

Analysis of complex survey samples.

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Abstract

I present software for analysing complex survey samples in R. The sampling scheme can be explicitly described or represented by replication weights. Variance estimation uses either replication or linearisation.

1 Introduction

Analysis of complex survey samples has traditionally been the province of specialised software. This is partly due to the computational burden of large surveys, but the philosophical separation between survey statistics and much of the rest of the discipline is also important. In most areas of statistics the data are regarded as random, and the statistician must model their distribution (or the distribution of statistics computed from them). In traditional ‘design-based’ survey statistics the population data are regarded as fixed and the randomness comes entirely from the sampling procedure.

The advantage of the design-based view is that the sampling procedure is under the control of the analyst, and can in principle be known perfectly, the exception to George Box’s dictum that all models are wrong.

In this paper I describe a package of R code for analysing complex surveys. Before describing the features of the package I will present a short overview of the methods used in the `survey` package. Books covering survey statistics in more detail include Cochran (1977) and Levy & Lemeshow (1999). Examples of analyses across multiple computer packages are given at http://www.ats.ucla.edu/stat/survey/survey_howtochoose.htm.

2 Statistical methods

In the case of simple random sampling from a large population a survey sample will be nearly an independent and identically distributed sample from an unknown distribution. The law of large numbers and central limit theorem justify most of the same analyses from a design-based viewpoint as they do from a model-based viewpoint.

The complications in a complex survey sample result from

stratification Dividing the population into relatively homogenous groups (strata) and sampling a predetermined number from each stratum will increase precision for a given sample size

clustering Dividing the population into groups and sampling from a random subset of these groups (eg geographical locations) will decrease precision for a given sample size but often increase precision for a given cost.

unequal sampling Sampling small subpopulations more heavily will tend to increase precision relative to a simple random sample of the same size.

finite population Sampling all of a population or stratum results in an estimate with no variability, and sampling a substantial fraction of a stratum results in decreased variability in comparison to a sample from an infinite population.

I have described these in terms of their effect on the design of the survey. More important to the programmer is their effect on the analysis. Analysing a stratified sample as if it were a simple random sample will overestimate the standard errors, analysing a cluster sample as if it were a simple random sample will usually underestimate the standard errors, as will analysing an unequal probability sample as if it were a simple random sample. Note that the *design effect* and *misspecification effect* agree (qualitatively) for stratification and clustering but not for unequal probability sampling.

Clustering can be carried on to multiple levels: e.g., sampling individuals from families within neighbourhoods within cities. The largest clusters, which are sampled independently within a stratum, are called PSUs (primary sampling units). As they are sampled independently they are a fundamental part of the statistical analysis.

2.1 Weighting

When units are sampled with unequal probability it is necessary to give them correspondingly unequal weights in the analysis. Suppose 100 individuals are sampled from each state of the USA. The 100 people sampled from California represent a population of 34,000,000 people; the 100 sampled from Iowa represent only 2,900,000 people. Thus, each Californian must receive nearly 12 times as much weight in a valid analysis.

This *inverse-probability weighting* has generally the same effect on point estimates as the more familiar inverse-variance weighting, but very different effects on standard errors. In addition, the general principle in regression modelling that misspecified weights cause no bias does not apply here: it relies on the assumption that the model correctly specifies the mean, which is not permissible in a design-based analysis. In some circumstances a model-based analysis may be able to omit the weights and thus gain more precision (DuMouchel & Duncan, 1983).

2.2 Variances

Two widely used and fairly general techniques for variance estimation are Taylor series linearisation and replication weights. The former is based on reducing the variance estimation problem to estimating the variance of a mean, the latter is based on the same ideas as the jackknife. These two approaches are discussed in more detail below and are implemented in the `survey` package.

Other variance estimation techniques for surveys include the method of random groups and PSU-level bootstrapping. The method of random groups is based on sampling within PSUs. It is described by Wolter (1985), a comprehensive reference (at that date) on survey variance estimation. Bootstrapping at the PSU level, along with BRR and the jackknife methods, is discussed in Chapter 6 of Shao & Tu (1995).

2.2.1 Variances by linearisation

Taylor series linearisation estimators are very similar to the sandwich variance estimators widely used in biostatistics and econometrics. Survey-oriented presentations of the theory are given by Binder (1983), and Chapter 6 of Wolter (1985).

The principle is simple. Consider estimating the variance of the population total of a variable Y . Write Y_{sij} for observation j in PSU i in stratum s and π_{sij} for its sampling probability.

