

# Package ‘survey’

July 23, 2025

**Title** Analysis of Complex Survey Samples

## Description

Summary statistics, two-sample tests, rank tests, generalised linear models, cumulative link models, Cox models, loglinear models, and general maximum pseudolikelihood estimation for multi-stage stratified, cluster-sampled, unequally weighted survey samples. Variances by Taylor series linearisation or replicate weights. Post-stratification, calibration, and raking. Two-phase subsampling designs. Graphics. PPS sampling without replacement. Small-area estimation.

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**Author** Thomas Lumley, Peter Gao, Ben Schneider

**Maintainer** ``Thomas Lumley" <t.lumley@auckland.ac.nz>

**License** GPL-2 | GPL-3

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anova.svyglm	<i>Model comparison for glms.</i>
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**Description**

A method for the [anova](#) function, for use on [svyglm](#) and [svycoxph](#) objects. With a single model argument it produces a sequential anova table, with two arguments it compares the two models.

## Usage

```
## S3 method for class 'svyglm'
anova(object, object2 = NULL, test = c("F", "Chisq"),
  method = c("LRT", "Wald"), tolerance = 1e-05, ..., force = FALSE)
## S3 method for class 'svycoxph'
anova(object, object2=NULL, test=c("F", "Chisq"),
  method=c("LRT", "Wald"), tolerance=1e-5, ..., force=FALSE)
## S3 method for class 'svyglm'
AIC(object, ..., k=2, null_has_intercept=TRUE)
## S3 method for class 'svyglm'
BIC(object, ..., maximal)
## S3 method for class 'svyglm'
extractAIC(fit, scale, k=2, ..., null_has_intercept=TRUE)
## S3 method for class 'svrepglm'
extractAIC(fit, scale, k=2, ..., null_has_intercept=TRUE)
```

## Arguments

<code>object, fit</code>	A <a href="#">svyglm</a> or <a href="#">svycoxph</a> object.
<code>object2</code>	Optionally, another <a href="#">svyglm</a> or <a href="#">svycoxph</a> object.
<code>test</code>	Use (linear combination of) F or chi-squared distributions for p-values. F is usually preferable.
<code>method</code>	Use weighted deviance difference (LRT) or Wald tests to compare models
<code>tolerance</code>	For models that are not symbolically nested, the tolerance for deciding that a term is common to the models.
<code>...</code>	For AIC and BIC, optionally more <a href="#">svyglm</a> objects
<code>scale</code>	not used
<code>null_has_intercept</code>	Does the null model for AIC have an intercept or not? Must be FALSE if any of the models are intercept-only.
<code>force</code>	Force the tests to be done by explicit projection even if the models are symbolically nested (eg, for debugging)
<code>maximal</code>	A <a href="#">svyglm</a> model that object (and ... if supplied) are nested in.
<code>k</code>	Multiplier for effective df in AIC. Usually 2. There is no choice of k that will give BIC

## Details

The reference distribution for the LRT depends on the misspecification effects for the parameters being tested (Rao and Scott, 1984). If the models are symbolically nested, so that the relevant parameters can be identified just by manipulating the model formulas, `anova` is equivalent to [regTermTest](#). If the models are nested but not symbolically nested, more computation using the design matrices is needed to determine the projection matrix on to the parameters being tested. In the examples below, `model1` and `model2` are symbolically nested in `model0` because `model0` can be obtained just by deleting terms from the formulas. On the other hand, `model2` is nested in `model1`

but not symbolically nested: knowing that the model is nested requires knowing what design matrix columns are produced by `stype` and `as.numeric(stype)`. Other typical examples of models that are nested but not symbolically nested are linear and spline models for a continuous covariate, or models with categorical versions of a variable at different resolutions (eg, smoking yes/no or smoking never/former/current).

A saddlepoint approximation is used for the LRT with numerator df greater than 1.

AIC is defined using the Rao-Scott approximation to the weighted loglikelihood (Lumley and Scott, 2015). It replaces the usual penalty term  $p$ , which is the null expectation of the log likelihood ratio, by the trace of the generalised design effect matrix, which is the expectation under complex sampling. For computational reasons everything is scaled so the weights sum to the sample size.

BIC is a BIC for the (approximate) multivariate Gaussian models on regression coefficients from the maximal model implied by each submodel (ie, the models that say some coefficients in the maximal model are zero) (Lumley and Scott, 2015). It corresponds to comparing the models with a Wald test and replacing the sample size in the penalty by an effective sample size. For computational reasons, the models must not only be nested, the names of the coefficients must match.

`extractAIC` for a model with a Gaussian link uses the actual AIC based on maximum likelihood estimation of the variance parameter as well as the regression parameters.

## Value

Object of class `seqanova.svyglm` if one model is given, otherwise of class `regTermTest` or `regTermTestLRT`

## Note

At the moment, AIC works only for models including an intercept.

## References

- Rao, JNK, Scott, AJ (1984) "On Chi-squared Tests For Multiway Contingency Tables with Proportions Estimated From Survey Data" *Annals of Statistics* 12:46-60.
- Lumley, T., & Scott, A. (2014). "Tests for Regression Models Fitted to Survey Data". *Australian and New Zealand Journal of Statistics*, 56 (1), 1-14.
- Lumley T, Scott AJ (2015) "AIC and BIC for modelling with complex survey data" *J Surv Stat Methodol* 3 (1): 1-18.

## See Also

[regTermTest](#), [pchisqsum](#)

## Examples

```
data(api)
dclus2<-svydesign(id=~dnum+snum, weights=~pw, data=apiclus2)

model0<-svyglm(I(sch.wide=="Yes")~ell+meals+mobility, design=dclus2, family=quasibinomial())
model1<-svyglm(I(sch.wide=="Yes")~ell+meals+mobility+as.numeric(stype),
  design=dclus2, family=quasibinomial())
model2<-svyglm(I(sch.wide=="Yes")~ell+meals+mobility+stype, design=dclus2, family=quasibinomial())
```

```

anova(model2)
anova(model0,model2)
anova(model1, model2)

anova(model1, model2, method="Wald")

AIC(model0,model1, model2)
BIC(model0, model2,maximal=model2)

## AIC for linear model is different because it considers the variance
## parameter

model0<-svyglm(api00~ell+meals+mobility, design=dclus2)
model1<-svyglm(api00~ell+meals+mobility+as.numeric(stype),
  design=dclus2)
model2<-svyglm(api00~ell+meals+mobility+stype, design=dclus2)
modelnull<-svyglm(api00~1, design=dclus2)

AIC(model0, model1, model2)

AIC(model0, model1, model2,modelnull, null_has_intercept=FALSE)

## from ?twophase
data(nwtco)
dcchs<-twophase(id=list(~seqno,~seqno), strata=list(NULL,~rel),
  subset=~I(in.subcohort | rel), data=nwtco)
a<-svycoxph(Surv(edrel,rel)~factor(stage)+factor(histol)+I(age/12), design=dcchs)
b<-update(a, .~-I(age/12)+poly(age,3))
## not symbolically nested models
anova(a,b)

```

---

api

---

*Student performance in California schools*


---

## Description

The Academic Performance Index is computed for all California schools based on standardised testing of students. The data sets contain information for all schools with at least 100 students and for various probability samples of the data.

## Usage

```
data(api)
```

## Format

The full population data in apipop are a data frame with 6194 observations on the following 37 variables.

**cds** Unique identifier  
**stype** Elementary/Middle/High School  
**name** School name (15 characters)  
**sname** School name (40 characters)  
**snum** School number  
**dname** District name  
**dnum** District number  
**cname** County name  
**cnum** County number  
**flag** reason for missing data  
**pcttest** percentage of students tested  
**api00** API in 2000  
**api99** API in 1999  
**target** target for change in API  
**growth** Change in API  
**sch.wide** Met school-wide growth target?  
**comp.imp** Met Comparable Improvement target  
**both** Met both targets  
**awards** Eligible for awards program  
**meals** Percentage of students eligible for subsidized meals  
**ell** 'English Language Learners' (percent)  
**yr.rnd** Year-round school  
**mobility** percentage of students for whom this is the first year at the school  
**acs.k3** average class size years K-3  
**acs.46** average class size years 4-6  
**acs.core** Number of core academic courses  
**pct.resp** percent where parental education level is known  
**not.hsg** percent parents not high-school graduates  
**hsg** percent parents who are high-school graduates  
**some.col** percent parents with some college  
**col.grad** percent parents with college degree  
**grad.sch** percent parents with postgraduate education  
**avg.ed** average parental education level  
**full** percent fully qualified teachers  
**emer** percent teachers with emergency qualifications  
**enroll** number of students enrolled  
**api.stu** number of students tested.

The other data sets contain additional variables *pw* for sampling weights and *fpc* to compute finite population corrections to variance.

## Details

apipop is the entire population, apisrs is a simple random sample, apiclus1 is a cluster sample of school districts, apistrat is a sample stratified by stype, and apiclus2 is a two-stage cluster sample of schools within districts. The sampling weights in apiclus1 are incorrect (the weight should be 757/15) but are as obtained from UCLA.

## Source

Data were obtained from the survey sampling help pages of UCLA Academic Technology Services; these pages are no longer on line.

## References

The API program has been discontinued at the end of 2018, and the archive page at the California Department of Education is now gone. The Wikipedia article has links to past material at the Internet Archive. [https://en.wikipedia.org/wiki/Academic\\_Performance\\_Index\\_\(California\\_public\\_schools\)](https://en.wikipedia.org/wiki/Academic_Performance_Index_(California_public_schools))

## Examples

```
library(survey)
data(api)
mean(api00$api00)
sum(api00$enroll, na.rm=TRUE)

#stratified sample
dstrat<-svydesign(id=~1,strata=~stype, weights=~pw, data=apistrat, fpc=~fpc)
summary(dstrat)
svymean(~api00, dstrat)
svytotal(~enroll, dstrat, na.rm=TRUE)

# one-stage cluster sample
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
summary(dclus1)
svymean(~api00, dclus1)
svytotal(~enroll, dclus1, na.rm=TRUE)

# two-stage cluster sample
dclus2<-svydesign(id=~dnum+snum, fpc=~fpc1+fpc2, data=apiclus2)
summary(dclus2)
svymean(~api00, dclus2)
svytotal(~enroll, dclus2, na.rm=TRUE)

# two-stage `with replacement'
dclus2wr<-svydesign(id=~dnum+snum, weights=~pw, data=apiclus2)
summary(dclus2wr)
svymean(~api00, dclus2wr)
svytotal(~enroll, dclus2wr, na.rm=TRUE)

# convert to replicate weights
```

```

rclus1<-as.svrepdesign(dclus1)
summary(rclus1)
svymean(~api00, rclus1)
svytotal(~enroll, rclus1, na.rm=TRUE)

# post-stratify on school type
pop.types<-xtabs(~stype, data=apipop)

rclus1p<-postStratify(rclus1, ~stype, pop.types)
dclus1p<-postStratify(dclus1, ~stype, pop.types)
summary(dclus1p)
summary(rclus1p)

svymean(~api00, dclus1p)
svytotal(~enroll, dclus1p, na.rm=TRUE)

svymean(~api00, rclus1p)
svytotal(~enroll, rclus1p, na.rm=TRUE)

```

as.fpc

*Package sample and population size data***Description**

This function creates an object to store the number of clusters sampled within each stratum (at each stage of multistage sampling) and the number of clusters available in the population. It is called by svydesign, not directly by the user.

**Usage**

```
as.fpc(df, strata, ids, pps=FALSE)
```

**Arguments**

df	A data frame or matrix with population size information
strata	A data frame giving strata at each stage
ids	A data frame giving cluster ids at each stage
pps	if TRUE, fpc information may vary within a stratum and must be specified as a proportion rather than a population sizes

**Details**

The population size information may be specified as the number of clusters in the population or as the proportion of clusters sampled.

**Value**

An object of class survey\_fpc

**See Also**

[svydesign](#), [svyrecvar](#)

---

as.svrepdesign

*Convert a survey design to use replicate weights*

---

**Description**

Creates a replicate-weights survey design object from a traditional strata/cluster survey design object. JK1 and JK<sub>n</sub> are jackknife methods, BRR is Balanced Repeated Replicates and Fay is Fay's modification of this, bootstrap is Canty and Davison's bootstrap, subbootstrap is Rao and Wu's  $(n - 1)$  bootstrap, and mrbbootstrap is Preston's multistage rescaled bootstrap. With a `svyimputationList` object, the same replicate weights will be used for each imputation if the sampling weights are all the same and `separate.replicates=FALSE`.

**Usage**

```
as.svrepdesign(design,...)
## Default S3 method:
as.svrepdesign(design, type=c("auto", "JK1", "JKn", "BRR", "bootstrap",
  "subbootstrap", "mrbbootstrap", "Fay"),
  fay.rho = 0, fpc=NULL, fpctype=NULL, ..., compress=TRUE,
  mse=getOption("survey.replicates.mse"))
## S3 method for class 'svyimputationList'
as.svrepdesign(design, type=c("auto", "JK1", "JKn", "BRR", "bootstrap",
  "subbootstrap", "mrbbootstrap", "Fay"),
  fay.rho = 0, fpc=NULL, fpctype=NULL, separate.replicates=FALSE, ..., compress=TRUE,
  mse=getOption("survey.replicates.mse"))
```

**Arguments**

<code>design</code>	Object of class <code>survey.design</code> or <code>svyimputationList</code> . Must not have been post-stratified/raked/calibrated in R
<code>type</code>	Type of replicate weights. "auto" uses JK <sub>n</sub> for stratified, JK1 for unstratified designs
<code>fay.rho</code>	Tuning parameter for Fay's variance method
<code>fpc, fpctype, ...</code>	Passed to <code>jk1weights</code> , <code>jkweights</code> , <code>brrweights</code> , <code>bootweights</code> , <code>subbootweights</code> , or <code>mrbweights</code> .
<code>separate.replicates</code>	Compute replicate weights separately for each design (useful for the bootstrap types, which are not deterministic)
<code>compress</code>	Use a compressed representation of the replicate weights matrix.
<code>mse</code>	if TRUE, compute variances from sums of squares around the point estimate, rather than the mean of the replicates

**Value**

Object of class `svyrep.design`.

**References**

- Canty AJ, Davison AC. (1999) Resampling-based variance estimation for labour force surveys. *The Statistician* 48:379-391
- Judkins, D. (1990), "Fay's Method for Variance Estimation," *Journal of Official Statistics*, 6, 223-239.
- Preston J. (2009) Rescaled bootstrap for stratified multistage sampling. *Survey Methodology* 35(2) 227-234
- Rao JNK, Wu CFJ. Bootstrap inference for sample surveys. *Proc Section on Survey Research Methodology*. 1993 (866–871)

**See Also**

[brrweights](#), [svydesign](#), [svrepdesign](#), [bootweights](#), [subbootweights](#), [mrbweights](#)

**Examples**

```
data(scd)
scddes<-svydesign(data=scd, prob=~1, id=~ambulance, strata=~ESA,
nest=TRUE, fpc=rep(5,6))
scdnofpc<-svydesign(data=scd, prob=~1, id=~ambulance, strata=~ESA,
nest=TRUE)

# convert to BRR replicate weights
scd2brr <- as.svrepdesign(scdnofpc, type="BRR")
scd2fay <- as.svrepdesign(scdnofpc, type="Fay",fay.rho=0.3)
# convert to JKn weights
scd2jkn <- as.svrepdesign(scdnofpc, type="JKn")

# convert to JKn weights with finite population correction
scd2jknf <- as.svrepdesign(scddes, type="JKn")

## with user-supplied hadamard matrix
scd2brr1 <- as.svrepdesign(scdnofpc, type="BRR", hadamard.matrix=paley(11))

svyratio(~alive, ~arrests, design=scd2brr)
svyratio(~alive, ~arrests, design=scd2brr1)
svyratio(~alive, ~arrests, design=scd2fay)
svyratio(~alive, ~arrests, design=scd2jkn)
svyratio(~alive, ~arrests, design=scd2jknf)

data(api)
## one-stage cluster sample
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
## convert to JK1 jackknife
rclus1<-as.svrepdesign(dclus1)
## convert to bootstrap
```

```

bclus1<-as.svrepdesign(dclus1,type="bootstrap", replicates=100)

svymean(~api00, dclus1)
svytotal(~enroll, dclus1)

svymean(~api00, rclus1)
svytotal(~enroll, rclus1)

svymean(~api00, bclus1)
svytotal(~enroll, bclus1)

dclus2<-svydesign(id = ~dnum + snum, fpc = ~fpc1 + fpc2, data = apiclus2)
mrbclus2<-as.svrepdesign(dclus2, type="mrb",replicates=100)
svytotal(~api00+stype, dclus2)
svytotal(~api00+stype, mrbclus2)

```

as.svydesign2

*Update to the new survey design format***Description**

The structure of survey design objects changed in version 2.9, to allow standard errors based on multistage sampling. `as.svydesign` converts an object to the new structure and `.svycheck` warns if an object does not have the new structure.

You can set `options(survey.want.obsolete=TRUE)` to suppress the warnings produced by `.svycheck` and `options(survey.ultimate.cluster=TRUE)` to always compute variances based on just the first stage of sampling.

**Usage**

```

as.svydesign2(object)
.svycheck(object)

```

**Arguments**

object                      produced by `svydesign`

**Value**

Object of class `survey.design2`

**See Also**

[svydesign](#), [svyrecvar](#)

---

barplot.svystat	<i>Barplots and Dotplots</i>
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---

## Description

Draws a barplot or dotplot based on results from a survey analysis. The default barplot method already works for results from [svytable](#).

## Usage

```
## S3 method for class 'svystat'
barplot(height, ...)
## S3 method for class 'svrepstat'
barplot(height, ...)
## S3 method for class 'svyby'
barplot(height,beside=TRUE, ...)

## S3 method for class 'svystat'
dotchart(x,...,pch=19)
## S3 method for class 'svrepstat'
dotchart(x,...,pch=19)
## S3 method for class 'svyby'
dotchart(x,...,pch=19)
```

## Arguments

height, x	Analysis result
beside	Grouped, rather than stacked, bars
...	Arguments to <a href="#">barplot</a> or <a href="#">dotchart</a>
pch	Overrides the default in <code>dotchart.default</code>

## Examples

```
data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)

a<-svymean(~stype, dclus1)
barplot(a)
barplot(a, names.arg=c("Elementary","High","Middle"), col="purple",
  main="Proportions of school level")

b<-svyby(~enroll+api.stu, ~stype, dclus1, svymean)
barplot(b,beside=TRUE,legend=TRUE)
dotchart(b)
```

bootweights

*Compute survey bootstrap weights***Description**

Bootstrap weights for infinite populations ('with replacement' sampling) are created by sampling with replacement from the PSUs in each stratum. `subbootweights()` samples  $n-1$  PSUs from the  $n$  available (Rao and Wu), `bootweights` samples  $n$  (Canty and Davison).

For multistage designs or those with large sampling fractions, `mrweights` implements Preston's multistage rescaled bootstrap. The multistage rescaled bootstrap is still useful for single-stage designs with small sampling fractions, where it reduces to a half-sample replicate method.

**Usage**

```
bootweights(strata, psu, replicates = 50, fpc = NULL,
            fpctype = c("population", "fraction", "correction"),
            compress = TRUE)
subbootweights(strata, psu, replicates = 50, compress = TRUE)
mrweights(clusters, stratas, fpcs, replicates=50,
          multicore=getOption("survey.multicore"))
```

**Arguments**

<code>strata</code>	Identifier for sampling strata (top level only)
<code>stratas</code>	data frame of strata for all stages of sampling
<code>psu</code>	Identifier for primary sampling units
<code>clusters</code>	data frame of identifiers for sampling units at each stage
<code>replicates</code>	Number of bootstrap replicates
<code>fpc</code>	Finite population correction (top level only)
<code>fpctype</code>	Is <code>fpc</code> the population size, sampling fraction, or 1-sampling fraction?
<code>fpcs</code>	<code>survey_fpc</code> object with population and sample size at each stage
<code>compress</code>	Should the replicate weights be compressed?
<code>multicore</code>	Use the <code>multicore</code> package to generate the replicates in parallel

**Value**

A set of replicate weights

**warning**

With `multicore=TRUE` the resampling procedure does not use the current random seed, so the results cannot be exactly reproduced even by using `set.seed()`

**Note**

These bootstraps are strictly appropriate only when the first stage of sampling is a simple or stratified random sample of PSUs with or without replacement, and not (eg) for PPS sampling. The functions will not enforce simple random sampling, so they can be used (approximately) for data that have had non-response corrections and other weight adjustments. It is preferable to apply these adjustments after creating the bootstrap replicate weights, but that may not be possible with public-use data.

**References**

- Canty AJ, Davison AC. (1999) Resampling-based variance estimation for labour force surveys. *The Statistician* 48:379-391
- Judkins, D. (1990), "Fay's Method for Variance Estimation" *Journal of Official Statistics*, 6, 223-239.
- Preston J. (2009) Rescaled bootstrap for stratified multistage sampling. *Survey Methodology* 35(2) 227-234
- Rao JNK, Wu CFJ. Bootstrap inference for sample surveys. *Proc Section on Survey Research Methodology*. 1993 (866–871)

**See Also**

[as.svrepdesign](#)

---

brrweights

---

*Compute replicate weights*


---

**Description**

Compute replicate weights from a survey design. These functions are usually called from [as.svrepdesign](#) rather than directly by the user.

**Usage**

```
brrweights(strata, psu, match = NULL,
           small = c("fail", "split", "merge"),
           large = c("split", "merge", "fail"),
           fay.rho=0, only.weights=FALSE,
           compress=TRUE, hadamard.matrix=NULL)
jk1weights(psu, fpc=NULL,
           fpctype=c("population", "fraction", "correction"),
           compress=TRUE)
jknweights(strata, psu, fpc=NULL,
           fpctype=c("population", "fraction", "correction"),
           compress=TRUE,
           lonely.psu=getOption("survey.lonely.psu"))
```

## Arguments

<code>strata</code>	Stratum identifiers
<code>psu</code>	PSU (cluster) identifier
<code>match</code>	Optional variable to use in matching.
<code>small</code>	How to handle strata with only one PSU
<code>large</code>	How to handle strata with more than two PSUs
<code>fpc</code>	Optional population (stratum) size or finite population correction
<code>fpctype</code>	How fpc is coded.
<code>fay.rho</code>	Parameter for Fay's extended BRR method
<code>only.weights</code>	If TRUE return only the matrix of replicate weights
<code>compress</code>	If TRUE, store the replicate weights in compressed form
<code>hadamard.matrix</code>	Optional user-supplied Hadamard matrix for brrweights
<code>lonely.psu</code>	Handling of non-certainty single-PSU strata

## Details

JK1 and JK<sub>n</sub> are jackknife schemes for unstratified and stratified designs respectively. The finite population correction may be specified as a single number, a vector with one entry per stratum, or a vector with one entry per observation (constant within strata). When `fpc` is a vector with one entry per stratum it may not have names that differ from the stratum identifiers (it may have no names, in which case it must be in the same order as `unique(strata)`). To specify population stratum sizes use `fpctype="population"`, to specify sampling fractions use `fpctype="fraction"` and to specify the correction directly use `fpctype="correction"`

The only reason not to use `compress=TRUE` is that it is new and there is a greater possibility of bugs. It reduces the number of rows of the replicate weights matrix from the number of observations to the number of PSUs.

In BRR variance estimation each stratum is split in two to give half-samples. Balanced replicated weights are needed, where observations in two different strata end up in the same half stratum as often as in different half-strata. BRR, strictly speaking, is defined only when each stratum has exactly two PSUs. A stratum with one PSU can be merged with another such stratum, or can be split to appear in both half samples with half weight. The latter approach is appropriate for a PSU that was deterministically sampled.

A stratum with more than two PSUs can be split into multiple smaller strata each with two PSUs or the PSUs can be merged to give two superclusters within the stratum.

When merging small strata or grouping PSUs in large strata the `match` variable is used to sort PSUs before merging, to give approximate matching on this variable.

If you want more control than this you should probably construct your own weights using the Hadamard matrices produced by [hadamard](#)

**Value**

For `brrweights` with only `.weights=FALSE` a list with elements

<code>weights</code>	two-column matrix indicating the weight for each half-stratum in one particular set of split samples
<code>wstrata</code>	New stratum variable incorporating merged or split strata
<code>strata</code>	Original strata for distinct PSUs
<code>psu</code>	Distinct PSUs
<code>npairs</code>	Dimension of Hadamard matrix used in BRR construction
<code>sampler</code>	function returning replicate weights
<code>compress</code>	Indicates whether the sampler returns per PSU or per observation weights

For `jk1weights` and `jkweights` a data frame of replicate weights and the scale and `rscale` arguments to [svrVar](#).

**References**

Levy and Lemeshow "Sampling of Populations". Wiley.  
 Shao and Tu "The Jackknife and Bootstrap". Springer.

**See Also**

[hadamard](#), [as.svrepdesign](#), [svrVar](#), [surveyoptions](#)

**Examples**

```
data(scd)
scdnofpc<-svydesign(data=scd, prob=~1, id=~ambulance, strata=~ESA,
nest=TRUE)

## convert to BRR replicate weights
scd2brr <- as.svrepdesign(scdnofpc, type="BRR")
svymean(~alive, scd2brr)
svyratio(~alive, ~arrests, scd2brr)

## with user-supplied hadamard matrix
scd2brr1 <- as.svrepdesign(scdnofpc, type="BRR", hadamard.matrix=paley(11))
svymean(~alive, scd2brr1)
svyratio(~alive, ~arrests, scd2brr1)
```

calibrate

*Calibration (GREG) estimators***Description**

Calibration, generalized raking, or GREG estimators generalise post-stratification and raking by calibrating a sample to the marginal totals of variables in a linear regression model. This function reweights the survey design and adds additional information that is used by svyrecvar to reduce the estimated standard errors.

**Usage**

```
calibrate(design,...)
## S3 method for class 'survey.design2'
calibrate(design, formula, population,
          aggregate.stage=NULL, stage=0, variance=NULL,
          bounds=c(-Inf,Inf), calfun=c("linear","raking","logit"),
          maxit=50,epsilon=1e-7,verbose=FALSE,force=FALSE,trim=NULL,
          bounds.const=FALSE, sparse=FALSE,...)
## S3 method for class 'svyrep.design'
calibrate(design, formula, population,compress=NA,
          aggregate.index=NULL, variance=NULL, bounds=c(-Inf,Inf),
          calfun=c("linear","raking","logit"),
          maxit=50, epsilon=1e-7, verbose=FALSE,force=FALSE,trim=NULL,
          bounds.const=FALSE, sparse=FALSE,...)
## S3 method for class 'twophase'
calibrate(design, phase=2,formula, population,
          calfun=c("linear","raking","logit","rrz"),...)
grake(mm,ww,calfun,eta=rep(0,NCOL(mm)),bounds,population,epsilon,
      verbose,maxit,variance=NULL)
cal_names(formula,design,...)
```

**Arguments**

design	Survey design object
formula	Model formula for calibration model, or list of formulas for each margin
population	Vectors of population column totals for the model matrix in the calibration model, or list of such vectors for each cluster, or list of tables for each margin. Required except for two-phase designs
compress	compress the resulting replicate weights if TRUE or if NA and weights were previously compressed
stage	See Details below
variance	Coefficients for variance in calibration model (heteroskedasticity parameters) (see Details below)

<code>aggregate.stage</code>	An integer. If not NULL, make calibration weights constant within sampling units at this stage.
<code>aggregate.index</code>	A vector or one-sided formula. If not NULL, make calibration weights constant within levels of this variable
<code>bounds</code>	Bounds for the calibration weights, optional except for <code>calfun="logit"</code>
<code>bounds.const</code>	Should be TRUE if bounds have been specified as constant values rather than multiplicative values
<code>trim</code>	Weights outside this range will be trimmed to these bounds.
<code>...</code>	Options for other methods
<code>calfun</code>	Calibration function: see below
<code>maxit</code>	Number of iterations
<code>epsilon</code>	Tolerance in matching population total. Either a single number or a vector of the same length as population
<code>verbose</code>	Print lots of uninteresting information
<code>force</code>	Return an answer even if the specified accuracy was not achieved
<code>phase</code>	Phase of a two-phase design to calibrate (only <code>phase=2</code> currently implemented.)
<code>mm</code>	Model matrix
<code>ww</code>	Vector of weights
<code>eta</code>	Starting values for iteration
<code>sparse</code>	Use sparse matrices for faster computation

## Details

The formula argument specifies a model matrix, and the population argument is the population column sums of this matrix. The function `cal_names` shows what the column names of this model matrix will be.

For the important special case where the calibration totals are (possibly overlapping) marginal tables of factor variables, as in classical raking, the formula and population arguments may be lists in the same format as the input to [rake](#).

If the population argument has a `names` attribute it will be checked against the names produced by `model.matrix(formula)` and reordered if necessary. This protects against situations where the (locale-dependent) ordering of factor levels is not what you expected.

Numerical instabilities may result if the sampling weights in the design object are wrong by multiple orders of magnitude. The code now attempts to rescale the weights first, but it is better for the user to ensure that the scale is reasonable.

The `calibrate` function implements linear, bounded linear, raking, bounded raking, and logit calibration functions. All except unbounded linear calibration use the Newton-Raphson algorithm described by Deville et al (1993). This algorithm is exposed for other uses in the `grake` function. Unbounded linear calibration uses an algorithm that is less sensitive to collinearity. The calibration function may be specified as a string naming one of the three built-in functions or as an object of class `calfun`, allowing user-defined functions. See [make.calfun](#) for details.

The bounds argument can be specified as global upper and lower bounds e.g. `bounds=c(0.5, 2)` or as a list with lower and upper vectors e.g. `bounds=list(lower=lower, upper=upper)`. This allows for individual boundary constraints for each unit. The lower and upper vectors must be the same length as the input data. The bounds can be specified as multiplicative values or constant values. If constant, `bounds.const` must be set to `TRUE`.

Calibration with bounds, or on highly collinear data, may fail. If `force=TRUE` the approximately calibrated design object will still be returned (useful for examining why it failed). A failure in calibrating a set of replicate weights when the sampling weights were successfully calibrated will give only a warning, not an error.

When calibration to the desired set of bounds is not possible, another option is to trim weights. To do this set bounds to a looser set of bounds for which calibration is achievable and set `trim` to the tighter bounds. Weights outside the bounds will be trimmed to the bounds, and the excess weight distributed over other observations in proportion to their sampling weight (and so this may put some other observations slightly over the trimming bounds). The projection matrix used in computing standard errors is based on the feasible bounds specified by the bounds argument. See also `trimWeights`, which trims the final weights in a design object rather than the calibration adjustments.

For two-phase designs `calfun="rrz"` estimates the sampling probabilities using logistic regression as described by Robins et al (1994). `estWeights` will do the same thing.

Calibration may result in observations within the last-stage sampling units having unequal weight even though they necessarily are sampled together. Specifying `aggregate.stage` ensures that the calibration weight adjustments are constant within sampling units at the specified stage; if the original sampling weights were equal the final weights will also be equal. The algorithm is as described by Vanderhoeft (2001, section III.D). Specifying `aggregate.index` does the same thing for replicate weight designs; a warning will be given if the original weights are not constant within levels of `aggregate.index`.

In a model with two-stage sampling, population totals may be available for the PSUs actually sampled, but not for the whole population. In this situation, calibrating within each PSU reduces with second-stage contribution to variance. This generalizes to multistage sampling. The stage argument specifies which stage of sampling the totals refer to. Stage 0 is full population totals, stage 1 is totals for PSUs, and so on. The default, `stage=NULL` is interpreted as stage 0 when a single population vector is supplied and stage 1 when a list is supplied. Calibrating to PSU totals will fail (with a message about an exactly singular matrix) for PSUs that have fewer observations than the number of calibration variables.

The variance in the calibration model may depend on covariates. If `variance=NULL` the calibration model has constant variance. If `variance` is not `NULL` it specifies a linear combination of the columns of the model matrix and the calibration variance is proportional to that linear combination. Alternatively `variance` can be specified as a vector of values the same length as the input data specifying a heteroskedasticity parameter for each unit.

The design matrix specified by formula (after any aggregation) must be of full rank, with one exception. If the population total for a column is zero and all the observations are zero the column will be ignored. This allows the use of factors where the population happens to have no observations at some level.

In a two-phase design, population may be omitted when `phase=2`, to specify calibration to the phase-one sample. If the two-phase design object was constructed using the more memory-efficient

method="approx" argument to [twophase](#), calibration of the first phase of sampling to the population is not supported.

### Value

A survey design object.

### References

- Breslow NE, Lumley T, Ballantyne CM, Chambless LE, Kulich M. Using the whole cohort in the analysis of case-cohort data. *Am J Epidemiol.* 2009;169(11):1398-1405. doi:10.1093/aje/kwp055
- Deville J-C, Sarndal C-E, Sautory O (1993) Generalized Raking Procedures in Survey Sampling. *JASA* 88:1013-1020
- Kalton G, Flores-Cervantes I (2003) "Weighting methods" *J Official Stat* 19(2) 81-97
- Lumley T, Shaw PA, Dai JY (2011) "Connections between survey calibration estimators and semi-parametric models for incomplete data" *International Statistical Review.* 79:200-220. (with discussion 79:221-232)
- Sarndal C-E, Swensson B, Wretman J. "Model Assisted Survey Sampling". Springer. 1991.
- Rao JNK, Yung W, Hidiroglou MA (2002) Estimating equations for the analysis of survey data using poststratification information. *Sankhya* 64 Series A Part 2, 364-378.
- Robins JM, Rotnitzky A, Zhao LP. (1994) Estimation of regression coefficients when some regressors are not always observed. *Journal of the American Statistical Association*, 89, 846-866.
- Vanderhoeft C (2001) Generalized Calibration at Statistics Belgium. *Statistics Belgium Working Paper* No 3.

