropolitan statistical area

Library Multistage Sample (library_multistage_sample):

These data represent a two-stage sample (PSUs and SSUs), where the first stage sample is selected using unequal probability sampling without replacement (PPSWOR) and the second stage sample is selected using simple random sampling without replacement (SRSWOR).

Includes the same variables as `library_census`, but with additional design variables.

- `PSU_ID`: A unique identifier for primary sampling units
- `SSU_ID`: A unique identifier for secondary sampling units
- `SAMPLING_PROB`: Overall inclusion probability
- `PSU_SAMPLING_PROB`: Inclusion probability for the PSU
- `SSU_SAMPLING_PROB`: Inclusion probability for the SSU
- `PSU_POP_SIZE`: The number of PSUs in the population
- `SSU_POP_SIZE`: The number of population SSUs within the PSU

Library Stratified Systematic Sample (library_stsys_sample):

These data represent a stratified systematic sample.

Includes the same variables as `library_census`, but with additional design variables.

- `SAMPLING_STRATUM`: Unique identifier for sampling strata
- `STRATUM_POP_SIZE`: The population size in the stratum
- `SAMPLING_SORT_ORDER`: The sort order used before selecting a random systematic sample
- `SAMPLING_PROB`: Overall inclusion probability

References

Pelczar, M., Soffronoff, J., Nielsen, E., Li, J., & Mabile, S. (2022). Data File Documentation: Public Libraries in the United States Fiscal Year 2020. Institute of Museum and Library Services: Washington, D.C.

lou_pums_microdata *ACS PUMS Data for Louisville*

Description

Person-level microdata from the American Community Survey (ACS) 2015-2019 public-use microdata sample (PUMS) data for Louisville, KY. This microdata sample represents all adults (persons aged 18 or over) in Louisville, KY.

These data include replicate weights to use for variance estimation.

Usage

```
data(lou_pums_microdata)
```

Format

A data frame with 80 rows and 85 variables

- **UNIQUE_ID**: Unique identifier for records
- **AGE**: Age in years (copied from the AGEP variable in the ACS microdata)
- **RACE_ETHNICITY**: Race and Hispanic/Latino ethnicity derived from RAC1P and HISP variables of ACS microdata and collapsed to a smaller number of categories.
- **SEX**: Male or Female
- **EDUC_ATTAINMENT**: Highest level of education attained ('Less than high school' or 'High school or beyond') derived from SCHL variable in ACS microdata and collapsed to a smaller number of categories.
- **PWGTP**: Weights for the full-sample
- **PWGTP1-PWGTP80**: 80 columns of replicate weights created using the Successive Differences Replication (SDR) method.

Examples

```
## Not run:
data(lou_pums_microdata)

# Prepare the data for analysis with the survey package
library(survey)

lou_pums_rep_design <- survey::svrepdesign(
  data = lou_pums_microdata,
  variables = ~ UNIQUE_ID + AGE + SEX + RACE_ETHNICITY + EDUC_ATTAINMENT,
  weights = ~ PWGTP, repweights = "PWGTP\\d{1,2}",
  type = "successive-difference",
  mse = TRUE
)

# Estimate population proportions
svymean(~ SEX, design = lou_pums_rep_design)

## End(Not run)
```

Description

A survey measuring Covid-19 vaccination status and a handful of demographic variables, based on a simple random sample of 1,000 residents of Louisville, Kentucky with an approximately 50% response rate.

These data were created using simulation.

Usage

```
data(lou_vax_survey)
```

Format

A data frame with 1,000 rows and 6 variables

RESPONSE_STATUS Response status to the survey ('Respondent' or 'Nonrespondent')

RACE_ETHNICITY Race and Hispanic/Latino ethnicity derived from RAC1P and HISP variables of ACS microdata and collapsed to a smaller number of categories.

SEX Male or Female

EDUC_ATTAINMENT Highest level of education attained ('Less than high school' or 'High school or beyond') derived from SCHL variable in ACS microdata and collapsed to a smaller number of categories.

VAX_STATUS Covid-19 vaccination status ('Vaccinated' or 'Unvaccinated')

SAMPLING_WEIGHT Sampling weight: equal for all cases since data come from a simple random sample

lou_vax_survey_control_totals

Control totals for the Louisville Vaccination Survey

Description

Control totals to use for raking or post-stratification for the Louisville Vaccination Survey data. Control totals are population size estimates from the ACS 2015-2019 5-year Public Use Microdata Sample (PUMS) for specific demographic categories among adults in Jefferson County, KY.

These data were created using simulation.

Usage

```
data(lou_vax_survey_control_totals)
```

Format

A nested list object with two lists, `poststratification` and `raking`, each of which contains two elements: `estimates` and `variance-covariance`.

poststratification Control totals for the combination of `RACE_ETHNICITY`, `SEX`, and `EDUC_ATTAINMENT`.

- `estimates`: A numeric vector of estimated population totals.
- `variance-covariance`: A variance-covariance matrix for the estimated population totals.

raking Separate control totals for each of `RACE_ETHNICITY`, `SEX`, and `EDUC_ATTAINMENT`.

- `estimates`: A numeric vector of estimated population totals.
- `variance-covariance`: A variance-covariance matrix for the estimated population totals.

`make_gen_boot_factors` *Creates replicate factors for the generalized survey bootstrap*

Description

Creates replicate factors for the generalized survey bootstrap method. The generalized survey bootstrap is a method for forming bootstrap replicate weights from a textbook variance estimator, provided that the variance estimator can be represented as a quadratic form whose matrix is positive semidefinite (this covers a large class of variance estimators).

Usage

```
make_gen_boot_factors(Sigma, num_replicates, tau = "auto")
```

Arguments

| | |
|-----------------------------|---|
| <code>Sigma</code> | The matrix of the quadratic form used to represent the variance estimator. Must be positive semidefinite. |
| <code>num_replicates</code> | The number of bootstrap replicates to create. |
| <code>tau</code> | Either "auto", or a single number. This is the rescaling constant used to avoid negative weights through the transformation $\frac{w+\tau-1}{\tau}$, where w is the original weight and τ is the rescaling constant tau. If <code>tau="auto"</code> , the rescaling factor is determined automatically as follows: if all of the adjustment factors are nonnegative, then <code>tau</code> is set equal to 1; otherwise, <code>tau</code> is set to the smallest value needed to rescale the adjustment factors such that they are all at least 0.01. |

Value

A matrix with the same number of rows as `Sigma`, and the number of columns equal to `num_replicates`. The object has an attribute named `tau` which can be retrieved by calling `attr(which = 'tau')` on the object. The value `tau` is a rescaling factor which was used to avoid negative weights.

In addition, the object has attributes named `scale` and `rscales` which can be passed directly to [svrepdesign](#). Note that the value of `scale` is τ^2/B , while the value of `rscales` is vector of length B , with every entry equal to 1.

Statistical Details

Let $v(\hat{T}_y)$ be the textbook variance estimator for an estimated population total \hat{T}_y of some variable y . The base weight for case i in our sample is w_i , and we let \check{y}_i denote the weighted value $w_i y_i$. Suppose we can represent our textbook variance estimator as a quadratic form: $v(\hat{T}_y) = \check{y}'\Sigma\check{y}^T$, for some $n \times n$ matrix Σ . The only constraint on Σ is that, for our sample, it must be symmetric and positive semidefinite.