Inverse-probability weighting gives a contribution to the total from each PSU

$$Y_{si\cdot} = \sum_j \frac{1}{\pi_{sij}} Y_{sij},$$

and as PSUs are sampled independently within strata the variance of the stratum total can be estimated by the empirical variance of the PSU totals. If n_s is the number of PSUs sampled in the n th stratum then

$$\begin{aligned} Y_{s\cdot\cdot} &= \sum_{i=1}^{n_s} Y_{si\cdot} \\ \bar{Y}_{s\cdot\cdot} &= \frac{1}{n_s} \sum_{i=1}^{n_s} Y_{si\cdot} \\ \widehat{\text{var}}[\bar{Y}_{s\cdot\cdot}] &= \frac{1}{n_s - 1} \sum_{i=1}^{n_s} (Y_{si\cdot} - \bar{Y}_{s\cdot\cdot})^2. \end{aligned}$$

This variance will be too large when sampling an appreciable fraction of a population. When a simple random sample of PSUs is taken in each stratum, with no further subsampling, the variance can be multiplied by a finite population correction $1 - f_s$, where f_s is the proportion of PSUs sampled in stratum s . For other sampling designs the correct finite population adjustments will differ. Bellhouse (1985) describes algorithms for doing this if the necessary design details are available. A reviewer points out that in cases where finite-population

corrections are substantial it is also important to note that estimation usually assumes the PSUs are sampled with replacement, which is, of course, not typically the case.

Finally, adding up estimates for each of S strata gives a total and an estimate of its variance:

$$Y_{\dots} = \sum_{s=1}^S Y_{s..}$$

$$\widehat{\text{var}}[Y_{\dots}] = \sum_{s=1}^s (1 - f_s) \frac{1}{n_s - 1} \sum_{i=1}^{n_s} (Y_{si.} - \bar{Y}_{s..})^2.$$

Now, in most cases a statistic can be written as the solution $\hat{\theta}$ of an estimating equation

$$\sum_{i=1}^n U(X_i; \theta) = 0$$

where $\theta \mapsto U(X; \theta)$ is differentiable (a notable exception being quantiles). The variance V_U of

$$\sum_{i=1}^n U(X_i; \theta)$$

can be estimated in the same way as the variance of any other population total, and an asymptotic approximation to the variance of $\hat{\theta}$ is then

$$\left(\sum_{i=1}^n \frac{\partial U_i}{\partial \theta} \right)^{-1} V_U \left(\sum_{i=1}^n \frac{\partial U_i}{\partial \theta} \right)^{-1}.$$

With inverse-probability weighting we estimate θ by solving

$$\sum_{i=1}^n \tilde{U}_i(X_i, \theta) = \sum_{i=1}^n \frac{1}{\pi_i} U(X_i; \theta) = 0$$

where π_i is the sampling probability for the i th case. The asymptotic approximation to the variance of $\hat{\theta}$ is then

$$\left(\sum_{i=1}^n \frac{\partial \tilde{U}_i}{\partial \theta} \right)^{-1} V_{\tilde{U}} \left(\sum_{i=1}^n \frac{\partial \tilde{U}_i}{\partial \theta} \right)^{-1}.$$

Estimating the variance of $\hat{\theta}$ is a matter of estimating the mean of $\partial \tilde{U} / \partial \theta$ and the variance of the mean of $\tilde{U}(\theta)$ at $\hat{\theta}$, which can be done using standard methods for means in complex samples.

Survey sampling implementations of these sandwich variances differ from those in other areas of statistics only in the handling of stratification and finite-population corrections. The resulting variance estimators are approximately unbiased but may be quite variable and as a result tend to lead to confidence intervals that are too short in small samples.

2.2.2 Variances by subsampling

A second class of variance estimators is based on the jackknife. Chapters 3 and 4 of Wolter (1985) discuss these estimators from a survey statistics viewpoint. A different viewpoint is presented in Chapter 6 of Shao & Tu (1995).

In unstratified surveys one PSU at a time is deleted and the others reweighted to keep the same total weight (known as the JK1 jackknife). For stratified designs the JK_n jackknife removes one PSU at a time, but reweights only the other PSUs in the same stratum.

The Balanced Repeated Replicates estimator is intended for surveys with exactly two PSUs in each stratum. Subsamples are constructed by giving weights of 2 to one PSU in a stratum and 0 to the other. While in principle the BRR estimator would require 2^L sets of computations for L strata, it is possible to construct small, balanced sets of half-samples that give exactly the same variance for a linear statistic and similar variance for nonlinear statistics. These sets of replicates are constructed according to Plackett–Burman (Plackett & Burman, 1946) designs. The number of replicates in a Plackett–Burman design is always a multiple of four. It is conjectured that designs exist for any multiple of four, which would imply that at most $L + 4$ replicates are sufficient (known to be true for L up to 423). Given a design with m replicates it is easy to construct one with $2m$ replicates, thus designs with at most $2L$ replicates can easily be provided. A library of Hadamard matrices, from which Plackett–Burman designs can be constructed, is available at <http://www.research.att.com/~njas/hadamard/> and Wolter (1985) provides designs for $m \leq 100$.