### See Also

[postStratify](#), [rake](#) for other ways to use auxiliary information

[twophase](#) and `vignette("epi")` for an example of calibration in two-phase designs

`survey/tests/kalton.R` for examples replicating those in Kalton & Flores-Cervantes (2003)

[make.calfun](#) for user-defined calibration distances.

[trimWeights](#) to trim final weights rather than calibration adjustments.

### Examples

```
data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)

cal_names(~stype, dclus1)

pop.totals<-c(`(Intercept)`=6194, stypeH=755, stypeM=1018)

## For a single factor variable this is equivalent to
## postStratify

(dclus1g<-calibrate(dclus1, ~stype, pop.totals))
```

```

svymean(~api00, dclus1g)
svytotal(~enroll, dclus1g)
svytotal(~stype, dclus1g)

## Make weights constant within school district
(dclus1agg<-calibrate(dclus1, ~stype, pop.totals, aggregate=1))
svymean(~api00, dclus1agg)
svytotal(~enroll, dclus1agg)
svytotal(~stype, dclus1agg)

## Now add sch.wide
cal_names(~stype+sch.wide, dclus1)
(dclus1g2 <- calibrate(dclus1, ~stype+sch.wide, c(pop.totals, sch.wideYes=5122)))

svymean(~api00, dclus1g2)
svytotal(~enroll, dclus1g2)
svytotal(~stype, dclus1g2)

## Finally, calibrate on 1999 API and school type

cal_names(~stype+api99, dclus1)
(dclus1g3 <- calibrate(dclus1, ~stype+api99, c(pop.totals, api99=3914069)))

svymean(~api00, dclus1g3)
svytotal(~enroll, dclus1g3)
svytotal(~stype, dclus1g3)

## Same syntax with replicate weights
rclus1<-as.svrepdesign(dclus1)

(rclus1g3 <- calibrate(rclus1, ~stype+api99, c(pop.totals, api99=3914069)))

svymean(~api00, rclus1g3)
svytotal(~enroll, rclus1g3)
svytotal(~stype, rclus1g3)

(rclus1agg3 <- calibrate(rclus1, ~stype+api99, c(pop.totals, api99=3914069), aggregate.index=~dnum))

svymean(~api00, rclus1agg3)
svytotal(~enroll, rclus1agg3)
svytotal(~stype, rclus1agg3)

###
## Bounded weights
range(weights(dclus1g3)/weights(dclus1))
dclus1g3b <- calibrate(dclus1, ~stype+api99, c(pop.totals, api99=3914069), bounds=c(0.6,1.6))
range(weights(dclus1g3b)/weights(dclus1))

svymean(~api00, dclus1g3b)
svytotal(~enroll, dclus1g3b)

```

```

svytotal(~stype, dclus1g3b)

## Individual boundary constraints as constant values
# the first weight will be bounded at 40, the rest free to move
bnds <- list(
  lower = rep(-Inf, nrow(apiclus1)),
  upper = c(40, rep(Inf, nrow(apiclus1)-1)))
head(weights(dclus1g3))
dclus1g3b1 <- calibrate(dclus1, ~stype+api99, c(pop.totals, api99=3914069),
  bounds=bnds, bounds.const=TRUE)
head(weights(dclus1g3b1))
svytotal(~api.stu, dclus1g3b1)

## trimming
dclus1tr <- calibrate(dclus1, ~stype+api99, c(pop.totals, api99=3914069),
  bounds=c(0.5,2), trim=c(2/3,3/2))
svymean(~api00+api99+enroll, dclus1tr)
svytotal(~stype,dclus1tr)
range(weights(dclus1tr)/weights(dclus1))

rclus1tr <- calibrate(rclus1, ~stype+api99, c(pop.totals, api99=3914069),
  bounds=c(0.5,2), trim=c(2/3,3/2))
svymean(~api00+api99+enroll, rclus1tr)
svytotal(~stype,rclus1tr)

## Input in the same format as rake() for classical raking
pop.table <- xtabs(~stype+sch.wide,apipop)
pop.table2 <- xtabs(~stype+comp.imp,apipop)
dclus1r<-rake(dclus1, list(~stype+sch.wide, ~stype+comp.imp),
  list(pop.table, pop.table2))
gclus1r<-calibrate(dclus1, formula=list(~stype+sch.wide, ~stype+comp.imp),
  population=list(pop.table, pop.table2),calfun="raking")
svymean(~api00+stype, dclus1r)
svymean(~api00+stype, gclus1r)

## generalised raking
dclus1g3c <- calibrate(dclus1, ~stype+api99, c(pop.totals,
  api99=3914069), calfun="raking")
range(weights(dclus1g3c)/weights(dclus1))

(dclus1g3d <- calibrate(dclus1, ~stype+api99, c(pop.totals,
  api99=3914069), calfun=cal.logit, bounds=c(0.5,2.5)))
range(weights(dclus1g3d)/weights(dclus1))

## Ratio estimators are calibration estimators
dstrat<-svydesign(id=~1,strata=~stype, weights=~pw, data=apistrat, fpc=~fpc)
svytotal(~api.stu,dstrat)

common<-svyratio(~api.stu, ~enroll, dstrat, separate=FALSE)
predict(common, total=3811472)

```

```

pop<-3811472
## equivalent to (common) ratio estimator
dstratg1<-calibrate(dstrat,~enroll-1, pop, variance=1)
svytotal(~api.stu, dstratg1)

# Alternatively specifying the heteroskedasticity parameters directly
dstratgh <- calibrate(dstrat,~enroll-1, pop, variance=apistrat$enroll)
svytotal(~api.stu, dstratgh)

```

---

compressWeights	<i>Compress replicate weight matrix</i>
-----------------	---

---

## Description

Many replicate weight matrices have redundant rows, such as when weights are the same for all observations in a PSU. This function produces a compressed form. Methods for `as.matrix` and `as.vector` extract and expand the weights.

## Usage

```

compressWeights(rw, ...)
## S3 method for class 'svyrep.design'
compressWeights(rw,...)
## S3 method for class 'repweights_compressed'
as.matrix(x,...)
## S3 method for class 'repweights_compressed'
as.vector(x,...)

```

## Arguments

<code>rw</code>	A set of replicate weights or a <code>svyrep.design</code> object
<code>x</code>	A compressed set of replicate weights
<code>...</code>	For future expansion

## Value

An object of class `repweights_compressed` or a `svyrep.design` object with `repweights` element of class `repweights_compressed`

## See Also

[jknweights](#), [as.svrepdesign](#)

## Examples

```
data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
rclus1c<-as.svrepdesign(dclus1,compress=TRUE)
rclus1<-as.svrepdesign(dclus1,compress=FALSE)
```

---

confint.svyglm

*Confidence intervals for regression parameters*

---

## Description

Computes confidence intervals for regression parameters in `svyglm` objects. The default is a Wald-type confidence interval, adding and subtracting a multiple of the standard error. The method="likelihood" is an interval based on inverting the Rao-Scott likelihood ratio test. That is, it is an interval where the working model deviance is lower than the threshold for the Rao-Scott test at the specified level.

## Usage

```
## S3 method for class 'svyglm'
confint(object, parm, level = 0.95, method = c("Wald", "likelihood"), ddf = NULL, ...)
```

## Arguments

object	svyglm object
parm	numeric or character vector indicating which parameters to construct intervals for.
level	desired coverage
method	See description above
ddf	Denominator degrees of freedom for "likelihood" method, to use a t distribution rather than normal. If NULL, use object\$df.residual
...	for future expansion

## Value

A matrix of confidence intervals

## References

J. N. K. Rao and Alistair J. Scott (1984) On Chi-squared Tests For Multiway Contingency Tables with Proportions Estimated From Survey Data. *Annals of Statistics* 12:46-60

## See Also

[confint](#)

## Examples

```
data(api)
dclus2<-svydesign(id=~dnum+snum, fpc=~fpc1+fpc2, data=apiclus2)

m<-svyglm(I(comp.imp=="Yes")~stype*emer+ell, design=dclus2, family=quasibinomial)
confint(m)
confint(m, method="like",ddf=NULL, parm=c("ell","emer"))
```

---

crowd

*Household crowding*


---

## Description

A tiny dataset from the VPLX manual.

## Usage

```
data(crowd)
```

## Format

A data frame with 6 observations on the following 5 variables.

**rooms** Number of rooms in the house  
**person** Number of people in the household  
**weight** Sampling weight  
**cluster** Cluster number  
**stratum** Stratum number

## Source

Manual for VPLX, Census Bureau.

## Examples

```
data(crowd)

## Example 1-1
i1.1<-as.svrepdesign(svydesign(id=~cluster, weight=~weight,data=crowd))
i1.1<-update(i1.1, room.ratio=rooms/person,
overcrowded=factor(person>rooms))
svymean(~rooms+person+room.ratio,i1.1)
svytotal(~rooms+person+room.ratio,i1.1)
svymean(~rooms+person+room.ratio,subset(i1.1,overcrowded==TRUE))
svytotal(~rooms+person+room.ratio,subset(i1.1,overcrowded==TRUE))

## Example 1-2
```

```
i1.2<-as.svrepdesign(svydesign(id=~cluster,weight=~weight,strata=~stratum, data=crowd))
svymean(~rooms+person,i1.2)
svytotal(~rooms+person,i1.2)
```

---

dimnames.DBIsvydesign *Dimensions of survey designs*

---

## Description

dimnames returns variable names and row names for the data variables in a design object and dim returns dimensions. For multiple imputation designs there is a third dimension giving the number of imputations. For database-backed designs the second dimension includes variables defined by update. The first dimension excludes observations with zero weight.

## Usage

```
## S3 method for class 'survey.design'
dim(x)
## S3 method for class 'svyimputationList'
dim(x)
## S3 method for class 'survey.design'
dimnames(x)
## S3 method for class 'DBIsvydesign'
dimnames(x)
## S3 method for class 'svyimputationList'
dimnames(x)
```

## Arguments

x                      Design object

## Value

A vector of numbers for dim, a list of vectors of strings for dimnames.

## See Also

[update.DBIsvydesign, with.svyimputationList](#)

## Examples

```
data(api)
dclus1 <- svydesign(ids=~dnum,weights=~pw,data=apiclus1,fpc=~fpc)
dim(dclus1)
dimnames(dclus1)
colnames(dclus1)
```

---

election

*US 2004 presidential election data at state or county level*


---

### Description

A sample of voting data from US states or counties (depending on data availability), sampled with probability proportional to number of votes. The sample was drawn using Tille's splitting method, implemented in the "sampling" package.

### Usage

```
data(election)
```

### Format

election is a data frame with 4600 observations on the following 8 variables.

County A factor specifying the state or country

TotPrecincts Number of precincts in the state or county

PrecinctsReporting Number of precincts supplying data

Bush Votes for George W. Bush

Kerry Votes for John Kerry

Nader Votes for Ralph Nader

votes Total votes for those three candidates

p Sampling probability, proportional to votes

election\_pps is a sample of 40 counties or states taken with probability proportional to the number of votes. It includes the additional column wt with the sampling weights.

election\_insample indicates which rows of election were sampled.

election\_jointprob are the pairwise sampling probabilities and election\_jointHR are approximate pairwise sampling probabilities using the Hartley-Rao approximation.

### Source

.

### Examples

```
data(election)
## high positive correlation between totals
plot(Bush~Kerry,data=election,log="xy")
## high negative correlation between proportions
plot(I(Bush/votes)~I(Kerry/votes), data=election)

## Variances without replacement
## Horvitz-Thompson type
```

```

dpps_br<- svydesign(id=~1, fpc=~p, data=election_pps, pps="brewer")
dpps_ov<- svydesign(id=~1, fpc=~p, data=election_pps, pps="overton")
dpps_hr<- svydesign(id=~1, fpc=~p, data=election_pps, pps=HR(sum(election$p^2)/40))
dpps_hr1<- svydesign(id=~1, fpc=~p, data=election_pps, pps=HR())
dpps_ht<- svydesign(id=~1, fpc=~p, data=election_pps, pps=ppsmat(election_jointprob))
## Yates-Grundy type
dpps_yg<- svydesign(id=~1, fpc=~p, data=election_pps, pps=ppsmat(election_jointprob),variance="YG")
dpps_hryg<- svydesign(id=~1, fpc=~p, data=election_pps, pps=HR(sum(election$p^2)/40),variance="YG")

## The with-replacement approximation
dppswr <-svydesign(id=~1, probs=~p, data=election_pps)

svytotal(~Bush+Kerry+Nader, dpps_ht)
svytotal(~Bush+Kerry+Nader, dpps_yg)
svytotal(~Bush+Kerry+Nader, dpps_hr)
svytotal(~Bush+Kerry+Nader, dpps_hryg)
svytotal(~Bush+Kerry+Nader, dpps_hr1)
svytotal(~Bush+Kerry+Nader, dpps_br)
svytotal(~Bush+Kerry+Nader, dpps_ov)
svytotal(~Bush+Kerry+Nader, dppswr)

```

---

estweights

*Estimated weights for missing data*


---

## Description

Creates or adjusts a two-phase survey design object using a logistic regression model for second-phase sampling probability. This function should be particularly useful in reweighting to account for missing data.

## Usage

```

estWeights(data,formula,...)
## S3 method for class 'twophase'
estWeights(data,formula=NULL, working.model=NULL,...)
## S3 method for class 'data.frame'
estWeights(data,formula=NULL, working.model=NULL,
            subset=NULL, strata=NULL,...)

```

## Arguments

<code>data</code>	twophase design object or data frame
<code>formula</code>	Predictors for estimating weights
<code>working.model</code>	Model fitted to complete (ie phase 1) data
<code>subset</code>	Subset of data frame with complete data (ie phase 1). If NULL use all complete cases
<code>strata</code>	Stratification (if any) of phase 2 sampling
<code>...</code>	for future expansion

## Details

If data is a data frame, `estWeights` first creates a two-phase design object. The `strata` argument is used only to compute finite population corrections, the same variables must be included in `formula` to compute stratified sampling probabilities.

With a two-phase design object, `estWeights` estimates the sampling probabilities using logistic regression as described by Robins et al (1994) and adds information to the object to enable correct sandwich standard errors to be computed.

An alternative to specifying `formula` is to specify `working.model`. The estimating functions from this model will be used as predictors of the sampling probabilities, which will increase efficiency to the extent that the working model and the model of interest estimate the same parameters (Kulich & Lin 2004).

The effect on a two-phase design object is very similar to `calibrate`, and is identical when `formula` specifies a saturated model.

## Value

A two-phase survey design object.

## References

Breslow NE, Lumley T, Ballantyne CM, Chambless LE, Kulich M. (2009) Using the Whole Cohort in the Analysis of Case-Cohort Data. *Am J Epidemiol.* 2009 Jun 1;169(11):1398-405.

Robins JM, Rotnitzky A, Zhao LP. (1994) Estimation of regression coefficients when some regressors are not always observed. *Journal of the American Statistical Association*, 89, 846-866.

Kulich M, Lin DY (2004). Improving the Efficiency of Relative-Risk Estimation in Case-Cohort Studies. *Journal of the American Statistical Association*, Vol. 99, pp.832-844

Lumley T, Shaw PA, Dai JY (2011) "Connections between survey calibration estimators and semi-parametric models for incomplete data" *International Statistical Review.* 79:200-220. (with discussion 79:221-232)

## See Also

[postStratify](#), [calibrate](#), [twophase](#)

## Examples

```
data(airquality)

## ignoring missingness, using model-based standard error
summary(lm(log(Ozone)~Temp+Wind, data=airquality))

## Without covariates to predict missingness we get
## same point estimates, but different (sandwich) standard errors
daq<-estWeights(airquality, formula=~1, subset=~I(!is.na(Ozone)))
summary(svyglm(log(Ozone)~Temp+Wind, design=daq))

## Reweighting based on weather, month
d2aq<-estWeights(airquality, formula=~Temp+Wind+Month,
```

```
subset=~I(!is.na(Ozone)))
summary(svyglm(log(Ozone)~Temp+Wind,design=d2aq))
```

fpc

*Small survey example*

## Description

The fpc data frame has 8 rows and 6 columns. It is artificial data to illustrate survey sampling estimators.

## Usage

```
data(fpc)
```

## Format

This data frame contains the following columns:

**stratid** Stratum ids

**psuid** Sampling unit ids

**weight** Sampling weights

**nh** number sampled per stratum

**Nh** population size per stratum

**x** data

## Source

<https://www.stata-press.com/data/r7/fpc.dta>

## Examples

```
data(fpc)
fpc
```

```
withoutfpc<-svydesign(weights=~weight, ids=~psuid, strata=~stratid, variables=~x,
  data=fpc, nest=TRUE)
```

```
withoutfpc
svymean(~x, withoutfpc)
```

```
withfpc<-svydesign(weights=~weight, ids=~psuid, strata=~stratid,
  fpc=~Nh, variables=~x, data=fpc, nest=TRUE)
```

```
withfpc
svymean(~x, withfpc)
```

```
## Other equivalent forms
withfpc<-svydesign(prob=~I(1/weight), ids=~psuid, strata=~stratid,
fpc=~Nh, variables=~x, data=fpc, nest=TRUE)

svymean(~x, withfpc)

withfpc<-svydesign(weights=~weight, ids=~psuid, strata=~stratid,
fpc=~I(nh/Nh), variables=~x, data=fpc, nest=TRUE)

svymean(~x, withfpc)

withfpc<-svydesign(weights=~weight, ids=~interaction(stratid,psuid),
strata=~stratid, fpc=~I(nh/Nh), variables=~x, data=fpc)

svymean(~x, withfpc)

withfpc<-svydesign(ids=~psuid, strata=~stratid, fpc=~Nh,
variables=~x,data=fpc,nest=TRUE)

svymean(~x, withfpc)

withfpc<-svydesign(ids=~psuid, strata=~stratid,
fpc=~I(nh/Nh), variables=~x, data=fpc, nest=TRUE)

svymean(~x, withfpc)
```

---

ftable.svystat

*Lay out tables of survey statistics*


---

## Description

Reformat the output of survey computations to a table.

## Usage

```
## S3 method for class 'svystat'
ftable(x, rownames,...)
## S3 method for class 'svrepstat'
ftable(x, rownames,...)
## S3 method for class 'svyby'
ftable(x,...)
```

## Arguments

x                      Output of functions such as svymean,svrepmean, svyby

rownames	List of vectors of strings giving dimension names for the resulting table (see examples)
...	Arguments for future expansion

**Value**

An object of class "ftable"

**See Also**

[ftable](#)

**Examples**

```
data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)

a<-svymean(~interaction(stype,comp.imp), design=dclus1)
b<-ftable(a, rownames=list(stype=c("E","H","M"),comp.imp=c("No","Yes")))
b

a<-svymean(~interaction(stype,comp.imp), design=dclus1, deff=TRUE)
b<-ftable(a, rownames=list(stype=c("E","H","M"),comp.imp=c("No","Yes")))
round(100*b,1)

rclus1<-as.svrepdesign(dclus1)
a<-svytotal(~interaction(stype,comp.imp), design=rclus1)
b<-ftable(a, rownames=list(stype=c("E","H","M"),comp.imp=c("No","Yes")))
b
round(b)

a<-svyby(~api99 + api00, ~stype + sch.wide, rclus1, svymean, keep.var=TRUE)
ftable(a)
print(ftable(a),digits=2)

b<-svyby(~api99 + api00, ~stype + sch.wide, rclus1, svymean, keep.var=TRUE, deff=TRUE)
print(ftable(b),digits=2)

d<-svyby(~api99 + api00, ~stype + sch.wide, rclus1, svymean, keep.var=TRUE, vartype=c("se","cvpct"))
round(ftable(d),1)
```

---

hadamard

*Hadamard matrices*


---

**Description**

Returns a Hadamard matrix of dimension larger than the argument.

**Usage**

```
hadamard(n)
```

**Arguments**

n                      lower bound for size

**Details**

For most  $n$  the matrix comes from [paley](#). The  $36 \times 36$  matrix is from Plackett and Burman (1946) and the  $28 \times 28$  is from Sloane's library of Hadamard matrices.

Matrices of dimension every multiple of 4 are thought to exist, but this function doesn't know about all of them, so it will sometimes return matrices that are larger than necessary. The excess is at most 4 for  $n < 180$  and at most 5% for  $n > 100$ .

**Value**

A Hadamard matrix

**Note**

Strictly speaking, a Hadamard matrix has entries  $+1$  and  $-1$  rather than  $1$  and  $0$ , so  $2 \times \text{hadamard}(n) - 1$  is a Hadamard matrix

**References**

Sloane NJA. A Library of Hadamard Matrices <http://neilsloane.com/hadamard/>

Plackett RL, Burman JP. (1946) The Design of Optimum Multifactorial Experiments *Biometrika*, Vol. 33, No. 4 pp. 305-325

Cameron PJ (2005) Hadamard Matrices <http://designtheory.org/library/encyc/topics/had.pdf>. In: The Encyclopedia of Design Theory <http://designtheory.org/library/encyc/>

**See Also**

[brrweights](#), [paley](#)

**Examples**

```
par(mfrow=c(2,2))
## Sylvester-type
image(hadamard(63),main=quote("Sylvester: " * 64 == 2^6))
## Paley-type
image(hadamard(59),main=quote("Paley: " * 60 == 59 + 1))
## from NJ Sloane's library
image(hadamard(27),main=quote("Stored: " * 28))
## For n=90 we get 96 rather than the minimum possible size, 92.
image(hadamard(90),main=quote("Constructed: " * 96 == 2^3 * (11 + 1)))

par(mfrow=c(1,1))
```

```
plot(2:150,sapply(2:150,function(i) ncol(hadamard(i))),type="S",
     ylab="Matrix size",xlab="n",xlim=c(1,150),ylim=c(1,150))
abline(0,1,lty=3)
lines(2:150, 2:150-(2:150 %% 4)+4,col="purple",type="S",lty=2)
legend(c(x=10,y=140),legend=c("Actual size","Minimum possible size"),
       col=c("black","purple"),bty="n",lty=c(1,2))
```

---

hospital	<i>Sample of obstetric hospitals</i>
----------	--------------------------------------

---

## Description

The hospital data frame has 15 rows and 5 columns.

## Usage

```
data(hospital)
```

## Format

This data frame contains the following columns:

**hospno** Hospital id  
**oblevel** level of obstetric care  
**weighta** Weights, as given by the original reference  
**tothosp** total hospitalisations  
**births** births  
**weightats** Weights, as given in the source

## Source

Previously at <http://www.ats.ucla.edu/stat/books/sop/hospsamp.dta>

## References

Levy and Lemeshow. "Sampling of Populations" (3rd edition). Wiley.

## Examples

```
data(hospital)
hospdes<-svydesign(strata=~oblevel, id=~hospno, weights=~weighta,
fpc=~tothosp, data=hospital)
hosprep<-as.svrepdesign(hospdes)

svytotal(~births, design=hospdes)
svytotal(~births, design=hosprep)
```

---

HR

*Wrappers for specifying PPS designs*


---

## Description

The Horvitz-Thompson estimator and the Hartley-Rao approximation require information in addition to the sampling probabilities for sampled individuals. These functions allow this information to be supplied.

## Usage

```
HR(psum=NULL, strata = NULL)
ppsmat(jointprob, tolerance = 1e-04)
ppscov(probcov, weighted=FALSE)
```

## Arguments

psum	The sum of squared sampling probabilities for the population, divided by the sample size, as a single number or as a vector for stratified sampling
strata	Stratum labels, of the same length as psum, if psum is a vector
jointprob	Matrix of pairwise sampling probabilities for the sampled individuals
tolerance	Tolerance for deciding that the covariance of sampling indicators is zero
probcov	Covariance of the sampling indicators (often written 'Delta'), or weighted covariance if weighted=TRUE
weighted	If TRUE, the probcov argument is the covariance divided by pairwise sampling probabilities

## Value

An object of class HR,ppsmat, ppsdelta, or ppsdcheck suitable for supplying as the pps argument to [svydesign](#).

## See Also

[election](#) for examples of PPS designs

## Examples

```
HR(0.1)
```

make.calfun

*Calibration metrics***Description**

Create calibration metric for use in [calibrate](#). The function  $F$  is the link function described in section 2 of Deville et al. To create a new calibration metric, specify  $F - 1$  and its derivative. The package provides `cal.linear`, `cal.raking`, `cal.logit`, which are standard, and `cal.sinh` from the CALMAR2 macro, for which  $F$  is the derivative of the inverse hyperbolic sine.

**Usage**

```
make.calfun(Fm1, dF, name)
```

**Arguments**

Fm1	Function $F - 1$ taking a vector $u$ and a vector of length 2, bounds.
dF	Derivative of Fm1 wrt $u$ : arguments $u$ and bounds
name	Character string to use as name

**Value**

An object of class "calfun"

**References**

Deville J-C, Sarndal C-E, Sautory O (1993) Generalized Raking Procedures in Survey Sampling. JASA 88:1013-1020

Deville J-C, Sarndal C-E (1992) Calibration Estimators in Survey Sampling. JASA 87: 376-382

**See Also**

[calibrate](#)

**Examples**

```
str(cal.linear)
cal.linear$Fm1
cal.linear$dF

hellinger <- make.calfun(Fm1=function(u, bounds) ((1-u/2)^2)-1,
                        dF= function(u, bounds) (1-u/2)^-3 ,
                        name="hellinger distance")

hellinger

data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
```

```
svymean(~api00,calibrate(dclus1, ~api99, pop=c(6194, 3914069),
  calfun=hellinger))

svymean(~api00,calibrate(dclus1, ~api99, pop=c(6194, 3914069),
  calfun=cal.linear))

svymean(~api00,calibrate(dclus1, ~api99, pop=c(6194,3914069),
  calfun=cal.raking))
```

---

marginpred

*Standardised predictions (predictive margins) for regression models.*


---

## Description

Reweights the design (using [calibrate](#)) so that the adjustment variables are uncorrelated with the variables in the model, and then performs predictions by calling `predict`. When the adjustment model is saturated this is equivalent to direct standardization on the adjustment variables.

The `svycoxph` and `svykm1ist` methods return survival curves.

## Usage

```
marginpred(model, adjustfor, predictat, ...)
## S3 method for class 'svycoxph'
marginpred(model, adjustfor, predictat, se=FALSE, ...)
## S3 method for class 'svykm1ist'
marginpred(model, adjustfor, predictat, se=FALSE, ...)
## S3 method for class 'svyglm'
marginpred(model, adjustfor, predictat, ...)
```

## Arguments

<code>model</code>	A regression model object of a class that has a <code>marginpred</code> method
<code>adjustfor</code>	Model formula specifying adjustment variables, which must be in the design object of the model
<code>predictat</code>	A data frame giving values of the variables in <code>model</code> to predict at
<code>se</code>	Estimate standard errors for the survival curve (uses a lot of memory if the sample size is large)
<code>...</code>	Extra arguments, passed to the <code>predict</code> method for <code>model</code>

## See Also

[svypredmeans](#) for the method of Graubard and Korn implemented in SUDAAN.

[calibrate](#)

[predict.svycoxph](#)

## Examples

```
## generate data with apparent group effect from confounding
set.seed(42)
df<-data.frame(x=rnorm(100))
df$time<-rexp(100)*exp(df$x-1)
df$status<-1
df$group<-(df$x+rnorm(100))>0
des<-svydesign(id=~1,data=df)
newdf<-data.frame(group=c(FALSE,TRUE), x=c(0,0))

## Cox model
m0<-svycoxph(Surv(time,status)~group,design=des)
m1<-svycoxph(Surv(time,status)~group+x,design=des)
## conditional predictions, unadjusted and adjusted
cpred0<-predict(m0, type="curve", newdata=newdf, se=TRUE)
cpred1<-predict(m1, type="curve", newdata=newdf, se=TRUE)
## adjusted marginal prediction
mpred<-marginpred(m0, adjustfor=~x, predictat=newdf, se=TRUE)

plot(cpred0)
lines(cpred1[[1]],col="red")
lines(cpred1[[2]],col="red")
lines(mpred[[1]],col="blue")
lines(mpred[[2]],col="blue")

## Kaplan--Meier
s2<-svykm(Surv(time,status>0)~group, design=des)
p2<-marginpred(s2, adjustfor=~x, predictat=newdf,se=TRUE)
plot(s2)
lines(p2[[1]],col="green")
lines(p2[[2]],col="green")

## logistic regression
logisticm <- svyglm(group~time, family=quasibinomial, design=des)
newdf$time<-c(0.1,0.8)
logisticpred <- marginpred(logisticm, adjustfor=~x, predictat=newdf)
```

## Description

The MU284 population comes from Sarndal et al, and the complete data are available from Statlib. These data are a two-stage sample from the population, analyzed on page 143 of the book.

## Usage

```
data(mu284)
```

**Format**

A data frame with 15 observations on the following 5 variables.

id1 identifier for PSU  
 n1 number of PSUs in population  
 id2 identifier for second-stage unit  
 y1 variable to be analysed  
 n2 number of second-stage units in this PSU

**Source**

Carl Erik Sarndal, Bengt Swensson, Jan Wretman. (1991) "Model Assisted Survey Sampling" Springer.

(downloaded from StatLib, which is no longer active)

**Examples**

```
data(mu284)
(dmu284<-svydesign(id=~id1+id2,fpc=~n1+n2, data=mu284))
(ytotal<-svytotal(~y1, dmu284))
vcov(ytotal)
```

---

myco

---

*Association between leprosy and BCG vaccination*


---

**Description**

These data are in a paper by JNK Rao and colleagues, on score tests for complex survey data. External information (not further specified) suggests the functional form for the Age variable.

**Usage**

```
data("myco")
```

**Format**

A data frame with 516 observations on the following 6 variables.

Age Age in years at the midpoint of six age strata  
 Scar Presence of a BCG vaccination scar  
 n Sampled number of cases (and thus controls) in the age stratum  
 Ncontrol Number of non-cases in the population  
 wt Sampling weight  
 leprosy case status 0/1

## Details

The data are a simulated stratified case-control study drawn from a population study conducted in a region of Malawi (Clayton and Hills, 1993, Table 18.1). The goal was to examine whether BCG vaccination against tuberculosis protects against leprosy (the causative agents are both species of *Mycobacterium*). Rao et al have a typographical error: the number of non-cases in the population in the 25-30 age stratum is given as 4981 but 5981 matches both the computational output and the data as given by Clayton and Hills.

## Source

JNK Rao, AJ Scott, and Skinner, C. (1998). QUASI-SCORE TESTS WITH SURVEY DATA. *Statistica Sinica*, 8(4), 1059-1070.

Clayton, D., & Hills, M. (1993). *Statistical Models in Epidemiology*. OUP

## Examples

```
data(myco)
dmyco<-svydesign(id=~1, strata=~interaction(Age,leprosy),weights=~wt,data=myco)

m_full<-svyglm(leprosy~I((Age+7.5)^-2)+Scar, family=quasibinomial, design=dmyco)
m_age<-svyglm(leprosy~I((Age+7.5)^-2), family=quasibinomial, design=dmyco)
anova(m_full,m_age)

## unweighted model does not match
m_full
glm(leprosy~I((Age+7.5)^-2)+Scar, family=binomial, data=myco)
```

---

newsvyquantile

*Quantiles under complex sampling.*


---

## Description

Estimates quantiles and confidence intervals for them. This function was completely re-written for version 4.1 of the survey package, and has a wider range of ways to define the quantile. See the vignette for a list of them.

## Usage

```
svyquantile(x, design, quantiles, ...)
## S3 method for class 'survey.design'
svyquantile(x, design, quantiles, alpha = 0.05,
            interval.type = c("mean", "beta", "xlogit", "asin", "score"),
            na.rm = FALSE, ci=TRUE, se = ci,
            qrule=c("math", "school", "shahvaish", "hf1", "hf2", "hf3",
                    "hf4", "hf5", "hf6", "hf7", "hf8", "hf9"),
            df = NULL, ...)
```

```
## S3 method for class 'svyrep.design'
svyquantile(x, design, quantiles, alpha = 0.05,
            interval.type = c("mean", "beta", "xlogit", "asin", "quantile"),
            na.rm = FALSE, ci = TRUE, se=ci,
            qrule=c("math", "school", "shahvaish", "hf1", "hf2", "hf3",
                    "hf4", "hf5", "hf6", "hf7", "hf8", "hf9"),
            df = NULL, return.replicates=FALSE,...)
```

## Arguments

<code>x</code>	A one-sided formula describing variables to be used
<code>design</code>	Design object
<code>quantiles</code>	Numeric vector specifying which quantiles are requested
<code>alpha</code>	Specified confidence interval coverage
<code>interval.type</code>	See Details below
<code>na.rm</code>	Remove missing values?
<code>ci, se</code>	Return an estimated confidence interval and standard error?
<code>qrule</code>	Rule for defining the quantiles: either a character string specifying one of the built-in rules, or a function
<code>df</code>	Degrees of freedom for confidence interval estimation: NULL specifies <code>degf(design)</code>
<code>return.replicates</code>	Return replicate estimates of the quantile (only for <code>interval.type="quantile"</code> )
<code>...</code>	For future expansion

## Details

The  $p$ th quantile is defined as the value where the estimated cumulative distribution function is equal to  $p$ . As with quantiles in unweighted data, this definition only pins down the quantile to an interval between two observations, and a rule is needed to interpolate. The default is the mathematical definition, the lower end of the quantile interval; `qrule="school"` uses the midpoint of the quantile interval; "hf1" to "hf9" are weighted analogues of `type=1` to 9 in [quantile](#). See the vignette "Quantile rules" for details and for how to write your own.