The bootstrapping process creates B sets of replicate weights, where the b -th set of replicate weights is a vector of length n denoted $\mathbf{a}^{(b)}$, whose k -th value is denoted $a_k^{(b)}$. This yields B replicate estimates of the population total, $\hat{T}_y^{*(b)} = \sum_{k \in S} a_k^{(b)} \check{y}_k$, for $b = 1, \dots, B$, which can be used to estimate sampling variance.

$$v_B(\hat{T}_y) = \frac{\sum_{b=1}^B \left(\hat{T}_y^{*(b)} - \hat{T}_y \right)^2}{B}$$

This bootstrap variance estimator can be written as a quadratic form:

$$v_B(\hat{T}_y) = \check{\mathbf{y}}' \Sigma_B \check{\mathbf{y}}$$

where

$$\Sigma_B = \frac{\sum_{b=1}^B (\mathbf{a}^{(b)} - \mathbf{1}_n) (\mathbf{a}^{(b)} - \mathbf{1}_n)'}{B}$$

Note that if the vector of adjustment factors $\mathbf{a}^{(b)}$ has expectation $\mathbf{1}_n$ and variance-covariance matrix Σ , then we have the bootstrap expectation $E_*(\Sigma_B) = \Sigma$. Since the bootstrap process takes the sample values \check{y} as fixed, the bootstrap expectation of the variance estimator is $E_*(\check{\mathbf{y}}' \Sigma_B \check{\mathbf{y}}) = \check{\mathbf{y}}' \Sigma \check{\mathbf{y}}$. Thus, we can produce a bootstrap variance estimator with the same expectation as the textbook variance estimator simply by randomly generating $\mathbf{a}^{(b)}$ from a distribution with the following two conditions:

Condition 1: $E_*(\mathbf{a}) = \mathbf{1}_n$

Condition 2: $E_*(\mathbf{a} - \mathbf{1}_n) (\mathbf{a} - \mathbf{1}_n)' = \Sigma$

While there are multiple ways to generate adjustment factors satisfying these conditions, the simplest general method is to simulate from a multivariate normal distribution: $\mathbf{a} \sim MVN(\mathbf{1}_n, \Sigma)$. This is the method used by this function.

Details on Rescaling to Avoid Negative Adjustment Factors

Let $\mathbf{A} = [\mathbf{a}^{(1)} \dots \mathbf{a}^{(b)} \dots \mathbf{a}^{(B)}]$ denote the $(n \times B)$ matrix of bootstrap adjustment factors. To eliminate negative adjustment factors, Beaumont and Patak (2012) propose forming a rescaled matrix of nonnegative replicate factors \mathbf{A}^S by rescaling each adjustment factor $a_k^{(b)}$ as follows:

$$a_k^{S,(b)} = \frac{a_k^{(b)} + \tau - 1}{\tau}$$

where $\tau \geq 1 - a_k^{(b)} \geq 1$ for all k in $\{1, \dots, n\}$ and all b in $\{1, \dots, B\}$.

The value of τ can be set based on the realized adjustment factor matrix \mathbf{A} or by choosing τ prior to generating the adjustment factor matrix \mathbf{A} so that τ is likely to be large enough to prevent negative bootstrap weights.

If the adjustment factors are rescaled in this manner, it is important to adjust the scale factor used in estimating the variance with the bootstrap replicates, which becomes $\frac{\tau^2}{B}$ instead of $\frac{1}{B}$.

$$\text{Prior to rescaling: } v_B(\hat{T}_y) = \frac{1}{B} \sum_{b=1}^B (\hat{T}_y^{*(b)} - \hat{T}_y)^2$$

$$\text{After rescaling: } v_B(\hat{T}_y) = \frac{\tau^2}{B} \sum_{b=1}^B (\hat{T}_y^{S*(b)} - \hat{T}_y)^2$$

When sharing a dataset that uses rescaled weights from a generalized survey bootstrap, the documentation for the dataset should instruct the user to use replication scale factor $\frac{\tau^2}{B}$ rather than $\frac{1}{B}$ when estimating sampling variances.

References

The generalized survey bootstrap was first proposed by Bertail and Combris (1997). See Beaumont and Patak (2012) for a clear overview of the generalized survey bootstrap. The generalized survey bootstrap represents one strategy for forming replication variance estimators in the general framework proposed by Fay (1984) and Dippo, Fay, and Morganstein (1984).

- Beaumont, Jean-François, and Zdenek Patak. 2012. “On the Generalized Bootstrap for Sample Surveys with Special Attention to Poisson Sampling: Generalized Bootstrap for Sample Surveys.” *International Statistical Review* 80 (1): 127–48. <https://doi.org/10.1111/j.1751-5823.2011.00166.x>.

- Bertail, and Combris. 1997. “Bootstrap Généralisé d’un Sondage.” *Annales d’Économie Et de Statistique*, no. 46: 49. <https://doi.org/10.2307/20076068>.

- Dippo, Cathryn, Robert Fay, and David Morganstein. 1984. “Computing Variances from Complex Samples with Replicate Weights.” In, 489–94. Alexandria, VA: American Statistical Association. http://www.asarms.org/Proceedings/papers/1984_094.pdf.

- Fay, Robert. 1984. “Some Properties of Estimates of Variance Based on Replication Methods.” In, 495–500. Alexandria, VA: American Statistical Association. http://www.asarms.org/Proceedings/papers/1984_095.pdf.

See Also

The function `make_quad_form_matrix` can be used to represent several common variance estimators as a quadratic form’s matrix, which can then be used as an input to `make_gen_boot_factors()`.

Examples

```
## Not run:
  library(survey)

# Load an example dataset that uses unequal probability sampling ----
```

```

data('election', package = 'survey')

# Create matrix to represent the Horvitz-Thompson estimator as a quadratic form ----
n <- nrow(election_pps)
pi <- election_jointprob
horvitz_thompson_matrix <- matrix(nrow = n, ncol = n)
for (i in seq_len(n)) {
  for (j in seq_len(n)) {
    horvitz_thompson_matrix[i,j] <- 1 - (pi[i,i] * pi[j,j])/pi[i,j]
  }
}

## Equivalently:

horvitz_thompson_matrix <- make_quad_form_matrix(
  variance_estimator = "Horvitz-Thompson",
  joint_probs = election_jointprob
)

# Make generalized bootstrap adjustment factors ----

bootstrap_adjustment_factors <- make_gen_boot_factors(
  Sigma = horvitz_thompson_matrix,
  num_replicates = 80,
  tau = 'auto'
)

# Determine replication scale factor for variance estimation ----
tau <- attr(bootstrap_adjustment_factors, 'tau')
B <- ncol(bootstrap_adjustment_factors)
replication_scaling_constant <- tau^2 / B

# Create a replicate design object ----
election_pps_bootstrap_design <- svrepdesign(
  data = election_pps,
  weights = 1 / diag(election_jointprob),
  repweights = bootstrap_adjustment_factors,
  combined.weights = FALSE,
  type = "other",
  scale = attr(bootstrap_adjustment_factors, 'scale'),
  rscales = attr(bootstrap_adjustment_factors, 'rscales')
)

# Compare estimates to Horvitz-Thompson estimator ----

election_pps_ht_design <- svydesign(
  id = ~1,
  fpc = ~p,
  data = election_pps,
  pps = ppsmat(election_jointprob),
  variance = "HT"
)

```

```
svytotal(x = ~ Bush + Kerry,
         design = election_pps_bootstrap_design)
svytotal(x = ~ Bush + Kerry,
         design = election_pps_ht_design)

## End(Not run)
```

make_quad_form_matrix *Represent a variance estimator as a quadratic form*

Description

Common variance estimators for estimated population totals can be represented as a quadratic form. Given a choice of variance estimator and information about the sample design, this function constructs the matrix of the quadratic form.

In notation, let $v(\hat{Y}) = \check{y}'\Sigma\check{y}$, where \check{y} is the vector of weighted values, $y_i/\pi_i, i = 1, \dots, n$. This function constructs the $n \times n$ matrix of the quadratic form, Σ .