Fay’s method (Judkins, 1990) is a modification of BRR where a parameter $\rho \in [0, 1)$ is chosen and weights of $2 - \rho$ and ρ are used for the two PSUs in each stratum. This has the advantage of using all the data and may give more stable estimates if ρ is chosen correctly. Fay’s method reduces to BRR if $\rho = 0$.

As an alternative to replicates constructed by the analyst, some recent US government surveys provide replicate weights instead of information on PSUs. These replicate weights are typically generated by one of the methods described above, but may then be modified for various reasons. One important use of replicate weights is to preserve privacy: it may be possible to disguise the PSUs and so prevent the identification of individuals in small PSUs.

A general formula for variance estimation from replicate weights is

$$\text{var}[\hat{\theta}] = C \sum_i c_i (\hat{\theta}(w_i) - \bar{\theta})^{\otimes 2} \quad (1)$$

where $\otimes 2$ indicates the outer product of a vector with itself. Here $\hat{\theta}(w_i)$ is the estimate of θ with the i th set of weights, $\bar{\theta}$ is the average of the replicate estimates of θ , c_i is a replication-specific constant and C is an overall scaling factor. The full-sample estimate $\hat{\theta}$ is sometimes used instead of $\bar{\theta}$. If the average weight for each observation is the same as its sampling weight there is no difference for linear statistics and it is not clear which is better for nonlinear statistics.

If L is the number of strata, n the total number of PSUs and n_s the number of PSUs in stratum s the constants are:

	C	c_i
JK1	$(n - 1)/n$	1
JKn	1	$(n_s - 1)/n_s$
BRR	$1/L$	1
Fay	$1/(L(1 - \rho)^2)$	1

Only the jackknife methods can readily incorporate a finite-population correction. Each replicate is specific to a stratum, so the constant c_i can be multiplied by the finite-population correction for that stratum.

2.3 Poststratification and raking

Stratified sampling requires a stratified *sampling frame*, that is, full prior knowledge of the stratum for every primary sampling unit in the population. It is often the case that the size of each population stratum is known (eg from Census data) and that the stratum for each sampled unit can be determined easily, but that a stratified sampling frame is prohibitively expensive.

Much of the efficiency of stratified sampling can then be recovered by scaling the sampling weights so that the total weight for each sample stratum is the same as the stratum size in the population. Variance estimation using replicate weights is still straightforward: the same scaling is performed on each set of replicates. Variances by linearisation are more complicated, at least in small samples.

In some situations the joint population distribution of a number of stratifying factors is not known but their marginal distributions are known. It would be desirable to post-stratify on each of these factors, but matching the marginal distribution of one factor may unmatch the marginal distribution of others. However, it is typically the case that iteratively post-stratifying on each factor in turn will lead to a converging sets of weights where the marginal distribution of each factor matches the population margins. This iterative algorithm is called *raking*.

Convergence will always occur if the sample joint distribution of the factors has no empty cells. If there are empty cells then convergence will occur whenever there is a joint distribution with the desired margins and the same pattern of empty cells.

2.4 Subpopulations

A subpopulation of a survey cannot simply be treated as a smaller survey. The subpopulation may have fewer PSUs in some strata, resulting in a random, rather than fixed, sample size. Conceptually, the correct analysis involves keeping the entire sample but assigning zero weight to observations not in the subpopulation. This strategy maintains, for example, the equivalence between separate regression models in subpopulations and a common regression with interactions.

A subpopulation of a survey design specified by replicate weights, on the other hand, can simply be analysed as a subset. The replicate weights are based on the design of the full sample and are still correct.

There is a minor computational ambiguity in using zero weights versus sub-setting: should observations with no weight still contribute to constraints in constrained models? For example, in fitting a linear model to binomial data, should the coefficients be restricted so that fitted proportions are in $[0, 1]$ even for cases with zero weight? There is no entirely satisfactory answer, but it is certainly simpler for cases with zero weight not to participate even in constraints.

3 The survey package

The **survey** package consists entirely of interpreted R code. This paper describes version 2.2. Future versions will be available at the Comprehensive R Archive Network (<http://cran.r-project.org>).

The **survey** package has two main purposes. The first is to bind the necessary design metadata to the data so that the correct analysis adjustments can be performed reliably and automatically. This is done by constructor functions **svydesign** and **svrepdesign** that create objects containing a data frame and design information. Extracting subsets of the data must preserve the metadata and also allow for accurate subpopulation estimates, so methods for "`[`", `subset`, `update`, and the `na.action` commands are provided.

The second main purpose is to provide valid variance estimates for statistics computed on these objects. The **svyCprod** function abstracts the computations needed for Taylor series linearisation and **svrVar** does a similar job for replicate weights. The `withReplicates()` function computes replicate-weight variances for arbitrary statistics specified by functions or expressions.