By default, confidence intervals are estimated using Woodruff's (1952) method, which involves computing the quantile, estimating a confidence interval for the proportion of observations below the quantile, and then transforming that interval using the estimated CDF. In that context, the `interval.type` argument specifies how the confidence interval for the proportion is computed, matching [svyciprop](#). In contrast to `oldsvyquantile`, NaN is returned if a confidence interval endpoint on the probability scale falls outside  $[0, 1]$ .

There are two exceptions. For `svydesign` objects, `interval.type="score"` asks for the Francisco & Fuller confidence interval based on inverting a score test. According to Dorfmann & Valliant, this interval has inferior performance to the "beta" and "logit" intervals; it is provided for compatibility.

For replicate-weight designs, `interval.type="quantile"` ask for an interval based directly on the replicates of the quantile. This interval is not valid for jackknife-type replicates, though it should perform well for bootstrap-type replicates, BRR, and SDR.

The `df` argument specifies degrees of freedom for a t-distribution approximation to distributions of means. The default is the design degrees of freedom. Specify `df=Inf` to use a Normal distribution (eg, for compatibility).

When the standard error is requested, it is estimated by dividing the confidence interval length by the number of standard errors in a t confidence interval with the specified alpha. For example, with `alpha=0.05` and `df=Inf` the standard error is estimated as the confidence interval length divided by  $2 \times 1.96$ .

## Value

An object of class "newsvyquantile", except that with a replicate-weights design and `interval.type="quantile"` and `return.replicates=TRUE` it's an object of class "svrepstat"

## References

- Dorfman A, Valliant R (1993) Quantile variance estimators in complex surveys. Proceedings of the ASA Survey Research Methods Section. 1993: 866-871
- Francisco CA, Fuller WA (1986) Estimation of the distribution function with a complex survey. Technical Report, Iowa State University.
- Hyndman, R. J. and Fan, Y. (1996) Sample quantiles in statistical packages, The American Statistician 50, 361-365.
- Shah BV, Vaish AK (2006) Confidence Intervals for Quantile Estimation from Complex Survey Data. Proceedings of the Section on Survey Research Methods.
- Woodruff RS (1952) Confidence intervals for medians and other position measures. JASA 57, 622-627.

## See Also

`vignette("qrule", package = "survey")` [oldsvyquantile](#) [quantile](#)

## Examples

```
data(api)
## population
quantile(apiop$api00, c(.25, .5, .75))

## one-stage cluster sample
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
rclus1<-as.svrepdesign(dclus1)
bclus1<-as.svrepdesign(dclus1, type="boot")

svyquantile(~api00, dclus1, c(.25, .5, .75))
svyquantile(~api00, dclus1, c(.25, .5, .75), interval.type="beta")

svyquantile(~api00, rclus1, c(.25, .5, .75))
svyquantile(~api00, rclus1, c(.25, .5, .75), interval.type="quantile")
svyquantile(~api00, bclus1, c(.25, .5, .75), interval.type="quantile")
```

```
svyquantile(~api00+ell, dclus1, c(.25,.5,.75), qrule="math")
svyquantile(~api00+ell, dclus1, c(.25,.5,.75), qrule="school")
svyquantile(~api00+ell, dclus1, c(.25,.5,.75), qrule="hf8")
```

---

nhanes

*Cholesterol data from a US survey*


---

## Description

Data extracted from NHANES 2009-2010 on high cholesterol.

## Usage

```
data(nhanes)
```

## Format

A data frame with 8591 observations on the following 7 variables.

SDMVPSU Primary sampling units

SDMVSTRA Sampling strata

WTMEC2YR Sampling weights

HI\_CHOL Numeric vector: 1 for total cholesterol over 240mg/dl, 0 under 240mg/dl

race 1=Hispanic, 2=non-Hispanic white, 3=non-Hispanic black, 4=other

agecat Age group (0,19] (19,39] (39,59] (59,Inf]

RIAGENDR Gender: 1=male, 2=female

## Source

Previously at <https://www.cdc.gov/nchs/nhanes/search/datapage.aspx?Component=laboratory&CycleBeginYear>

## Examples

```
data(nhanes)
design <- svydesign(id=~SDMVPSU, strata=~SDMVSTRA, weights=~WTMEC2YR, nest=TRUE, data=nhanes)
design
```

---

nonresponse

---

*Experimental: Construct non-response weights*


---

## Description

Functions to simplify the construction of non-response weights by combining strata with small numbers or large weights.

## Usage

```
nonresponse(sample.weights, sample.counts, population)
sparseCells(object, count=0, totalweight=Inf, nrweight=1.5)
neighbours(index, object)
joinCells(object, a, ...)
## S3 method for class 'nonresponse'
weights(object, ...)
```

## Arguments

sample.weights	table of sampling weight by stratifying variables
sample.counts	table of sample counts by stratifying variables
population	table of population size by stratifying variables
object	object of class "nonresponse"
count	Cells with fewer sampled units than this are "sparse"
nrweight	Cells with higher non-response weight than this are "sparse"
totalweight	Cells with average sampling weight times non-response weight higher than this are "sparse"
index	Number of a cell whose neighbours are to be found
a, ...	Cells to join

## Details

When a stratified survey is conducted with imperfect response it is desirable to rescale the sampling weights to reflect the nonresponse. If some strata have small sample size, high non-response, or already had high sampling weights it may be desirable to get less variable non-response weights by averaging non-response across strata. Suitable strata to collapse may be similar on the stratifying variables and/or on the level of non-response.

nonresponse() combines stratified tables of population size, sample size, and sample weight into an object. sparseCells identifies cells that may need combining. neighbours describes the cells adjacent to a specified cell, and joinCells collapses the specified cells. When the collapsing is complete, use weights() to extract the nonresponse weights.

## Value

nonresponse and joinCells return objects of class "nonresponse", neighbours and sparseCells return objects of class "nonresponseSubset"

## Examples

```
data(api)
## pretend the sampling was stratified on three variables
poptable<-xtabs(~sch.wide+comp.imp+stype,data=apipop)
sample.count<-xtabs(~sch.wide+comp.imp+stype,data=apiclus1)
sample.weight<-xtabs(pw~sch.wide+comp.imp+stype, data=apiclus1)

## create a nonresponse object
nr<-nonresponse(sample.weight,sample.count, poptable)

## sparse cells
sparseCells(nr)

## Look at neighbours
neighbours(3,nr)
neighbours(11,nr)

## Collapse some contiguous cells
nr1<-joinCells(nr,3,5,7)

## sparse cells now
sparseCells(nr1)
nr2<-joinCells(nr1,3,11,8)

nr2

## one relatively sparse cell
sparseCells(nr2)
## but nothing suitable to join it to
neighbours(3,nr2)

## extract the weights
weights(nr2)
```

---

oldsvyquantile

*Deprecated implementation of quantiles*

---

## Description

Compute quantiles for data from complex surveys. `oldsvyquantile` is the version of the function from before version 4.1 of the package, available for backwards compatibility. See [svyquantile](#) for the current version

## Usage

```
## S3 method for class 'survey.design'
oldsvyquantile(x, design, quantiles, alpha=0.05,
  ci=FALSE, method = "linear", f = 1,
  interval.type=c("Wald","score","betaWald"), na.rm=FALSE,se=ci,
```

```

    ties=c("discrete","rounded"), df=NULL,...)
## S3 method for class 'svyrep.design'
oldsvyquantile(x, design, quantiles,
  method = "linear", interval.type=c("probability","quantile"), f = 1,
  return.replicates=FALSE, ties=c("discrete","rounded"),na.rm=FALSE,
  alpha=0.05,df=NULL,...)

```

## Arguments

<code>x</code>	A formula, vector or matrix
<code>design</code>	survey.design or svyrep.design object
<code>quantiles</code>	Quantiles to estimate
<code>method</code>	see <a href="#">approxfun</a>
<code>f</code>	see <a href="#">approxfun</a>
<code>ci</code>	Compute a confidence interval? (relatively slow; needed for <a href="#">svyby</a> )
<code>se</code>	Compute standard errors from the confidence interval length?
<code>alpha</code>	Level for confidence interval
<code>interval.type</code>	See Details below
<code>ties</code>	See Details below
<code>df</code>	Degrees of freedom for a t-distribution. Inf requests a Normal distribution, NULL uses <a href="#">degf</a> . Not relevant for type="betaWald"
<code>return.replicates</code>	Return the replicate means?
<code>na.rm</code>	Remove NAs?
<code>...</code>	arguments for future expansion

## Details

The definition of the CDF and thus of the quantiles is ambiguous in the presence of ties. With `ties="discrete"` the data are treated as genuinely discrete, so the CDF has vertical steps at tied observations. With `ties="rounded"` all the weights for tied observations are summed and the CDF interpolates linearly between distinct observed values, and so is a continuous function. Combining `interval.type="betaWald"` and `ties="discrete"` is (close to) the proposal of Shah and Vaish(2006) used in some versions of SUDAAN.

Interval estimation for quantiles is complicated, because the influence function is not continuous. Linearisation cannot be used directly, and computing the variance of replicates is valid only for some designs (eg BRR, but not jackknife). The `interval.type` option controls how the intervals are computed.

For `survey.design` objects the default is `interval.type="Wald"`. A 95% Wald confidence interval is constructed for the proportion below the estimated quantile. The inverse of the estimated CDF is used to map this to a confidence interval for the quantile. This is the method of Woodruff (1952). For "betaWald" the same procedure is used, but the confidence interval for the proportion is computed using the exact binomial cdf with an effective sample size proposed by Korn & Graubard (1998).

If `interval.type="score"` we use a method described by Binder (1991) and due originally to Francisco and Fuller (1986), which corresponds to inverting a robust score test. At the upper and lower limits of the confidence interval, a test of the null hypothesis that the cumulative distribution function is equal to the target quantile just rejects. This was the default before version 2.9. It is much slower than "Wald", and Dorfman & Valliant (1993) suggest it is not any more accurate.

Standard errors are computed from these confidence intervals by dividing the confidence interval length by  $2 \times \text{qnorm}(\alpha/2)$ .

For replicate-weight designs, ordinary replication-based standard errors are valid for BRR and Fay's method, and for some bootstrap-based designs, but not for jackknife-based designs. `interval.type="quantile"` gives these replication-based standard errors. The default, `interval.type="probability"` computes confidence on the probability scale and then transforms back to quantiles, the equivalent of `interval.type="Wald"` for survey.design objects (with  $\alpha=0.05$ ).

There is a `confint` method for `svyquantile` objects; it simply extracts the pre-computed confidence interval.

## Value

returns a list whose first component is the quantiles and second component is the confidence intervals. For replicate weight designs, returns an object of class `svyrepstat`.

## Author(s)

Thomas Lumley

## References

- Binder DA (1991) Use of estimating functions for interval estimation from complex surveys. *Proceedings of the ASA Survey Research Methods Section* 1991: 34-42
- Dorfman A, Valliant R (1993) Quantile variance estimators in complex surveys. *Proceedings of the ASA Survey Research Methods Section*. 1993: 866-871
- Korn EL, Graubard BI. (1998) Confidence Intervals For Proportions With Small Expected Number of Positive Counts Estimated From Survey Data. *Survey Methodology* 23:193-201.
- Francisco CA, Fuller WA (1986) Estimation of the distribution function with a complex survey. Technical Report, Iowa State University.
- Shao J, Tu D (1995) *The Jackknife and Bootstrap*. Springer.
- Shah BV, Vaish AK (2006) Confidence Intervals for Quantile Estimation from Complex Survey Data. *Proceedings of the Section on Survey Research Methods*.
- Woodruff RS (1952) Confidence intervals for medians and other position measures. *JASA* 57, 622-627.

## See Also

[svykm](#) for quantiles of survival curves  
[svyciprop](#) for confidence intervals on proportions.

## Examples

```

data(api)
## population
quantile(apipop$api00,c(.25,.5,.75))

## one-stage cluster sample
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
oldsvyquantile(~api00, dclus1, c(.25,.5,.75),ci=TRUE)
oldsvyquantile(~api00, dclus1, c(.25,.5,.75),ci=TRUE,interval.type="betaWald")
oldsvyquantile(~api00, dclus1, c(.25,.5,.75),ci=TRUE,df=NULL)

dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
(qapi<-oldsvyquantile(~api00, dclus1, c(.25,.5,.75),ci=TRUE, interval.type="score"))
SE(qapi)

#stratified sample
dstrat<-svydesign(id=~1, strata=~stype, weights=~pw, data=apistrat, fpc=~fpc)
oldsvyquantile(~api00, dstrat, c(.25,.5,.75),ci=TRUE)

#stratified sample, replicate weights
# interval="probability" is necessary for jackknife weights
rstrat<-as.svrepdesign(dstrat)
oldsvyquantile(~api00, rstrat, c(.25,.5,.75), interval.type="probability")

# BRR method
data(scd)
repweights<-2*cbind(c(1,0,1,0,1,0), c(1,0,0,1,0,1), c(0,1,1,0,0,1),
                    c(0,1,0,1,1,0))
scdrep<-svrepdesign(data=scd, type="BRR", repweights=repweights)
oldsvyquantile(~arrests+alive, design=scdrep, quantile=0.5, interval.type="quantile")
oldsvyquantile(~arrests+alive, design=scdrep, quantile=0.5, interval.type="quantile",df=NULL)

```

---

open.DBIsvydesign

*Open and close DBI connections*


---

## Description

A database-backed survey design object contains a connection to a database. This connection will be broken if the object is saved and reloaded, and the connection should ideally be closed with `close` before quitting R (although it doesn't matter for SQLite connections). The connection can be reopened with `open`.

## Usage

```

## S3 method for class 'DBIsvydesign'
open(con, ...)

```

```
## S3 method for class 'DBIsvydesign'
close(con, ...)
```

### Arguments

con	Object of class DBIsvydesign
...	Other options, to be passed to dbConnect or dbDisconnect.

### Value

The same survey design object with the connection opened or closed.

### See Also

[svydesign](#)  
DBI package

### Examples

```
## Not run:
library(RSQLite)
dbclus1<-svydesign(id=~dnum, weights=~pw, fpc=~fpc,
data="apiclus1",dbtype="SQLite",
dbname=system.file("api.db",package="survey"))

dbclus1
close(dbclus1)
dbclus1
try(svymean(~api00, dbclus1))

dbclus1<-open(dbclus1)
open(dbclus1)
svymean(~api00, dbclus1)

## End(Not run)
```

---

paley

*Paley-type Hadamard matrices*


---

### Description

Computes a Hadamard matrix of dimension  $(p + 1) \times 2^k$ , where p is a prime, and p+1 is a multiple of 4, using the Paley construction. Used by [hadamard](#).

### Usage

```
paley(n, nmax = 2 * n, prime=NULL, check=!is.null(prime))

is.hadamard(H, style=c("0/1", "+-"), full.orthogonal.balance=TRUE)
```

**Arguments**

n	Minimum size for matrix
nmax	Maximum size for matrix. Ignored if prime is specified.
prime	Optional. A prime at least as large as n, such that prime+1 is divisible by 4.
check	Check that the resulting matrix is of Hadamard type
H	Matrix
style	"0/1" for a matrix of 0s and 1s, "+-" for a matrix of $\pm 1$ .
full.orthogonal.balance	Require full orthogonal balance?

**Details**

The Paley construction gives a Hadamard matrix of order  $p+1$  if  $p$  is prime and  $p+1$  is a multiple of 4. This is then expanded to order  $(p+1) \times 2^k$  using the Sylvester construction.

paley knows primes up to 7919. The user can specify a prime with the prime argument, in which case a matrix of order  $p+1$  is constructed.

If check=TRUE the code uses is.hadamard to check that the resulting matrix really is of Hadamard type, in the same way as in the example below. As this test takes  $n^3$  time it is preferable to just be sure that prime really is prime.

A Hadamard matrix including a row of 1s gives BRR designs where the average of the replicates for a linear statistic is exactly the full sample estimate. This property is called full orthogonal balance.

**Value**

For paley, a matrix of zeros and ones, or NULL if no matrix smaller than nmax can be found.

For is.hadamard, TRUE if H is a Hadamard matrix.

**References**

Cameron PJ (2005) Hadamard Matrices. In: The Encyclopedia of Design Theory

**See Also**

[hadamard](#)

**Examples**

```
M<-paley(11)

is.hadamard(M)
## internals of is.hadamard(M)
H<-2*M-1
## HH^T is diagonal for any Hadamard matrix
H%*%t(H)
```

pchisqsum

*Distribution of quadratic forms***Description**

The distribution of a quadratic form in  $p$  standard Normal variables is a linear combination of  $p$  chi-squared distributions with 1df. When there is uncertainty about the variance, a reasonable model for the distribution is a linear combination of F distributions with the same denominator.

**Usage**

```
pchisqsum(x, df, a, lower.tail = TRUE,
  method = c("satterthwaite", "integration", "saddlepoint"))
pFsum(x, df, a, ddf=Inf, lower.tail = TRUE,
  method = c("saddlepoint", "integration", "satterthwaite"), ...)
```

**Arguments**

<code>x</code>	Observed values
<code>df</code>	Vector of degrees of freedom
<code>a</code>	Vector of coefficients
<code>ddf</code>	Denominator degrees of freedom
<code>lower.tail</code>	lower or upper tail?
<code>method</code>	See Details below
<code>...</code>	arguments to <code>pchisqsum</code>

**Details**

The "satterthwaite" method uses Satterthwaite's approximation, and this is also used as a fall-back for the other methods. The accuracy is usually good, but is more variable depending on  $a$  than the other methods and is anticonservative in the right tail (eg for upper tail probabilities less than  $10^{-5}$ ). The Satterthwaite approximation requires all  $a > 0$ .

"integration" requires the `CompQuadForm` package. For `pchisqsum` it uses Farebrother's algorithm if all  $a > 0$ . For `pFsum` or when some  $a < 0$  it inverts the characteristic function using the algorithm of Davies (1980). These algorithms are highly accurate for the lower tail probability, but they obtain the upper tail probability by subtraction from 1 and so fail completely when the upper tail probability is comparable to machine epsilon or smaller.

If the `CompQuadForm` package is not present, a warning is given and the saddlepoint approximation is used.

"saddlepoint" uses Kuonen's saddlepoint approximation. This is moderately accurate even very far out in the upper tail or with some  $a = 0$  and does not require any additional packages. The relative error in the right tail is uniformly bounded for all  $x$  and decreases as  $p$  increases. This method is implemented in pure R and so is slower than the "integration" method.

The distribution in `pFsum` is standardised so that a likelihood ratio test can use the same  $x$  value as in `pchisqsum`. That is, the linear combination of chi-squareds is multiplied by `ddf` and then divided by an independent chi-squared with `ddf` degrees of freedom.

**Value**

Vector of cumulative probabilities

**References**

- Chen, T., & Lumley T. (2019). Numerical evaluation of methods approximating the distribution of a large quadratic form in normal variables. *Computational Statistics and Data Analysis*, 139, 75-81.
- Davies RB (1973). "Numerical inversion of a characteristic function" *Biometrika* 60:415-7
- Davies RB (1980) "Algorithm AS 155: The Distribution of a Linear Combination of chi-squared Random Variables" *Applied Statistics*, Vol. 29, No. 3 (1980), pp. 323-333
- P. Duchesne, P. Lafaye de Micheaux (2010) "Computing the distribution of quadratic forms: Further comparisons between the Liu-Tang-Zhang approximation and exact methods", *Computational Statistics and Data Analysis*, Volume 54, (2010), 858-862
- Farebrother R.W. (1984) "Algorithm AS 204: The distribution of a Positive Linear Combination of chi-squared random variables". *Applied Statistics* Vol. 33, No. 3 (1984), p. 332-339
- Kuonen D (1999) Saddlepoint Approximations for Distributions of Quadratic Forms in Normal Variables. *Biometrika*, Vol. 86, No. 4 (Dec., 1999), pp. 929-935

**See Also**

[pchisq](#)

**Examples**

```
x <- 2.7*rnorm(1001)^2+rnorm(1001)^2+0.3*rnorm(1001)^2
x.thin<-sort(x)[1+(0:50)*20]
p.invert<-pchisqsum(x.thin,df=c(1,1,1),a=c(2.7,1,.3),method="int",lower=FALSE)
p.satt<-pchisqsum(x.thin,df=c(1,1,1),a=c(2.7,1,.3),method="satt",lower=FALSE)
p.sadd<-pchisqsum(x.thin,df=c(1,1,1),a=c(2.7,1,.3),method="sad",lower=FALSE)

plot(p.invert, p.satt,type="l",log="xy")
abline(0,1,lty=2,col="purple")
plot(p.invert, p.sadd,type="l",log="xy")
abline(0,1,lty=2,col="purple")

pchisqsum(20, df=c(1,1,1),a=c(2.7,1,.3), lower.tail=FALSE,method="sad")
pFsum(20, df=c(1,1,1),a=c(2.7,1,.3), ddf=49,lower.tail=FALSE,method="sad")
pFsum(20, df=c(1,1,1),a=c(2.7,1,.3), ddf=1000,lower.tail=FALSE,method="sad")
```

---

poisson\_sampling

*Specify Poisson sampling design*

---

**Description**

Specify a design where units are sampled independently from the population, with known probabilities. This design is often used theoretically, but is rarely used in practice because the sample size is variable. This function calls [ppscov](#) to specify a sparse sampling covariance matrix.

**Usage**

```
poisson_sampling(p)
```

**Arguments**

`p`                      Vector of sampling probabilities

**Value**

Object of class `ppsdcheck`

**See Also**

[ppscov](#), [svydesign](#)

**Examples**

```
data(api)
apipop$prob<-with(apipop, 200*api00/sum(api00))
insample<-as.logical(rbinom(nrow(apipop),1,apipop$prob))
apipois<-apipop[insample,]
despois<-svydesign(id=~1, prob=~prob, pps=poisson_sampling(apipois$prob), data=apipois)

svytotal(~api00, despois)

## SE formula
sqrt(sum( (apipois$api00*weights(despois))^2*(1-apipois$prob)))
```

---

postStratify	<i>Post-stratify a survey</i>
--------------	-------------------------------

---

**Description**

Post-stratification adjusts the sampling and replicate weights so that the joint distribution of a set of post-stratifying variables matches the known population joint distribution. Use [rake](#) when the full joint distribution is not available.

**Usage**

```
postStratify(design, strata, population, partial = FALSE, ...)
## S3 method for class 'svyrep.design'
postStratify(design, strata, population, partial = FALSE, compress=NULL,...)
## S3 method for class 'survey.design'
postStratify(design, strata, population, partial = FALSE, ...)
```

**Arguments**

design	A survey design with replicate weights
strata	A formula or data frame of post-stratifying variables, which must not contain missing values.
population	A <a href="#">table</a> , <a href="#">xtabs</a> or <code>data.frame</code> with population frequencies
partial	if TRUE, ignore population strata not present in the sample
compress	Attempt to compress the replicate weight matrix? When NULL will attempt to compress if the original weight matrix was compressed
...	arguments for future expansion

**Details**

The population totals can be specified as a table with the strata variables in the margins, or as a data frame where one column lists frequencies and the other columns list the unique combinations of strata variables (the format produced by `as.data.frame` acting on a `table` object). A table must have named `dimnames` to indicate the variable names.

Compressing the replicate weights will take time and may even increase memory use if there is actually little redundancy in the weight matrix (in particular if the post-stratification variables have many values and cut across PSUs).

If a `svydesign` object is to be converted to a replication design the post-stratification should be performed after conversion.

The variance estimate for replication designs follows the same procedure as Valliant (1993) described for estimating totals. Rao et al (2002) describe this procedure for estimating functions (and also the GREG or g-calibration procedure, see [calibrate](#))

**Value**

A new survey design object.

**Note**

If the sampling weights are already post-stratified there will be no change in point estimates after `postStratify` but the standard error estimates will decrease to correctly reflect the post-stratification.

**References**

- Valliant R (1993) Post-stratification and conditional variance estimation. *JASA* 88: 89-96
- Rao JNK, Yung W, Hidiroglou MA (2002) Estimating equations for the analysis of survey data using poststratification information. *Sankhya* 64 Series A Part 2, 364-378.

**See Also**

[rake](#), [calibrate](#) for other things to do with auxiliary information

[compressWeights](#) for information on compressing weights

## Examples

```
data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
rclus1<-as.svrepdesign(dclus1)

svymean(~api00, rclus1)
svytotal(~enroll, rclus1)

# post-stratify on school type
pop.types <- data.frame(stype=c("E","H","M"), Freq=c(4421,755,1018))
#or: pop.types <- xtabs(~stype, data=apipop)
#or: pop.types <- table(stype=apipop$stype)

rclus1p<-postStratify(rclus1, ~stype, pop.types)
summary(rclus1p)
svymean(~api00, rclus1p)
svytotal(~enroll, rclus1p)

## and for svydesign objects
dclus1p<-postStratify(dclus1, ~stype, pop.types)
summary(dclus1p)
svymean(~api00, dclus1p)
svytotal(~enroll, dclus1p)
```

---

psrsq

*Pseudo-Rsquareds*


---

## Description

Compute the Nagelkerke and Cox–Snell pseudo-rsquared statistics, primarily for logistic regression. A generic function with methods for `glm` and [svyglm](#). The method for `svyglm` objects uses the design-based estimators described by Lumley (2017)

## Usage

```
psrsq(object, method = c("Cox-Snell", "Nagelkerke"), ...)
```

## Arguments

<code>object</code>	A regression model ( <code>glm</code> or <code>svyglm</code> )
<code>method</code>	Which statistic to compute
<code>...</code>	For future expansion

## Value

Numeric value

References

Lumley T (2017) "Pseudo-R2 statistics under complex sampling" Australian and New Zealand Journal of Statistics DOI: 10.1111/anzs.12187 (preprint: <https://arxiv.org/abs/1701.07745>)

See Also

[AIC.svyglm](#)

Examples

```
data(api)
dclus2<-svydesign(id=~dnum+snum, weights=~pw, data=apiclus2)

model1<-svyglm(I(sch.wide=="Yes")~ell+meals+mobility+as.numeric(stype),
  design=dclus2, family=quasibinomial())

psrsq(model1, type="Nagelkerke")
```

---

rake	<i>Raking of replicate weight design</i>
------	--

---

Description

Raking uses iterative post-stratification to match marginal distributions of a survey sample to known population margins.

Usage

```
rake(design, sample.margins, population.margins, control = list(maxit = 10, epsilon = 1, verbose=FALSE), compress=NULL)
```

Arguments

- design                   A survey object
- sample.margins   list of formulas or data frames describing sample margins, which must not contain missing values
- population.margins   list of tables or data frames describing corresponding population margins
- control               maxit controls the number of iterations. Convergence is declared if the maximum change in a table entry is less than epsilon. If epsilon<1 it is taken to be a fraction of the total sampling weight.
- compress             If design has replicate weights, attempt to compress the new replicate weight matrix? When NULL, will attempt to compress if the original weight matrix was compressed

## Details

The `sample.margins` should be in a format suitable for [postStratify](#).

Raking (aka iterative proportional fitting) is known to converge for any table without zeros, and for any table with zeros for which there is a joint distribution with the given margins and the same pattern of zeros. The ‘margins’ need not be one-dimensional.

The algorithm works by repeated calls to [postStratify](#) (iterative proportional fitting), which is efficient for large multiway tables. For small tables [calibrate](#) will be faster, and also allows raking to population totals for continuous variables, and raking with bounded weights.

## Value

A raked survey design.

## See Also

[postStratify](#), [compressWeights](#)  
[calibrate](#) for other ways to use auxiliary information.

## Examples

```
data(api)
dclus1 <- svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
rclus1 <- as.svrepdesign(dclus1)

svymean(~api00, rclus1)
svytotal(~enroll, rclus1)

## population marginal totals for each stratum
pop.types <- data.frame(stype=c("E","H","M"), Freq=c(4421,755,1018))
pop.schwide <- data.frame(sch.wide=c("No","Yes"), Freq=c(1072,5122))

rclus1r <- rake(rclus1, list(~stype,~sch.wide), list(pop.types, pop.schwide))

svymean(~api00, rclus1r)
svytotal(~enroll, rclus1r)

## marginal totals correspond to population
xtabs(~stype, apipop)
svytable(~stype, rclus1r, round=TRUE)
xtabs(~sch.wide, apipop)
svytable(~sch.wide, rclus1r, round=TRUE)

## joint totals don't correspond
xtabs(~stype+sch.wide, apipop)
svytable(~stype+sch.wide, rclus1r, round=TRUE)

## Do it for a design without replicate weights
dclus1r<-rake(dclus1, list(~stype,~sch.wide), list(pop.types, pop.schwide))

svymean(~api00, dclus1r)
```

```

svytotal(~enroll, dclus1r)

## compare to raking with calibrate()
dclus1gr<-calibrate(dclus1, ~stype+sch.wide, pop=c(6194, 755,1018,5122),
  calfun="raking")
svymean(~stype+api00, dclus1r)
svymean(~stype+api00, dclus1gr)

## compare to joint post-stratification
## (only possible if joint population table is known)
##
pop.table <- xtabs(~stype+sch.wide,apipop)
rclus1ps <- postStratify(rclus1, ~stype+sch.wide, pop.table)
svytable(~stype+sch.wide, rclus1ps, round=TRUE)

svymean(~api00, rclus1ps)
svytotal(~enroll, rclus1ps)

## Example of raking with partial joint distributions
pop.imp<-data.frame(comp.imp=c("No","Yes"),Freq=c(1712,4482))
dclus1r2<-rake(dclus1, list(~stype+sch.wide, ~comp.imp),
  list(pop.table, pop.imp))
svymean(~api00, dclus1r2)

## compare to calibrate() syntax with tables
dclus1r2<-calibrate(dclus1, formula=list(~stype+sch.wide, ~comp.imp),
  population=list(pop.table, pop.imp),calfun="raking")
svymean(~api00, dclus1r2)

```

regTermTest

*Wald test for a term in a regression model***Description**

Provides Wald test and working Wald and working likelihood ratio (Rao-Scott) test of the hypothesis that all coefficients associated with a particular regression term are zero (or have some other specified values). Particularly useful as a substitute for [anova](#) when not fitting by maximum likelihood.

**Usage**

```

regTermTest(model, test.terms, null=NULL,df=NULL,
method=c("Wald","WorkingWald","LRT"), lrt.approximation="saddlepoint")

```

**Arguments**

model                    A model object with [coef](#) and [vcov](#) methods

<code>test.terms</code>	Character string or one-sided formula giving name of term or terms to test
<code>null</code>	Null hypothesis values for parameters. Default is zeros
<code>df</code>	Denominator degrees of freedom for an F test. If NULL these are estimated from the model. Use Inf for a chi-squared test.
<code>method</code>	If "Wald", the Wald-type test; if "LRT" the Rao-Scott test based on the estimated log likelihood ratio; If "WorkingWald" the Wald-type test using the variance matrix under simple random sampling
<code>lrt.approximation</code>	method for approximating the distribution of the LRT and Working Wald statistic; see <a href="#">pchisqsum</a> .

## Details

The Wald test uses a chisquared or F distribution. The two working-model tests come from the (mis-specified) working model where the observations are independent and the weights are frequency weights. For categorical data, this is just the model fitted to the estimated population crosstabulation. The Rao-Scott LRT statistic is the likelihood ratio statistic in this model. The working Wald test statistic is the Wald statistic in this model. The working-model tests do not have a chi-squared sampling distribution: we use a linear combination of chi-squared or F distributions as in [pchisqsum](#). I believe the working Wald test is what SUDAAN refers to as a "Satterthwaite adjusted Wald test".

To match other software you will typically need to use `lrt.approximation="satterthwaite"`

## Value

An object of class `regTermTest` or `regTermTestLRT`.