Usage

```
make_quad_form_matrix(
  variance_estimator = "Yates-Grundy",
  joint_probs = NULL,
  cluster_ids = NULL,
  strata_ids = NULL,
  strata_pop_sizes = NULL,
  sort_order = NULL
)
```

Arguments

variance_estimator

The name of the variance estimator whose quadratic form matrix should be created. See the section "Variance Estimators" below. Options include:

- **"Yates-Grundy"**: The Yates-Grundy variance estimator based on first-order and second-order inclusion probabilities. If this is used, the argument `joint_probs` must also be used.
- **"Horvitz-Thompson"**: The Horvitz-Thompson variance estimator based on first-order and second-order inclusion probabilities. If this is used, the argument `joint_probs` must also be used.
- **"Stratified Multistage SRS"**: The usual stratified multistage variance estimator based on estimating the variance of cluster totals within strata at each stage. If this option is used, then it is necessary to also use the arguments `strata_ids`, `cluster_ids`, `strata_samp_sizes`, and `strata_pop_sizes`.

- **"Ultimate Cluster"**: The usual variance estimator based on estimating the variance of first-stage cluster totals within first-stage strata. If this option is used, then it is necessary to also use the arguments `strata_ids`, `cluster_ids`, `strata_samp_sizes`. Optionally, to use finite population correction factors, one can also use the argument `strata_pop_sizes`.
- **"SD1"**: The non-circular successive-differences variance estimator described by Ash (2014), sometimes used for variance estimation for systematic sampling.
- **"SD2"**: The circular successive-differences variance estimator described by Ash (2014). This estimator is the basis of the "successive-differences replication" estimator commonly used for variance estimation for systematic sampling.

| | |
|-------------------------------|---|
| <code>joint_probs</code> | Only used if <code>variance_estimator = "Horvitz-Thompson"</code> or <code>variance_estimator = "Yates-Grundy"</code> . This should be a matrix of joint inclusion probabilities. Element <code>[i, i]</code> of the matrix is the first-order inclusion probability of unit <code>i</code> , while element <code>[i, j]</code> is the joint inclusion probability of units <code>i</code> and <code>j</code> . |
| <code>cluster_ids</code> | Required unless <code>variance_estimator</code> equals <code>"Horvitz-Thompson"</code> or <code>"Yates-Grundy"</code> . This should be a matrix or data frame of cluster IDs. If there are multiple stages of sampling, then <code>cluster_ids</code> can have multiple columns, with one column for each level of sampling to be accounted for by the variance estimator. |
| <code>strata_ids</code> | Required if <code>variance_estimator</code> equals <code>"Stratified Multistage SRS"</code> or <code>"Ultimate Cluster"</code> . This should be a matrix or data frame of strata IDs. If there are multiple stages of sampling, then <code>strata_ids</code> can have multiple columns, with one column for each level of sampling to be accounted for by the variance estimator. |
| <code>strata_pop_sizes</code> | Required if <code>variance_estimator</code> equals <code>"Stratified Multistage SRS"</code> , but can optionally be used if <code>variance_estimator</code> equals <code>"Ultimate Cluster"</code> , <code>"SD1"</code> , or <code>"SD2"</code> . If there are multiple stages of sampling, then <code>strata_pop_sizes</code> can have multiple columns, with one column for each level of sampling to be accounted for by the variance estimator. |
| <code>sort_order</code> | Required if <code>variance_estimator</code> equals <code>"SD1"</code> or <code>"SD2"</code> . This should be a vector that orders the rows of data into the order used for sampling. |

Value

The matrix of the quadratic form representing the variance estimator.

Arguments required for each variance estimator

Below are the arguments that are required or optional for each variance estimator.

| <code>variance_estimator</code> | <code>joint_probs</code> | <code>cluster_ids</code> | <code>strata_ids</code> | <code>strata_pop_sizes</code> | <code>sort_order</code> |
|---------------------------------|--------------------------|--------------------------|-------------------------|-------------------------------|-------------------------|
| Yates-Grundy | Required | | | | |
| Horvitz-Thompson | Required | | | | |
| Stratified Multistage SRS | | Required | Required | Required | |
| Ultimate Cluster | | Required | Required | Optional | |
| SD1 | | Required | Optional | Optional | Required |

SD2

Required Optional

Optional Required

Variance Estimators

The **Horvitz-Thompson** variance estimator:

$$v(\hat{Y}) = \sum_{i \in s} \sum_{j \in s} \left(1 - \frac{\pi_i \pi_j}{\pi_{ij}}\right) \frac{y_i}{\pi_i} \frac{y_j}{\pi_j}$$

The **Yates-Grundy** variance estimator:

$$v(\hat{Y}) = -\frac{1}{2} \sum_{i \in s} \sum_{j \in s} \left(1 - \frac{\pi_i \pi_j}{\pi_{ij}}\right) \left(\frac{y_i}{\pi_i} - \frac{y_j}{\pi_j}\right)^2$$

The **Stratified Multistage SRS** variance estimator is the recursive variance estimator proposed by Bellhouse (1985) and used in the 'survey' package's function `svyrecvar`. The estimator can be used for any number of sampling stages. For illustration, we describe its use for two sampling stages.

$$v(\hat{Y}) = \hat{V}_1 + \hat{V}_2$$

where

$$\hat{V}_1 = \sum_{h=1}^H \left(1 - \frac{n_h}{N_h}\right) \frac{n_h}{n_h - 1} \sum_{i=1}^{n_h} (y_{hi.} - \bar{y}_{hi.})^2$$

and

$$\hat{V}_2 = \sum_{h=1}^H \frac{n_h}{N_h} \sum_{i=1}^{n_h} v_{hi.}(y_{hi.})$$

where n_h is the number of sampled clusters in stratum h , N_h is the number of population clusters in stratum h , $y_{hi.}$ is the weighted cluster total in cluster i of stratum h , $\bar{y}_{hi.}$ is the mean weighted cluster total of stratum h , ($\bar{y}_{hi.} = \frac{1}{n_h} \sum_{i=1}^{n_h} y_{hi.}$), and $v_{hi.}(y_{hi.})$ is the estimated sampling variance of $y_{hi.}$.

The **Ultimate Cluster** variance estimator is simply the stratified multistage SRS variance estimator, but ignoring variances from later stages of sampling.

$$v(\hat{Y}) = \hat{V}_1$$

This is the variance estimator used in the 'survey' package when the user specifies option `(survey.ultimate.cluster = TRUE)` or uses `svyrecvar(..., one.stage = TRUE)`. When the first-stage sampling fractions are small, analysts often omit the finite population corrections ($1 - \frac{n_h}{N_h}$) when using the ultimate cluster estimator.

The **SD1** and **SD2** variance estimators are "successive difference" estimators sometimes used for systematic sampling designs. Ash (2014) describes each estimator as follows:

$$\hat{v}_{SD1}(\hat{Y}) = \left(1 - \frac{n}{N}\right) \frac{n}{2(n-1)} \sum_{k=2}^n (\check{y}_k - \check{y}_{k-1})^2$$

$$\hat{v}_{SD2}(\hat{Y}) = \left(1 - \frac{n}{N}\right) \frac{1}{2} \left[\sum_{k=2}^n (\check{y}_k - \check{y}_{k-1})^2 + (\check{y}_n - \check{y}_1)^2 \right]$$

where $\check{y}_k = y_k/\pi_k$ is the weighted value of unit k with selection probability π_k . The SD1 estimator is recommended by Wolter (1984). The SD2 estimator is the basis of the successive difference replication estimator commonly used for systematic sampling designs. See Ash (2014) for details.

For multistage samples, SD1 and SD2 are applied to the clusters at each stage, separately by stratum. For later stages of sampling, the variance estimate from a stratum is multiplied by the product of sampling fractions from earlier stages of sampling. For example, at a third stage of sampling, the variance estimate from a third-stage stratum is multiplied by $\frac{n_1}{N_1} \frac{n_2}{N_2}$, which is the product of sampling fractions from the first-stage stratum and second-stage stratum.