Computation of the statistics themselves is performed largely by existing R functions, the **survey** package merely providing wrappers. For example, **svyglm** and **svrepglm** construct calls to `glm` to fit generalised linear models and then modify the resulting objects to give correct variances. This approach makes it easy to extend the package, at some cost in speed and memory use.

3.1 Sampling design and Taylor series linearisation

The **svydesign** function constructs an object that specifies the strata, PSUs, sampling weights or probabilities, and finite population correction for a survey sample.

The resulting objects can be used in the statistical functions whose names begin `svy`: `svymean`, `svyvar`, `svyquantile`, `svytable`, `svyglm`, `svycoxph`, `svymle`. Standard errors are computed using Taylor series linearisation (where available).

The modelling functions **svyglm** and **svycoxph** require that all the variables in the model are contained in the survey design object. This would be good practice in any case; it is required to avoid scoping problems, as these functions work by constructing and evaluating calls to the ordinary `glm` and `coxph`

functions.

Fairly general pseudolikelihood estimation can be done with `svymle`. This function takes a loglikelihood and a set of linear predictors for some or all of its parameters, and maximises the estimated population loglikelihood

$$\hat{\ell}(\theta) = \sum_{i=1}^n \frac{1}{\pi_i} \ell_i(\theta)$$

where $\ell_i(\theta)$ is the loglikelihood of the i th observation.

3.2 Replicate weight designs

The `svrepdesign` function describes surveys specified solely in terms of replicate weights. A sampling design object can be converted to a replicate-weight design using `as.svrepdesign`. There are two basic classes of replicate weights: BRR and jackknife, but arbitrary designs can be specified by giving the replicate weights and the scaling parameters `scale` and `rscales` (C and c_i respectively, in equation 1). Poststratification is available in the `postStratify` function and raking in the `rake` function.

When converting from a sampling design object the functions `jk1weights`, `jkweights` and `brrweights` are used to construct replicate weights, and these can be called directly by the user. In constructing BRR weights the package uses precomputed Hadamard matrices with dimension 8, 16, 20, 24, 36, 72, and 256, and then doubles the dimension of these matrices as necessary to create other sizes.

The survey replicate objects produced by `as.svrepdesign` or `svrepdesign` can be used in the statistical functions whose names begin `svrep`: `svrepmean`, `svreptable`, `svrepglm`, and in the `withReplicates` function. The `withReplicates` function allows arbitrary statistics to be analysed, but requires more coding to use.

Fay's variance estimator can be specified when the design is constructed, thus fixing ρ , and giving a design of type "Fay". It may also be specified for designs of type "BRR" at analysis time, allowing different ρ to be used.

A finite population correction for jackknife weights can be specified by multiplying `rscales` (c_i in equation 1) by the correction (1-sampling fraction in the stratum). This is done automatically by `as.svrepdesign` with `type="JK1"` or `type="JKn"` if the original design contains a finite population correction.

4 How to use the package

The first step is to create an appropriate design object that contains the data variables and the metadata needed for valid estimation.

1. If you have design information (weights or sampling probabilities, PSU and stratum identifiers) and want to use Taylor series linearisation, use `svydesign`

2. If you have design information and want to use jackknife or BRR methods, use `svydesign` to create a `survey.design` object and then use `as.svrepdesign` to convert it to a replication-weights object.
3. If you have replication weights rather than design information use `svrepdesign`

Data processing to create new variables may be done either before or after the design object is created. It may be easier to do this before, as after the design object is created the `update` function provides the only access for adding variables. Data processing to remove observations should be done after the object is created, as otherwise the design information will not be updated correctly.

The analysis functions usually take as arguments this design object and a model formula specifying variables to be used. Names of analysis functions for objects created with `svydesign` begin with “svy”, and the functions for objects created with `svrepdesign` or `as.svrepdesign` begin with “svr”.

5 Examples

5.1 California School Performance

California public schools test their students each year. School-level summaries of the results of these tests in schools with more than 100 students are made publically available by the Department of Education at <http://www.cde.ca.gov/psaa/api>. Here we analyse three subsamples, from files published by Academic Technology Services at UCLA (http://www.ats.ucla.edu/stat/stata/Library/svy_survey.htm): a stratified independent sample, a one-stage cluster sample and a two-stage cluster sample. For each subsample we compute the means of two variables, and fit a linear regression model.

First we build `survey.design` objects and use the Taylor series linearisation methods, then we convert these to use jackknife-based replication weights. Finally we show how post-stratification and raking affect the estimation of the means.