## Note

The "LRT" method will not work if the model had starting values supplied for the regression coefficients. Instead, fit the two models separately and use `anova(model1, model2, force=TRUE)`

## References

- Rao, JNK, Scott, AJ (1984) "On Chi-squared Tests For Multiway Contingency Tables with Proportions Estimated From Survey Data" *Annals of Statistics* 12:46-60.
- Lumley T, Scott A (2012) "Partial likelihood ratio tests for the Cox model under complex sampling" *Statistics in Medicine* 17 JUL 2012. DOI: 10.1002/sim.5492
- Lumley T, Scott A (2014) "Tests for Regression Models Fitted to Survey Data" *Australian and New Zealand Journal of Statistics* 56:1-14 DOI: 10.1111/anzs.12065

## See Also

[anova](#), [vcov](#), [contrasts](#), [pchisqsum](#)

## Examples

```
data(esoph)
model1 <- glm(cbind(ncases, ncontrols) ~ agegp + tobgp *
  alcgp, data = esoph, family = binomial())
anova(model1)

regTermTest(model1, "tobgp")
regTermTest(model1, "tobgp:alcgp")
regTermTest(model1, ~alcgp+tobgp:alcgp)

data(api)
dclus2<-svydesign(id=~dnum+snum, weights=~pw, data=apiclus2)
model2<-svyglm(I(sch.wide=="Yes")~ell+meals+mobility, design=dclus2, family=quasibinomial())
regTermTest(model2, ~ell)
regTermTest(model2, ~ell, df=NULL)
regTermTest(model2, ~ell, method="LRT", df=Inf)
regTermTest(model2, ~ell+meals, method="LRT", df=NULL)

regTermTest(model2, ~ell+meals, method="WorkingWald", df=NULL)
```

---

salamander

*Salamander mating data set from McCullagh and Nelder (1989)*


---

## Description

This data set presents the outcome of three experiments conducted at the University of Chicago in 1986 to study interbreeding between populations of mountain dusky salamanders (McCullagh and Nelder, 1989, Section 14.5). The analysis here is from Lumley (1998, section 5.3)

## Usage

```
data(salamander)
```

## Format

A data frame with the following columns:

**Mate** Whether the salamanders mated (1) or did not mate (0).

**Cross** Cross between female and male type. A factor with four levels: R/R, R/W, W/R, and W/W. The type of the female salamander is listed first and the male is listed second. Rough Butt is represented by R and White Side is represented by W. For example, Cross=W/R indicates a White Side female was crossed with a Rough Butt male.

**Male** Identification number of the male salamander. A factor.

**Female** Identification number of the female salamander. A factor.

## References

McCullagh P. and Nelder, J. A. (1989) *Generalized Linear Models*. Chapman and Hall/CRC. Lumley T (1998) PhD thesis, University of Washington

## Examples

```
data(salamander)
salamander$mixed<-with(salamander, Cross=="W/R" | Cross=="R/W")
salamander$RWvsWR<-with(salamander, ifelse(mixed,
      ((Cross=="R/W")-(Cross=="W/R"))/2,
      0))
xsalamander<-xdesign(id=list(~Male, ~Female), data=salamander,
      overlap="unbiased")

## Adjacency matrix
## Blocks 1 and 2 are actually the same salamanders, but
## it's traditional to pretend they are independent.
image(xsalamander$adjacency)

## R doesn't allow family=binomial(identity)
success <- svyglm(Mate~mixed+RWvsWR, design=xsalamander,
      family=quasi(link="identity", variance="mu(1-mu)"))
summary(success)
```

---

scd

---

*Survival in cardiac arrest*


---

## Description

These data are from Section 12.2 of Levy and Lemeshow. They describe (a possibly apocryphal) study of survival in out-of-hospital cardiac arrest. Two out of five ambulance stations were sampled from each of three emergency service areas.

## Usage

```
data(scd)
```

## Format

This data frame contains the following columns:

**ESA** Emergency Service Area (strata)

**ambulance** Ambulance station (PSU)

**arrests** estimated number of cardiac arrests

**alive** number reaching hospital alive

## Source

Levy and Lemeshow. "Sampling of Populations" (3rd edition). Wiley.

## Examples

```
data(scd)

## survey design objects
scddes<-svydesign(data=scd, prob=~1, id=~ambulance, strata=~ESA,
nest=TRUE, fpc=rep(5,6))
scdnofpc<-svydesign(data=scd, prob=~1, id=~ambulance, strata=~ESA,
nest=TRUE)

# convert to BRR replicate weights
scd2brr <- as.svrepdesign(scdnofpc, type="BRR")
# or to Rao-Wu bootstrap
scd2boot <- as.svrepdesign(scdnofpc, type="subboot")

# use BRR replicate weights from Levy and Lemeshow
repweights<-2*cbind(c(1,0,1,0,1,0), c(1,0,0,1,0,1), c(0,1,1,0,0,1),
c(0,1,0,1,1,0))
scdrep<-svrepdesign(data=scd, type="BRR", repweights=repweights)

# ratio estimates
svyratio(~alive, ~arrests, design=scddes)
svyratio(~alive, ~arrests, design=scdnofpc)
svyratio(~alive, ~arrests, design=scd2brr)
svyratio(~alive, ~arrests, design=scd2boot)
svyratio(~alive, ~arrests, design=scdrep)

# or a logistic regression
summary(svyglm(cbind(alive,arrests~1), family=quasibinomial, design=scdnofpc))
summary(svyglm(cbind(alive,arrests~1), family=quasibinomial, design=scdrep))

# Because no sampling weights are given, can't compute design effects
# without replacement: use deff="replace"

svymean(~alive+arrests, scddes, deff=TRUE)
svymean(~alive+arrests, scddes, deff="replace")
```

---

SE

---

*Extract standard errors*


---

## Description

Extracts standard errors from an object. The default method is for objects with a [vcov](#) method.

## Usage

```
SE(object, ...)
## Default S3 method:
SE(object,...)
## S3 method for class 'svrepstat'
SE(object,...)
```

Arguments

- object           An object
- ...             Arguments for future expansion

Value

Vector of standard errors.

See Also

[vcov](#)

---

smoothArea	<i>Small area estimation via basic area level model</i>
------------	---

---

Description

Generates small area estimates by smoothing direct estimates using an area level model

Usage

```
svysmoothArea(  
  formula,  
  domain,  
  design = NULL,  
  adj.mat = NULL,  
  X.domain = NULL,  
  direct.est = NULL,  
  domain.size = NULL,  
  transform = c("identity", "logit", "log"),  
  pc.u = 1,  
  pc.alpha = 0.01,  
  pc.u.phi = 0.5,  
  pc.alpha.phi = 2/3,  
  level = 0.95,  
  n.sample = 250,  
  var.tol = 1e-10,  
  return.samples = FALSE,...  
)
```

Arguments

- formula           An object of class 'formula' describing the model to be fitted. If direct.est is specified, the right hand side of the formula is not necessary.
- domain           One-sided formula specifying factors containing domain labels
- design            An object of class "svydesign" containing the data for the model

adj.mat	Adjacency matrix with rownames matching the domain labels. If set to NULL, the IID spatial effect will be used.
X.domain	Data frame of areal covariates. One of the column names needs to match the name of the domain variable, in order to be linked to the data input. Currently only supporting time-invariant covariates.
direct.est	Data frame of direct estimates, with first column containing the domain variable, second column containing direct estimate, and third column containing the variance of direct estimate.
domain.size	Data frame of domain sizes. One of the column names needs to match the name of the domain variable, in order to be linked to the data input and there must be a column names 'size' containing domain sizes.
transform	Optional transformation applied to the direct estimates before fitting area level model. The default option is no transformation, but logit and log are implemented.
pc.u	Hyperparameter U for the PC prior on precisions. See the INLA documentation for more details on the parameterization.
pc.alpha	Hyperparameter alpha for the PC prior on precisions.
pc.u.phi	Hyperparameter U for the PC prior on the mixture probability phi in BYM2 model.
pc.alpha.phi	Hyperparameter alpha for the PC prior on the mixture probability phi in BYM2 model.
level	The specified level for the posterior credible intervals
n.sample	Number of draws from posterior used to compute summaries
var.tol	Tolerance parameter; if variance of an area's direct estimator is below this value, that direct estimator is dropped from model
return.samples	If TRUE, return matrix of posterior samples of area level quantities
...	for future methods

## Details

The basic area level model is a Bayesian version of the Fay-Herriot model (Fay & Herriot, 1979). It treats direct estimates of small area quantities as response data and explicitly models differences between areas using covariate information and random effects. The Fay-Herriot model can be viewed as a two-stage model: in the first stage, a sampling model represents the sampling variability of a direct estimator and in the second stage, a linking model describes the between area differences in small area quantities. More detail is given in section 4 of Mercer et al (2015).

## Value

A `svysae` object

## References

Fay, Robert E., and Roger A. Herriot. (1979). Estimates of Income for Small Places: An Application of James-Stein Procedures to Census Data. *Journal of the American Statistical Association* 74 (366a): 269-77.

Mercer LD, Wakefield J, Pantazis A, Lutambi AM, Masanja H, Clark S. Space-Time Smoothing of Complex Survey Data: Small Area Estimation for Child Mortality. *Ann Appl Stat.* 2015 Dec;9(4):1889-1905. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4959836/>

### See Also

The survey-sae vignette

### Examples

```
## artificial data from SUMMER package
## Uses too many cores for a CRAN example

## Not run:
hasSUMMER<-tryCatch({
  data("DemoData2",package="SUMMER")
  data("DemoMap2", package="SUMMER")
}, error=function(e) FALSE)

if (!isFALSE(hasSUMMER)){
  library(survey)
  des0 <- svydesign(ids = ~clustid+id, strata = ~strata,
    weights = ~weights, data = DemoData2, nest = TRUE)
  Xmat <- aggregate(age~region, data = DemoData2, FUN = mean)

  cts.cov.res <- svysmoothArea(tobacco.use ~ age,
    domain = ~region,
    design = des0,
    adj.mat = DemoMap2$Amat,
    X.domain = Xmat,
    pc.u = 1,
    pc.alpha = 0.01,
    pc.u.phi = 0.5,
    pc.alpha.phi = 2/3)

  print(cts.cov.res)
  plot(cts.cov.res)
}

## End(Not run)
```

### Description

Generates small area estimates by smoothing direct estimates using a basic unit level model. This model assumes sampling is ignorable (no selection bias). It's a Bayesian linear (family="gaussian") or generalised linear (family="binomial") mixed model for the unit-level data with individual-level covariates and area-level random effects.

**Usage**

```
svsmoothUnit(
  formula,
  domain,
  design,
  family = c("gaussian", "binomial"),
  X.pop = NULL,
  adj.mat = NULL,
  domain.size = NULL,
  pc.u = 1,
  pc.alpha = 0.01,
  pc.u.phi = 0.5,
  pc.alpha.phi = 2/3,
  level = 0.95,
  n.sample = 250,
  return.samples = FALSE,
  X.pop.weights = NULL,...
)
```

**Arguments**

formula	An object of class 'formula' describing the model to be fitted.
domain	One-sided formula specifying factors containing domain labels
design	An object of class "survey.design" containing the data for the model
family	of the response variable, currently supports 'binomial' (default with logit link function) or 'gaussian'.
X.pop	Data frame of population unit-level covariates. One of the column name needs to match the domain specified, in order to be linked to the data input. Currently only supporting time-invariant covariates.
adj.mat	Adjacency matrix with rownames matching the domain labels. If set to NULL, the IID spatial effect will be used.
domain.size	Data frame of domain sizes. One of the column names needs to match the name of the domain variable, in order to be linked to the data input and there must be a column names 'size' containing domain sizes. The default option is no transformation, but logit and log are implemented.
pc.u	Hyperparameter U for the PC prior on precisions. See the INLA documentation for more details on the parameterization.
pc.alpha	Hyperparameter alpha for the PC prior on precisions.
pc.u.phi	Hyperparameter U for the PC prior on the mixture probability phi in BYM2 model.
pc.alpha.phi	Hyperparameter alpha for the PC prior on the mixture probability phi in BYM2 model.
level	The specified level for the posterior credible intervals
n.sample	Number of draws from posterior used to compute summaries

return.samples If TRUE, return matrix of posterior samples of area level quantities  
X.pop.weights Optional vector of weights to use when aggregating unit level predictions  
... for future expansion

**Value**

A svysae object

**References**

Battese, G. E., Harter, R. M., & Fuller, W. A. (1988). An Error-Components Model for Prediction of County Crop Areas Using Survey and Satellite Data. Journal of the American Statistical Association, 83(401), 28-36.

**See Also**

The survey-sae vignette

---

stratsample	<i>Take a stratified sample</i>
-------------	---------------------------------

---

**Description**

This function takes a stratified sample without replacement from a data set.

**Usage**

```
stratsample(strata, counts)
```

**Arguments**

strata Vector of stratum identifiers; will be coerced to character  
counts named vector of stratum sample sizes, with names corresponding to the values of as.character(strata)

**Value**

vector of indices into strata giving the sample

**See Also**

[sample](#)  
The "sampling" package has many more sampling algorithms.

**Examples**

```
data(api)
s<-stratsample(apiop$type, c("E"=5,"H"=4,"M"=2))
table(apiop$type[s])
```

---

subset.survey.design    *Subset of survey*


---

## Description

Restrict a survey design to a subpopulation, keeping the original design information about number of clusters, strata. If the design has no post-stratification or calibration data the subset will use proportionately less memory.

## Usage

```
## S3 method for class 'survey.design'
subset(x, subset, ...)
## S3 method for class 'svyrep.design'
subset(x, subset, ...)
```

## Arguments

x	A survey design object
subset	An expression specifying the subpopulation
...	Arguments not used by this method

## Value

A new survey design object

## See Also

[svydesign](#)

## Examples

```
data(fpc)
dfpc<-svydesign(id=~psuid, strat=~stratid, weight=~weight, data=fpc, nest=TRUE)
dsub<-subset(dfpc, x>4)
summary(dsub)
svymean(~x, design=dsub)

## These should give the same domain estimates and standard errors
svyby(~x, ~I(x>4), design=dfpc, svymean)
summary(svyglm(x~I(x>4)+0, design=dfpc))

data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
rclus1<-as.svrepdesign(dclus1)
svymean(~enroll, subset(dclus1, sch.wide=="Yes" & comp.imp=="Yes"))
svymean(~enroll, subset(rclus1, sch.wide=="Yes" & comp.imp=="Yes"))
```

## Description

This help page documents the options that control the behaviour of the survey package.

## Details

All the options for the survey package have names beginning with "survey". Four of them control standard error estimation.

`options("survey.replicates.mse")` controls the default in `svrepdesign` and `as.svrepdesign` for computing variances. When `options("survey.replicates.mse")` is TRUE, the default is to create replicate weight designs that compute variances centered at the point estimate, rather than at the mean of the replicates. The option can be overridden by specifying the `mse` argument explicitly in `svrepdesign` and `as.svrepdesign`. The default is FALSE.

When `options("survey.ultimate.cluster")` is TRUE, standard error estimation is based on independence of PSUs at the first stage of sampling, without using any information about subsequent stages. When FALSE, finite population corrections and variances are estimated recursively. See [svyrecvar](#) for more information. This option makes no difference unless first-stage finite population corrections are specified, in which case setting the option to TRUE gives the wrong answer for a multistage study. The only reason to use TRUE is for compatibility with other software that gives the wrong answer.

Handling of strata with a single PSU that are not certainty PSUs is controlled by `options("survey.lonely.psu")`. The default setting is "fail", which gives an error. Use "remove" to ignore that PSU for variance computation, "adjust" to center the stratum at the population mean rather than the stratum mean, and "average" to replace the variance contribution of the stratum by the average variance contribution across strata. As of version 3.4-2 `as.svrepdesign` also uses this option.

The variance formulas for domain estimation give well-defined, positive results when a stratum contains only one PSU with observations in the domain, but are not unbiased. If `options("survey.adjust.domain.lonely")` is TRUE and `options("survey.lonely.psu")` is "average" or "adjust" the same adjustment for lonely PSUs will be used within a domain. Note that this adjustment is not available for replicate-weight designs, nor (currently) for raked, post-stratified, or calibrated designs.

The fourth option is `options("survey.want.obsolete")`. This controls the warnings about using the deprecated pre-2.9.0 survey design objects.

The behaviour of replicate-weight designs for self-representing strata is controlled by `options("survey.drop.replicates")`. When TRUE, various optimizations are used that take advantage of the fact that these strata do not contribute to the variance. The only reason ever to use FALSE is if there is a bug in the code for these optimizations.

The fifth option controls the use of multiple processors with the `multicore` package. This option should not affect the values computed by any of the survey functions. If TRUE, all functions that are able to use multiple processors will do so by default. Using multiple processors may speed up calculations, but need not, especially if the computer is short on memory. The best strategy is probably to experiment with explicitly requesting `multicore=TRUE` in functions that support it, to see if there is an increase in speed before setting the global option.

survey.use\_rcpp controls whether the new C++ code for standard errors is used (vs the old R code). The factory setting is TRUE and the only reason to use FALSE is for comparisons.

---

surveysummary

*Summary statistics for sample surveys*


---

## Description

Compute means, variances, ratios and totals for data from complex surveys.

## Usage

```
## S3 method for class 'survey.design'
svymean(x, design, na.rm=FALSE, deff=FALSE, influence=FALSE,...)
## S3 method for class 'survey.design2'
svymean(x, design, na.rm=FALSE, deff=FALSE, influence=FALSE,...)
## S3 method for class 'twophase'
svymean(x, design, na.rm=FALSE, deff=FALSE,...)
## S3 method for class 'svyrep.design'
svymean(x, design, na.rm=FALSE, rho=NULL,
  return.replicates=FALSE, deff=FALSE,...)
## S3 method for class 'survey.design'
svyvar(x, design, na.rm=FALSE,...)
## S3 method for class 'svyrep.design'
svyvar(x, design, na.rm=FALSE, rho=NULL,
  return.replicates=FALSE,..., estimate.only=FALSE)
## S3 method for class 'survey.design'
svytotal(x, design, na.rm=FALSE, deff=FALSE, influence=FALSE,...)
## S3 method for class 'survey.design2'
svytotal(x, design, na.rm=FALSE, deff=FALSE, influence=FALSE,...)
## S3 method for class 'twophase'
svytotal(x, design, na.rm=FALSE, deff=FALSE,...)
## S3 method for class 'svyrep.design'
svytotal(x, design, na.rm=FALSE, rho=NULL,
  return.replicates=FALSE, deff=FALSE,...)
## S3 method for class 'svystat'
coef(object,...)
## S3 method for class 'svrepstat'
coef(object,...)
## S3 method for class 'svystat'
vcov(object,...)
## S3 method for class 'svrepstat'
vcov(object,...)
## S3 method for class 'svystat'
confint(object, parm, level = 0.95, df = Inf,...)
## S3 method for class 'svrepstat'
confint(object, parm, level = 0.95, df = Inf,...)
```

```
cv(object,...)
deff(object, quietly=FALSE,...)
make.formula(names)
```

### Arguments

<code>x</code>	A formula, vector or matrix
<code>design</code>	<code>survey.design</code> or <code>svyrep.design</code> object
<code>na.rm</code>	Should cases with missing values be dropped?
<code>influence</code>	Should a matrix of influence functions be returned (primarily to support <a href="#">svyby</a> )
<code>rho</code>	parameter for Fay's variance estimator in a BRR design
<code>return.replicates</code>	Return the replicate means/totals?
<code>deff</code>	Return the design effect (see below)
<code>object</code>	The result of one of the other survey summary functions
<code>quietly</code>	Don't warn when there is no design effect computed
<code>estimate.only</code>	Don't compute standard errors (useful when <code>svyvar</code> is used to estimate the design effect)
<code>parm</code>	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
<code>level</code>	the confidence level required.
<code>df</code>	degrees of freedom for t-distribution in confidence interval, use <code>degf(design)</code> for number of PSUs minus number of strata
<code>...</code>	additional arguments to methods, not currently used
<code>names</code>	vector of character strings

### Details

These functions perform weighted estimation, with each observation being weighted by the inverse of its sampling probability. Except for the table functions, these also give precision estimates that incorporate the effects of stratification and clustering.

Factor variables are converted to sets of indicator variables for each category in computing means and totals. Combining this with the [interaction](#) function, allows crosstabulations. See [ftable.svystat](#) for formatting the output.

With `na.rm=TRUE`, all cases with missing data are removed. With `na.rm=FALSE` cases with missing data are not removed and so will produce missing results. When using replicate weights and `na.rm=FALSE` it may be useful to set `options(na.action="na.pass")`, otherwise all replicates with any missing results will be discarded.

The `svytotal` and `svreptotal` functions estimate a population total. Use `predict` on [svyratio](#) and [svyglm](#), to get ratio or regression estimates of totals.

`svyvar` estimates the population variance. The object returned includes the full matrix of estimated population variances and covariances, but by default only the diagonal elements are printed. To display the whole matrix use `as.matrix(v)` or `print(v, covariance=TRUE)`.

The design effect compares the variance of a mean or total to the variance from a study of the same size using simple random sampling without replacement. Note that the design effect will be incorrect if the weights have been rescaled so that they are not reciprocals of sampling probabilities. To obtain an estimate of the design effect comparing to simple random sampling with replacement, which does not have this requirement, use `deff="replace"`. This with-replacement design effect is the square of Kish's "deft".

The design effect for a subset of a design conditions on the size of the subset. That is, it compares the variance of the estimate to the variance of an estimate based on a simple random sample of the same size as the subset, taken from the subpopulation. So, for example, under stratified random sampling the design effect in a subset consisting of a single stratum will be 1.0.

The `cv` function computes the coefficient of variation of a statistic such as ratio, mean or total. The default method is for any object with methods for [SE](#) and `coef`.

`make.formula` makes a formula from a vector of names. This is useful because formulas as the best way to specify variables to the survey functions.

## Value

Objects of class "svystat" or "svrepstat", which are vectors with a "var" attribute giving the variance and a "statistic" attribute giving the name of the statistic.

These objects have methods for `vcov`, `SE`, `coef`, `confint`, `svycontrast`.

## Author(s)

Thomas Lumley

## See Also

[svydesign](#), [as.svrepdesign](#), [svrepdesign](#) for constructing design objects.

[degf](#) to extract degrees of freedom from a design.

[svyquantile](#) for quantiles

[ftable.svystat](#) for more attractive tables

[svyciprop](#) for more accurate confidence intervals for proportions near 0 or 1.

[svyttest](#) for comparing two means.

[svycontrast](#) for linear and nonlinear functions of estimates.

## Examples

```
data(api)

## one-stage cluster sample
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)

svymean(~api00, dclus1, deff=TRUE)
svymean(~factor(stype),dclus1)
svymean(~interaction(stype, comp.imp), dclus1)
svyquantile(~api00, dclus1, c(.25,.5,.75))
svytotal(~enroll, dclus1, deff=TRUE)
```

```

svyratio(~api.stu, ~enroll, dclus1)

v<-svyvar(~api00+api99, dclus1)
v
print(v, cov=TRUE)
as.matrix(v)

# replicate weights - jackknife (this is slower)
dstrat<-svydesign(id=~1, strata=~stype, weights=~pw,
  data=apistrat, fpc=~fpc)
jkstrat<-as.svrepdesign(dstrat)

svymean(~api00, jkstrat)
svymean(~factor(stype), jkstrat)
svyvar(~api00+api99, jkstrat)

svyquantile(~api00, jkstrat, c(.25,.5,.75))
svytotal(~enroll, jkstrat)
svyratio(~api.stu, ~enroll, jkstrat)

# coefficients of variation
cv(svytotal(~enroll, dstrat))
cv(svyratio(~api.stu, ~enroll, jkstrat))

# extracting information from the results
coef(svytotal(~enroll, dstrat))
vcov(svymean(~api00+api99, jkstrat))
SE(svymean(~enroll, dstrat))
confint(svymean(~api00+api00, dclus1))
confint(svymean(~api00+api00, dclus1), df=degf(dclus1))

# Design effect
svymean(~api00, dstrat, deff=TRUE)
svymean(~api00, dstrat, deff="replace")
svymean(~api00, jkstrat, deff=TRUE)
svymean(~api00, jkstrat, deff="replace")
(a<-svytotal(~enroll, dclus1, deff=TRUE))
deff(a)

## weights that are *already* calibrated to population size
sum(weights(dclus1))
nrow(apipop)
cdclus1<- svydesign(id=~dnum, weights=~pw, data=apiclus1,
  fpc=~fpc, calibrate.formula=~1)
SE(svymean(~enroll, dclus1))
## not equal to SE(mean)
SE(svytotal(~enroll, dclus1))/nrow(apipop)
## equal to SE(mean)
SE(svytotal(~enroll, cdclus1))/nrow(apipop)

```

svrepdesign

*Specify survey design with replicate weights***Description**

Some recent large-scale surveys specify replication weights rather than the sampling design (partly for privacy reasons). This function specifies the data structure for such a survey.

**Usage**

```
svrepdesign(variables , repweights , weights, data, degf=NULL,...)
## Default S3 method:
svrepdesign(variables = NULL, repweights = NULL, weights = NULL,
  data = NULL, degf=NULL, type = c("BRR", "Fay", "JK1", "JKn", "bootstrap",
    "ACS", "successive-difference", "JK2", "other"),
  combined.weights=TRUE, rho = NULL, bootstrap.average=NULL,
  scale=NULL, rscales=NULL, fpc=NULL, fpctype=c("fraction", "correction"),
  mse=getOption("survey.replicates.mse"),...)
## S3 method for class 'imputationList'
svrepdesign(variables=NULL,
  repweights, weights, data, degf=NULL,
  mse=getOption("survey.replicates.mse"),...)
## S3 method for class 'character'
svrepdesign(variables=NULL, repweights=NULL,
  weights=NULL, data=NULL, degf=NULL,
  type=c("BRR", "Fay", "JK1", "JKn", "bootstrap", "ACS", "successive-difference", "JK2", "other"),
  combined.weights=TRUE, rho=NULL, bootstrap.average=NULL, scale=NULL, rscales=NULL,
  fpc=NULL, fpctype=c("fraction", "correction"), mse=getOption("survey.replicates.mse"),
  dbtype="SQLite", dbname,...)

## S3 method for class 'svyrep.design'
image(x, ...,
  col=grey(seq(.5, 1, length=30)), type.=c("rep", "total"))
```

**Arguments**

<code>variables</code>	formula or data frame specifying variables to include in the design (default is all)
<code>repweights</code>	formula or data frame specifying replication weights, or character string specifying a regular expression that matches the names of the replication weight variables
<code>weights</code>	sampling weights
<code>data</code>	data frame to look up variables in formulas, or character string giving name of database table
<code>degf</code>	Design degrees of freedom; use NULL to have the function work this out for you

<code>type</code>	Type of replication weights
<code>combined.weights</code>	TRUE if the repweights already include the sampling weights. This is usually the case.
<code>rho</code>	Shrinkage factor for weights in Fay's method
<code>bootstrap.average</code>	For <code>type="bootstrap"</code> , if the bootstrap weights have been averaged, gives the number of iterations averaged over
<code>scale, rscales</code>	Scaling constant for variance, see Details below
<code>fpc, fpctype</code>	Finite population correction information
<code>mse</code>	If TRUE, compute variances based on sum of squares around the point estimate, rather than the mean of the replicates
<code>dbname</code>	name of database, passed to <code>DBI::dbConnect()</code>
<code>dbtype</code>	Database driver: see Details
<code>x</code>	survey design with replicate weights
<code>...</code>	Other arguments to <a href="#">image</a>
<code>col</code>	Colors
<code>type.</code>	"rep" for only the replicate weights, "total" for the replicate and sampling weights combined.

## Details

In the BRR method, the dataset is split into halves, and the difference between halves is used to estimate the variance. In Fay's method, rather than removing observations from half the sample they are given weight  $\rho$  in one half-sample and  $2-\rho$  in the other. The ideal BRR analysis is restricted to a design where each stratum has two PSUs, however, it has been used in a much wider class of surveys. The `scale` and `rscales` arguments will be ignored (with a warning) if they are specified.

The JK1 and JK<sub>n</sub> types are both jackknife estimators deleting one cluster at a time. JK<sub>n</sub> is designed for stratified and JK1 for unstratified designs.

The successive-difference weights in the American Community Survey automatically use `scale = 4/ncol(repweights)` and `rscales=rep(1, ncol(repweights))`. This can be specified as `type="ACS"` or `type="successive-difference"`. The `scale` and `rscales` arguments will be ignored (with a warning) if they are specified.

JK2 weights (`type="JK2"`), as in the California Health Interview Survey, automatically use `scale=1`, `rscales=rep(1, ncol(repweights))`. The `scale` and `rscales` arguments will be ignored (with a warning) if they are specified.

Averaged bootstrap weights ("mean bootstrap") are used for some surveys from Statistics Canada. Yee et al (1999) describe their construction and use for one such survey.

The variance is computed as the sum of squared deviations of the replicates from their mean. This may be rescaled: `scale` is an overall multiplier and `rscales` is a vector of replicate-specific multipliers for the squared deviations. That is, `rscales` should have one entry for each column of `repweights`. If thereplication weights incorporate the sampling weights (`combined.weights=TRUE`) or for `type="other"` these must be specified, otherwise they can be guessed from the weights.

A finite population correction may be specified for `type="other"`, `type="JK1"` and `type="JKn"`. `fpc` must be a vector with one entry for each replicate. To specify sampling fractions use `fpctype="fraction"` and to specify the correction directly use `fpctype="correction"`

The design degrees of freedom are returned by `degf`. By default they are computed from the numerical rank of the repweights. This is slow for very large data sets and you can specify a value instead.

`repweights` may be a character string giving a regular expression for the replicate weight variables. For example, in the California Health Interview Survey public-use data, the sampling weights are `"rakedw0"` and the replicate weights are `"rakedw1"` to `"rakedw80"`. The regular expression `"rakedw[1-9]"` matches the replicate weight variables (and not the sampling weight variable).

`data` may be a character string giving the name of a table or view in a relational database that can be accessed through the DBI interface. For DBI interfaces `dbtype` should be the name of the database driver and `dbname` should be the name by which the driver identifies the specific database (eg file name for SQLite).

The appropriate database interface package must already be loaded (eg `RSQLite` for SQLite). The survey design object will contain the replicate weights, but actual variables will be loaded from the database only as needed. Use `close` to close the database connection and `open` to reopen the connection, eg, after loading a saved object.

The database interface does not attempt to modify the underlying database and so can be used with read-only permissions on the database.

To generate your own replicate weights either use `as.svrepdesign` on a `survey.design` object, or see `brrweights`, `bootweights`, `jk1weights` and `jkweights`

The `model.frame` method extracts the observed data.

## Value

Object of class `svyrep.design`, with methods for `print`, `summary`, `weights`, `image`.

## Note

To use replication-weight analyses on a survey specified by sampling design, use `as.svrepdesign` to convert it.

## References

Levy and Lemeshow. "Sampling of Populations". Wiley.

Shao and Tu. "The Jackknife and Bootstrap." Springer.

Yee et al (1999). Bootstrat Variance Estimation for the National Population Health Survey. Proceedings of the ASA Survey Research Methodology Section. [https://web.archive.org/web/20151110170959/http://www.amstat.org/sections/SRMS/Proceedings/papers/1999\\_136.pdf](https://web.archive.org/web/20151110170959/http://www.amstat.org/sections/SRMS/Proceedings/papers/1999_136.pdf)

## See Also

`as.svrepdesign`, `svydesign`, `brrweights`, `bootweights`

## Examples

```
data(scd)
# use BRR replicate weights from Levy and Lemeshow
repweights<-2*cbind(c(1,0,1,0,1,0), c(1,0,0,1,0,1), c(0,1,1,0,0,1),
c(0,1,0,1,1,0))
scdrep<-svrepdesign(data=scd, type="BRR", repweights=repweights, combined.weights=FALSE)
svyratio(~alive, ~arrests, scdrep)

## Not run:
## Needs RSQLite
library(RSQLite)
db_rclus1<-svrepdesign(weights=~pw, repweights="wt[1-9]+", type="JK1", scale=(1-15/757)*14/15,
data="apiclus1rep", dbtype="SQLite", dbname=system.file("api.db",package="survey"), combined=FALSE)
svymean(~api00+api99,db_rclus1)

summary(db_rclus1)

## closing and re-opening a connection
close(db_rclus1)
db_rclus1
try(svymean(~api00+api99,db_rclus1))
db_rclus1<-open(db_rclus1)
svymean(~api00+api99,db_rclus1)

## End(Not run)
```

---

svrVar

---

*Compute variance from replicates*


---

## Description

Compute an appropriately scaled empirical variance estimate from replicates. The `mse` argument specifies whether the sums of squares should be centered at the point estimate (`mse=TRUE`) or the mean of the replicates. It is usually taken from the `mse` component of the design object.

## Usage

```
svrVar(thetas, scale, rscales, na.action=getOption("na.action"),
mse=getOption("survey.replicates.mse"),coef)
```

## Arguments

<code>thetas</code>	matrix whose rows are replicates (or a vector of replicates)
<code>scale</code>	Overall scaling factor

<code>rscales</code>	Scaling factor for each squared deviation
<code>na.action</code>	How to handle replicates where the statistic could not be estimated
<code>mse</code>	if TRUE, center at the point estimated, if FALSE center at the mean of the replicates
<code>coef</code>	The point estimate, required only if <code>mse==TRUE</code>

**Value**

covariance matrix.

**See Also**

[svrepdesign](#), [as.svrepdesign](#), [brrweights](#), [jk1weights](#), [jknweights](#)

---

svy.varcoef

*Sandwich variance estimator for glms*


---

**Description**

Computes the sandwich variance estimator for a generalised linear model fitted to data from a complex sample survey. Designed to be used internally by [svyglm](#).