References

Ash, S. (2014). "Using successive difference replication for estimating variances." **Survey Methodology**, Statistics Canada, 40(1), 47–59.

Bellhouse, D.R. (1985). "Computing Methods for Variance Estimation in Complex Surveys." **Journal of Official Statistics**, Vol.1, No.3.

See Also

For a two-phase design, the function `make_twophase_quad_form` combines the quadratic form matrix from each phase.

Examples

```
## Not run:
# Example 1: The Horvitz-Thompson Estimator
library(survey)
data("election", package = "survey")

ht_quad_form_matrix <- make_quad_form_matrix(variance_estimator = "Horvitz-Thompson",
                                             joint_probs = election_jointprob)

##_ Produce variance estimate
wtd_y <- as.matrix(election_pps$wt * election_pps$Bush)
t(wtd_y) %*% ht_quad_form_matrix %*% wtd_y

##_ Compare against result from 'survey' package
svytotal(x = ~ Bush,
         design = svydesign(data=election_pps,
                           variance = "HT",
                           pps = ppsmat(election_jointprob),
                           ids = ~ 1, fpc = ~ p)) |> vcov()

# Example 2: Stratified multistage Sample ----

data("mu284", package = 'survey')
multistage_srswor_design <- svydesign(data = mu284,
                                     ids = ~ id1 + id2,
                                     fpc = ~ n1 + n2)
```

```

multistage_srs_quad_form <- make_quad_form_matrix(
  variance_estimator = "Stratified Multistage SRS",
  cluster_ids = mu284[,c('id1', 'id2')],
  strata_ids = matrix(1, nrow = nrow(mu284), ncol = 2),
  strata_pop_sizes = mu284[,c('n1', 'n2')]
)

wtd_y <- as.matrix(weights(multistage_srswor_design) * mu284$y1)
t(wtd_y) %%% multistage_srs_quad_form %%% wtd_y

svytotal(x = ~ y1, design = multistage_srswor_design) |> vcov()

# Example 3: Successive-differences estimator ----

data('library_stsys_sample', package = 'svrep')

sd1_quad_form <- make_quad_form_matrix(
  variance_estimator = 'SD1',
  cluster_ids = library_stsys_sample[, 'FSCSKEY', drop=FALSE],
  strata_ids = library_stsys_sample[, 'SAMPLING_STRATUM', drop=FALSE],
  strata_pop_sizes = library_stsys_sample[, 'STRATUM_POP_SIZE', drop=FALSE],
  sort_order = library_stsys_sample[['SAMPLING_SORT_ORDER']]
)

wtd_y <- as.matrix(library_stsys_sample[['TOTCIR']] /
  library_stsys_sample$SAMPLING_PROB)
wtd_y[is.na(wtd_y)] <- 0

t(wtd_y) %%% sd1_quad_form %%% wtd_y

## End(Not run)

```

```
make_rwyb_bootstrap_weights
```

Create bootstrap replicate weights for a general survey design, using the Rao-Wu-Yue-Beaumont bootstrap method

Description

Creates bootstrap replicate weights for a multistage stratified sample design using the method of Beaumont and Émond (2022), which is a generalization of the Rao-Wu-Yue bootstrap.

The design may have different sampling methods used at different stages. Each stage of sampling may potentially use unequal probabilities (with or without replacement) and may potentially use Poisson sampling.

Usage

```
make_rwyb_bootstrap_weights(
```

```

num_replicates = 100,
samp_unit_ids,
strata_ids,
samp_unit_sel_probs,
samp_method_by_stage = rep("PPSWOR", times = ncol(samp_unit_ids)),
allow_final_stage_singletons = TRUE,
output = "weights"
)

```

Arguments

num_replicates Positive integer giving the number of bootstrap replicates to create

samp_unit_ids Matrix or data frame of sampling unit IDs for each stage of sampling

strata_ids Matrix or data frame of strata IDs for each sampling unit at each stage of sampling

samp_unit_sel_probs Matrix or data frame of selection probabilities for each sampling unit at each stage of sampling.

samp_method_by_stage A vector with length equal to the number of stages of sampling, corresponding to the number of columns in `samp_unit_ids`. This describes the method of sampling used at each stage. Each element should be one of the following:

- "SRSWOR" - Simple random sampling, without replacement
- "SRSWR" - Simple random sampling, with replacement
- "PPSWOR" - Unequal probabilities of selection, without replacement
- "PPSWR" - Unequal probabilities of selection, with replacement
- "Poisson" - Poisson sampling: each sampling unit is selected into the sample at most once, with potentially different probabilities of inclusion for each sampling unit.

allow_final_stage_singletons Logical value indicating whether to allow non-certainty singleton strata at the final sampling stage (rather than throw an error message). If TRUE, the sampling unit in a non-certainty singleton stratum will have its final-stage adjustment factor calculated as if it was selected with certainty at the final stage (i.e., its adjustment factor will be 1), and then its final bootstrap weight will be calculated by combining this adjustment factor with its final-stage selection probability.

output Either "weights" (the default) or "factors". Specifying `output = "factors"` returns a matrix of replicate adjustment factors which can later be multiplied by the full-sample weights to produce a matrix of replicate weights. Specifying `output = "weights"` returns the matrix of replicate weights, where the full-sample weights are inferred using `samp_unit_sel_probs`.

Details

Beaumont and Émond (2022) describe a general algorithm for forming bootstrap replicate weights for multistage stratified samples, based on the method of Rao-Wu-Yue, with extensions to sampling

without replacement and use of unequal probabilities of selection (i.e., sampling with probability proportional to size) as well as Poisson sampling. These methods are guaranteed to produce non-negative replicate weights and provide design-unbiased and design-consistent variance estimates for totals, for designs where sampling uses one or more of the following methods:

- "SRSWOR" - Simple random sampling, without replacement
- "SRSWR" - Simple random sampling, with replacement
- "PPSWR" - Unequal probabilities of selection, with replacement
- "Poisson" - Poisson sampling: each sampling unit is selected into the sample at most once, with potentially different probabilities of inclusion for each sampling unit.

For designs where at least one stage's strata have sampling without replacement with unequal probabilities of selection ("PPSWOR"), the bootstrap method of Beaumont and Émond (2022) is guaranteed to produce nonnegative weights, but is not design-unbiased, since the method only approximates the joint selection probabilities which would be needed for unbiased estimation.

Unless any stages use simple random sampling without replacement, the resulting bootstrap replicate weights are guaranteed to all be strictly positive, which may be useful for calibration or analyses of domains with small sample sizes. If any stages use simple random sampling without replacement, it is possible for some replicate weights to be zero.

If there is survey nonresponse, it may be useful to represent the response/nonresponse as an additional stage of sampling, where sampling is conducted with Poisson sampling where each unit's "selection probability" at that stage is its response propensity (which typically has to be estimated).

Value

A matrix of with the same number of rows as `samp_unit_ids` and the number of columns equal to the value of the argument `num_replicates`. Specifying `output = "factors"` returns a matrix of replicate adjustment factors which can later be multiplied by the full-sample weights to produce a matrix of replicate weights. Specifying `output = "weights"` returns the matrix of replicate weights, where the full-sample weights are inferred using `samp_unit_sel_probs`.

References

Beaumont, J.-F.; Émond, N. (2022). "A Bootstrap Variance Estimation Method for Multistage Sampling and Two-Phase Sampling When Poisson Sampling Is Used at the Second Phase." *Stats*, 5: 339–357. <https://doi.org/10.3390/stats5020019>

Rao, J.N.K.; Wu, C.F.J.; Yue, K. (1992). "Some recent work on resampling methods for complex surveys." *Surv. Methodol.*, 18: 209–217.

See Also

If the survey design can be accurately represented using `svydesign`, then it is easier to simply use `as_bootstrap_design` with argument `type = "Rao-Wu-Yue-Beaumont"`.