Stratified Independent Sample

First consider a sample stratified by level of school (elementary, middle, high), in the data frame `strat`. The variable `snum` identifies a school, `stype` is the level of school, `fpc` is the number of schools in the stratum, and `pw` is the sampling weights. The initial step is to define a survey design object containing the data and metadata.

```
> dstrat<-svydesign(ids=~snum, strata=~stype, fpc=~fpc, data=strat, weight=~pw)
> dstrat
Stratified Independent Sampling design
svydesign(ids = ~snum, strata = ~stype, fpc = ~fpc, data = strat,
          weight = ~pw)
```

The summary method for such an object shows more detail about the design

```
> summary(dstrat)
Stratified Independent Sampling design
svydesign(ids = ~snum, strata = ~stype, fpc = ~fpc, data = strat,
  weight = ~pw)
Probabilities:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.02262 0.02262 0.03587 0.04014 0.05339 0.06623
Stratum sizes:
      E H M
obs      100 50 50
design.PSU 100 50 50
actual.PSU 100 50 50
Population stratum sizes (PSUs):
  strata  N
1      E 4421
2      H  755
3      M 1018
Data variables:
 [1] "cds"      "stype"      "name"      "sname"     "snum"      "dname"
 [7] "dnum"      "cname"     "cnum"      "flag"      "pcttest"   "api00"
[13] "api99"     "target"    "growth"    "sch.wide"  "comp.imp"  "both"
[19] "awards"    "meals"     "ell"       "yr.rnd"   "mobility"  "acs.k3"
[25] "acs.46"    "acs.core"  "pct.resp"  "not.hsg"  "hsg"       "some.col"
[31] "col.grad"  "grad.sch"  "avg.ed"    "full"     "emer"      "enroll"
[37] "api.stu"   "pw"        "fpc"
```

and we can now estimate the mean API performance score, the total enrollment across the state, and the relationship between API score and some measures of social disadvantage

```
> svymean(~api00+I(api00-api99), dstrat)
      mean      SE
api00      662.287 9.4089
I(api00 - api99) 32.893 2.0511
> svytotal(~enroll, dstrat)
      total      SE
enroll 3687178 114642
> summary(svyglm(api00~ell+meals+mobility, design=dstrat))
```

```
Call:
svyglm(formula = api00 ~ ell + meals + mobility, design = dstrat)
```

```
Survey design:
svydesign(id = ~1, strata = ~stype, weights = ~pw, data = apistrat,
  fpc = ~fpc)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	820.8873	10.0777	81.456	<2e-16 ***
ell	-0.4806	0.3920	-1.226	0.222
meals	-3.1415	0.2839	-11.064	<2e-16 ***
mobility	0.2257	0.3932	0.574	0.567

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Cluster sample

Next we consider sampling 15 school districts and taking all the schools in each of these districts, `strat`. The variable `snum` identifies a school, `stype` is the level of school, `fpc` is the number of schools in the stratum, and `pw` is the sampling weights. The initial step is to define a survey design object containing the data and metadata.

```
> dclus1<-svydesign(ids=~dnum, fpc=~fpc, data=clus1, weight=~pw)
```

```
> dclus1
```

```
1 - level Cluster Sampling design
```

```
With ( 15 ) clusters.
```

```
svydesign(ids = ~dnum, fpc = ~fpc, data = clus1, weight = ~pw)
```

```
> summary(dclus1)
```

```
1 - level Cluster Sampling design
```

```
With ( 15 ) clusters.
```

```
svydesign(ids = ~dnum, fpc = ~fpc, data = clus1, weight = ~pw)
```

```
Probabilities:
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.02954	0.02954	0.02954	0.02954	0.02954	0.02954

```
Population size (PSUs): 757
```

```
Data variables:
```

[1]	"cds"	"stype"	"name"	"sname"	"snum"	"dname"	"dnum"
[8]	"cname"	"cnum"	"flag"	"pcttest"	"api00"	"api99"	"target"
[15]	"growth"	"sch.wide"	"comp.imp"	"both"	"awards"	"meals"	"ell"
[22]	"yr.rnd"	"mobility"	"acs.k3"	"acs.46"	"acs.core"	"pct.resp"	"not.hsg"
[29]	"hsg"	"some.col"	"col.grad"	"grad.sch"	"avg.ed"	"full"	"emer"
[36]	"enroll"	"api.stu"	"fpc"	"pw"	"strat"		

and then perform the same analyses as for the stratified study

```
> svymean(~api00+I(api00-api99), dclus1)
```

	mean	SE
api00	644.169	23.5422
I(api00 - api99)	37.191	3.0852

```
> svytotal(~enroll, dclus1)
```

total	SE
-------	----

```

enroll 3404940 932235
> summary(svyglm(api00~ell+meals+mobility, design=dclus1))

Call:
svyglm(formula = api00 ~ ell + meals + mobility, design = dclus1)

Survey design:
svydesign(id = ~dnum, weights = ~pw, data = apiclus1, fpc = ~fpc)

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) 819.2791    21.3900  38.302  <2e-16 ***
ell          -0.5167     0.3240  -1.595   0.113
meals        -3.1232     0.2781 -11.231  <2e-16 ***
mobility     -0.1689     0.4449  -0.380   0.705
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Two-stage cluster sample

Finally we consider a two-stage cluster-sampled design in which 40 school districts are sampled and then up to five schools from each district.