**Usage**

```
svy.varcoef(glm.object, design)
```

**Arguments**

<code>glm.object</code>	A <a href="#">glm</a> object
<code>design</code>	A <code>survey.design</code> object

**Value**

A variance matrix

**Author(s)**

Thomas Lumley

**See Also**

[svyglm](#), [svydesign](#), [svyCprod](#)

svyby

*Survey statistics on subsets***Description**

Compute survey statistics on subsets of a survey defined by factors.

**Usage**

```
svyby(formula, by ,design,...)
## Default S3 method:
svyby(formula, by, design, FUN, ..., deff=FALSE,keep.var = TRUE,
keep.names = TRUE,verbose=FALSE, vartype=c("se","ci","ci","cv","cvpct","var"),
drop.empty.groups=TRUE, covmat=FALSE, return.replicates=FALSE,
na.rm.by=FALSE, na.rm.all=FALSE, stringsAsFactors=TRUE,
multicore=getOption("survey.multicore"))
## S3 method for class 'survey.design2'
svyby(formula, by, design, FUN, ..., deff=FALSE,keep.var = TRUE,
keep.names = TRUE,verbose=FALSE, vartype=c("se","ci","ci","cv","cvpct","var"),
drop.empty.groups=TRUE, covmat=FALSE, influence=covmat,
na.rm.by=FALSE, na.rm.all=FALSE, stringsAsFactors=TRUE,
multicore=getOption("survey.multicore"))

## S3 method for class 'svyby'
SE(object,...)
## S3 method for class 'svyby'
deff(object,...)
## S3 method for class 'svyby'
coef(object,...)
## S3 method for class 'svyby'
confint(object, parm, level = 0.95,df =Inf,...)
unwtd.count(x, design, ...)
svybys(formula, bys, design, FUN, ...)
```

**Arguments**

formula, x	A formula specifying the variables to pass to FUN (or a matrix, data frame, or vector)
by	A formula specifying factors that define subsets, or a list of factors.
design	A svydesign or svrepdesign object
FUN	A function taking a formula and survey design object as its first two arguments.
...	Other arguments to FUN. NOTE: if any of the names of these are partial matches to formula,by, or design, you must specify the formula,by, or design argument by name, not just by position.
deff	Request a design effect from FUN

<code>keep.var</code>	If FUN returns a <code>svystat</code> object, extract standard errors from it
<code>keep.names</code>	Define row names based on the subsets
<code>verbose</code>	If TRUE, print a label for each subset as it is processed.
<code>vartype</code>	Report variability as one or more of standard error, confidence interval, coefficient of variation, percent coefficient of variation, or variance
<code>drop.empty.groups</code>	If FALSE, report NA for empty groups, if TRUE drop them from the output
<code>na.rm.by</code>	If true, omit groups defined by NA values of the by variables
<code>.</code>	
<code>na.rm.all</code>	If true, check for groups with no non-missing observations for variables defined by formula and treat these groups as empty. Doesn't make much sense without <code>na.rm=TRUE</code>
<code>covmat</code>	If TRUE, compute covariances between estimates for different subsets. Allows <a href="#">svycontrast</a> to be used on output. Requires that FUN supports either <code>return.replicates=TRUE</code> or <code>influence=TRUE</code>
<code>return.replicates</code>	Only for replicate-weight designs. If TRUE, return all the replicates as the "replicates" attribute of the result
<code>influence</code>	Return the influence functions of the result
<code>multicore</code>	Use multicore package to distribute subsets over multiple processors?
<code>stringsAsFactors</code>	Convert any string variables in formula to factors before calling FUN, so that the factor levels will be the same in all groups (See Note below). Potentially slow.
<code>parm</code>	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
<code>level</code>	the confidence level required.
<code>df</code>	degrees of freedom for t-distribution in confidence interval, use <code>degf(design)</code> for number of PSUs minus number of strata
<code>object</code>	An object of class "svyby"
<code>bys</code>	one-sided formula with each term specifying a grouping (rather than being combined to give a grouping)

## Details

The variance type "ci" asks for confidence intervals, which are produced by `confint`. In some cases additional options to FUN will be needed to produce confidence intervals, for example, `svyquantile` needs `ci=TRUE` or `keep.var=FALSE`.

`unwtd.count` is designed to be passed to `svyby` to report the number of non-missing observations in each subset. Observations with exactly zero weight will also be counted as missing, since that's how subsets are implemented for some designs.

Parallel processing with `multicore=TRUE` is useful only for fairly large problems and on computers with sufficient memory. The `multicore` package is incompatible with some GUIs, although the Mac Aqua GUI appears to be safe.

The variant `svybys` creates a separate table for each term in `bys` rather than creating a joint table.

**Value**

An object of class "svyby": a data frame showing the factors and the results of FUN.

For `unwtd.count`, the unweighted number of non-missing observations in the data matrix specified by `x` for the design.

**Note**

The function works by making a lot of calls of the form `FUN(formula, subset(design, by==i))`, where `formula` is re-evaluated in each subset, so it is unwise to use data-dependent terms in `formula`. In particular, `svyby(~factor(a), ~b, design=d, svymean)`, will create factor variables whose levels are only those values of `a` present in each subset. If `a` is a character variable then `svyby(~a, ~b, design=d, svymean)` creates factor variables implicitly and so has the same problem. Either use [update.survey.design](#) to add variables to the design object instead or specify the levels explicitly in the call to `factor`. The `stringsAsFactors=TRUE` option converts all character variables to factors, which can be slow, set it to `FALSE` if you have predefined factors where necessary.

**Note**

Asking for a design effect (`deff=TRUE`) from a function that does not produce one will cause an error or incorrect formatting of the output. The same will occur with `keep.var=TRUE` if the function does not compute a standard error.

**See Also**

[svytable](#) and [ftable.svystat](#) for contingency tables, [ftable.svyby](#) for pretty-printing of `svyby`

**Examples**

```
data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)

svyby(~api99, ~stype, dclus1, svymean)
svyby(~api99, ~stype, dclus1, svyquantile, quantiles=0.5, ci=TRUE, vartype="ci")
## without ci=TRUE svyquantile does not compute standard errors
svyby(~api99, ~stype, dclus1, svyquantile, quantiles=0.5, keep.var=FALSE)
svyby(~api99, list(school.type=apiclus1$stype), dclus1, svymean)
svyby(~api99+api00, ~stype, dclus1, svymean, deff=TRUE, vartype="ci")
svyby(~api99+api00, ~stype+sch.wide, dclus1, svymean, keep.var=FALSE)
## report raw number of observations
svyby(~api99+api00, ~stype+sch.wide, dclus1, unwtd.count, keep.var=FALSE)

rclus1<-as.svrepdesign(dclus1)

svyby(~api99, ~stype, rclus1, svymean)
svyby(~api99, ~stype, rclus1, svyquantile, quantiles=0.5)
svyby(~api99, list(school.type=apiclus1$stype), rclus1, svymean, vartype="cv")
svyby(~enroll, ~stype, rclus1, svytotal, deff=TRUE)
svyby(~api99+api00, ~stype+sch.wide, rclus1, svymean, keep.var=FALSE)
##report raw number of observations
```

```

svyby(~api99+api00, ~stype+sch.wide, rclus1, unwtd.count, keep.var=FALSE)

## comparing subgroups using covmat=TRUE
mns<-svyby(~api99, ~stype, rclus1, svymean,covmat=TRUE)
vcov(mns)
svycontrast(mns, c(E = 1, M = -1))

str(svyby(~api99, ~stype, rclus1, svymean,return.replicates=TRUE))

tots<-svyby(~enroll, ~stype, dclus1, svytotals,covmat=TRUE)
vcov(tots)
svycontrast(tots, quote(E/H))

## comparing subgroups uses the delta method unless replicates are present
meanlogs<-svyby(~log(enroll),~stype,svymean, design=rclus1,covmat=TRUE)
svycontrast(meanlogs, quote(exp(E-H)))
meanlogs<-svyby(~log(enroll),~stype,svymean, design=rclus1,covmat=TRUE,return.replicates=TRUE)
svycontrast(meanlogs, quote(exp(E-H)))

## extractor functions
(a<-svyby(~enroll, ~stype, rclus1, svytotals, deff=TRUE, verbose=TRUE,
  vartype=c("se","cv","cvpct","var"))
deff(a)
SE(a)
cv(a)
coef(a)
confint(a, df=degf(rclus1))

## ratio estimates
svyby(~api.stu, by=~stype, denominator=~enroll, design=dclus1, svyratio)

ratios<-svyby(~api.stu, by=~stype, denominator=~enroll, design=dclus1, svyratio,covmat=TRUE)
vcov(ratios)

## empty groups
svyby(~api00,~comp.imp+sch.wide,design=dclus1,svymean)
svyby(~api00,~comp.imp+sch.wide,design=dclus1,svymean,drop.empty.groups=FALSE)

## Multiple tables
svybys(~api00,~comp.imp+sch.wide,design=dclus1,svymean)

```

## Description

Estimates the population cumulative distribution function for specified variables. In contrast to [svyquantile](#), this does not do any interpolation: the result is a right-continuous step function.

## Usage

```
svycdf(formula, design, na.rm = TRUE, ...)
## S3 method for class 'svycdf'
print(x, ...)
## S3 method for class 'svycdf'
plot(x, xlab=NULL, ...)
```

## Arguments

formula	one-sided formula giving variables from the design object
design	survey design object
na.rm	remove missing data (case-wise deletion)?
...	other arguments to <a href="#">plot.stepfun</a>
x	object of class svycdf
xlab	a vector of x-axis labels or NULL for the default labels

## Value

An object of class svycdf, which is a list of step functions (of class [stepfun](#))

## See Also

[svyquantile](#), [svyhist](#), [plot.stepfun](#)

## Examples

```
data(api)
dstrat <- svydesign(id = ~1, strata = ~stype, weights = ~pw, data = apistrat,
  fpc = ~fpc)
cdf.est<-svycdf(~enroll+api00+api99, dstrat)
cdf.est
## function
cdf.est[[1]]
## evaluate the function
cdf.est[[1]](800)
cdf.est[[2]](800)

## compare to population and sample CDFs.
opar<-par(mfrow=c(2,1))
cdf.pop<-ecdf(apipop$enroll)
cdf.samp<-ecdf(apistrat$enroll)
plot(cdf.pop,main="Population vs sample", xlab="Enrollment")
lines(cdf.samp,col.points="red")
```

```
plot(cdf.pop, main="Population vs estimate", xlab="Enrollment")
lines(cdf.est[[1]],col.points="red")

par(opar)
```

svyciprop

*Confidence intervals for proportions***Description**

Computes confidence intervals for proportions using methods that may be more accurate near 0 and 1 than simply using `confint(svymean())`.

**Usage**

```
svyciprop(formula, design, method = c("logit", "likelihood", "asin", "beta",
"mean", "xlogit"), level = 0.95, df=degf(design),...)
```

**Arguments**

<code>formula</code>	Model formula specifying a single binary variable
<code>design</code>	survey design object
<code>method</code>	See Details below. Partial matching is done on the argument.
<code>level</code>	Confidence level for interval
<code>df</code>	denominator degrees of freedom, for all methods except "beta". Use Inf for confidence intervals based on a Normal distribution, and for "likelihood" and "logit" use NULL for the default method in glms (currently <code>degf(design)-1</code> , but this may be improved in the future)
<code>...</code>	For "mean" and "asin", this is passed to <code>confint.svystat</code>

**Details**

The "logit" method fits a logistic regression model and computes a Wald-type interval on the log-odds scale, which is then transformed to the probability scale.

The "likelihood" method uses the (Rao-Scott) scaled chi-squared distribution for the loglikelihood from a binomial distribution.

The "asin" method uses the variance-stabilising transformation for the binomial distribution, the arcsine square root, and then back-transforms the interval to the probability scale

The "beta" method uses the incomplete beta function as in `binom.test`, with an effective sample size based on the estimated variance of the proportion. (Korn and Graubard, 1998)

The "xlogit" method uses a logit transformation of the mean and then back-transforms to the probability scale. This appears to be the method used by SUDAAN and SPSS COMPLEX SAMPLES.

The "mean" method is a Wald-type interval on the probability scale, the same as `confint(svymean())`

All methods undercover for probabilities close enough to zero or one, but "beta", "likelihood", "logit", and "logit" are noticeably better than the other two. None of the methods will work when the observed proportion is exactly 0 or 1.

The `confint` method extracts the confidence interval; the `vcov` and `SE` methods just report the variance or standard error of the mean.

## Value

The point estimate of the proportion, with the confidence interval as an attribute

## References

Rao, JNK, Scott, AJ (1984) "On Chi-squared Tests For Multiway Contingency Tables with Proportions Estimated From Survey Data" *Annals of Statistics* 12:46-60.

Korn EL, Graubard BI. (1998) Confidence Intervals For Proportions With Small Expected Number of Positive Counts Estimated From Survey Data. *Survey Methodology* 23:193-201.

## See Also

[svymean](#), [yrbs](#)

## Examples

```
data(api)
dclus1<-svydesign(id=~dnum, fpc=~fpc, data=apiclus1)

svyciprop(~I(ell==0), dclus1, method="li")
svyciprop(~I(ell==0), dclus1, method="lo")
svyciprop(~I(ell==0), dclus1, method="as")
svyciprop(~I(ell==0), dclus1, method="be")
svyciprop(~I(ell==0), dclus1, method="me")
svyciprop(~I(ell==0), dclus1, method="xl")

## reproduces Stata svy: mean
svyciprop(~I(ell==0), dclus1, method="me", df=degf(dclus1))
## reproduces Stata svy: prop
svyciprop(~I(ell==0), dclus1, method="lo", df=degf(dclus1))

rclus1<-as.svrepdesign(dclus1)
svyciprop(~I(emer==0), rclus1, method="li")
svyciprop(~I(emer==0), rclus1, method="lo")
svyciprop(~I(emer==0), rclus1, method="as")
svyciprop(~I(emer==0), rclus1, method="be")
svyciprop(~I(emer==0), rclus1, method="me")
```

---

svycontrast*Linear and nonlinear contrasts of survey statistics*

---

## Description

Computes linear or nonlinear contrasts of estimates produced by survey functions (or any object with `coef` and `vcov` methods).

## Usage

```
svycontrast(stat, contrasts, add=FALSE, ...)
```

## Arguments

<code>stat</code>	object of class <code>svrepstat</code> or <code>svystat</code>
<code>contrasts</code>	A vector or list of vectors of coefficients, or a call or list of calls
<code>add</code>	keep all the coefficients of the input in the output?
<code>...</code>	For future expansion

## Details

If `contrasts` is a list, the element names are used as names for the returned statistics.

If an element of `contrasts` is shorter than `coef(stat)` and has names, the names are used to match up the vectors and the remaining elements of `contrasts` are assumed to be zero. If the names are not legal variable names (eg `0.1`) they must be quoted (eg `"0.1"`)

If `contrasts` is a "call" or list of "call"s, and `stat` is a `svrepstat` object including replicates, the replicates are transformed and used to compute the variance. If `stat` is a `svystat` object or a `svrepstat` object without replicates, the delta-method is used to compute variances, and the calls must use only functions that `deriv` knows how to differentiate. If the names are not legal variable names they must be quoted with backticks (eg ``0.1``).

If `stats` is a `svyvar` object, the estimates are elements of a matrix and the names are the row and column names pasted together with a colon.

## Value

Object of class `svrepstat` or `svystat` or `svyvar`

## See Also

[regTermTest](#), [svyglm](#)

## Examples

```

data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)

a <- svytotal(~api00+enroll+api99, dclus1)
svycontrast(a, list(avg=c(0.5,0,0.5), diff=c(1,0,-1)))
## if contrast vectors have names, zeroes may be omitted
svycontrast(a, list(avg=c(api00=0.5,api99=0.5), diff=c(api00=1,api99=-1)))

## nonlinear contrasts
svycontrast(a, quote(api00/api99))
svyratio(~api00, ~api99, dclus1)

## Example: standardised skewness coefficient
moments<-svymean(~I(api00^3)+I(api00^2)+I(api00), dclus1)
svycontrast(moments,
quote((`I(api00^3)`-3*`I(api00^2)`*`I(api00)`+ 3*`I(api00)`*`I(api00)`^2-`I(api00)`^3)/
      (`I(api00^2)`-`I(api00)`^2)^1.5))

## Example: geometric means
## using delta method
meanlogs <- svymean(~log(api00)+log(api99), dclus1)
svycontrast(meanlogs,
  list(api00=quote(exp(`log(api00)`)), api99=quote(exp(`log(api99)`))))

## using delta method
rclus1<-as.svrepdesign(dclus1)
meanlogs <- svymean(~log(api00)+log(api99), rclus1)
svycontrast(meanlogs,
  list(api00=quote(exp(`log(api00)`)),
    api99=quote(exp(`log(api99)`))))

## why is add=TRUE useful?

(totals<-svyby(~enroll,~stype,design=dclus1,svytotal,covmat=TRUE))
totals1<-svycontrast(totals, list(total=c(1,1,1)), add=TRUE)

svycontrast(totals1, list(quote(E/total), quote(H/total), quote(M/total)))

totals2<-svycontrast(totals, list(total=quote(E+H+M)), add=TRUE)
all.equal(as.matrix(totals1),as.matrix(totals2))

## more complicated svyby
means <- svyby(~api00+api99, ~stype+sch.wide, design=dclus1, svymean,covmat=TRUE)
svycontrast(means, quote(`E.No:api00`-`E.No:api99`))
svycontrast(means, quote(`E.No:api00`/`E.No:api99`))

## transforming replicates
meanlogs_r <- svymean(~log(api00)+log(api99), rclus1, return.replicates=TRUE)
svycontrast(meanlogs_r,
  list(api00=quote(exp(`log(api00)`)), api99=quote(exp(`log(api99)`))))

```

```
## converting covariances to correlations
vmat <-svyvar(~api00+ell,dclus1)
print(vmat,cov=TRUE)
cov2cor(as.matrix(vmat))[1,2]
svycontrast(vmat, quote(`api00:ell`/sqrt(`api00:api00`*`ell:ell`)))
```

svycoplot

*Conditioning plots of survey data***Description**

Draws conditioned scatterplots ('Trellis' plots) of survey data using hexagonal binning or transparency.

**Usage**

```
svycoplot(formula, design, style = c("hexbin", "transparent"), basecol =
"black", alpha = c(0, 0.8),hexscale=c("relative","absolute"), ...)
```

**Arguments**

formula	A graph formula suitable for <a href="#">xyplot</a>
design	A survey design object
style	Hexagonal binning or transparent color?
basecol	The fully opaque 'base' color for creating transparent colors. This may also be a function; see <a href="#">svyplot</a> for details
alpha	Minimum and maximum opacity
hexscale	Scale hexagons separate for each panel (relative) or across all panels (absolute)
...	Other arguments passed to <a href="#">grid.hexagons</a> or <a href="#">xyplot</a>

**Value**

An object of class `trellis`

**Note**

As with all 'Trellis' graphs, this function creates an object but does not draw the graph. When used inside a function or non-interactively you need to `print()` the result to create the graph.

**See Also**

[svyplot](#)

## Examples

```
data(api)
dclus2<-svydesign(id=~dnum+snum, weights=~pw,
                 data=apiclus2, fpc=~fpc1+fpc2)

svycoplot(api00~api99|sch.wide*comp.imp, design=dclus2, style="hexbin")
svycoplot(api00~api99|sch.wide*comp.imp, design=dclus2, style="hexbin", hexscale="absolute")

svycoplot(api00~api99|sch.wide, design=dclus2, style="trans")

svycoplot(api00~meals|stype,design=dclus2,
          style="transparent",
          basecol=function(d) c("darkred","purple","forestgreen")[as.numeric(d$stype)],
          alpha=c(0,1))
```

---

svycoxph

*Survey-weighted Cox models.*


---

## Description

Fit a proportional hazards model to data from a complex survey design.

## Usage

```
svycoxph(formula, design, subset=NULL, rescale=TRUE, ...)
## S3 method for class 'svycoxph'
predict(object, newdata, se=FALSE,
        type=c("lp", "risk", "terms", "curve"),...)
## S3 method for class 'svycoxph'
AIC(object, ..., k = 2)
```

## Arguments

formula	Model formula. Any <code>cluster()</code> terms will be ignored.
design	survey.design object. Must contain all variables in the formula
subset	Expression to select a subpopulation
rescale	Rescale weights to improve numerical stability
object	A <code>svycoxph</code> object
newdata	New data for prediction
se	Compute standard errors? This takes a lot of memory for <code>type="curve"</code>
type	"curve" does predicted survival curves. The other values are passed to <code>predict.coxph()</code>
...	For AIC, more models to compare the AIC of. For <code>svycoxph</code> , other arguments passed to <code>coxph</code> .
k	The penalty per parameter that would be used under independent sampling: AIC has <code>k=2</code>

## Details

The main difference between `svycoxph` function and the `robust=TRUE` option to `coxph` in the `survival` package is that this function accounts for the reduction in variance from stratified sampling and the increase in variance from having only a small number of clusters.

Note that `strata` terms in the model formula describe subsets that have a separate baseline hazard function and need not have anything to do with the stratification of the sampling.

The AIC method uses the same approach as `AIC.svyglm`, though the relevance of the criterion this optimises is a bit less clear than for generalised linear models.

The standard errors for predicted survival curves are available only by linearization, not by replicate weights (at the moment). Use `withReplicates` to get standard errors with replicate weights. Predicted survival curves are not available for stratified Cox models.

The standard errors use the delta-method approach of Williams (1995) for the Nelson-Aalen estimator, modified to handle the Cox model following Tsiatis (1981). The standard errors agree closely with `survfit.coxph` for independent sampling when the model fits well, but are larger when the model fits poorly. I believe the standard errors are equivalent to those of Lin (2000), but I don't know of any implementation that would allow a check.

## Value

An object of class `svycoxph` for `svycoxph`, an object of class `svykm` or `svykmList` for `predict(, type="curve")`.

## Warning

The standard error calculation for survival curves uses memory proportional to the sample size times the square of the number of events.

## Author(s)

Thomas Lumley

## References

- Binder DA. (1992) Fitting Cox's proportional hazards models from survey data. *Biometrika* 79: 139-147
- Lin D-Y (2000) On fitting Cox's proportional hazards model to survey data. *Biometrika* 87: 37-47
- Tsiatis AA (1981) A Large Sample Study of Cox's Regression Model. *Annals of Statistics* 9(1) 93-108
- Williams RL (1995) "Product-Limit Survival Functions with Correlated Survival Times" *Lifetime Data Analysis* 1: 171-186

## See Also

`coxph`, `predict.coxph`

`svykm` for estimation of Kaplan-Meier survival curves and for methods that operate on survival curves.

`regTermTest` for Wald and (Rao-Scott) likelihood ratio tests for one or more parameters.

## Examples

```
## Somewhat unrealistic example of nonresponse bias.
data(pbc, package="survival")

pbc$randomized<-with(pbc, !is.na(trt) & trt>0)
biasmodel<-glm(randomized~age*edema,data=pbc,family=binomial)
pbc$randprob<-fitted(biasmodel)
if (is.null(pbc$albumin)) pbc$albumin<-pbc$alb ##pre2.9.0

dpbc<-svydesign(id=~1, prob=~randprob, strata=~edema, data=subset(pbc,randomized))
rpbc<-as.svrepdesign(dpbc)

(model<-svycoxph(Surv(time,status>0)~log(bili)+protime+albumin,design=dpbc))

svycoxph(Surv(time,status>0)~log(bili)+protime+albumin,design=rpbc)

s<-predict(model,se=TRUE, type="curve",
  newdata=data.frame(bili=c(3,9), protime=c(10,10), albumin=c(3.5,3.5)))
plot(s[[1]],ci=TRUE,col="sienna")
lines(s[[2]], ci=TRUE,col="royalblue")
quantile(s[[1]], ci=TRUE)
confint(s[[2]], parm=365*(1:5))
```

---

svyCprod

*Computations for survey variances*


---

## Description

Computes the sum of products needed for the variance of survey sample estimators. `svyCprod` is used for survey design objects from before version 2.9, `onestage` is called by `svyrecvar` for post-2.9 design objects.

## Usage

```
svyCprod(x, strata, psu, fpc, nPSU, certainty=NULL, postStrata=NULL,
  lonely.psu=getOption("survey.lonely.psu"))
onestage(x, strata, clusters, nPSU, fpc,
  lonely.psu=getOption("survey.lonely.psu"), stage=0, cal)
```

## Arguments

<code>x</code>	A vector or matrix
<code>strata</code>	A vector of stratum indicators (may be NULL for <code>svyCprod</code> )
<code>psu</code>	A vector of cluster indicators (may be NULL)
<code>clusters</code>	A vector of cluster indicators
<code>fpc</code>	A data frame ( <code>svyCprod</code> ) or vector ( <code>onestage</code> ) of population stratum sizes, or NULL

nPSU	Table (svyprod) or vector (onestage) of original sample stratum sizes (or NULL)
certainty	logical vector with stratum names as names. If TRUE and that stratum has a single PSU it is a certainty PSU
postStrata	Post-stratification variables
lonely.psu	One of "remove", "adjust", "fail", "certainty", "average". See Details below
stage	Used internally to track the depth of recursion
cal	Used to pass calibration information at stages below the population

## Details

The observations for each cluster are added, then centered within each stratum and the outer product is taken of the row vector resulting for each cluster. This is added within strata, multiplied by a degrees-of-freedom correction and by a finite population correction (if supplied) and added across strata.

If there are fewer clusters (PSUs) in a stratum than in the original design extra rows of zeroes are added to `x` to allow the correct subpopulation variance to be computed.

See [postStratify](#) for information about post-stratification adjustments.

The variance formula gives 0/0 if a stratum contains only one sampling unit. If the `certainty` argument specifies that this is a PSU sampled with probability 1 (a "certainty" PSU) then it does not contribute to the variance (this is correct only when there is no subsampling within the PSU – otherwise it should be defined as a pseudo-stratum). If `certainty` is FALSE for this stratum or is not supplied the result depends on `lonely.psu`.

The options are "fail" to give an error, "remove" or "certainty" to give a variance contribution of 0 for the stratum, "adjust" to center the stratum at the grand mean rather than the stratum mean, and "average" to assign strata with one PSU the average variance contribution from strata with more than one PSU. The choice is controlled by setting `options(survey.lonely.psu)`. If this is not done the factory default is "fail". Using "adjust" is conservative, and it would often be better to combine strata in some intelligent way. The properties of "average" have not been investigated thoroughly, but it may be useful when the lonely PSUs are due to a few strata having PSUs missing completely at random.

The "remove" and "certainty" options give the same result, but "certainty" is intended for situations where there is only one PSU in the population stratum, which is sampled with certainty (also called 'self-representing' PSUs or strata). With "certainty" no warning is generated for strata with only one PSU. Ordinarily, `svydesign` will detect certainty PSUs, making this option unnecessary.

For strata with a single PSU in a subset (domain) the variance formula gives a value that is well-defined and positive, but not typically correct. If `options("survey.adjust.domain.lonely")` is TRUE and `options("survey.lonely.psu")` is "adjust" or "average", and no post-stratification or G-calibration has been done, strata with a single PSU in a subset will be treated like those with a single PSU in the sample. I am not aware of any theoretical study of this procedure, but it should at least be conservative.

## Value

A covariance matrix

**Author(s)**

Thomas Lumley

**References**

Binder, David A. (1983). On the variances of asymptotically normal estimators from complex surveys. *International Statistical Review*, 51, 279- 292.

**See Also**

[svydesign](#), [svyrecvar](#), [surveyoptions](#), [postStratify](#)

---

svycralpha

*Cronbach's alpha*


---

**Description**

Compute Cronbach's alpha coefficient of reliability from survey data. The formula is equation (2) of Cronbach (1951) only with design-based estimates of the variances.

**Usage**

```
svycralpha(formula, design, na.rm = FALSE)
```

**Arguments**

formula	One-sided formula giving the variables that make up the total score
design	survey design object
na.rm	TRUE to remove missing values

**Value**

A number

**References**

Cronbach LJ (1951). "Coefficient alpha and the internal structure of tests". *Psychometrika*. 16 (3): 297-334. doi:10.1007/bf02310555.

**Examples**

```
data(api)
dstrat<-svydesign(id = ~1, strata = ~stype, weights = ~pw, data = apistrat,
  fpc = ~fpc)
svycralpha(~ell+mobility+avg.ed+emer+meals, dstrat)
```

svydesign

*Survey sample analysis.***Description**

Specify a complex survey design.

**Usage**

```
svydesign(ids, probs=NULL, strata = NULL, variables = NULL, fpc=NULL,
data = NULL, nest = FALSE, check.strata = !nest, weights=NULL,pps=FALSE,...)
## Default S3 method:
svydesign(ids, probs=NULL, strata = NULL, variables = NULL,
  fpc=NULL,data = NULL, nest = FALSE, check.strata = !nest, weights=NULL,
  pps=FALSE,calibrate.formula=NULL,variance=c("HT","YG"),...)
## S3 method for class 'imputationList'
svydesign(ids, probs = NULL, strata = NULL, variables = NULL,
  fpc = NULL, data, nest = FALSE, check.strata = !nest, weights = NULL, pps=FALSE,
  calibrate.formula=NULL,...)
## S3 method for class 'character'
svydesign(ids, probs = NULL, strata = NULL, variables = NULL,
  fpc = NULL, data, nest = FALSE, check.strata = !nest, weights = NULL, pps=FALSE,
  calibrate.formula=NULL,dbtype = "SQLite", dbname, ...)
```

**Arguments**

ids	Formula or data frame specifying cluster ids from largest level to smallest level, ~0 or ~1 is a formula for no clusters.
probs	Formula or data frame specifying cluster sampling probabilities
strata	Formula or vector specifying strata, use NULL for no strata
variables	Formula or data frame specifying the variables measured in the survey. If NULL, the data argument is used.
fpc	Finite population correction: see Details below
weights	Formula or vector specifying sampling weights as an alternative to prob
data	Data frame to look up variables in the formula arguments, or database table name, or imputationList object, see below
nest	If TRUE, relabel cluster ids to enforce nesting within strata
check.strata	If TRUE, check that clusters are nested in strata
.	
pps	"brewer" to use Brewer's approximation for PPS sampling without replacement. "overton" to use Overton's approximation. An object of class <a href="#">HR</a> to use the Hartley-Rao approximation. An object of class <a href="#">ppsmat</a> to use the Horvitz-Thompson estimator.

<code>calibrate.formula</code>	model formula specifying how the weights are <i>*already*</i> calibrated (raked, post-stratified).
<code>dbtype</code>	name of database driver to pass to <code>dbDriver</code>
<code>dbname</code>	name of database (eg file name for SQLite)
<code>variance</code>	For pps without replacement, use <code>variance="YG"</code> for the Yates-Grundy estimator instead of the Horvitz-Thompson estimator
<code>...</code>	for future expansion

## Details

The `svydesign` object combines a data frame and all the survey design information needed to analyse it. These objects are used by the survey modelling and summary functions. The `id` argument is always required, the `strata`, `fpc`, `weights` and `probs` arguments are optional. If these variables are specified they must not have any missing values.

By default, `svydesign` assumes that all PSUs, even those in different strata, have a unique value of the `id` variable. This allows some data errors to be detected. If your PSUs reuse the same identifiers across strata then set `nest=TRUE`.

The finite population correction (`fpc`) is used to reduce the variance when a substantial fraction of the total population of interest has been sampled. It may not be appropriate if the target of inference is the process generating the data rather than the statistics of a particular finite population.

The finite population correction can be specified either as the total population size in each stratum or as the fraction of the total population that has been sampled. In either case the relevant population size is the sampling units. That is, sampling 100 units from a population stratum of size 500 can be specified as 500 or as  $100/500=0.2$ . The exception is for PPS sampling without replacement, where the sampling probability (which will be different for each PSU) must be used.

If population sizes are specified but not sampling probabilities or weights, the sampling probabilities will be computed from the population sizes assuming simple random sampling within strata.

For multistage sampling the `id` argument should specify a formula with the cluster identifiers at each stage. If subsequent stages are stratified strata should also be specified as a formula with stratum identifiers at each stage. The population size for each level of sampling should also be specified in `fpc`. If `fpc` is not specified then sampling is assumed to be with replacement at the top level and only the first stage of cluster is used in computing variances. If `fpc` is specified but for fewer stages than `id`, sampling is assumed to be complete for subsequent stages. The variance calculations for multistage sampling assume simple or stratified random sampling within clusters at each stage except possibly the last.

For PPS sampling without replacement it is necessary to specify the probabilities for each stage of sampling using the `fpc` arguments, and an overall weight argument should not be given. At the moment, multistage or stratified PPS sampling without replacement is supported only with `pps="brewer"`, or by giving the full joint probability matrix using `ppsmat`. [Cluster sampling is supported by all methods, but not subsampling within clusters].

The `dim`, `"["`, `"[<-"` and `na.action` methods for `survey.design` objects operate on the dataframe specified by `variables` and ensure that the design information is properly updated to correspond to the new data frame. With the `"[<-"` method the new value can be a `survey.design` object instead of a data frame, but only the data frame is used. See also `subset.survey.design` for a simple way to select subpopulations.

The `model.frame` method extracts the observed data.

If the strata with only one PSU are not self-representing (or they are, but `svydesign` cannot tell based on `fpc`) then the handling of these strata for variance computation is determined by `options("survey.lonely.psu")`. See [svyCprod](#) for details.