Use `estimate_boot_reps_for_target_cv` to help choose the number of bootstrap replicates.


```

                                ids = ~ 1)

## Create bootstrap replicate weights
set.seed(2022)
bootstrap_replicate_weights <- make_rwyb_bootstrap_weights(
  num_replicates = 5000,
  samp_unit_ids = pps_wor_design$cluster,
  strata_ids = pps_wor_design$strata,
  samp_unit_sel_probs = pps_wor_design$prob,
  samp_method_by_stage = c("PPSWOR")
)

## Create a replicate design object with the survey package
bootstrap_rep_design <- svrepdesign(
  data = pps_wor_design$variables,
  repweights = bootstrap_replicate_weights,
  weights = weights(pps_wor_design, type = "sampling"),
  type = "bootstrap"
)

## Compare std. error estimates from bootstrap versus linearization
data.frame(
  'Statistic' = c('total', 'mean'),
  'SE (bootstrap)' = c(SE(svytotal(x = ~ Bush, design = bootstrap_rep_design)),
                      SE(svymean(x = ~ I(Bush/votes),
                                   design = bootstrap_rep_design))),
  'SE (Overton\'s PPS approximation)' = c(SE(svytotal(x = ~ Bush,
                                                    design = pps_wor_design)),
                                          SE(svymean(x = ~ I(Bush/votes),
                                                    design = pps_wor_design))),
  check.names = FALSE
)

## End(Not run)

```

```
make_twophase_quad_form
```

Combine quadratic forms from each phase of a two phase design

Description

This function combines quadratic forms from each phase of a two phase design, so that the combined variance of the entire two-phase sampling design can be estimated.

Usage

```
make_twophase_quad_form(
  sigma_1,
  sigma_2,
  phase_2_joint_probs,
```



```

    ensure_psd = TRUE
  )

```

Arguments

| | |
|---------------------|---|
| sigma_1 | The quadratic form for the first phase variance estimator, subsetted to only include cases selected in the phase two sample. |
| sigma_2 | The quadratic form for the second phase variance estimator, conditional on the selection of the first phase sample. |
| phase_2_joint_probs | The matrix of conditional joint inclusion probabilities for the second phase, given the selected first phase sample. |
| ensure_psd | If TRUE (the default), ensures that the result is a positive semidefinite matrix. This is necessary if the quadratic form is used as an input for replication methods such as the generalized bootstrap. For details, see the help section entitled "Ensuring the Result is Positive Semidefinite". |

Value

A quadratic form matrix that can be used to estimate the sampling variance from a two-phase sample design.

Statistical Details

The two-phase variance estimator has a quadratic form matrix Σ_{ab} given by:

$$\Sigma_{ab} = W_b^{-1}(\Sigma_{a'} \circ D_b)W_b^{-1} + \Sigma_b$$

The first term estimates the variance contribution from the first phase of sampling, while the second term estimates the variance contribution from the second phase of sampling.

The full quadratic form of the variance estimator is:

$$v(\hat{t}_y) = \check{y}' \Sigma_{ab} \check{y}$$

where the weighted variable $\check{y}_k = \frac{y_k}{\pi_{ak}\pi_{bk}}$, is formed using the first phase inclusion probability, denoted π_{ak} , and the conditional second phase inclusion probability (given the selected first phase sample), denoted π_{bk} .

The notation for this estimator is as follows:

- n_a denotes the first phase sample size.
- n_b denotes the second phase sample size.
- Σ_a denotes the matrix of dimension $n_a \times n_a$ representing the quadratic form for the variance estimator used for the full first-phase design.
- $\Sigma_{a'}$ denotes the matrix of dimension $n_b \times n_b$ formed by subsetting the rows and columns of Σ_a to only include cases selected in the second-phase sample.

- Σ_b denotes the matrix of dimension $n_b \times n_b$ representing the Horvitz-Thompson estimator of variance for the second-phase sample, conditional on the selected first-phase sample.
- D_b denotes the $n_b \times n_b$ matrix of weights formed by the inverses of the second-phase joint inclusion probabilities, with element kl equal to π_{bkl}^{-1} , where π_{bkl} is the conditional probability that units k and l are included in the second-phase sample, given the selected first-phase sample. Note that this matrix will often not be positive semidefinite, and so the two-phase variance estimator has a quadratic form which is not necessarily positive semidefinite.
- W_b denotes the diagonal $n_b \times n_b$ matrix whose k -th diagonal entry is the second-phase weight π_{bk}^{-1} , where π_{bk} is the conditional probability that unit k is included in the second-phase sample, given the selected first-phase sample.

Ensuring the Result is Positive semidefinite

Note that the matrix $(\Sigma_{a'} \circ D_b)$ may not be positive semidefinite, since the matrix D_b is not guaranteed to be positive semidefinite. If $(\Sigma_{a'} \circ D_b)$ is found not to be positive semidefinite, then it is approximated by the nearest positive semidefinite matrix in the Frobenius norm, using the method of Higham (1988).

This approximation is discussed by Beaumont and Patak (2012) in the context of forming replicate weights for two-phase samples. The authors argue that this approximation should lead to only a small overestimation of variance.

Since $(\Sigma_{a'} \circ D_b)$ is a real, symmetric matrix, this is equivalent to "zeroing out" negative eigenvalues. To be more precise, denote $A = (\Sigma_{a'} \circ D_b)$. Then we can form the spectral decomposition $A = \Gamma \Lambda \Gamma'$, where Λ is the diagonal matrix whose entries are eigenvalues of A . The method of Higham (1988) is to approximate A with $\hat{A} = \Gamma \Lambda_+ \Gamma'$, where the ii -th entry of Λ_+ is $\max(\Lambda_{ii}, 0)$.

References

See Section 7.5 of Tillé (2020) or Section 9.3 of Särndal, Swensson, and Wretman (1992) for an overview of variance estimation for two-phase sampling. In the case where the Horvitz-Thompson variance estimator is used for both phases, the method used in this function is equivalent to equation (9.3.8) of Särndal, Swensson, and Wretman (1992) and equation (7.7) of Tillé (2020). However, this function can be used for any combination of first-phase and second-phase variance estimators, provided that the joint inclusion probabilities from the second-phase design are available and are all nonzero.

- Beaumont, Jean-François, and Zdenek Patak. (2012). "On the Generalized Bootstrap for Sample Surveys with Special Attention to Poisson Sampling: Generalized Bootstrap for Sample Surveys." *International Statistical Review* 80 (1): 127–48.
- Higham, N. J. (1988). "Computing a nearest symmetric positive semidefinite matrix." *Linear Algebra and Its Applications*, 103, 103–118.

- Särndal, C.-E., Swensson, B., & Wretman, J. (1992). *Model Assisted Survey Sampling*. Springer New York.
- Tillé, Y. (2020). *Sampling and estimation from finite populations*. (I. Hekimi, Trans.). Wiley.

See Also

For each phase of sampling, the function [make_quad_form_matrix](#) can be used to create the appropriate quadratic form matrix.