```

> dclus2<-svydesign(ids=~dnum+snum, data=clus2, weight=~pw)
> dclus2
2 - level Cluster Sampling design
With ( 40,126 ) clusters.
svydesign(ids = ~dnum + snum, data = clus2, weight = ~pw)
> summary(dclus2)
2 - level Cluster Sampling design
With ( 40,126 ) clusters.
svydesign(ids = ~dnum + snum, data = clus2, weight = ~pw)
Probabilities:
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.02034 0.02034 0.02034 0.02034 0.02034 0.02034
Data variables:
 [1] "cds"      "stype"    "name"     "sname"    "snum"     "dname"    "dnum"
 [8] "cname"    "cnum"     "flag"     "pcttest"  "api00"    "api99"    "target"
[15] "growth"   "sch.wide" "comp.imp" "both"     "awards"   "meals"    "ell"
[22] "yr.rnd"   "mobility" "acs.k3"   "acs.46"   "acs.core" "pct.resp" "not.hsg"
[29] "hsg"      "some.col" "col.grad" "grad.sch" "avg.ed"   "full"     "emer"
[36] "enroll"   "api.stu"  "pw"
> svymean(~api00+I(api00-api99), dclus2)
              mean      SE
api00          703.810 23.1481
I(api00 - api99) 26.365  3.2776

```

```

> svytotal(~enroll, dclus2, na.rm=TRUE)
      total      SE
enroll 2927501 409261
> summary(svyglm(api00~ell+meals+mobility, design=dclus2))
svydesign(id = ~dnum + snum, weights = ~pw, data = apiclus2)

Call:
svyglm(formula = api00 ~ ell + meals + mobility, design = dclus2)

Deviance Residuals:
      Min       1Q   Median       3Q      Max
-19.17319  -4.87463  -0.05346   6.05140  23.33656

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  821.4515    27.8954  29.448 < 2e-16 ***
ell          -1.3000     1.1559  -1.125  0.262920
meals        -2.9221     0.7666  -3.812  0.000218 ***
mobility      0.5799     0.5975   0.971  0.333679
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Note that no finite population correction has been specified. The package does not currently support finite population corrections for multistage sampling.

Jackknife for stratified independent sample

The default replicate weight method for the stratified sample is the “JKn” stratified jackknife.

```

> rstrat<-as.svrepdesign(dstrat)
> rstrat
Survey with replicate weights:
Call: as.svrepdesign(dstrat)
> summary(rstrat)
Survey with replicate weights:
Call: as.svrepdesign(dstrat)
Stratified cluster jackknife (JKn) with 200 replicates.
Variables:
 [1] "cds"      "stpe"      "name"      "sname"     "snum"      "dname"     "dnum"
 [8] "cname"    "cnum"      "flag"      "pcttest"   "api00"     "api99"     "target"
[15] "growth"   "sch.wide"  "comp.imp"  "both"      "awards"    "meals"     "ell"
[22] "yr.rnd"   "mobility"  "acs.k3"    "acs.46"    "acs.core"  "pct.resp"  "not.hsg"
[29] "hsg"      "some.col"  "col.grad"  "grad.sch"  "avg.ed"    "full"      "emer"
[36] "enroll"   "api.stu"   "pw"        "fpc"

```

and then perform the same analyses

```

> svrepmean(~api00+I(api00-api99), rstrat)
              mean      SE
api00          662.287  9.4089
I(api00 - api99)  32.893  2.0511
> svreptotal(~enroll, rstrat)
              total      SE
enroll 3687178 114642
> summary(svrepglm(api00~ell+meals+mobility, design=rstrat))

```

Call:

```
svrepglm(formula = api00 ~ ell + meals + mobility, design = rstrat)
```

Survey design:

```
as.svrepdesign(dstrat)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	820.8873	10.5190	78.038	<2e-16 ***
ell	-0.4806	0.4060	-1.184	0.238
meals	-3.1415	0.2939	-10.691	<2e-16 ***
mobility	0.2257	0.4515	0.500	0.618

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

5.1.1 Jackknife for two-stage cluster sample

For the unstratified two-stage cluster sample the default replicate weights method is the unstratified (JK1) jackknife.