`data` may be a character string giving the name of a table or view in a relational database that can be accessed through the DBI interfaces. For DBI interfaces `dbtype` should be the name of the database driver and `dbname` should be the name by which the driver identifies the specific database (eg file name for SQLite).

The appropriate database interface package must already be loaded (eg `RSQLite` for SQLite). The survey design object will contain only the design meta-data, and actual variables will be loaded from the database as needed. Use [close](#) to close the database connection and [open](#) to reopen the connection, eg, after loading a saved object.

The database interface does not attempt to modify the underlying database and so can be used with read-only permissions on the database.

If `data` is an `imputationList` object (from the "mitools" package), `svydesign` will return a `svyimputationList` object containing a set of designs. Use [with.svyimputationList](#) to do analyses on these designs and `MIcombine` to combine the results.

## Value

An object of class `survey.design`.

## Author(s)

Thomas Lumley

## See Also

[as.svrepdesign](#) for converting to replicate weight designs, [subset.survey.design](#) for domain estimates, [update.survey.design](#) to add variables.

`mitools` package for using multiple imputations

[svyrecvar](#) for details of variance estimation

[election](#) for examples of PPS sampling without replacement.

## Examples

```
data(api)
# stratified sample
dstrat<-svydesign(id=~1,strata=~stype, weights=~pw, data=apistrat, fpc=~fpc)
# one-stage cluster sample
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
# two-stage cluster sample: weights computed from population sizes.
dclus2<-svydesign(id=~dnum+snum, fpc=~fpc1+fpc2, data=apiclus2)

## multistage sampling has no effect when fpc is not given, so
## these are equivalent.
dclus2wr<-svydesign(id=~dnum+snum, weights=weights(dclus2), data=apiclus2)
dclus2wr2<-svydesign(id=~dnum, weights=weights(dclus2), data=apiclus2)
```

```
## syntax for stratified cluster sample
##(though the data weren't really sampled this way)
svydesign(id=~dnum, strata=~stype, weights=~pw, data=apistrat,
nest=TRUE)

## PPS sampling without replacement
data(election)
dpps<- svydesign(id=~1, fpc=~p, data=election_pps, pps="brewer")

##database example: requires RSQLite
## Not run:
library(RSQLite)
dbclus1<-svydesign(id=~dnum, weights=~pw, fpc=~fpc,
data="apiclus1",dbtype="SQLite", dbname=system.file("api.db",package="survey"))

## End(Not run)

## pre-calibrated weights
cdclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc,
  calibration.formula=~1)
```

---

svyfactanal

---

*Factor analysis in complex surveys (experimental).*


---

## Description

This function fits a factor analysis model or SEM, by maximum weighted likelihood.

## Usage

```
svyfactanal(formula, design, factors,
  n = c("none", "sample", "degf", "effective", "min.effective"), ...)
```

## Arguments

formula	Model formula specifying the variables to use
design	Survey design object
factors	Number of factors to estimate
n	Sample size to be used for testing: see below
...	Other arguments to pass to <a href="#">factanal</a> .

## Details

The population covariance matrix is estimated by [svyvar](#) and passed to [factanal](#)

Although fitting these models requires only the estimated covariance matrix, inference requires a sample size. With `n="sample"`, the sample size is taken to be the number of observations; with `n="degf"`, the survey degrees of freedom as returned by [degf](#). Using "sample" corresponds to standardizing weights to have mean 1, and is known to result in anti-conservative tests.

The other two methods estimate an effective sample size for each variable as the sample size where the standard error of a variance of a Normal distribution would match the design-based standard error estimated by [svyvar](#). With `n="min.effective"` the minimum sample size across the variables is used; with `n="effective"` the harmonic mean is used. For `svyfactanal` the test of model adequacy is optional, and the default choice, `n="none"`, does not do the test.

## Value

An object of class `factanal`

## References

.

## See Also

[factanal](#)

The `lavaan.survey` package fits structural equation models to complex samples using similar techniques.

## Examples

```
data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)

svyfactanal(~api99+api00+hsg+meals+ell+emer, design=dclus1, factors=2)

svyfactanal(~api99+api00+hsg+meals+ell+emer, design=dclus1, factors=2, n="effective")

##Population dat for comparison
factanal(~api99+api00+hsg+meals+ell+emer, data=apipop, factors=2)
```

---

svyglm

*Survey-weighted generalised linear models.*

---

## Description

Fit a generalised linear model to data from a complex survey design, with inverse-probability weighting and design-based standard errors.

**Usage**

```
## S3 method for class 'survey.design'
svyglm(formula, design, subset=NULL,
family=stats::gaussian(),start=NULL, rescale=TRUE, ..., deff=FALSE,
influence=FALSE)
## S3 method for class 'svyrep.design'
svyglm(formula, design, subset=NULL,
family=stats::gaussian(),start=NULL, rescale=NULL, ..., rho=NULL,
return.replicates=FALSE, na.action,multicore=getOption("survey.multicore"))
## S3 method for class 'svyglm'
summary(object, correlation = FALSE, df.resid=NULL,
...)
## S3 method for class 'svyglm'
predict(object,newdata=NULL,total=NULL,
        type=c("link","response","terms"),
        se.fit=(type != "terms"),vcov=FALSE,...)
## S3 method for class 'svrepglm'
predict(object,newdata=NULL,total=NULL,
        type=c("link","response","terms"),
        se.fit=(type != "terms"),vcov=FALSE,
        return.replicates=!is.null(object$replicates),...)
```

**Arguments**

formula	Model formula
design	Survey design from <a href="#">svydesign</a> or <a href="#">svrepdesign</a> . Must contain all variables in the formula
subset	Expression to select a subpopulation
family	family object for glm
start	Starting values for the coefficients (needed for some uncommon link/family combinations)
rescale	Rescaling of weights, to improve numerical stability. The default rescales weights to sum to the sample size. Use FALSE to not rescale weights. For replicate-weight designs, use TRUE to rescale weights to sum to 1, as was the case before version 3.34.
...	Other arguments passed to glm or summary.glm
rho	For replicate BRR designs, to specify the parameter for Fay's variance method, giving weights of rho and 2-rho
return.replicates	Return the replicates as the replicates component of the result? (for predict, only possible if they were computed in the svyglm fit)
deff	Estimate the design effects
influence	Return influence functions
object	A svyglm object

correlation	Include the correlation matrix of parameters?
na.action	Handling of NAs
multicore	Use the multicore package to distribute replicates across processors?
df.resid	Optional denominator degrees of freedom for Wald tests
newdata	new data frame for prediction
total	population size when predicting population total
type	linear predictor (link) or response
se.fit	if TRUE, return variances of predictions
vcov	if TRUE and se=TRUE return full variance-covariance matrix of predictions

### Details

For binomial and Poisson families use `family=quasibinomial()` and `family=quasipoisson()` to avoid a warning about non-integer numbers of successes. The ‘quasi’ versions of the family objects give the same point estimates and standard errors and do not give the warning.

If `df.resid` is not specified the df for the null model is computed by [degf](#) and the residual df computed by subtraction. This is recommended by Korn and Graubard and is correct for PSU-level covariates but is potentially very conservative for individual-level covariates. To get tests based on a Normal distribution use `df.resid=Inf`, and to use number of PSUs-number of strata, specify `df.resid=degf(design)`.

Parallel processing with `multicore=TRUE` is helpful only for fairly large data sets and on computers with sufficient memory. It may be incompatible with GUIs, although the Mac Aqua GUI appears to be safe.

`predict` gives fitted values and sampling variability for specific new values of covariates. When `newdata` are the population mean it gives the regression estimator of the mean, and when `newdata` are the population totals and `total` is specified it gives the regression estimator of the population total. Regression estimators of mean and total can also be obtained with [calibrate](#).

### Value

`svyglm` returns an object of class `svyglm`. The `predict` method returns an object of class `svyestat`

### Note

`svyglm` always returns ‘model-robust’ standard errors; the Horvitz-Thompson-type standard errors used everywhere in the survey package are a generalisation of the model-robust ‘sandwich’ estimators. In particular, a quasi-Poisson `svyglm` will return correct standard errors for relative risk regression models.

### Note

This function does not return the same standard error estimates for the regression estimator of population mean and total as some textbooks, or SAS. However, it does give the same standard error estimator as estimating the mean or total with calibrated weights.

In particular, under simple random sampling with or without replacement there is a simple rescaling of the mean squared residual to estimate the mean squared error of the regression estimator.

The standard error estimate produced by `predict.svyglm` has very similar (asymptotically identical) expected value to the textbook estimate, and has the advantage of being applicable when the supplied newdata are not the population mean of the predictors. The difference is small when the sample size is large, but can be appreciable for small samples.

You can obtain the other standard error estimator by calling `predict.svyglm` with the covariates set to their estimated (rather than true) population mean values.

### Author(s)

Thomas Lumley

### References

Lumley T, Scott A (2017) "Fitting Regression Models to Survey Data" *Statistical Science* 32: 265-278

### See Also

[glm](#), which is used to do most of the work.

[regTermTest](#), for multiparameter tests

[calibrate](#), for an alternative way to specify regression estimators of population totals or means

[svyttest](#) for one-sample and two-sample t-tests.

### Examples

```
data(api)

dstrat<-svydesign(id=~1,strata=~stype, weights=~pw, data=apistat, fpc=~fpc)
dclus2<-svydesign(id=~dnum+snum, weights=~pw, data=apiclus2)
rstrat<-as.svrepdesign(dstrat)
rclus2<-as.svrepdesign(dclus2)

summary(svyglm(api00~ell+meals+mobility, design=dstrat))
summary(svyglm(api00~ell+meals+mobility, design=dclus2))
summary(svyglm(api00~ell+meals+mobility, design=rstrat))
summary(svyglm(api00~ell+meals+mobility, design=rclus2))

## use quasibinomial, quasipoisson to avoid warning messages
summary(svyglm(sch.wide~ell+meals+mobility, design=dstrat,
  family=quasibinomial()))

## Compare regression and ratio estimation of totals
api.ratio <- svyratio(~api.stu,~enroll, design=dstrat)
pop<-data.frame(enroll=sum(apipop$enroll, na.rm=TRUE))
npop <- nrow(apipop)
predict(api.ratio, pop$enroll)

## regression estimator is less efficient
```

```

api.reg <- svyglm(api.stu~enroll, design=dstrat)
predict(api.reg, newdata=pop, total=npop)
## same as calibration estimator
svytotal(~api.stu, calibrate(dstrat, ~enroll, pop=c(npop, pop$enroll)))

## svyglm can also reproduce the ratio estimator
api.reg2 <- svyglm(api.stu~enroll-1, design=dstrat,
                  family=quasi(link="identity",var="mu"))
predict(api.reg2, newdata=pop, total=npop)

## higher efficiency by modelling variance better
api.reg3 <- svyglm(api.stu~enroll-1, design=dstrat,
                  family=quasi(link="identity",var="mu^3"))
predict(api.reg3, newdata=pop, total=npop)
## true value
sum(apipop$api.stu)

```

svygofchisq

*Test of fit to known probabilities***Description**

A Rao-Scott-type version of the chi-squared test for goodness of fit to prespecified proportions. The test statistic is the chi-squared statistic applied to the estimated population table, and the reference distribution is a Satterthwaite approximation: the test statistic divided by the estimated scale is compared to a chi-squared distribution with the estimated df.

**Usage**

```
svygofchisq(formula, p, design, ...)
```

**Arguments**

formula	Formula specifying a single factor variable
p	Vector of probabilities for the categories of the factor, in the correct order (will be rescaled to sum to 1)
design	Survey design object
...	Other arguments to pass to <a href="#">svytotal</a> , such as <code>na.rm</code>

**Value**

An object of class `htest`

**See Also**

[chisq.test](#), [svychisq](#), [pchisqsum](#)

**Examples**

```
data(api)
dclus2<-svydesign(id=~dnum+snum, fpc=~fpc1+fpc2, data=apiclus2)

true_p <- table(apipop$stype)

svygofchisq(~stype,dclus2,p=true_p)
svygofchisq(~stype,dclus2,p=c(1/3,1/3,1/3))
```

svyhist

*Histograms and boxplots***Description**

Histograms and boxplots weighted by the sampling weights.

**Usage**

```
svyhist(formula, design, breaks = "Sturges",
        include.lowest = TRUE, right = TRUE, xlab = NULL,
        main = NULL, probability = TRUE, freq = !probability, ...)
svyboxplot(formula, design, all.outliers=FALSE,...)
```

**Arguments**

formula	One-sided formula for svyhist, two-sided for svyboxplot
design	A survey design object
xlab	x-axis label
main	Main title
probability, freq	Y-axis is probability density or frequency
all.outliers	Show all outliers in the boxplot, not just extremes
breaks, include.lowest, right	As for <a href="#">hist</a>
...	Other arguments to <a href="#">hist</a> or <a href="#">bxp</a>

**Details**

The histogram breakpoints are computed as if the sample were a simple random sample of the same size.

The grouping variable in svyboxplot, if present, must be a factor.

The boxplot whiskers go to the maximum and minimum observations or to 1.5 interquartile ranges beyond the end of the box, whichever is closer. The maximum and minimum are plotted as outliers if they are beyond the ends of the whiskers, but other outlying points are not plotted unless all.outliers=TRUE. svyboxplot requires a two-sided formula; use variable~1 for a single boxplot.

Value

As for hist, except that when probability=FALSE, the return value includes a component count\_scale giving a scale factor between density and counts, assuming equal bin widths.

See Also

[svyplot](#)

Examples

```
data(api)
dstrat <- svydesign(id = ~1, strata = ~stype, weights = ~pw, data = apistrat,
  fpc = ~fpc)
opar<-par(mfrow=c(1,3))
svyhist(~enroll, dstrat, main="Survey weighted",col="purple",ylim=c(0,1.3e-3))
hist(apistrat$enroll, main="Sample unweighted",col="purple",prob=TRUE,ylim=c(0,1.3e-3))
hist(apipop$enroll, main="Population",col="purple",prob=TRUE,ylim=c(0,1.3e-3))

par(mfrow=c(1,1))
svyboxplot(enroll~stype,dstrat,all.outliers=TRUE)
svyboxplot(enroll~1,dstrat)
par(opar)
```

---

svyivreg	<i>Two-stage least-squares for instrumental variable regression</i>
----------	---

---

Description

Estimates regressions with endogenous covariates using two-stage least squares. The function uses ivreg from the AER package for the main computations, and follows the syntax of that function.

Usage

```
svyivreg(formula, design, ...)
```

Arguments

formula	formula specification(s) of the regression relationship and the instruments. See Details for details
design	A survey design object
...	For future expansion

**Details**

Regressors and instruments for `svyivreg` are specified in a formula with two parts on the right-hand side, e.g.,  $y \sim x_1 + x_2 \mid z_1 + z_2 + z_3$ , where  $x_1$  and  $x_2$  are the regressors and  $z_1$ ,  $z_2$ , and  $z_3$  are the instruments. Note that exogenous regressors have to be included as instruments for themselves. For example, if there is one exogenous regressor  $ex$  and one endogenous regressor  $en$  with instrument  $in$ , the appropriate formula would be  $y \sim ex + en \mid ex + in$ . Equivalently, this can be specified as  $y \sim ex + en \mid . - en + in$ , i.e., by providing an update formula with a `.` in the second part of the formula.

**Value**

An object of class `svyivreg`

**References**

<https://notstatschat.rbind.io/2019/07/16/adding-new-functions-to-the-survey-package/>

**See Also**

[ivreg](#)

---

svykappa	<i>Cohen's kappa for agreement</i>
----------	------------------------------------

---

**Description**

Computes the unweighted kappa measure of agreement between two raters and the standard error. The measurements must both be factor variables in the survey design object.

**Usage**

```
svykappa(formula, design, ...)
```

**Arguments**

- |         |   |
|---------|---|
| formula | one-sided formula giving two measurements   |
| design  | survey design object  |
| ...     | passed to <code>svymean</code> internally (such as <code>return.replicates</code> or <code>influence</code> ) |

**Value**

Object of class `svystat`

**See Also**

[svycontrast](#)

## Examples

```
data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
svykappa(~comp.imp+sch.wide, dclus1)

dclus1<-update(dclus1, stypecopy=stype)
svykappa(~stype+stypecopy,dclus1)

(kappas<-svyby(~comp.imp+sch.wide,~stype,design=dclus1, svykappa, covmat=TRUE))
svycontrast(kappas, quote(E/H))
```

---

svykm	<i>Estimate survival function.</i>
-------	------------------------------------

---

## Description

Estimates the survival function using a weighted Kaplan-Meier estimator.

## Usage

```
svykm(formula, design, se=FALSE, ...)
## S3 method for class 'svykm'
plot(x,xlab="time",ylab="Proportion surviving",
     ylim=c(0,1),ci=NULL,lty=1,...)
## S3 method for class 'svykm'
lines(x,xlab="time",type="s",ci=FALSE,lty=1,...)
## S3 method for class 'svykmlist'
plot(x, pars=NULL, ci=FALSE,...)
## S3 method for class 'svykm'
quantile(x, probs=c(0.75,0.5,0.25),ci=FALSE,level=0.95,...)
## S3 method for class 'svykm'
confint(object,parm,level=0.95,...)
```

## Arguments

formula	Two-sided formula. The response variable should be a right-censored Surv object
design	survey design object
se	Compute standard errors? This is slow for moderate to large data sets
...	in plot and lines methods, graphical parameters
x	a svykm or svykmlist object
xlab, ylab, ylim, type	as for plot
lty	Line type, see <a href="#">par</a>

<code>ci</code>	Plot (or return, for <code>quantile</code> ) the confidence interval
<code>pars</code>	A list of vectors of graphical parameters for the separate curves in a <code>svykm</code> object
<code>object</code>	A <code>svykm</code> object
<code>parm</code>	vector of times to report confidence intervals
<code>level</code>	confidence level
<code>probs</code>	survival probabilities for computing survival quantiles (note that these are the complement of the usual <code>quantile</code> input, so 0.9 means 90% surviving, not 90% dead)

## Details

When standard errors are computed, the survival curve is actually the Aalen (hazard-based) estimator rather than the Kaplan-Meier estimator.

The standard error computations use memory proportional to the sample size times the square of the number of events. This can be a lot.

In the case of equal-probability cluster sampling without replacement the computations are essentially the same as those of Williams (1995), and the same linearization strategy is used for other designs.

Confidence intervals are computed on the  $\log(\text{survival})$  scale, following the default in `survival` package, which was based on simulations by Link(1984).

Confidence intervals for quantiles use Woodruff's method: the interval is the intersection of the horizontal line at the specified quantile with the pointwise confidence band around the survival curve.

## Value

For `svykm`, an object of class `svykm` for a single curve or `svykm`list for multiple curves.

## References

Link, C. L. (1984). Confidence intervals for the survival function using Cox's proportional hazards model with covariates. *Biometrics* 40, 601-610.

Williams RL (1995) "Product-Limit Survival Functions with Correlated Survival Times" *Lifetime Data Analysis* 1: 171-186

Woodruff RS (1952) Confidence intervals for medians and other position measures. *JASA* 57, 622-627.

## See Also

`predict.svycoxph` for survival curves from a Cox model

**Examples**

```

data(pbc, package="survival")
pbc$randomized <- with(pbc, !is.na(trt) & trt>0)
biasmodel<-glm(randomized~age*edema,data=pbc)
pbc$randprob<-fitted(biasmodel)

dpbc<-svydesign(id=~1, prob=~randprob, strata=~edema, data=subset(pbc,randomized))

s1<-svykm(Surv(time,status>0)~1, design=dpbc)
s2<-svykm(Surv(time,status>0)~I(bili>6), design=dpbc)

plot(s1)
plot(s2)
plot(s2, lwd=2, pars=list(lty=c(1,2),col=c("purple","forestgreen"))))

quantile(s1, probs=c(0.9,0.75,0.5,0.25,0.1))

s3<-svykm(Surv(time,status>0)~I(bili>6), design=dpbc,se=TRUE)
plot(s3[[2]],col="purple")

confint(s3[[2]], parm=365*(1:5))
quantile(s3[[1]], ci=TRUE)

```

svyloglin

*Loglinear models***Description**

Fit and compare hierarchical loglinear models for complex survey data.

**Usage**

```

svyloglin(formula, design, ...)
## S3 method for class 'svyloglin'
update(object,formula,...)
## S3 method for class 'svyloglin'
anova(object,object1,...,integrate=FALSE)
## S3 method for class 'anova.svyloglin'
print(x,pval=c("F","saddlepoint","lincom","chisq"),...)
## S3 method for class 'svyloglin'
coef(object,...,intercept=FALSE)

```

**Arguments**

formula	Model formula
design	survey design object
object, object1	loglinear model from svyloglin

pval	p-value approximation: see Details
integrate	Compute the exact asymptotic p-value (slow)?
...	not used
intercept	Report the intercept?
x	anova object

## Details

The loglinear model is fitted to a multiway table with probabilities estimated by [svymean](#) and with the sample size equal to the observed sample size, treating the resulting table as if it came from iid multinomial sampling, as described by Rao and Scott. The variance-covariance matrix does not include the intercept term, and so by default neither does the `coef` method. A Newton-Raphson algorithm is used, rather than iterative proportional fitting, so starting values are not needed.

The `anova` method computes the quantities that would be the score (Pearson) and likelihood ratio chi-squared statistics if the data were an iid sample. It computes four p-values for each of these, based on the exact asymptotic distribution (see [pchisqsum](#)), a saddlepoint approximation to this distribution, a scaled chi-squared distribution, and a scaled F-distribution. When testing the two-way interaction model against the main-effects model in a two-way table the score statistic and p-values match the Rao-Scott tests computed by [svychisq](#).

The `anova` method can only compare two models if they are for exactly the same multiway table (same variables and same order). The `update` method will help with this. It is also much faster to use `update` than `svyloglin` for a large data set: its time complexity depends only on the size of the model, not on the size of the data set.

It is not possible to fit a model using a variable created inline, eg `I(x<10)`, since the multiway table is based on all variables used in the formula.

## Value

Object of class "svyloglin"

## References

Rao, JNK, Scott, AJ (1984) "On Chi-squared Tests For Multiway Contingency Tables with Proportions Estimated From Survey Data" *Annals of Statistics* 12:46-60.

## See Also

[svychisq](#), [svyglm](#), [pchisqsum](#)

## Examples

```
data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
a<-svyloglin(~stype+comp.imp,dclus1)
b<-update(a,~.^2)
an<-anova(a,b)
an
print(an, pval="saddlepoint")
```

```
## Wald test
regTermTest(b, ~stype:comp.imp)

## linear-by-linear association
d<-update(a,~.+as.numeric(stype):as.numeric(comp.imp))
an1<-anova(a,d)
an1
```

---

svylogrank	<i>Compare survival distributions</i>
------------	---------------------------------------

---

## Description

Computes a weighted version of the logrank test for comparing two or more survival distributions. The generalization to complex samples is based on the characterization of the logrank test as the score test in a Cox model. Under simple random sampling with replacement, this function with  $\rho=0$  and  $\gamma=0$  is almost identical to the robust score test in the survival package. The  $\rho=0$  and  $\gamma=0$  version was proposed by Rader (2014).

## Usage

```
svylogrank(formula, design, rho=0,gamma=0,method=c("small","large","score"), ...)
```

## Arguments

formula	Model formula with a single predictor. The predictor must be a factor if it has more than two levels.
design	A survey design object
rho, gamma	Coefficients for the Harrington/Fleming G-rho-gamma tests. The default is the logrank test, $\rho=1$ gives a generalised Wilcoxon test
method	"small" works faster when a matrix with dimension number of events by number of people fits easily in memory; "large" works faster for large data sets; "score" works by brute-force construction of an expanded data set, and is for debugging
...	for future expansion.

## Value

A vector containing the z-statistic for comparing each level of the variable to the lowest, the chisquared statistic for the logrank test, and the p-value.

## References

Rader, Kevin Andrew. 2014. Methods for Analyzing Survival and Binary Data in Complex Surveys. Doctoral dissertation, Harvard University.<http://nrs.harvard.edu/urn-3:HUL.InstRepos:12274283>

**See Also**

[svykm](#), [svycoxph](#).

**Examples**

```
library("survival")
data(nwtco)
## stratified on case status
dcchs<-twophase(id=list(~seqno,~seqno), strata=list(NULL,~rel),
               subset=~I(in.subcohort | rel), data=nwtco, method="simple")
svylogrank(Surv(edrel,rel)~factor(stage),design=dcchs)

data(pbc, package="survival")
pbc$randomized <- with(pbc, !is.na(trt) & trt>0)
biasmodel<-glm(randomized~age*edema,data=pbc)
pbc$randprob<-fitted(biasmodel)
dpbc<-svydesign(id=~1, prob=~randprob, strata=~edema, data=subset(pbc,randomized))

svylogrank(Surv(time,status==2)~trt,design=dpbc)

svylogrank(Surv(time,status==2)~trt,design=dpbc,rho=1)

rpbc<-as.svrepdesign(dpbc)
svylogrank(Surv(time,status==2)~trt,design=rpbc)
```

---

svymle

---

*Maximum pseudolikelihood estimation in complex surveys*


---

**Description**

Maximises a user-specified likelihood parametrised by multiple linear predictors to data from a complex sample survey and computes the sandwich variance estimator of the coefficients. Note that this function maximises an estimated population likelihood, it is not the sample MLE.

**Usage**

```
svymle(loglike, gradient = NULL, design, formulas, start = NULL, control
= list(), na.action="na.fail", method=NULL, lower=NULL, upper=NULL, influence=FALSE,...)
## S3 method for class 'svymle'
summary(object, stderr=c("robust", "model"),...)
```

**Arguments**

loglike	vectorised loglikelihood function
gradient	Derivative of loglike. Required for variance computation and helpful for fitting
design	a survey.design object

<code>formulas</code>	A list of formulas specifying the variable and linear predictors: see Details below
<code>start</code>	Starting values for parameters
<code>control</code>	control options for the optimiser: see the help page for the optimiser you are using.
<code>lower, upper</code>	Parameter bounds for bobyqa
<code>influence</code>	Return the influence functions (primarily for svyby)
<code>na.action</code>	Handling of NAs
<code>method</code>	"nlm" to use nlm, "uobyqa" or "bobyqa" to use those optimisers from the minqa package; otherwise passed to <a href="#">optim</a>
<code>...</code>	Arguments to loglike and gradient that are not to be optimised over.
<code>object</code>	svymle object
<code>stderr</code>	Choice of standard error estimator. The default is a standard sandwich estimator. See Details below.

## Details

Optimization is done by [nlm](#) by default or if `method=="nlm"`. Otherwise [optim](#) is used and `method` specifies the method and `control` specifies control parameters.

The design object contains all the data and design information from the survey, so all the formulas refer to variables in this object. The `formulas` argument needs to specify the response variable and a linear predictor for each freely varying argument of `loglike`.

Consider for example the [dnorm](#) function, with arguments `x`, `mean`, `sd` and `log`, and suppose we want to estimate the mean of `y` as a linear function of a variable `z`, and to estimate a constant standard deviation. The `log` argument must be fixed at `FALSE` to get the loglikelihood. A `formulas` argument would be `list(~y, mean=~z, sd=~1)`. Note that the data variable `y` must be the first argument to `dnorm` and the first formula and that all the other formulas are labelled. It is also permitted to have the data variable as the left-hand side of one of the formulas: eg `list(mean=y~z, sd=~1)`.

The two optimisers from the `minqa` package do not use any derivatives to be specified for optimisation, but they do assume that the function is smooth enough for a quadratic approximation, ie, that two derivatives exist.

The usual variance estimator for MLEs in a survey sample is a 'sandwich' variance that requires the score vector and the information matrix. It requires only sampling assumptions to be valid (though some model assumptions are required for it to be useful). This is the `stderr="robust"` option, which is available only when the `gradient` argument was specified.

If the model is correctly specified and the sampling is at random conditional on variables in the model then standard errors based on just the information matrix will be approximately valid. In particular, for independent sampling where weights and strata depend on variables in the model the `stderr="model"` should work fairly well.

## Value

An object of class `svymle`

**Author(s)**

Thomas Lumley

**See Also**[svydesign](#), [svyglm](#)**Examples**

```

data(api)

dstrat<-svydesign(id=~1, strata=~stype, weight=~pw, fpc=~fpc, data=apistrat)

## fit with glm
m0 <- svyglm(api00~api99+ell,family="gaussian",design=dstrat)
## fit as mle (without gradient)
m1 <- svymle(loglike=dnorm,gradient=NULL, design=dstrat,
  formulas=list(mean=api00~api99+ell, sd=~1),
  start=list(c(80,1,0),c(20)), log=TRUE)
## with gradient
gr<- function(x,mean,sd,log){
  dm<-2*(x - mean)/(2*sd^2)
  ds<-(x-mean)^2*(2*(2 * sd))/(2*sd^2)^2 - sqrt(2*pi)/(sd*sqrt(2*pi))
  cbind(dm,ds)
}
m2 <- svymle(loglike=dnorm,gradient=gr, design=dstrat,
  formulas=list(mean=api00~api99+ell, sd=~1),
  start=list(c(80,1,0),c(20)), log=TRUE, method="BFGS")

summary(m0)
summary(m1,stderr="model")
summary(m2)

## Using offsets
m3 <- svymle(loglike=dnorm,gradient=gr, design=dstrat,
  formulas=list(mean=api00~api99+offset(ell)+ell, sd=~1),
  start=list(c(80,1,0),c(20)), log=TRUE, method="BFGS")

## demonstrating multiple linear predictors

m3 <- svymle(loglike=dnorm,gradient=gr, design=dstrat,
  formulas=list(mean=api00~api99+offset(ell)+ell, sd=~stype),
  start=list(c(80,1,0),c(20,0,0)), log=TRUE, method="BFGS")

## More complicated censored lognormal data example
## showing that the response variable can be multivariate

data(pbc, package="survival")
pbc$randomized <- with(pbc, !is.na(trt) & trt>0)

```

```

biasmodel<-glm(randomized~age*edema,data=pbpc)
pbpc$randprob<-fitted(biasmodel)
dpbc<-svydesign(id=~1, prob=~randprob, strata=~edema,
  data=subset(pbc,randomized))

## censored logNormal likelihood
lcens<-function(x,mean,sd){
  ifelse(x[,2]==1,
    dnorm(log(x[,1]),mean,sd,log=TRUE),
    pnorm(log(x[,1]),mean,sd,log=TRUE,lower.tail=FALSE)
  )
}

gcens<- function(x,mean,sd){

  dz<- -dnorm(log(x[,1]),mean,sd)/pnorm(log(x[,1]),mean,sd,lower.tail=FALSE)

  dm<-ifelse(x[,2]==1,
    2*(log(x[,1]) - mean)/(2*sd^2),
    dz*-1/sd)
  ds<-ifelse(x[,2]==1,
    (log(x[,1])-mean)^2*(2*(2 * sd))/(2*sd^2)^2 - sqrt(2*pi)/(sd*sqrt(2*pi)),
    dz*-(log(x[,1])-mean)/(sd*sd))
  cbind(dm,ds)
}

m<-svymle(loglike=lcens, gradient=gcens, design=dpbc, method="newuoa",
  formulas=list(mean=I(cbind(time,status>0))~bili+protime+albumin,
    sd=~1),
  start=list(c(10,0,0,0),c(1)))

summary(m)

## the same model, but now specifying the lower bound of zero on the
## log standard deviation

mbox<-svymle(loglike=lcens, gradient=gcens, design=dpbc, method="bobyqa",
  formulas=list(mean=I(cbind(time,status>0))~bili+protime+albumin, sd=~1),
  lower=list(c(-Inf,-Inf,-Inf,-Inf),0), upper=Inf,
  start=list(c(10,0,0,0),c(1)))

## The censored lognormal model is now available in svysurvreg()

summary(svysurvreg(Surv(time,status>0)~bili+protime+albumin,
  design=dpbc,dist="lognormal"))

## compare svymle scale value after log transformation
svycontrast(m, quote(log(`sd.(Intercept)`)))

```

svynls

*Probability-weighted nonlinear least squares***Description**

Fits a nonlinear model by probability-weighted least squares. Uses `nls` to do the fitting, but estimates design-based standard errors with either linearisation or replicate weights. See [nls](#) for documentation of model specification and fitting.

**Usage**

```
svynls(formula, design, start, weights=NULL, ...)
```

**Arguments**

<code>formula</code>	Nonlinear model specified as a formula; see <a href="#">nls</a>
<code>design</code>	Survey design object
<code>start</code>	starting values, passed to <a href="#">nls</a>
<code>weights</code>	Non-sampling weights, eg precision weights to give more efficient estimation in the presence of heteroscedasticity.
<code>...</code>	Other arguments to <code>nls</code> (especially, <code>start</code> ). Also supports <code>return.replicates</code> for replicate-weight designs and <code>influence</code> for other designs.

**Value**

Object of class `svynls`. The fitted `nls` object is included as the `fit` element.