Examples

```
## Not run:

## ----- Example 1 -----##
## First phase is a stratified multistage sample      ##
## Second phase is a simple random sample           ##
##-----##
data('library_multistage_sample', package = 'svrep')

# Load first-phase sample
twophase_sample <- library_multistage_sample

# Select second-phase sample
set.seed(2022)

twophase_sample[['SECOND_PHASE_SELECTION']] <- sampling::srswor(
  n = 100,
  N = nrow(twophase_sample)
) |> as.logical()

# Declare survey design
twophase_design <- twophase(
  method = "full",
  data = twophase_sample,
  # Identify the subset of first-phase elements
  # which were selected into the second-phase sample
  subset = ~ SECOND_PHASE_SELECTION,
  # Describe clusters, probabilities, and population sizes
  # at each phase of sampling
  id = list(~ PSU_ID + SSU_ID,
            ~ 1),
  probs = list(~ PSU_SAMPLING_PROB + SSU_SAMPLING_PROB,
               NULL),
  fpc = list(~ PSU_POP_SIZE + SSU_POP_SIZE,
             NULL)
)

# Get quadratic form matrix for the first phase design
first_phase_sigma <- get_design_quad_form(
  design = twophase_design$phase1$full,
```

```

    variance_estimator = "Stratified Multistage SRS"
  )

# Subset to only include cases sampled in second phase

first_phase_sigma <- first_phase_sigma[twophase_design$subset,
                                       twophase_design$subset]

# Get quadratic form matrix for the second-phase design
second_phase_sigma <- get_design_quad_form(
  design = twophase_design$phase2,
  variance_estimator = "Ultimate Cluster"
)

# Get second-phase joint probabilities
n <- twophase_design$phase2$fpc$sampsize[1,1]
N <- twophase_design$phase2$fpc$popsize[1,1]

second_phase_joint_probs <- matrix((n/N)*((n-1)/(N-1)),
                                   nrow = n, ncol = n)
diag(second_phase_joint_probs) <- rep(n/N, times = n)

# Get quadratic form for entire two-phase variance estimator
twophase_quad_form <- make_twophase_quad_form(
  sigma_1 = first_phase_sigma,
  sigma_2 = second_phase_sigma,
  phase_2_joint_probs = second_phase_joint_probs
)

# Use for variance estimation

rep_factors <- make_gen_boot_factors(
  Sigma = twophase_quad_form,
  num_replicates = 500
)

library(survey)

combined_weights <- 1/twophase_design$prob

twophase_rep_design <- svrepdesign(
  data = twophase_sample |>
  subset(SECOND_PHASE_SELECTION),
  type = 'other',
  repweights = rep_factors,
  weights = combined_weights,
  combined.weights = FALSE,
  scale = attr(rep_factors, 'scale'),
  rscales = attr(rep_factors, 'rscales')
)

svymean(x = ~ LIBRARIA, design = twophase_rep_design)

```

```

## ----- Example 2 -----##
## First phase is a stratified systematic sample      ##
## Second phase is nonresponse, modeled as Poisson sampling ##
##-----##

data('library_stsys_sample', package = 'svrep')

# Determine quadratic form for full first-phase sample variance estimator

full_phase1_quad_form <- make_quad_form_matrix(
  variance_estimator = "SD2",
  cluster_ids = library_stsys_sample[, 'FSCSKEY', drop=FALSE],
  strata_ids = library_stsys_sample[, 'SAMPLING_STRATUM', drop=FALSE],
  strata_pop_sizes = library_stsys_sample[, 'STRATUM_POP_SIZE', drop=FALSE],
  sort_order = library_stsys_sample$SAMPLING_SORT_ORDER
)

# Identify cases included in phase two sample
# (in this example, respondents)
phase2_inclusion <- (
  library_stsys_sample$RESPONSE_STATUS == "Survey Respondent"
)
phase2_sample <- library_stsys_sample[phase2_inclusion,]

# Estimate response propensities

response_propensities <- glm(
  data = library_stsys_sample,
  family = quasibinomial('logit'),
  formula = phase2_inclusion ~ 1,
  weights = 1/library_stsys_sample$SAMPLING_PROB
) |>
  predict(type = "response",
          newdata = phase2_sample)

# Estimate conditional joint inclusion probabilities for second phase

phase2_joint_probs <- outer(response_propensities, response_propensities)
diag(phase2_joint_probs) <- response_propensities

# Determine quadratic form for variance estimator of second phase
# (Horvitz-Thompson estimator for nonresponse modeled as Poisson sampling)

phase2_quad_form <- make_quad_form_matrix(
  variance_estimator = "Horvitz-Thompson",
  joint_probs = phase2_joint_probs
)

# Create combined quadratic form for entire design

twophase_quad_form <- make_twophase_quad_form(
  sigma_1 = full_phase1_quad_form[phase2_inclusion, phase2_inclusion],

```

```

    sigma_2 = phase2_quad_form,
    phase_2_joint_probs = phase2_joint_probs
  )

  combined_weights <- 1/(phase2_sample$SAMPLING_PROB * response_propensities)

# Use for variance estimation

  rep_factors <- make_gen_boot_factors(
    Sigma = twophase_quad_form,
    num_replicates = 500
  )

  library(survey)

  twophase_rep_design <- svrepdesign(
    data = phase2_sample,
    type = 'other',
    repweights = rep_factors,
    weights = combined_weights,
    combined.weights = FALSE,
    scale = attr(rep_factors, 'scale'),
    rscales = attr(rep_factors, 'rscales')
  )

  svymean(x = ~ LIBRARIA, design = twophase_rep_design)

## End(Not run)

```

redistribute_weights *Redistribute weight from one group to another*

Description

Redistributes weight from one group to another: for example, from non-respondents to respondents. Redistribution is conducted for the full-sample weights as well as each set of replicate weights. This can be done separately for each combination of a set of grouping variables, for example to implement a nonresponse weighting class adjustment.

Usage

```
redistribute_weights(design, reduce_if, increase_if, by)
```

Arguments

| | |
|-----------|--|
| design | A survey design object, created with either the survey or srvyr packages. |
| reduce_if | An expression indicating which cases should have their weights set to zero. Must evaluate to a logical vector with only values of TRUE or FALSE. |

| | |
|-------------|--|
| increase_if | An expression indicating which cases should have their weights increased. Must evaluate to a logical vector with only values of TRUE or FALSE. |
| by | (Optional) A character vector with the names of variables used to group the redistribution of weights. For example, if the data include variables named "stratum" and "wt_class", one could specify <code>by = c("stratum", "wt_class")</code> . |

Value

The survey design object, but with updated full-sample weights and updated replicate weights. The resulting survey design object always has its value of `combined.weights` set to TRUE.

References

See Chapter 2 of Heeringa, West, and Berglund (2017) or Chapter 13 of Valliant, Dever, and Kreuter (2018) for an overview of nonresponse adjustment methods based on redistributing weights.

- Heeringa, S., West, B., Berglund, P. (2017). Applied Survey Data Analysis, 2nd edition. Boca Raton, FL: CRC Press. "Applied Survey Data Analysis, 2nd edition." Boca Raton, FL: CRC Press.

- Valliant, R., Dever, J., Kreuter, F. (2018). "Practical Tools for Designing and Weighting Survey Samples, 2nd edition." New York: Springer.

Examples

```
# Load example data
suppressPackageStartupMessages(library(survey))
data(api)

dclus1 <- svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
dclus1$variables$response_status <- sample(x = c("Respondent", "Nonrespondent",
                                                "Ineligible", "Unknown eligibility"),
                                           size = nrow(dclus1),
                                           replace = TRUE)

rep_design <- as.svrepdesign(dclus1)

# Adjust weights for cases with unknown eligibility
ue_adjusted_design <- redistribute_weights(
  design = rep_design,
  reduce_if = response_status %in% c("Unknown eligibility"),
  increase_if = !response_status %in% c("Unknown eligibility"),
  by = c("stype")
)

# Adjust weights for nonresponse
nr_adjusted_design <- redistribute_weights(
  design = ue_adjusted_design,
  reduce_if = response_status %in% c("Nonrespondent"),
  increase_if = response_status == "Respondent",
  by = c("stype")
)
```

rescale_reps

*Rescale replicate factors to have specified lower bound***Description**

Rescale replicate factors to ensure that they all exceed a specified lower bound. The main use of this rescaling is to ensure that all replicate weights are strictly positive.

Note that this rescaling has no impact on variance estimates for totals, but variance estimates for nonlinear statistics will be affected by the rescaling.