```

> rclus2<-as.svrepdesign(dclus2)
> rclus2
Survey with replicate weights:
Call: as.svrepdesign(dclus2)
> summary(rclus2)
Survey with replicate weights:
Call: as.svrepdesign(dclus2)
Unstratified cluster jackknife (JK1) with 40 replicates.
Variables:
 [1] "cds"      "stype"    "name"     "sname"    "snum"     "dname"    "dnum"
 [8] "cname"    "cnum"     "flag"     "pcttest"  "api00"    "api99"    "target"
[15] "growth"   "sch.wide" "comp.imp" "both"     "awards"   "meals"    "ell"
[22] "yr.rnd"   "mobility" "acs.k3"   "acs.46"   "acs.core" "pct.resp" "not.hsg"
[29] "hsg"      "some.col" "col.grad" "grad.sch" "avg.ed"   "full"     "emer"

```

```

[36] "enroll" "api.stu" "pw"
> svrepmean(~api00+I(api00-api99), rclus2)
      mean      SE
api00      703.810 23.4023
I(api00 - api99) 26.365 3.3067
> svreptotal(~enroll, rclus2, na.rm=TRUE)
      total      SE
enroll 2927501 409261
> summary(svrepglm(api00~ell+meals+mobility, design=rclus2))

Call:
svrepglm(formula = api00 ~ ell + meals + mobility, design = rclus2)

Survey design:
as.svrepdesign(dclus2)

Coefficients:
      Estimate Std. Error t value Pr(>|t|)
(Intercept)  821.4515    31.3720  26.184 < 2e-16 ***
ell          -1.3000     1.3681  -0.950  0.34385
meals        -2.9221     0.8679  -3.367  0.00102 **
mobility      0.5799     0.7888   0.735  0.46369
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

5.1.2 Post-stratification and raking of cluster sample

We can post-stratify the two-stage cluster sample by school type to increase efficiency somewhat. In this example the population stratum sizes are computed from the known population data; in a real example they would be entered directly.

```

> pop.types<-xtabs(~stype,pop)
Error in eval(expr, envir, enclos) : Object "pop" not found
> pop.types<-xtabs(~stype,apipop)
> rclus2p<-postStratify(rclus2, ~stype, pop.types)
> rclus2p
Survey with replicate weights:
Call: postStratify(rclus2, ~stype, pop.types)
> svrepmean(~api00, rclus2p)
      mean      SE
api00  708.57  21.865

```

The full set of replicate weights can be displayed with the `image` function, and are given in Figure 1. The structure of JK1 weights can easily be seen in both images. On the right, the faint striping of the background indicates the

small adjustments in weights needed for post-stratification. The adjustments are largest in replicate number 31, which corresponds to a school district where all the sampled schools were high schools.

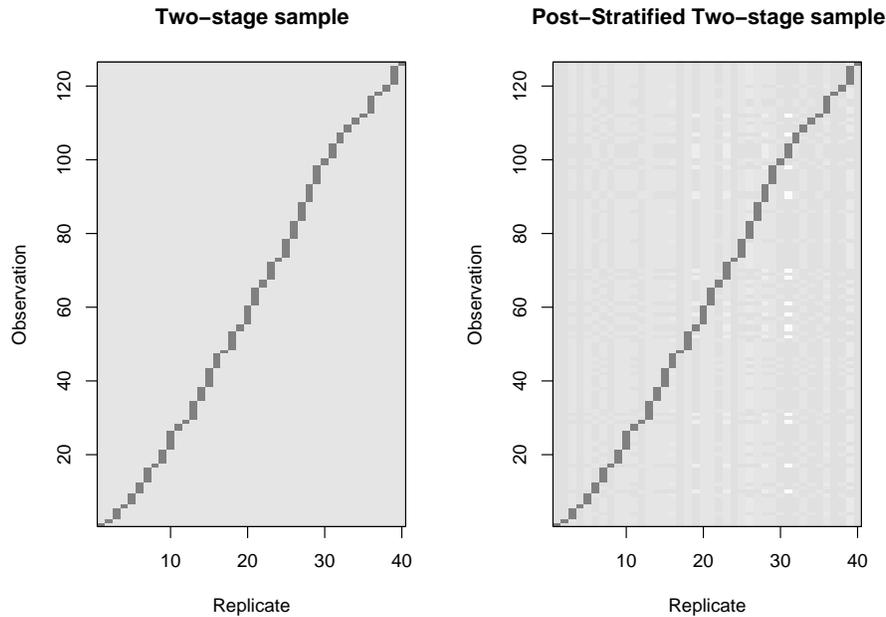


Figure 1: Replicate weights for two-stage cluster sample with and without post-stratification.