**See Also**

[svymle](#) for maximum likelihood with linear predictors on one or more parameters

**Examples**

```
set.seed(2020-4-3)
x<-rep(seq(0,50,1),10)
y<-((runif(1,10,20)*x)/(runif(1,0,10)+x))+rnorm(510,0,1)

pop_model<-nls(y~a*x/(b+x), start=c(a=15,b=5))

df<-data.frame(x=x,y=y)
df$p<-ifelse((y-fitted(pop_model))*(x-mean(x))>0, .4,.1)

df$strata<-ifelse(df$p==.4,"a","b")

in_sample<-stratsample(df$strata, round(table(df$strat)*c(0.4,0.1)))

sdf<-df[in_sample,]
des<-svydesign(id=~1, strata=~strata, prob=~p, data=sdf)
```

```
pop_model
(biased_sample<-nls(y~a*x/(b+x),data=sdf, start=c(a=15,b=5)))
(corrected <- svynls(y~a*x/(b+x), design=des, start=c(a=15,b=5)))
```

svyolr

*Proportional odds and related models***Description**

Fits cumulative link models: proportional odds, probit, complementary log-log, and cauchit.

**Usage**

```
svyolr(formula, design, ...)
## S3 method for class 'survey.design2'
svyolr(formula, design, start, subset=NULL,...,
        na.action = na.omit,method = c("logistic", "probit", "cloglog", "cauchit"))
## S3 method for class 'svyrep.design'
svyolr(formula,design,subset=NULL,...,return.replicates=FALSE,
        multicore=getOption("survey.multicore"))
## S3 method for class 'svyolr'
predict(object, newdata, type = c("class", "probs"), ...)
```

**Arguments**

formula	Formula: the response must be a factor with at least three levels
design	survey design object
subset	subset of the design to use; NULL for all of it
...	dots
start	Optional starting values for optimization
na.action	handling of missing values
multicore	Use multicore package to distribute computation of replicates across multiple processors?
method	Link function
return.replicates	return the individual replicate-weight estimates
object	object of class svyolr
newdata	new data for predictions
type	return vector of most likely class or matrix of probabilities

**Value**

An object of class svyolr

**Author(s)**

The code is based closely on `polr()` from the MASS package of Venables and Ripley.

**See Also**

[svyglm](#), [regTermTest](#)

**Examples**

```
data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
dclus1<-update(dclus1, mealcat=cut(meals,c(0,25,50,75,100)))

m<-svyolr(mealcat~avg.ed+mobility+stype, design=dclus1)
m

## Use regTermTest for testing multiple parameters
regTermTest(m, ~avg.ed+stype, method="LRT")

## predictions
summary(predict(m, newdata=apiclus2))
summary(predict(m, newdata=apiclus2, type="probs"))
```

---

svyplot

*Plots for survey data*


---

**Description**

Because observations in survey samples may represent very different numbers of units in the population ordinary plots can be misleading. The `svyplot` function produces scatterplots adjusted in various ways for sampling weights.

**Usage**

```
svyplot(formula, design,...)
## Default S3 method:
svyplot(formula, design, style = c("bubble", "hex", "grayhex", "subsample", "transparent"),
sample.size = 500, subset = NULL, legend = 1, inches = 0.05,
amount=NULL, basecol="black",
alpha=c(0, 0.8),xbins=30,...)
```

**Arguments**

<code>formula</code>	A model formula
<code>design</code>	A survey object ( <code>svydesign</code> or <code>svrepdesign</code> )
<code>style</code>	See Details below
<code>sample.size</code>	For <code>style="subsample"</code>

subset	expression using variables in the design object
legend	For style="hex" or "grayhex"
inches	Scale for bubble plots
amount	list with x and y components for amount of jittering to use in subsample plots, or NULL for the default amount
basecol	base color for transparent plots, or a function to compute the color (see below), or color for bubble plots
alpha	minimum and maximum opacity for transparent plots
xbins	Number of (x-axis) bins for hexagonal binning
...	Passed to plot methods

## Details

Bubble plots are scatterplots with circles whose area is proportional to the sampling weight. The two "hex" styles produce hexagonal binning scatterplots, and require the hexbin package from Bioconductor. The "transparent" style plots points with opacity proportional to sampling weight.

The subsample method uses the sampling weights to create a sample from approximately the population distribution and passes this to [plot](#)

Bubble plots are suited to small surveys, hexagonal binning and transparency to large surveys where plotting all the points would result in too much overlap.

basecol can be a function taking one data frame argument, which will be passed the data frame of variables from the survey object. This could be memory-intensive for large data sets.

## Value

None

## References

Korn EL, Graubard BI (1998) "Scatterplots with Survey Data" The American Statistician 52: 58-69

Lumley T, Scott A (2017) "Fitting Regression Models to Survey Data" Statistical Science 32: 265-278

## See Also

[symbols](#) for other options (such as colour) for bubble plots.

[svytable](#) for plots of discrete data.

## Examples

```
data(api)
dstrat<-svydesign(id=~1,strata=~stype, weights=~pw, data=apistrat, fpc=~fpc)

svyplot(api00~api99, design=dstrat, style="bubble")
svyplot(api00~api99, design=dstrat, style="transparent",pch=19)
```

```
## these two require the hexbin package
svyplot(api00~api99, design=dstrat, style="hex", xlab="1999 API",ylab="2000 API")
svyplot(api00~api99, design=dstrat, style="grayhex",legend=0)

dclus2<-svydesign(id=~dnum+snum, weights=~pw,
                 data=apiclus2, fpc=~fpc1+fpc2)
svyplot(api00~api99, design=dclus2, style="subsample")
svyplot(api00~api99, design=dclus2, style="subsample",
        amount=list(x=25,y=25))

svyplot(api00~api99, design=dstrat,
        basecol=function(df){c("goldenrod","tomato","sienna")[as.numeric(df$type)]},
        style="transparent",pch=19,alpha=c(0,1))
legend("topleft",col=c("goldenrod","tomato","sienna"), pch=19, legend=c("E","H","M"))

## For discrete data, estimate a population table and plot the table.
plot(svytable(~sch.wide+comp.imp+stype,design=dstrat))
fourfoldplot(svytable(~sch.wide+comp.imp+stype,design=dstrat,round=TRUE))

## To draw on a hexbin plot you need grid graphics, eg,
library(grid)
h<-svyplot(api00~api99, design=dstrat, style="hex", xlab="1999 API",ylab="2000 API")
s<-svysmooth(api00~api99,design=dstrat)
grid.polyline(s$api99$x,s$api99$y,vp=h$plot.vp@hexVp.on,default.units="native",
             gp=gpar(col="red",lwd=2))
```

---

svyprcomp

*Sampling-weighted principal component analysis*


---

## Description

Computes principal components using the sampling weights.

## Usage

```
svyprcomp(formula, design, center = TRUE, scale. = FALSE, tol = NULL, scores = FALSE, ...)
## S3 method for class 'svyprcomp'
biplot(x, cols=c("black","darkred"),xlabs=NULL,
       weight=c("transparent","scaled","none"),
       max.alpha=0.5,max.cex=0.5,xlim=NULL,ylim=NULL,pc.biplot=FALSE,
       expand=1,xlab=NULL,ylab=NULL, arrow.len=0.1, ...)
```

## Arguments

formula	model formula describing variables to be used
design	survey design object.
center	Center data before analysis?

<code>scale.</code>	Scale to unit variance before analysis?
<code>tol</code>	Tolerance for omitting components from the results; a proportion of the standard deviation of the first component. The default is to keep all components.
<code>scores</code>	Return scores on each component? These are needed for biplot.
<code>x</code>	A <code>svyprcomp</code> object
<code>cols</code>	Base colors for observations and variables respectively
<code>xlabs</code>	Formula, or character vector, giving labels for each observation
<code>weight</code>	How to display the sampling weights: "scaled" changes the size of the point label, "transparent" uses opacity proportional to sampling weight, "none" changes neither.
<code>max.alpha</code>	Opacity for the largest sampling weight, or for all points if <code>weight!="transparent"</code>
<code>max.cex</code>	Character size (as a multiple of <code>par("cex")</code> ) for the largest sampling weight, or for all points if <code>weight!="scaled"</code>
<code>xlim, ylim, xlab, ylab</code>	Graphical parameters
<code>expand, arrow.len</code>	See <a href="#">biplot</a>
<code>pc.biplot</code>	See <code>link{biplot.prcomp}</code>
<code>...</code>	Other arguments to <a href="#">prcomp</a> , or graphical parameters for biplot

### Value

`svyprcomp` returns an object of class `svyprcomp`, similar to class `prcomp` but including design information

### See Also

[prcomp](#), [biplot.prcomp](#)

### Examples

```
data(api)
dclus2<-svydesign(id=~dnum+snum, fpc=~fpc1+fpc2, data=apiclus2)

pc <- svyprcomp(~api99+api00+ell+hsg+meals+emer, design=dclus2,scale=TRUE,scores=TRUE)
pc
biplot(pc, xlabs=~dnum, weight="none")

biplot(pc, xlabs=~dnum,max.alpha=1)

biplot(pc, weight="scaled",max.cex=1.5, xlabs=~dnum)
```

svypredmeans

*Predictive marginal means***Description**

Predictive marginal means for a generalised linear model, using the method of Korn and Graubard (1999) and matching the results of SUDAAN. The predictive marginal mean for one level of a factor is the probability-weighted average of the fitted values for the model on new data where all the observations are set to that level of the factor but have whatever values of adjustment variables they really have.

**Usage**

```
svypredmeans(adjustmodel, groupfactor, predictat=NULL)
```

**Arguments**

adjustmodel	A generalised linear model fit by <code>svyglm</code> with the adjustment variable but without the factor for which predictive means are wanted
groupfactor	A one-sided formula specifying the factor for which predictive means are wanted. Can use, eg, <code>~interaction(race, sex)</code> for combining variables. This does not have to be a factor, but it will be modelled linearly if it isn't
predictat	A vector of the values of groupfactor where you want predictions. If groupfactor is a factor, these must be values in the data, but if it is numeric you can interpolate/extrapolate

**Value**

An object of class `svystat` with the predictive marginal means and their covariance matrix.

**Note**

It is possible to supply an adjustment model with only an intercept, but the results are then the same as `svymean`

It makes no sense to have a variable in the adjustment model that is part of the grouping factor, and will give an error message or NA.

**References**

Graubard B, Korn E (1999) "Predictive Margins with Survey Data" *Biometrics* 55:652-659

Bieler, Brown, Williams, & Brogan (2010) "Estimating Model-Adjusted Risks, Risk Differences, and Risk Ratios From Complex Survey Data" *Am J Epi* DOI: 10.1093/aje/kwp440

**See Also**[svyglm](#)

Worked example using National Health Interview Survey data: <https://gist.github.com/tslumley/2e74cd0ac12a671d2724>

**Examples**

```
data(nhanes)
nhanes_design <- svydesign(id=~SDMVPSU, strata=~SDMVSTRA, weights=~WTMEC2YR, nest=TRUE,data=nhanes)
agesexmodel<-svyglm(HI_CHOL~agecat+RIAGENDR, design=nhanes_design,family=quasibinomial)
## high cholesterol by race/ethnicity, adjusted for demographic differences
means<-svypredmeans(agesexmodel, ~factor(race))
means
## relative risks compared to non-Hispanic white
svycontrast(means,quote(`1`/^2`))
svycontrast(means,quote(`3`/^2`))

data(api)
dstrat<-svydesign(id=~1,strata=~stype, weights=~pw, data=apistat, fpc=~fpc)
demog_model <- svyglm(api00~mobility+ell+hsg+meals, design=dstrat)
svypredmeans(demog_model,~enroll, predictat=c(100,300,1000,3000))
```

svyqqplot

*Quantile-quantile plots for survey data***Description**

Quantile-quantile plots either against a specified distribution function or comparing two variables from the same or different designs.

**Usage**

```
svyqqplot(formula, design, designx = NULL, na.rm = TRUE, qrule = "hf8",
  xlab = NULL, ylab = NULL, ...)
svyqqmath(x, design, null=qnorm, na.rm=TRUE, xlab="Expected",ylab="Observed",...)
```

**Arguments**

x, formula	A one-sided formula for svyqqmath or a two-sided formula for svyqqplot
design	Survey design object to look up variables
designx	Survey design object to look up the RHS variable in svyqqplot, if different from the LHS variable
null	Quantile function to compare the data quantiles to
na.rm	Remove missing values
qrule	How to define quantiles for svyqqplot – see <a href="#">svyquantile</a> for possible values

<code>xlab, ylab</code>	Passed to <code>plot</code> . For <code>svyqqplot</code> , if these are <code>NULL</code> they are replaced by the variable names
<code>...</code>	Graphical options to be passed to <code>plot</code>

**Value**

None

**See Also**[quantile qqnorm qqplot](#)**Examples**

```
data(api)

dstrat<-svydesign(id=~1, strata=~stype, weights=~pw, data=apistrat,
fpc=~fpc)

svyqqmath(~api99, design=dstrat)
svyqqplot(api00~api99, design=dstrat)

dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
opar<-par(mfrow=c(1,2))

## sample distributions very different
qqplot(apiclus1$enroll, apistrat$enroll); abline(0,1)

## estimated population distributions much more similar
svyqqplot(enroll~enroll, design=dstrat, designx=dclus1, qrule=survey::qrule_hf8); abline(0,1)
par(opar)
```

svyranktest

*Design-based rank tests***Description**

Design-based versions of k-sample rank tests. The built-in tests are all for location hypotheses, but the user could specify others.

**Usage**

```
svyranktest(formula, design,
  test = c("wilcoxon", "vanderWaerden", "median", "KruskalWallis"), ...)
```

**Arguments**

formula	Model formula $y \sim g$ for outcome variable $y$ and group $g$
design	A survey design object
test	Which rank test to use: Wilcoxon, van der Waerden's normal-scores test, Mood's test for the median, or a function $f(r, N)$ where $r$ is the rank and $N$ the estimated population size. "KruskalWallis" is a synonym for "wilcoxon" for more than two groups.
...	for future expansion

**Details**

These tests are for the null hypothesis that the population or superpopulation distributions of the response variable are different between groups, targeted at population or superpopulation alternatives. The 'ranks' are defined as quantiles of the pooled distribution of the variable, so they do not just go from 1 to  $N$ ; the null hypothesis does not depend on the weights, but the ranks do.

The tests reduce to the usual Normal approximations to the usual rank tests under iid sampling. Unlike the traditional rank tests, they are not exact in small samples.

**Value**

Object of class `htest`

Note that with more than two groups the `statistic` element of the return value holds the numerator degrees of freedom and the `parameter` element holds the test statistic.

**References**

Lumley, T., & Scott, A. J. (2013). Two-sample rank tests under complex sampling. *BIOMETRIKA*, 100 (4), 831-842.

**See Also**

[svytest](#), [svylogrank](#)

**Examples**

```
data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, fpc=~fpc, data=apiclus1)

svyranktest(ell~comp.imp, dclus1)
svyranktest(ell~comp.imp, dclus1, test="median")

svyranktest(ell~stype, dclus1)
svyranktest(ell~stype, dclus1, test="median")

str(svyranktest(ell~stype, dclus1))

## upper quartile
svyranktest(ell~comp.imp, dclus1, test=function(r,N) as.numeric(r>0.75*N))
```

```

quantiletest<-function(p){
  rval<-function(r,N) as.numeric(r>(N*p))
  attr(rval,"name")<-paste(p,"quantile")
  rval
}
svyranktest(ell~comp.imp, dclus1, test=quantiletest(0.5))
svyranktest(ell~comp.imp, dclus1, test=quantiletest(0.75))

## replicate weights

rclus1<-as.svrepdesign(dclus1)
svyranktest(ell~stype, rclus1)

```

---

svyratio

*Ratio estimation*


---

## Description

Ratio estimation and estimates of totals based on ratios for complex survey samples. Estimating domain (subpopulation) means can be done more easily with [svymean](#).

## Usage

```

## S3 method for class 'survey.design2'
svyratio(numerator=formula, denominator,
  design, separate=FALSE, na.rm=FALSE, formula, covmat=FALSE,
  deff=FALSE, influence=FALSE, ...)
## S3 method for class 'svyrep.design'
svyratio(numerator=formula, denominator, design,
  na.rm=FALSE, formula, covmat=FALSE, return.replicates=FALSE, deff=FALSE, ...)
## S3 method for class 'twophase'
svyratio(numerator=formula, denominator, design,
  separate=FALSE, na.rm=FALSE, formula, ...)
## S3 method for class 'svyratio'
predict(object, total, se=TRUE, ...)
## S3 method for class 'svyratio_separate'
predict(object, total, se=TRUE, ...)
## S3 method for class 'svyratio'
SE(object, ..., drop=TRUE)
## S3 method for class 'svyratio'
coef(object, ..., drop=TRUE)
## S3 method for class 'svyratio'
confint(object, parm, level = 0.95, df = Inf, ...)

```

**Arguments**

numerator, formula	formula, expression, or data frame giving numerator variable(s)
denominator	formula, expression, or data frame giving denominator variable(s)
design	survey design object
object	result of svyratio
total	vector of population totals for the denominator variables in object, or list of vectors of population stratum totals if separate=TRUE
se	Return standard errors?
separate	Estimate ratio separately for strata
na.rm	Remove missing values?
covmat	Compute the full variance-covariance matrix of the ratios
deff	Compute design effects
return.replicates	Return replicate estimates of ratios
influence	Return influence functions
drop	Return a vector rather than a matrix
parm	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
level	the confidence level required.
df	degrees of freedom for t-distribution in confidence interval, use degf(design) for number of PSUs minus number of strata
...	Other unused arguments for other methods

**Details**

The separate ratio estimate of a total is the sum of ratio estimates in each stratum. If the stratum totals supplied in the `total` argument and the strata in the design object both have names these names will be matched. If they do not have names it is important that the sample totals are supplied in the correct order, the same order as shown in the output of `summary(design)`.

When design is a two-phase design, stratification will be on the second phase.

**Value**

`svyratio` returns an object of class `svyratio`. The `predict` method returns a matrix of population totals and optionally a matrix of standard errors.

**Author(s)**

Thomas Lumley

**References**

Levy and Lemeshow. "Sampling of Populations" (3rd edition). Wiley

**See Also**[svydesign](#)[svymean](#) for estimating proportions and domain means[calibrate](#) for estimators related to the separate ratio estimator.**Examples**

```

data(scd)

## survey design objects
scddes<-svydesign(data=scd, prob=~1, id=~ambulance, strata=~ESA,
nest=TRUE, fpc=rep(5,6))
scdnofpc<-svydesign(data=scd, prob=~1, id=~ambulance, strata=~ESA,
nest=TRUE)

# convert to BRR replicate weights
scd2brr <- as.svrepdesign(scdnofpc, type="BRR")

# use BRR replicate weights from Levy and Lemeshow
repweights<-2*cbind(c(1,0,1,0,1,0), c(1,0,0,1,0,1), c(0,1,1,0,0,1),
c(0,1,0,1,1,0))
scdrep<-svrepdesign(data=scd, type="BRR", repweights=repweights)

# ratio estimates
svyratio(~alive, ~arrests, design=scddes)
svyratio(~alive, ~arrests, design=scdnofpc)
svyratio(~alive, ~arrests, design=scd2brr)
svyratio(~alive, ~arrests, design=scdrep)

data(api)
dstrat<-svydesign(id=~1, strata=~stype, weights=~pw, data=apistrat, fpc=~fpc)

## domain means are ratio estimates, but available directly
svyratio(~I(api.stu*(comp.imp=="Yes")), ~as.numeric(comp.imp=="Yes"), dstrat)
svymean(~api.stu, subset(dstrat, comp.imp=="Yes"))

## separate and combined ratio estimates of total
(sep<-svyratio(~api.stu, ~enroll, dstrat, separate=TRUE))
(com<-svyratio(~api.stu, ~enroll, dstrat))

stratum.totals<-list(E=1877350, H=1013824, M=920298)

predict(sep, total=stratum.totals)
predict(com, total=sum(unlist(stratum.totals)))

SE(com)
coef(com)
coef(com, drop=FALSE)
confint(com)

```

svyrecvar

*Variance estimation for multistage surveys***Description**

Compute the variance of a total under multistage sampling, using a recursive descent algorithm.

**Usage**

```
svyrecvar(x, clusters, stratas, fpcs, postStrata = NULL,
lonely.psu = getOption("survey.lonely.psu"),
one.stage=getOption("survey.ultimate.cluster"))
```

**Arguments**

<code>x</code>	Matrix of data or estimating functions
<code>clusters</code>	Data frame or matrix with cluster ids for each stage
<code>stratas</code>	Strata for each stage
<code>fpcs</code>	Information on population and sample size for each stage, created by <a href="#">as.fpc</a>
<code>postStrata</code>	post-stratification information as created by <a href="#">postStratify</a> or <a href="#">calibrate</a>
<code>lonely.psu</code>	How to handle strata with a single PSU
<code>one.stage</code>	If TRUE, compute a one-stage (ultimate-cluster) estimator

**Details**

The main use of this function is to compute the variance of the sum of a set of estimating functions under multistage sampling. The sampling is assumed to be simple or stratified random sampling within clusters at each stage except perhaps the last stage. The variance of a statistic is computed from the variance of estimating functions as described by Binder (1983).

Use `one.stage=FALSE` for compatibility with other software that does not perform multi-stage calculations, and set `options(survey.ultimate.cluster=TRUE)` to make this the default.

The idea of a recursive algorithm is due to Bellhouse (1985). Texts such as Cochran (1977) and Sarndal et al (1991) describe the decomposition of the variance into a single-stage between-cluster estimator and a within-cluster estimator, and this is applied recursively.

If `one.stage` is a positive integer it specifies the number of stages of sampling to use in the recursive estimator.

If `pps="brewer"`, standard errors are estimated using Brewer's approximation for PPS without replacement, option 2 of those described by Berger (2004). The `fpc` argument must then be specified in terms of sampling fractions, not population sizes (or omitted, but then the `pps` argument would have no effect and the with-replacement standard errors would be correct).

**Value**

A covariance matrix

## Note

A simple set of finite population corrections will only be exactly correct when each successive stage uses simple or stratified random sampling without replacement. A correction under general unequal probability sampling (eg PPS) would require joint inclusion probabilities (or, at least, sampling probabilities for units not included in the sample), information not generally available.

The quality of Brewer's approximation is excellent in Berger's simulations, but the accuracy may vary depending on the sampling algorithm used.

## References

- Bellhouse DR (1985) Computing Methods for Variance Estimation in Complex Surveys. *Journal of Official Statistics*. Vol.1, No.3, 1985
- Berger, Y.G. (2004), A Simple Variance Estimator for Unequal Probability Sampling Without Replacement. *Journal of Applied Statistics*, 31, 305-315.
- Binder, David A. (1983). On the variances of asymptotically normal estimators from complex surveys. *International Statistical Review*, 51, 279-292.
- Brewer KRW (2002) Combined Survey Sampling Inference (Weighing Basu's Elephants) [Chapter 9]
- Cochran, W. (1977) *Sampling Techniques*. 3rd edition. Wiley.
- Sarndal C-E, Swensson B, Wretman J (1991) *Model Assisted Survey Sampling*. Springer.

## See Also

[svrVar](#) for replicate weight designs

[svyCprod](#) for a description of how variances are estimated at each stage

## Examples

```
data(mu284)
dmu284<-svydesign(id=~id1+id2,fpc=~n1+n2, data=mu284)
svytotal(~y1, dmu284)

data(api)
# two-stage cluster sample
dclus2<-svydesign(id=~dnum+snum, fpc=~fpc1+fpc2, data=apiclus2)
summary(dclus2)
svymean(~api00, dclus2)
svytotal(~enroll, dclus2, na.rm=TRUE)

# bootstrap for multistage sample
mrbclus2<-as.svrepdesign(dclus2, type="mrb", replicates=100)
svytotal(~enroll, mrbclus2, na.rm=TRUE)

# two-stage `with replacement'
dclus2wr<-svydesign(id=~dnum+snum, weights=~pw, data=apiclus2)
summary(dclus2wr)
svymean(~api00, dclus2wr)
```

```
svytotal(~enroll, dclus2wr, na.rm=TRUE)
```

---

svyscoretest

*Score tests in survey regression models*


---

## Description

Performs two versions of the efficient score test. These are the same for a single parameter. In the working score test, different parameters are weighted according to the inverse of the estimated population Fisher information. In the pseudoscore test, parameters are weighted according to the inverse of their estimated covariance matrix.

## Usage

```
svyscoretest(model, drop.terms=NULL, add.terms=NULL,
method=c("working", "pseudoscore", "individual"), ddf=NULL,
lrt.approximation = "satterthwaite", ...)
## S3 method for class 'svyglm'
svyscoretest(model, drop.terms=NULL, add.terms=NULL,
method=c("working", "pseudoscore", "individual"), ddf=NULL,
lrt.approximation = "satterthwaite", fullrank=TRUE, ...)
```

## Arguments

<code>model</code>	A model of a class having a <code>svyscoretest</code> method (currently just <code>svyglm</code> )
<code>drop.terms</code>	Model formula giving terms to remove from <code>model</code>
<code>add.terms</code>	Model formula giving terms to add to <code>model</code>
<code>method</code>	The type of score test to use. For a single parameter they are equivalent. To report tests for each column separately use <code>individual</code>
<code>ddf</code>	denominator degrees of freedom for an F or linear combination of F distributions. Use <code>Inf</code> to get chi-squared distributions. <code>NULL</code> asks for the model residual degrees of freedom, which is conservative.
<code>lrt.approximation</code>	For the working score, the method for computing/approximating the null distribution: see <a href="#">pchisqsum</a>
<code>fullrank</code>	If <code>FALSE</code> and <code>method="individual"</code> , keep even linearly dependent columns of the efficient score
<code>...</code>	for future expansion

### Details

The working score test will be asymptotically equivalent to the Rao-Scott likelihood ratio test computed by [regTermTest](#) and [anova.svyglm](#). The paper by Rao, Scott and Skinner calls this a "naive" score test. The null distribution is a linear combination of chi-squared (or F) variables.

The pseudoscore test will be asymptotically equivalent to the Wald test computed by [regTermTest](#); it has a chi-squared (or F) null distribution.

If ddf is negative or zero, which can happen with large numbers of predictors and small numbers of PSUs, it will be changed to 1 with a warning.

### Value

For "pseudoscore" and "working" score methods, a named vector with the test statistic, degrees of freedom, and p-value. For "individual" an object of class "svystat"

### References

JNK Rao, AJ Scott, and C Rao, J., Scott, A., & Skinner, C. (1998). QUASI-SCORE TESTS WITH SURVEY DATA. *Statistica Sinica*, 8(4), 1059-1070.

### See Also

[regTermTest](#), [anova.svyglm](#)

### Examples

```
data(myco)
dmyco<-svydesign(id=~1, strata=~interaction(Age,leprosy),weights=~wt,data=myco)

m_full<-svyglm(leprosy~I((Age+7.5)^-2)+Scar, family=quasibinomial, design=dmyco)
svyscoretest(m_full, ~Scar)

svyscoretest(m_full,add.terms= ~I((Age+7.5)^-2):Scar)
svyscoretest(m_full,add.terms= ~factor(Age), method="pseudo")
svyscoretest(m_full,add.terms= ~factor(Age),method="individual",fullrank=FALSE)

svyscoretest(m_full,add.terms= ~factor(Age),method="individual")
```

---

svysmooth

---

*Scatterplot smoothing and density estimation*


---

### Description

Scatterplot smoothing and density estimation for probability-weighted data.

**Usage**

```
svysmooth(formula, design, ...)
## Default S3 method:
svysmooth(formula, design, method = c("locpoly", "quantreg"),
  bandwidth = NULL, quantile, df = 4, ...)
## S3 method for class 'svysmooth'
plot(x, which=NULL, type="l", xlabs=NULL, ylab=NULL,...)
## S3 method for class 'svysmooth'
lines(x,which=NULL,...)
make.panel.svysmooth(design,bandwidth=NULL)
```

**Arguments**

formula	One-sided formula for density estimation, two-sided for smoothing
design	Survey design object
method	local polynomial smoothing for the mean or regression splines for quantiles
bandwidth	Smoothing bandwidth for "locpoly" or NULL for automatic choice
quantile	quantile to be estimated for "quantreg"
df	Degrees of freedom for "quantreg"
which	Which plots to show (default is all)
type	as for plot
xlabs	Optional vector of x-axis labels
ylab	Optional y-axis label
...	More arguments
x	Object of class svysmooth

**Details**

svysmooth does one-dimensional smoothing. If formula has multiple predictor variables a separate one-dimensional smooth is performed for each one.

For method="locpoly" the extra arguments are passed to locpoly from the KernSmooth package, for method="quantreg" they are passed to rq from the quantreg package. The automatic choice of bandwidth for method="locpoly" uses the default settings for dpik and dpill in the KernSmooth package.

make.panel.svysmooth() makes a function that plots points and draws a weighted smooth curve through them, a weighted replacement for [panel.smooth](#) that can be passed to functions such as [termplot](#) or [plot.lm](#). The resulting function has a span argument that will set the bandwidth; if this is not specified the automatic choice will be used.

**Value**

An object of class svysmooth, a list of lists, each with x and y components.

**See Also**

[svyhist](#) for histograms

## Examples

```
data(api)
dstrat<-svydesign(id=~1,strata=~stype, weights=~pw, data=apistrat, fpc=~fpc)

smth<-svysmooth(api00~api99+ell,dstrat)
dens<-svysmooth(~api99, dstrat,bandwidth=30)
dens1<-svysmooth(~api99, dstrat)
qsmth<-svysmooth(api00~ell,dstrat, quantile=0.75, df=3,method="quantreg")

plot(smth)
plot(smth, which="ell",lty=2,ylim=c(500,900))
lines(qsmth, col="red")

svyhist(~api99,design=dstrat)
lines(dens,col="purple",lwd=3)
lines(dens1, col="forestgreen",lwd=2)

m<-svyglm(api00~sin(api99/100)+stype, design=dstrat)
termplot(m, data=model.frame(dstrat), partial.resid=TRUE, se=TRUE,
smooth=make.panel.svysmooth(dstrat))
```

---

svystandardize

*Direct standardization within domains*


---

## Description

In health surveys it is often of interest to standardize domains to have the same distribution of, eg, age as in a target population. The operation is similar to post-stratification, except that the totals for the domains are fixed at the current estimates, not at known population values. This function matches the estimates produced by the (US) National Center for Health Statistics.

## Usage

```
svystandardize(design, by, over, population, excluding.missing = NULL)
```

## Arguments

design	survey design object
by	A one-sided formula specifying the variables whose distribution will be standardised
over	A one-sided formula specifying the domains within which the standardisation will occur, or ~1 to use the whole population.
population	Desired population totals or proportions for the levels of combinations of variables in by
excluding.missing	Optionally, a one-sided formula specifying variables whose missing values should be dropped before calculating the domain totals.

**Value**

A new survey design object of the same type as the input.

**Note**

The standard error estimates do not exactly match the NCHS estimates

**References**

National Center for Health Statistics <https://www.cdc.gov/nchs/tutorials/NHANES/NHANESAnalyses/agestandardiz>

**See Also**

[postStratify](#), [svyby](#)

**Examples**

```
## matches http://www.cdc.gov/nchs/data/databriefs/db92_fig1.png
data(nhanes)
popage <- c( 55901 , 77670 , 72816 , 45364 )
design<-svydesign(id=~SDMVPSU, strata=~SDMVSTRA, weights=~WTMEC2YR, data=nhanes, nest=TRUE)
stdes<-svystandardize(design, by=~agecat, over=~race+RIAGENDR,
  population=popage, excluding.missing=~HI_CHOL)
svyby(~HI_CHOL, ~race+RIAGENDR, svymean, design=subset(stdes,
  agecat!="(0,19]"))
```

```
data(nhanes)
nhanes_design <- svydesign(ids = ~ SDMVPSU, strata = ~ SDMVSTRA,
  weights = ~ WTMEC2YR, nest = TRUE, data = nhanes)
```

```
## These are the same
nhanes_adj <- svystandardize(update(nhanes_design, all_adults = "1"),
  by = ~ agecat, over = ~ all_adults,
  population = c(55901, 77670, 72816, 45364),
  excluding.missing = ~ HI_CHOL)
svymean(~I(HI_CHOL == 1), nhanes_adj, na.rm = TRUE)
```

```
nhanes_adj <- svystandardize(nhanes_design,
  by = ~ agecat, over = ~ 1,
  population = c(55901, 77670, 72816, 45364),
  excluding.missing = ~ HI_CHOL)
svymean(~I(HI_CHOL == 1), nhanes_adj, na.rm = TRUE)
```

svysurvreg

*Fit accelerated failure models to survey data***Description**

This function calls `survreg` from the 'survival' package to fit accelerated failure (accelerated life) models to complex survey data, and then computes correct standard errors by linearisation. It has the same arguments as `survreg`, except that the second argument is `design` rather than `data`.

**Usage**

```
## S3 method for class 'survey.design'
svysurvreg(formula, design, weights=NULL, subset=NULL, ...)
```

**Arguments**

<code>formula</code>	Model formula
<code>design</code>	Survey design object, including two-phase designs
<code>weights</code>	Additional weights to multiply by the sampling weights. No, I don't know why you'd want to do that.
<code>subset</code>	subset to use in fitting (if needed)
<code>...</code>	Other arguments of <code>survreg</code>

**Value**

Object of class `svysurvreg`, with the same structure as a `survreg` object but with NA for the log-likelihood.