Usage

```
rescale_reps(x, tau = "auto", min_wgt = 0.01, digits = 2)
```

Arguments

| | |
|---------|--|
| x | Either a replicate survey design object, or a numeric matrix of replicate weights. |
| tau | Either "auto", or a single number. This is the rescaling constant used to avoid negative weights through the transformation $\frac{w+\tau-1}{\tau}$, where w is the original weight and τ is the rescaling constant tau. If tau="auto", the rescaling factor is determined automatically as follows: if all of the adjustment factors exceed the minimum value min_wgt, then tau is set equal to 1; otherwise, tau is set to the smallest value needed to rescale the adjustment factors such that they are all at least min_wgt. |
| min_wgt | Only used if tau='auto'. Specifies the minimum acceptable value for the rescaled weights. Must be at least zero and must be less than one. |
| digits | Only used if tau='auto'. Specifies the number of decimal places to use for choosing tau. Using a smaller number of digits is useful simply for producing easier-to-read documentation. |

Details

Let $\mathbf{A} = [\mathbf{a}^{(1)} \dots \mathbf{a}^{(b)} \dots \mathbf{a}^{(B)}]$ denote the $(n \times B)$ matrix of replicate adjustment factors. To eliminate negative adjustment factors, Beaumont and Patak (2012) propose forming a rescaled matrix of nonnegative replicate factors \mathbf{A}^S by rescaling each adjustment factor $a_k^{(b)}$ as follows:

$$a_k^{S,(b)} = \frac{a_k^{(b)} + \tau - 1}{\tau}$$

where $\tau \geq 1 - a_k^{(b)} \geq 1$ for all k in $\{1, \dots, n\}$ and all b in $\{1, \dots, B\}$.

The value of τ can be set based on the realized adjustment factor matrix \mathbf{A} or by choosing τ prior to generating the adjustment factor matrix \mathbf{A} so that τ is likely to be large enough to prevent negative adjustment factors.

If the adjustment factors are rescaled in this manner, it is important to adjust the scale factor used in estimating the variance with the bootstrap replicates. For example, for bootstrap replicates, the adjustment factor becomes $\frac{\tau^2}{B}$ instead of $\frac{1}{B}$.

$$\text{Prior to rescaling: } v_B(\hat{T}_y) = \frac{1}{B} \sum_{b=1}^B (\hat{T}_y^{*(b)} - \hat{T}_y)^2$$

$$\text{After rescaling: } v_B(\hat{T}_y) = \frac{\tau^2}{B} \sum_{b=1}^B (\hat{T}_y^{S*(b)} - \hat{T}_y)^2$$

Value

If the input is a numeric matrix, returns the rescaled matrix. If the input is a replicate survey design object, returns an updated replicate survey design object.

For a replicate survey design object, results depend on whether the object has a matrix of replicate factors rather than a matrix of replicate weights (which are the product of replicate factors and sampling weights). If the design object has `combined.weights=FALSE`, then the replication factors are adjusted. If the design object has `combined.weights=TRUE`, then the replicate weights are adjusted.

For a replicate survey design object, the scale element of the design object will be updated appropriately, and an element `tau` will also be added. If the input is a matrix instead of a survey design object, the result matrix will have an attribute named `tau` which can be retrieved using `attr(x, 'tau')`.

Examples

```
# Example 1: Rescaling a matrix of replicate weights

rep_wgts <- matrix(
  c(1.69742746694909, -0.230761178913411, 1.53333377634192,
    0.0495043413294782, 1.81820367441039, 1.13229198793703,
    1.62482013925955, 1.0866133494029, 0.28856654131668,
    0.581930729719006, 0.91827012312825, 1.49979905894482,
    1.26281337410693, 1.99327362761477, -0.25608700039304),
  nrow = 3, ncol = 5
)

rescaled_wgts <- rescale_reps(rep_wgts, tau = 'auto', min_wgt = 0.01)

print(rep_wgts)
print(rescaled_wgts)

# Example 2: Rescaling replicate weights of a survey design object
set.seed(2023)
library(survey)
data('mu284', package = 'survey')

## First create a bootstrap design object
svy_design_object <- svydesign(
```

```

data = mu284,
ids = ~ id1 + id2,
fpc = ~ n1 + n2
)

boot_design <- as_gen_boot_design(
  design = svy_design_object,
  variance_estimator = "Stratified Multistage SRS",
  replicates = 5, tau = 1
)

## Rescale the weights
rescaled_boot_design <- boot_design |>
  rescale_reps(tau = 'auto', min_wgt = 0.01)

boot_wgts <- weights(boot_design, "analysis")
rescaled_boot_wgts <- weights(rescaled_boot_design, 'analysis')

print(boot_wgts)
print(rescaled_boot_wgts)

```

stack_replicate_designs

Stack replicate designs, combining data and weights into a single object

Description

Stack replicate designs: combine rows of data, rows of replicate weights, and the respective full-sample weights. This can be useful when comparing estimates before and after a set of adjustments made to the weights. Another more delicate application is when combining sets of replicate weights from multiple years of data for a survey, although this must be done carefully based on guidance from a data provider.

Usage

```
stack_replicate_designs(..., .id = "Design_Name")
```

Arguments

... Replicate-weights survey design objects to combine. These can be supplied in one of two ways.

- Option 1 - A series of design objects, for example 'adjusted' = adjusted_design, 'orig' = orig_design.
- Option 2 - A list object containing design objects, for example list('nr' = nr_adjusted_design, 'ue' = ue_adjusted_design).

All objects must have the same specifications for type, rho, mse, scales, and rscales.

`.id` A single character value, which becomes the name of a new column of identifiers created in the output data to link each row to the design from which it was taken. The labels used for the identifiers are taken from named arguments.

Value

A replicate-weights survey design object, with class `svyrep.design` and `svyrep.stacked`. The resulting survey design object always has its value of `combined.weights` set to `TRUE`.

Examples

```
# Load example data, creating a replicate design object
suppressPackageStartupMessages(library(survey))
data(api)

dclus1 <- svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
dclus1$variables$response_status <- sample(x = c("Respondent", "Nonrespondent",
                                               "Ineligible", "Unknown eligibility"),
                                           size = nrow(dclus1),
                                           replace = TRUE)

orig_rep_design <- as.svrepdesign(dclus1)

# Adjust weights for cases with unknown eligibility
ue_adjusted_design <- redistribute_weights(
  design = orig_rep_design,
  reduce_if = response_status %in% c("Unknown eligibility"),
  increase_if = !response_status %in% c("Unknown eligibility"),
  by = c("stype")
)

# Adjust weights for nonresponse
nr_adjusted_design <- redistribute_weights(
  design = ue_adjusted_design,
  reduce_if = response_status %in% c("Nonrespondent"),
  increase_if = response_status == "Respondent",
  by = c("stype")
)

# Stack the three designs, using any of the following syntax options
stacked_design <- stack_replicate_designs(orig_rep_design, ue_adjusted_design, nr_adjusted_design,
                                          .id = "which_design")
stacked_design <- stack_replicate_designs('original' = orig_rep_design,
                                          'unknown eligibility adjusted' = ue_adjusted_design,
                                          'nonresponse adjusted' = nr_adjusted_design,
                                          .id = "which_design")
list_of_designs <- list('original' = orig_rep_design,
                       'unknown eligibility adjusted' = ue_adjusted_design,
                       'nonresponse adjusted' = nr_adjusted_design)
stacked_design <- stack_replicate_designs(list_of_designs, .id = "which_design")
```

summarize_rep_weights *Summarize the replicate weights*

Description

Summarize the replicate weights of a design

Usage

```
summarize_rep_weights(rep_design, type = "both", by)
```

Arguments

| | |
|------------|--|
| rep_design | A replicate design object, created with either the survey or srvyr packages. |
| type | Default is "both". Use type = "overall", for an overall summary of the replicate weights. Use type = "specific" for a summary of each column of replicate weights, with each column of replicate weights summarized in a given row of the summary. |
| by | Use type = "both" for a list containing both summaries, with the list containing the names "overall" and "both". (Optional) A character vector with the names of variables used to group the summaries. |

Value

If type = "both" (the default), the result is a list of data frames with names "overall" and "specific". If type = "overall", the result is a data frame providing an overall summary of the replicate weights.