Finally, to illustrate raking we consider the proportion of schools that met their school-wide growth target in the API program

```
> rclus2r<-rake(rclus2, list(~stype, ~sch.wide),
+             list(pop.types, xtabs(~sch.wide,data=apipop)))
```

As these two variables are far from independent in the population, there is some efficiency gain but not as much as if the population joint distribution of the two variables were used for post-stratification.

```
> popboth<-xtabs(~stype+sch.wide,data=pop)
> popboth
      sch.wide
stype No  Yes
E     472 3949
H     334  421
M     266  752
> rclus2p2<-postStratify(rclus2, ~stype+sch.wide, popboth)
```

```

> svrepmean(~api00, rclus2)
      mean    SE
api00 703.81 23.402
> svrepmean(~api00, rclus2p)
      mean    SE
api00 708.57 21.865
> svrepmean(~api00, rclus2r)
      mean    SE
api00 710.51 21.351
> svrepmean(~api00, rclus2p2)
      mean    SE
api00 710.54 20.587

```

5.2 Design specified only by replicates

In the example above we created replicate weights for a survey whose sampling design was known. The package can also be used to analyse data where replicate weights are supplied and the design is otherwise unspecified.

As an example, consider the Alcohol and Drug Services Study (ADSS) conducted for the Substance Abuse and Mental Health Services Administration. Data for this study are available from the Inter-University Consortium for Political and Social Research (<http://www.icpsr.umich.edu/>), as are descriptions of the design and analysis conducted by Westat (Mohadjer *et al*, 2000). This is a multistage survey of facilities providing treatment for substance abuse. The data file contains 2394 records and 991 variables. In this example we look at Phase I of the study, which involves stratified sampling of facilities. Phases II and III involve further subsampling of clients.

The data files contain 200 replicate weights that are based on a stratified jackknife (JKn) with modifications to reduce very large weights, account for nonresponse, and for other reasons. Separate files contain the finite population correction factors and the quantity we have called c_i or `rscales`.

The design is specified by:

```

adss<-svrepdesign(data = adssdata, repweights = adssdata[, 782:981],
  scale = 1, rscales = adssjack, type = "other",
  weights = ~PH1FW0, combined.weights = TRUE, fpc=adssfpc,
  fpctype="correction")

```

where `adssdata` is the data frame containing all the survey data, and `adssjack` and `adssfpc` are the stratified jackknife c_i and the finite population correction factors. The `combined.weights` option indicates that the replicate weights already incorporate the original sampling probabilities.

An example is given in the ADSS User's Manual (Westat, 2000) of computing the mean number of clients (B1J2) for each facility type (TYPCARE5). This could be done with a linear regression

```

model1<-svrepglm(B1J2~factor(TYPCARE5)-1,design=adss)

```

```

summary(model1)

Call:
svrepglm(formula = B1J2 ~ factor(TYPCARE5) - 1, design = adss)

Survey design:
svrepdesign(data = adssdata, repweights = adssdata[, 782:981],
  scale = 1, rscales = adssjack, type = "other", weights = ~PH1FW0,
  combined.weights = TRUE, fpc = adssfpc, fptype = "correction")

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
factor(TYPCARE5)1  14.6843     0.9901   14.83  <2e-16 ***
factor(TYPCARE5)2  27.5658     1.3572   20.31  <2e-16 ***
factor(TYPCARE5)3 250.3610     8.5202   29.38  <2e-16 ***
factor(TYPCARE5)4  92.0009     3.6443   25.25  <2e-16 ***
factor(TYPCARE5)5 114.1075    10.1071   11.29  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

This example illustrates the relationship between memory and speed for the survey package. It takes 5–6 seconds to run on a PC with 1Gb of memory, and 15 seconds on an Apple Powerbook with only 256Mb. Peak memory usage is about 290Mb. It is interesting to compare this with the estimate given by Dippo *et al* (1984) for CPU time on an IBM 370 mainframe running the early *NASSVAR* replicate-weights program. Their estimate for this analysis would be 54 CPU-seconds: twenty years advance in computing permits us to use an interpreted language on commodity hardware and still run nearly ten times faster.

5.3 Comparisons with other packages

The `survey` package provides much, but not all, of the survey analysis functionality of SUDAAN or of Stata with the add-on `survwgt` code of Winter (2002). The most important exceptions are tests for association in contingency tables. Most other software will compute variances either by Taylor linearisation or from replicates, but not both.

Other differences result from the underlying properties of R. The `survey` package is slow and requires a lot of memory to analyse large surveys, especially under Windows. It is harder to learn than menu-driven programs such as `WesVar`, but on the other hand is more flexible and easier to extend.

Despite the similarity of R and S-PLUS, the `survey` package would require some editing to be used with S-PLUS. The file `porting.to.S` gives suggestions and the LGPL license of the code is intended to remove any concerns about the use of the code on other systems.

5.4 Acknowledgements

This paper and software has been considerably improved by the comments of users and of the editors and reviews.

6 References

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