**Note**

The `residuals` method is identical to that for `survreg` objects except the `weighted` option defaults to `TRUE`

**Examples**

```
data(pbc, package="survival")
pbc$randomized <- with(pbc, !is.na(trt) & trt>0)
biasmodel<-glm(randomized~age*edema,data=pbc)
pbc$randprob<-fitted(biasmodel)
dpbc<-svydesign(id=~1, prob=~randprob, strata=~edema,
  data=subset(pbc,randomized))

model <- svysurvreg(Surv(time, status>0)~bili+protime+albumin, design=dpbc, dist="weibull")
summary(model)
```

svytable

*Contingency tables for survey data***Description**

Contingency tables and chisquared tests of association for survey data.

**Usage**

```
## S3 method for class 'survey.design'
svytable(formula, design, Ntotal = NULL, round = FALSE,...)
## S3 method for class 'svyrep.design'
svytable(formula, design,
Ntotal = sum(weights(design, "sampling")), round = FALSE,...)
## S3 method for class 'survey.design'
svychisq(formula, design,
  statistic = c("F", "Chisq", "Wald", "adjWald", "lincom",
    "saddlepoint", "wls-score"), na.rm=TRUE,...)
## S3 method for class 'svyrep.design'
svychisq(formula, design,
  statistic = c("F", "Chisq", "Wald", "adjWald", "lincom",
    "saddlepoint", "wls-score"), na.rm=TRUE,...)
## S3 method for class 'svytable'
summary(object,
  statistic = c("F", "Chisq", "Wald", "adjWald", "lincom", "saddlepoint"),...)
degf(design, ...)
## S3 method for class 'survey.design2'
degf(design, ...)
## S3 method for class 'svyrep.design'
degf(design, tol=1e-5,...)
```

**Arguments**

formula	Model formula specifying margins for the table (using + only)
design	survey object
statistic	See Details below
Ntotal	A population total or set of population stratum totals to normalise to.
round	Should the table entries be rounded to the nearest integer?
na.rm	Remove missing values
object	Output from svytable
...	For svytable these are passed to xtabs. Use exclude=NULL, na.action=na.pass to include NAs in the table
tol	Tolerance for <a href="#">qr</a> in computing the matrix rank

## Details

The `svytable` function computes a weighted crosstabulation. This is especially useful for producing graphics. It is sometimes easier to use `svytotal` or `svymean`, which also produce standard errors, design effects, etc.

The frequencies in the table can be normalised to some convenient total such as 100 or 1.0 by specifying the `Ntotal` argument. If the formula has a left-hand side the mean or sum of this variable rather than the frequency is tabulated.

The `Ntotal` argument can be either a single number or a data frame whose first column gives the (first-stage) sampling strata and second column the population size in each stratum. In this second case the `svytable` command performs ‘post-stratification’: tabulating and scaling to the population within strata and then adding up the strata.

As with other `xtabs` objects, the output of `svytable` can be processed by `f table` for more attractive display. The summary method for `svytable` objects calls `svychisq` for a test of independence.

`svychisq` computes first and second-order Rao-Scott corrections to the Pearson chisquared test, and two Wald-type tests.

The default (`statistic="F"`) is the Rao-Scott second-order correction. The p-values are computed with a Satterthwaite approximation to the distribution and with denominator degrees of freedom as recommended by Thomas and Rao (1990). The alternative `statistic="Chisq"` adjusts the Pearson chisquared statistic by a design effect estimate and then compares it to the chisquared distribution it would have under simple random sampling.

The `statistic="Wald"` test is that proposed by Koch et al (1975) and used by the SUDAAN software package. It is a Wald test based on the differences between the observed cells counts and those expected under independence. The adjustment given by `statistic="adjWald"` reduces the statistic when the number of PSUs is small compared to the number of degrees of freedom of the test. Thomas and Rao (1987) compare these tests and find the adjustment beneficial.

`statistic="lincom"` replaces the numerator of the Rao-Scott F with the exact asymptotic distribution, which is a linear combination of chi-squared variables (see `pchisqsum`, and `statistic="saddlepoint"` uses a saddlepoint approximation to this distribution. The `CompQuadForm` package is needed for `statistic="lincom"` but not for `statistic="saddlepoint"`. The saddlepoint approximation is especially useful when the p-value is very small (as in large-scale multiple testing problems).

`statistic="wls-score"` is an experimental implementation of the weighted least squares score test of Lipsitz et al (2015). It is not identical to that paper, for example, I think the denominator degrees of freedom need to be reduced by JK for a JxK table, not (J-1)(K-1). And it's very close to the "adjWald" test.

For designs using replicate weights the code is essentially the same as for designs with sampling structure, since the necessary variance computations are done by the appropriate methods of `svytotal` and `svymean`. The exception is that the degrees of freedom is computed as one less than the rank of the matrix of replicate weights (by `degf`).

At the moment, `svychisq` works only for 2-dimensional tables.

## Value

The table commands return an `xtabs` object, `svychisq` returns a `htest` object.

## Note

Rao and Scott (1984) leave open one computational issue. In computing ‘generalised design effects’ for these tests, should the variance under simple random sampling be estimated using the observed proportions or the the predicted proportions under the null hypothesis? `svychisq` uses the observed proportions, following simulations by Sribney (1998), and the choices made in Stata

## References

- Davies RB (1973). "Numerical inversion of a characteristic function" *Biometrika* 60:415-7
- P. Duchesne, P. Lafaye de Micheaux (2010) "Computing the distribution of quadratic forms: Further comparisons between the Liu-Tang-Zhang approximation and exact methods", *Computational Statistics and Data Analysis*, Volume 54, 858-862
- Koch, GG, Freeman, DH, Freeman, JL (1975) "Strategies in the multivariate analysis of data from complex surveys" *International Statistical Review* 43: 59-78
- Stuart R. Lipsitz, Garrett M. Fitzmaurice, Debajyoti Sinha, Nathanael Hevelone, Edward Giovannucci, and Jim C. Hu (2015) "Testing for independence in JxK contingency tables with complex sample survey data" *Biometrics* 71(3): 832-840
- Rao, JNK, Scott, AJ (1984) "On Chi-squared Tests For Multiway Contingency Tables with Proportions Estimated From Survey Data" *Annals of Statistics* 12:46-60.
- Sribney WM (1998) "Two-way contingency tables for survey or clustered data" *Stata Technical Bulletin* 45:33-49.
- Thomas, DR, Rao, JNK (1987) "Small-sample comparison of level and power for simple goodness-of-fit statistics under cluster sampling" *JASA* 82:630-636

## See Also

`svytotal` and `svymean` report totals and proportions by category for factor variables.

See `svyby` and `ftable.svystat` to construct more complex tables of summary statistics.

See `svyloglin` for loglinear models.

See `regTermTest` for Rao-Scott tests in regression models.

See <https://notstatschat.rbind.io/2019/06/08/design-degrees-of-freedom-brief-note/> for an explanation of the design degrees of freedom with replicate weights.

## Examples

```
data(api)
xtabs(~sch.wide+stype, data=apipop)

dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
summary(dclus1)

(tbl1 <- svytable(~sch.wide+stype, dclus1))
plot(tbl1)
fourfoldplot(svytable(~sch.wide+comp.imp+stype, design=dclus1, round=TRUE), conf.level=0)

svychisq(~sch.wide+stype, dclus1)
```

```
summary(tbl, statistic="Chisq")
svychisq(~sch.wide+stype, dclus1, statistic="adjWald")

rclus1 <- as.svrepdesign(dclus1)
summary(svytable(~sch.wide+stype, rclus1))
svychisq(~sch.wide+stype, rclus1, statistic="adjWald")
```

svyttest

*Design-based t-test***Description**

One-sample or two-sample t-test. This function is a wrapper for [svymean](#) in the one-sample case and for [svyglm](#) in the two-sample case. Degrees of freedom are `degf(design)-1` for the one-sample test and `degf(design)-2` for the two-sample case.

**Usage**

```
svyttest(formula, design, ...)
```

**Arguments**

<code>formula</code>	Formula, <code>outcome~group</code> for two-sample, <code>outcome~0</code> or <code>outcome~1</code> for one-sample. The group variable must be a factor or character with two levels, or be coded 0/1 or 1/2
<code>design</code>	survey design object
<code>...</code>	for methods

**Value**

Object of class `htest`

**See Also**

[t.test](#)

**Examples**

```
data(api)
dclus2<-svydesign(id=~dnum+snum, fpc=~fpc1+fpc2, data=apiclus2)
tt<-svyttest(enroll~comp.imp, dclus2)
tt
confint(tt, level=0.9)

svyttest(enroll~I(stype=="E"), dclus2)

svyttest(I(api00-api99)~0, dclus2)
```

---

trimWeights	<i>Trim sampling weights</i>
-------------	------------------------------

---

## Description

Trims very high or very low sampling weights to reduce the influence of outlying observations. In a replicate-weight design object, the replicate weights are also trimmed. The total amount trimmed is divided among the observations that were not trimmed, so that the total weight remains the same.

## Usage

```
trimWeights(design, upper = Inf, lower = -Inf, ...)
## S3 method for class 'survey.design2'
trimWeights(design, upper = Inf, lower = -Inf, strict=FALSE,...)
## S3 method for class 'svyrep.design'
trimWeights(design, upper = Inf, lower = -Inf,
strict=FALSE, compress=FALSE,...)
```

## Arguments

design	A survey design object
upper	Upper bound for weights
lower	Lower bound for weights
strict	The reapportionment of the ‘trimmings’ from the weights can push other weights over the limits. If trim=TRUE the function repeats the trimming iteratively to prevent this. For replicate-weight designs strict applies only to the trimming of the sampling weights.
compress	Compress the replicate weights after trimming.
...	Other arguments for future expansion

## Value

A new survey design object with trimmed weights.

## See Also

[calibrate](#) has a trim option for trimming the calibration adjustments.

## Examples

```
data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)

pop.totals<-c(`(Intercept)`=6194, stypeH=755, stypeM=1018,
api99=3914069)
dclus1g<-calibrate(dclus1, ~stype+api99, pop.totals)
```

```
summary(weights(dclus1g))
dclus1t<-trimWeights(dclus1g,lower=20, upper=45)
summary(weights(dclus1t))
dclus1tt<-trimWeights(dclus1g, lower=20, upper=45,strict=TRUE)
summary(weights(dclus1tt))

svymean(~api99+api00+stype, dclus1g)
svymean(~api99+api00+stype, dclus1t)
svymean(~api99+api00+stype, dclus1tt)
```

twophase

*Two-phase designs***Description**

In a two-phase design a sample is taken from a population and a subsample taken from the sample, typically stratified by variables not known for the whole population. The second phase can use any design supported for single-phase sampling. The first phase must currently be one-stage element or cluster sampling

**Usage**

```
twophase(id, strata = NULL, probs = NULL, weights = NULL, fpc = NULL,
subset, data, method=c("full","approx","simple"), pps=NULL)
twophasevar(x,design)
twophase2var(x,design)
```

**Arguments**

id	list of two formulas for sampling unit identifiers
strata	list of two formulas (or NULLs) for stratum identifies
probs	list of two formulas (or NULLs) for sampling probabilities
weights	Only for method="approx", list of two formulas (or NULLs) for sampling weights
fpc	list of two formulas (or NULLs) for finite population corrections
subset	formula specifying which observations are selected in phase 2
data	Data frame will all data for phase 1 and 2
method	"full" requires (much) more memory, but gives unbiased variance estimates for general multistage designs at both phases. "simple" or "approx" uses the standard error calculation from version 3.14 and earlier, which uses much less memory and is correct for designs with simple random sampling at phase one and stratified random sampling at phase two.
pps	With method="full", an optional list of two PPS specifications for <a href="#">svydesign</a> . At the moment, the phase-one element must be NULL
x	probability-weighted estimating functions
design	two-phase design

## Details

The population for the second phase is the first-phase sample. If the second phase sample uses stratified (multistage cluster) sampling without replacement and all the stratum and sampling unit identifier variables are available for the whole first-phase sample it is possible to estimate the sampling probabilities/weights and the finite population correction. These would then be specified as NULL.

Two-phase case-control and case-cohort studies in biostatistics will typically have simple random sampling with replacement as the first stage. Variances given here may differ slightly from those in the biostatistics literature where a model-based estimator of the first-stage variance would typically be used.

Variance computations are based on the conditioning argument in Section 9.3 of Sarndal et al. Method "full" corresponds exactly to the formulas in that reference. Method "simple" or "approx" (the two are the same) uses less time and memory but is exact only for some special cases. The most important special case is the two-phase epidemiologic designs where phase 1 is simple random sampling from an infinite population and phase 2 is stratified random sampling. See the tests directory for a worked example. The only disadvantage of method="simple" in these cases is that standardization of margins ([marginpred](#)) is not available.

For method="full", sampling probabilities must be available for each stage of sampling, within each phase. For multistage sampling this requires specifying either fpc or probs as a formula with a term for each stage of sampling. If no fpc or probs are specified at phase 1 it is treated as simple random sampling from an infinite population, and population totals will not be correctly estimated, but means, quantiles, and regression models will be correct.

The pps argument allows for PPS sampling at phase two (or eventually at phase one), and also for Poisson sampling at phase two as a model for non-response.

## Value

twophase returns an object of class twophase2 (for method="full") or twophase. The structure of twophase2 objects may change as unnecessary components are removed.

twophase2var and twophasevar return a variance matrix with an attribute containing the separate phase 1 and phase 2 contributions to the variance.

## References

- Sarndal CE, Swensson B, Wretman J (1992) "Model Assisted Survey Sampling" Springer.
- Breslow NE and Chatterjee N, Design and analysis of two-phase studies with binary outcome applied to Wilms tumour prognosis. "Applied Statistics" 48:457-68, 1999
- Breslow N, Lumley T, Ballantyne CM, Chambless LE, Kulick M. (2009) Improved Horvitz-Thompson estimation of model parameters from two-phase stratified samples: applications in epidemiology. Statistics in Biosciences. doi 10.1007/s12561-009-9001-6
- Lin, DY and Ying, Z (1993). Cox regression with incomplete covariate measurements. "Journal of the American Statistical Association" 88: 1341-1349.

## See Also

[svydesign](#), [svyrecvar](#) for multi\*stage\* sampling

`calibrate` for calibration (GREG) estimators.

`estWeights` for two-phase designs for missing data.

The "epi" and "phase1" vignettes for examples and technical details.

## Examples

```
## two-phase simple random sampling.
data(pbc, package="survival")
pbc$randomized<-with(pbc, !is.na(trt) & trt>0)
pbc$id<-1:nrow(pbc)
d2pbc<-twophase(id=list(~id,~id), data=pbc, subset=~randomized)
svymean(~bili, d2pbc)

## two-stage sampling as two-phase
data(mu284)
ii<-with(mu284, c(1:15, rep(1:5,n2[1:5]-3)))
mu284.1<-mu284[ii,]
mu284.1$id<-1:nrow(mu284.1)
mu284.1$sub<-rep(c(TRUE,FALSE),c(15,34-15))
dmu284<-svydesign(id=~id1+id2,fpc=~n1+n2, data=mu284)
## first phase cluster sample, second phase stratified within cluster
d2mu284<-twophase(id=list(~id1,~id),strata=list(NULL,~id1),
                  fpc=list(~n1,NULL),data=mu284.1,subset=~sub)
svytotal(~y1, dmu284)
svytotal(~y1, d2mu284)
svymean(~y1, dmu284)
svymean(~y1, d2mu284)

## case-cohort design: this example requires R 2.2.0 or later
library("survival")
data(nwtco)

## stratified on case status
dcchs<-twophase(id=list(~seqno,~seqno), strata=list(NULL,~rel),
               subset=~I(in.subcohort | rel), data=nwtco)
svycoxph(Surv(edrel,rel)~factor(stage)+factor(histol)+I(age/12), design=dcchs)

## Using survival::cch
subcoh <- nwtco$in.subcohort
selccoh <- with(nwtco, rel==1|subcoh==1)
ccoh.data <- nwtco[selccoh,]
ccoh.data$subcohort <- subcoh[selccoh]
cch(Surv(edrel, rel) ~ factor(stage) + factor(histol) + I(age/12), data =ccoh.data,
    subcoh = ~subcohort, id=~seqno, cohort.size=4028, method="LinYing")

## two-phase case-control
## Similar to Breslow & Chatterjee, Applied Statistics (1999) but with
## a slightly different version of the data set

nwtco$incc2<-as.logical(with(nwtco, ifelse(rel | instit==2,1,rbinom(nrow(nwtco),1,.1))))
dccb2<-twophase(id=list(~seqno,~seqno),strata=list(NULL,~interaction(rel,instit)),
```

```

    data=nwtco, subset=~incc2)
dccc8<-twophase(id=list(~seqno,~seqno),strata=list(NULL,~interaction(rel,stage,instit)),
    data=nwtco, subset=~incc2)
summary(glm(rel~factor(stage)*factor(histol),data=nwtco,family=binomial()))
summary(svyglm(rel~factor(stage)*factor(histol),design=dccc2,family=quasibinomial()))
summary(svyglm(rel~factor(stage)*factor(histol),design=dccc8,family=quasibinomial()))

## Stratification on stage is really post-stratification, so we should use calibrate()
gccc8<-calibrate(dccc2, phase=2, formula=~interaction(rel,stage,instit))
summary(svyglm(rel~factor(stage)*factor(histol),design=gccc8,family=quasibinomial()))

## For this saturated model calibration is equivalent to estimating weights.
pccc8<-calibrate(dccc2, phase=2,formula=~interaction(rel,stage,instit), calfun="rrz")
summary(svyglm(rel~factor(stage)*factor(histol),design=pccc8,family=quasibinomial()))

## Since sampling is SRS at phase 1 and stratified RS at phase 2, we
## can use method="simple" to save memory.
dccc8_simple<-twophase(id=list(~seqno,~seqno),strata=list(NULL,~interaction(rel,stage,instit)),
    data=nwtco, subset=~incc2,method="simple")
summary(svyglm(rel~factor(stage)*factor(histol),design=dccc8_simple,family=quasibinomial()))

```

---

update.survey.design    *Add variables to a survey design*

---

## Description

Update the data variables in a survey design, either with a formula for a new set of variables or with an expression for variables to be added.

## Usage

```

## S3 method for class 'survey.design'
update(object, ...)
## S3 method for class 'twophase'
update(object, ...)
## S3 method for class 'svyrep.design'
update(object, ...)
## S3 method for class 'DBIsvydesign'
update(object, ...)

```

## Arguments

object	a survey design object
...	Arguments tag=expr add a new variable tag computed by evaluating expr in the survey data.

**Details**

Database-backed objects may not have write access to the database and so `update` does not attempt to modify the database. The expressions are stored and are evaluated when the data is loaded.

If a set of new variables will be used extensively it may be more efficient to modify the database, either with SQL queries from the R interface or separately. One useful intermediate approach is to create a table with the new variables and a view that joins this table to the table of existing variables.

There is now a base-R function [transform](#) for adding new variables to a data frame, so I have added `transform` as a synonym for `update` for survey objects.

**Value**

A survey design object

**See Also**

[svydesign](#), [svrepdesign](#), [twophase](#)

**Examples**

```
data(api)
dstrat<-svydesign(id=~1,strata=~stype, weights=~pw, data=apistrat,
fpc=~fpc)
dstrat<-update(dstrat, apidiff=api00-api99)
svymean(~api99+api00+apidiff, dstrat)
```

---

weights.survey.design *Survey design weights*

---

**Description**

Extract weights from a survey design object.

**Usage**

```
## S3 method for class 'survey.design'
weights(object, ...)
## S3 method for class 'svyrep.design'
weights(object,
type=c("replication","sampling","analysis"), ...)
## S3 method for class 'survey_fpc'
weights(object,final=TRUE,...)
```

**Arguments**

<code>object</code>	Survey design object
<code>type</code>	Type of weights: "analysis" combines sampling and replication weights.
<code>final</code>	If FALSE return a data frame with sampling weights at each stage of sampling.
<code>...</code>	Other arguments ignored

**Value**

vector or matrix of weights

**See Also**

[svydesign](#), [svrepdesign](#), [as.fpc](#)

**Examples**

```
data(scd)

scddes<-svydesign(data=scd, prob=~1, id=~ambulance, strata=~ESA,
                 nest=TRUE, fpc=rep(5,6))
repweights<-2*cbind(c(1,0,1,0,1,0), c(1,0,0,1,0,1), c(0,1,1,0,0,1), c(0,1,0,1,1,0))
scdrep<-svrepdesign(data=scd, type="BRR", repweights=repweights)

weights(scdrep)
weights(scdrep, type="sampling")
weights(scdrep, type="analysis")
weights(scddes)
```

---

with.svyimputationList

*Analyse multiple imputations*

---

**Description**

Performs a survey analysis on each of the designs in a `svyimputationList` objects and returns a list of results suitable for `MIcombine`. The analysis may be specified as an expression or as a function.

**Usage**

```
## S3 method for class 'svyimputationList'
with(data, expr, fun, ...,multicore=getOption("survey.multicore"))
## S3 method for class 'svyimputationList'
subset(x, subset,...)
```

**Arguments**

<code>data, x</code>	A <code>svyimputationList</code> object
<code>expr</code>	An expression giving a survey analysis
<code>fun</code>	A function taking a survey design object as its argument
<code>...</code>	for future expansion
<code>multicore</code>	Use multicore package to distribute imputed data sets over multiple processors?
<code>subset</code>	An logical expression specifying the subset

**Value**

A list of the results from applying the analysis to each design object.

**See Also**

MIcombine, in the mitools package

**Examples**

```
library(mitools)
data.dir<-system.file("dta",package="mitools")
files.men<-list.files(data.dir,pattern="m\\.\\dta$",full=TRUE)
men<-imputationList(lapply(files.men, foreign::read.dta,
warn.missing.labels=FALSE))
files.women<-list.files(data.dir,pattern="f\\.\\dta$",full=TRUE)
women<-imputationList(lapply(files.women, foreign::read.dta,
warn.missing.labels=FALSE))
men<-update(men, sex=1)
women<-update(women,sex=0)
all<-rbind(men,women)

designs<-svydesign(id=~id, strata=~sex, data=all)
designs

results<-with(designs, svymean(~drkfre))

MIcombine(results)

summary(MIcombine(results))

repdesigns<-as.svrepdesign(designs, type="boot", replicates=50)
MIcombine(with(repdesigns, svymean(~drkfre)))
```

---

withPV.survey.design    *Analyse plausible values in surveys*

---

**Description**

Repeats an analysis for each of a set of 'plausible values' in a survey data set, returning a list suitable for mitools::MIcombine. The default method works for both standard and replicate-weight designs but not for two-phase designs.

**Usage**

```
## S3 method for class 'survey.design'
withPV(mapping, data, action, rewrite=TRUE, ...)
```

**Arguments**

mapping	A formula or list of formulas describing each variable in the analysis that has plausible values. The left-hand side of the formula is the name to use in the analysis; the right-hand side gives the names in the dataset.
data	A survey design object, as created by <code>svydesign</code> or <code>svrepdesign</code>
action	With <code>rewrite=TRUE</code> , a function taking a survey design object as its only argument, or a quoted expression. With <code>rewrite=FALSE</code> a function taking a survey design object as its only argument, or a quoted expression with <code>.DESIGN</code> referring to the survey design object to be used.
rewrite	Rewrite action before evaluating it (versus constructing new data sets)
...	For methods

**Value**

A list of the results returned by each evaluation of action, with the call as an attribute.

**See Also**

[with.svyimputationList](#)

**Examples**

```
if(require(mitools)){
  data(pisamaths, package="mitools")
  des<-svydesign(id=~SCHOOLID+STIDSTD, strata=~STRATUM, nest=TRUE,
    weights=~W_FSCHWT+condwt, data=pisamaths)

  oo<-options(survey.lonely.psu="remove")

  results<-withPV(list(maths~PV1MATH+PV2MATH+PV3MATH+PV4MATH+PV5MATH),
    data=des,
    action=quote(svyglm(maths~ST04Q01*(PCGIRLS+SMRATIO)+MATHEFF+OPENPS, design=des)),
    rewrite=TRUE)

  summary(MIcombine(results))
  options(oo)
}
```

---

withReplicates

---

*Compute variances by replicate weighting*


---

**Description**

Given a function or expression computing a statistic based on sampling weights, `withReplicates` evaluates the statistic and produces a replicate-based estimate of variance. `vcov.svrep.design` produces the variance estimate from a set of replicates and the design object.

**Usage**

```

withReplicates(design, theta,..., return.replicates=FALSE)
## S3 method for class 'svyrep.design'
withReplicates(design, theta, rho = NULL, ...,
               scale.weights=FALSE, return.replicates=FALSE)
## S3 method for class 'svrepvar'
withReplicates(design, theta, ..., return.replicates=FALSE)
## S3 method for class 'svrepstat'
withReplicates(design, theta, ..., return.replicates=FALSE)
## S3 method for class 'svyimputationList'
withReplicates(design, theta, ..., return.replicates=FALSE)
## S3 method for class 'svyrep.design'
vcov(object, replicates, centre,...)

```

**Arguments**

design	A survey design with replicate weights (eg from <a href="#">svrepdesign</a> ) or a suitable object with replicate parameter estimates
theta	A function or expression: see Details below
rho	If design uses BRR weights, rho optionally specifies the parameter for Fay's variance estimator.
...	Other arguments to theta
scale.weights	Divide the probability weights by their sum (can help with overflow problems)
return.replicates	Return the replicate estimates as well as the variance?
object	The replicate-weights design object used to create the replicates
replicates	A set of replicates
centre	The centering value for variance calculation. If object\$mse is TRUE this is the result of estimation using the sampling weights, and must be supplied. If object\$mse is FALSE the mean of the replicates is used and this argument is silently ignored.

**Details**

The method for `svyrep.design` objects evaluates a function or expression using the sampling weights and then each set of replicate weights. The method for `svrepvar` objects evaluates the function or expression on an estimated population covariance matrix and its replicates, to simplify multivariate statistics such as structural equation models.

For the `svyrep.design` method, if `theta` is a function its first argument will be a vector of weights and the second argument will be a data frame containing the variables from the design object. If it is an expression, the sampling weights will be available as the variable `.weights`. Variables in the design object will also be in scope. It is possible to use global variables in the expression, but unwise, as they may be masked by local variables inside `withReplicates`.

For the `svrepvar` method a function will get the covariance matrix as its first argument, and an expression will be evaluated with `.replicate` set to the variance matrix.

For the `svrepstat` method a function will get the point estimate, and an expression will be evaluated with `.replicate` set to each replicate. The method can only be used when the `svrepstat` object includes replicates.

The `svyimputationList` method runs `withReplicates` on each imputed design (which must be replicate-weight designs).

## Value

If `return.replicates=FALSE`, the weighted statistic, with the variance matrix as the "var" attribute. If `return.replicates=TRUE`, a list with elements `theta` for the usual return value and `replicates` for the replicates.

## See Also

[svrepdesign](#), [as.svrepdesign](#), [svrVar](#)

## Examples

```
data(scd)
repweights<-2*cbind(c(1,0,1,0,1,0), c(1,0,0,1,0,1), c(0,1,1,0,0,1),
c(0,1,0,1,1,0))
scdrep<-svrepdesign(data=scd, type="BRR", repweights=repweights)

a<-svratio(~alive, ~arrests, design=scdrep)
print(a$ratio)
print(a$var)
withReplicates(scdrep, quote(sum(.weights*alive)/sum(.weights*arrests)))
withReplicates(scdrep, function(w,data)
sum(w*data$alive)/sum(w*data$arrests))

data(api)
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
rclus1<-as.svrepdesign(dclus1)
varmat<-svyvar(~api00+api99+ell+meals+hsg+mobility,rclus1,return.replicates=TRUE)
withReplicates(varmat, quote( factanal(covmat=.replicate, factors=2)$unique) )

data(nhanes)
nhanesdesign <- svydesign(id=~SDMVPSU, strata=~SDMVSTRA, weights=~WTMEC2YR, nest=TRUE,data=nhanes)
logistic <- svyglm(HI_CHOL~race+agecat+RIAGENDR, design=as.svrepdesign(nhanesdesign),
family=quasibinomial, return.replicates=TRUE)
fitted<-predict(logistic, return.replicates=TRUE, type="response")
sensitivity<-function(pred,actual) mean(pred>0.1 & actual)/mean(actual)
withReplicates(fitted, sensitivity, actual=logistic$y)

## Not run:
library(quantreg)
data(api)
## one-stage cluster sample
dclus1<-svydesign(id=~dnum, weights=~pw, data=apiclus1, fpc=~fpc)
## convert to bootstrap
bclus1<-as.svrepdesign(dclus1,type="bootstrap", replicates=100)
```

```
## median regression
withReplicates(bclus1, quote(coef(rq(api00~api99, tau=0.5, weights=.weights))))

## End(Not run)

## pearson correlation
dstrat <- svydesign(id=~1, strata=~stype, weights=~pw, data=apistat, fpc=~fpc)
bstrat<- as.svrepdesign(dstrat, type="subbootstrap")

v <- svyvar(~api00+api99, bstrat, return.replicates=TRUE)
vcor<-cov2cor(as.matrix(v))[2,1]
vrepos<-v$replicates
correps<-apply(vrepos,1, function(v) v[2]/sqrt(v[1]*v[4]))

vcov(bstrat,correps, centre=vcor)
```

---

xdesign

---

*Crossed effects and other sparse correlations*


---

## Description

Defines a design object with multiple dimensions of correlation: observations that share any of the id variables are correlated, or you can supply an adjacency matrix or Matrix to specify which are correlated. Supports crossed designs (eg multiple raters of multiple objects) and non-nested observational correlation (eg observations sharing primary school or secondary school). Has methods for svymean, svytotal, svyglm (so far).

## Usage

```
xdesign(id = NULL, strata = NULL, weights = NULL, data, fpc = NULL,
adjacency = NULL, overlap = c("unbiased", "positive"), allow.non.binary = FALSE)
```

## Arguments

id	list of formulas specifying cluster identifiers for each clustering dimension (or NULL)
strata	Not implemented
weights	model formula specifying (sampling) weights
data	data frame containing all the variables
fpc	Not implemented
adjacency	Adjacency matrix or Matrix indicating which pairs of observations are correlated
overlap	See details below
allow.non.binary	If FALSE check that adjacency is a binary 0/1 or TRUE/FALSE matrix or Matrix.

## Details

Subsetting for these objects actually drops observations; it is not equivalent to just setting weights to zero as for survey designs. So, for example, a subset of a balanced design will not be a balanced design.

The `overlap` option controls double-counting of some variance terms. Suppose there are two clustering dimensions, `~a` and `~b`. If we compute variance matrices clustered on `a` and clustered on `b` and add them, observations that share both `a` and `b` will be counted twice, giving a positively biased estimator. We can subtract off a variance matrix clustered on combinations of `a` and `b` to give an unbiased variance estimator. However, the unbiased estimator is not guaranteed to be positive definite. In the references, Miglioretti and Heagerty use the `overlap="positive"` estimator and Cameron et al use the `overlap="unbiased"` estimator.

## Value

An object of class `xdesign`

## References

Miglioretti D, Heagerty PJ (2007) Marginal modeling of nonnested multilevel data using standard software. *Am J Epidemiol* 165(4):453-63

Cameron, A. C., Gelbach, J. B., & Miller, D. L. (2011). Robust Inference With Multiway Clustering. *Journal of Business & Economic Statistics*, 29(2), 238-249.

<https://notstatschat.rbind.io/2021/09/18/crossed-clustering-and-parallel-invention/>

## See Also

[salamander](#)

## Examples

```
## With one clustering dimension, is close to the with-replacement
## survey estimator, but not identical unless clusters are equal size
data(api)
dclus1r<-svydesign(id=~dnum, weights=~pw, data=apiclus1)
xclus1<-xdesign(id=list(~dnum), weights=~pw, data=apiclus1)
xclus1

svymean(~enroll,dclus1r)
svymean(~enroll,xclus1)

data(salamander)
xsalamander<-xdesign(id=list(~Male, ~Female), data=salamander,
  overlap="unbiased")
xsalamander
degf(xsalamander)
```

yrbs

*One variable from the Youth Risk Behaviors Survey, 2015.***Description**

Design information from the Youth Risk Behaviors Survey (YRBS), together with the single variable 'Never/Rarely wore bike helmet'. Used as an analysis example by CDC.

**Usage**

```
data("yrbs")
```

**Format**

A data frame with 15624 observations on the following 4 variables.

```
weight sampling weights
stratum sampling strata
psu primary sampling units
qn8 1=Yes, 2=No
```

**Source**

<https://ftp.cdc.gov/pub/Data/YRBS/2015smy/> for files

**References**

Centers for Disease Control and Prevention (2016) Software for Analysis of YRBS Data. [CRAN doesn't believe the URL is valid]

**Examples**

```
data(yrbs)

yrbs_design <- svydesign(id=~psu, weight=~weight, strata=~stratum,
  data=yrbs)
yrbs_design <- update(yrbs_design, qn8yes=2-qn8)

ci <- svyciprop(~qn8yes, yrbs_design, na.rm=TRUE, method="xlogit")
ci

## to print more digits: matches SUDAAN and SPSS exactly, per table 3 of reference
coef(ci)
SE(ci)
attr(ci,"ci")
```

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