The contents of the "overall" summary are the following:

- "nrows": Number of rows for the weights
- "ncols": Number of columns of replicate weights
- "degf_svy_pkg": The degrees of freedom according to the survey package in R
- "rank": The matrix rank as determined by a QR decomposition
- "avg_wgt_sum": The average column sum
- "sd_wgt_sums": The standard deviation of the column sums
- "min_rep_wgt": The minimum value of any replicate weight
- "max_rep_wgt": The maximum value of any replicate weight

If type = "specific", the result is a data frame providing a summary of each column of replicate weights, with each column of replicate weights described in a given row of the data frame. The contents of the "specific" summary are the following:

- "Rep_Column": The name of a given column of replicate weights. If columns are unnamed, the column number is used instead
- "N": The number of entries
- "N_NONZERO": The number of nonzero entries
- "SUM": The sum of the weights
- "MEAN": The average of the weights
- "CV": The coefficient of variation of the weights (standard deviation divided by mean)
- "MIN": The minimum weight
- "MAX": The maximum weight

Examples

```
# Load example data
suppressPackageStartupMessages(library(survey))
data(api)

dclus1 <- svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
dclus1$variables$response_status <- sample(x = c("Respondent", "Nonrespondent",
                                                "Ineligible", "Unknown eligibility"),
                                           size = nrow(dclus1),
                                           replace = TRUE)

rep_design <- as.svrepdesign(dclus1)

# Adjust weights for cases with unknown eligibility
ue_adjusted_design <- redistribute_weights(
  design = rep_design,
  reduce_if = response_status %in% c("Unknown eligibility"),
  increase_if = !response_status %in% c("Unknown eligibility"),
  by = c("stype")
)

# Summarize replicate weights

summarize_rep_weights(rep_design, type = "both")

# Summarize replicate weights by grouping variables

summarize_rep_weights(ue_adjusted_design, type = 'overall',
                      by = c("response_status"))

summarize_rep_weights(ue_adjusted_design, type = 'overall',
                      by = c("stype", "response_status"))

# Compare replicate weights

rep_wt_summaries <- lapply(list('original' = rep_design,
                               'adjusted' = ue_adjusted_design),
                           summarize_rep_weights,
                           type = "overall")
```

```
print(rep_wt_summaries)
```

| | |
|--------------|---|
| svyby_repwts | <i>Compare survey statistics calculated separately from different sets of replicate weights</i> |
|--------------|---|

Description

A modified version of the `svyby()` function from the `survey` package. Whereas `svyby()` calculates statistics separately for each subset formed by a specified grouping variable, `svyby_repwts()` calculates statistics separately for each replicate design, in addition to any additional user-specified grouping variables.

Usage

```
svyby_repwts(
  rep_designs,
  formula,
  by,
  FUN,
  ...,
  deff = FALSE,
  keep.var = TRUE,
  keep.names = TRUE,
  verbose = FALSE,
  vartype = c("se", "ci", "ci", "cv", "cvpct", "var"),
  drop.empty.groups = TRUE,
  return.replicates = FALSE,
  na.rm.by = FALSE,
  na.rm.all = FALSE,
  multicore = getOption("survey.multicore")
)
```

Arguments

| | |
|--------------------------|---|
| <code>rep_designs</code> | <p>The replicate-weights survey designs to be compared. Supplied either as:</p> <ul style="list-style-type: none"> • A named list of replicate-weights survey design objects, for example <code>list('nr' = nr_adjusted_design, 'ue' = ue_adjusted_design)</code>. • A 'stacked' replicate-weights survey design object created by <code>stack_replicate_designs()</code>. <p>The designs must all have the same number of columns of replicate weights, of the same type (bootstrap, JK_n, etc.)</p> |
| <code>formula</code> | A formula specifying the variables to pass to <code>FUN</code> |
| <code>by</code> | A formula specifying factors that define subsets |
| <code>FUN</code> | A function taking a formula and survey design object as its first two arguments. Usually a function from the <code>survey</code> package, such as <code>svytotal</code> or <code>svymean</code> . |

| | |
|-------------------|--|
| ... | Other arguments to FUN |
| deff | A value of TRUE or FALSE, indicating whether design effects should be estimated if possible. |
| keep.var | A value of TRUE or FALSE. If FUN returns a svystat object, indicates whether to extract standard errors from it. |
| keep.names | Define row names based on the subsets |
| verbose | If TRUE, print a label for each subset as it is processed. |
| vartype | Report variability as one or more of standard error, confidence interval, coefficient of variation, percent coefficient of variation, or variance |
| drop.empty.groups | If FALSE, report NA for empty groups, if TRUE drop them from the output |
| return.replicates | If TRUE, return all the replicates as the "replicates" attribute of the result. This can be useful if you want to produce custom summaries of the estimates from each replicate. |
| na.rm.by | If true, omit groups defined by NA values of the by variables |
| na.rm.all | If true, check for groups with no non-missing observations for variables defined by formula and treat these groups as empty |
| multicore | Use multicore package to distribute subsets over multiple processors? |

Value

An object of class "svyby": a data frame showing the grouping factors and results of FUN for each combination of the grouping factors. The first grouping factor always consists of indicators for which replicate design was used for an estimate.

Examples

```
## Not run:
suppressPackageStartupMessages(library(survey))
data(api)

dclus1 <- svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
dclus1$variables$response_status <- sample(x = c("Respondent", "Nonrespondent",
                                             "Ineligible", "Unknown eligibility"),
                                           size = nrow(dclus1),
                                           replace = TRUE)

orig_rep_design <- as.svrepdesign(dclus1)

# Adjust weights for cases with unknown eligibility
ue_adjusted_design <- redistribute_weights(
  design = orig_rep_design,
  reduce_if = response_status %in% c("Unknown eligibility"),
  increase_if = !response_status %in% c("Unknown eligibility"),
  by = c("stype")
)

# Adjust weights for nonresponse
```

```

nr_adjusted_design <- redistribute_weights(
  design = ue_adjusted_design,
  reduce_if = response_status %in% c("Nonrespondent"),
  increase_if = response_status == "Respondent",
  by = c("stype")
)

# Compare estimates from the three sets of replicate weights

list_of_designs <- list('original' = orig_rep_design,
  'unknown eligibility adjusted' = ue_adjusted_design,
  'nonresponse adjusted' = nr_adjusted_design)

##_ First compare overall means for two variables
means_by_design <- svyby_repwts(formula = ~ api00 + api99,
  FUN = svymean,
  rep_design = list_of_designs)

print(means_by_design)

##_ Next compare domain means for two variables
domain_means_by_design <- svyby_repwts(formula = ~ api00 + api99,
  by = ~ stype,
  FUN = svymean,
  rep_design = list_of_designs)

print(domain_means_by_design)

# Calculate confidence interval for difference between estimates

ests_by_design <- svyby_repwts(rep_designs = list('NR-adjusted' = nr_adjusted_design,
  'Original' = orig_rep_design),
  FUN = svymean, formula = ~ api00 + api99)

differences_in_estimates <- svycontrast(stat = ests_by_design, contrasts = list(
  'Mean of api00: NR-adjusted vs. Original' = c(1,-1,0,0),
  'Mean of api99: NR-adjusted vs. Original' = c(0,0,1,-1)
))

print(differences_in_estimates)

confint(differences_in_estimates, level = 0.95)

## End(Not run)

```


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