

# Package ‘surveyCV’

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**Type** Package

**Title** Cross Validation Based on Survey Design

**Version** 0.2.0

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**Description** Functions to generate K-fold cross validation (CV) folds and CV test error estimates that take into account how a survey dataset's sampling design was constructed (SRS, clustering, stratification, and/or unequal sampling weights). You can input linear and logistic regression models, along with data and a type of survey design in order to get an output that can help you determine which model best fits the data using K-fold cross validation. Our paper on “K-Fold Cross-Validation for Complex Sample Surveys” by Wieczorek, Guerin, and McMahon (2022) [doi:10.1002/sta4.454](https://doi.org/10.1002/sta4.454) explains why differing how we take folds based on survey design is useful.

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

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**LazyData** TRUE

**Depends** R (>= 4.0)

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**VignetteBuilder** knitr

**URL** <https://github.com/ColbyStatSvyRsch/surveyCV/>

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cv.svy	<i>CV for survey data</i>
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## Description

This is a cross validation function designed for survey samples taken using a SRS, stratified, clustered, or clustered-and-stratified sampling design. Returns survey CV estimates of the mean loss for each model (MSE for linear models, or binary cross-entropy for logistic models).

## Usage

```
cv.svy(
  Data,
  formulae,
  nfolds = 5,
  strataID = NULL,
  clusterID = NULL,
  nest = FALSE,
  fpcID = NULL,
  method = c("linear", "logistic"),
  weightsID = NULL,
  useSvyForFolds = TRUE,
  useSvyForFits = TRUE,
  useSvyForLoss = TRUE,
  na.rm = FALSE
)
```

**Arguments**

Data	Dataframe of dataset to be used for CV
formulae	Vector of formulas (as strings) for the GLMs to be compared in cross validation
nfolds	Number of folds to be used during cross validation, defaults to 5
strataID	String of the variable name used to stratify during sampling, must be the same as in the dataset used
clusterID	String of the variable name used to cluster during sampling, must be the same as in the dataset used
nest	Specify nest = TRUE if clusters are nested within strata, defaults to FALSE
fpcID	String of the variable name used for finite population corrections, must be the same as in the dataset used, see <a href="#">svydesign</a> for details
method	String, must be either "linear" or "logistic", determines type of model fit during cross validation, defaults to linear
weightsID	String of the variable name in the dataset that contains sampling weights
useSvyForFolds	Specify useSvyForFolds = TRUE (default) to take svydesign into account when making folds; should not be set FALSE except for running simulations to understand the properties of surveyCV
useSvyForFits	Specify useSvyForFits = TRUE (default) to take svydesign into account when fitting models on training sets; should not be set FALSE except for running simulations to understand the properties of surveyCV
useSvyForLoss	Specify useSvyForLoss = TRUE (default) to take svydesign into account when calculating loss over test sets; should not be set FALSE except for running simulations to understand the properties of surveyCV
na.rm	Whether to drop cases with missing values when taking 'svymean' of test losses

**Details**

If you have already created a `svydesign` object or fitted a `svyglm`, you will probably prefer the convenience wrapper functions [cv.svydesign](#) or [cv.svyglm](#).

For models other than linear or logistic regression, you can use [folds.svy](#) or [folds.svydesign](#) to generate CV fold IDs that respect any stratification or clustering in the survey design. You can then carry out K-fold CV as usual, taking care to also use the survey design features and survey weights when fitting models in each training set and also when evaluating models against each test set.

**Value**

Object of class `svyestat`, which is a named vector of survey CV estimates of the mean loss (MSE for linear models, or binary cross-entropy for logistic models) for each model, with names `".Model_1"`, `".Model_2"`, etc. corresponding to the models provided in `formulae`; and with a `var` attribute giving the variances. See [surveysummary](#) for details.

**See Also**

[surveysummary](#), [svydesign](#)

[cv.svydesign](#) for a wrapper to use with a `svydesign` object, or [cv.svyglm](#) for a wrapper to use with a `svyglm` object

## Examples

```

# Compare CV MSEs and their SEs under 3 linear models
# for a stratified sample and a one-stage cluster sample,
# using data from the `survey` package
library(survey)
data("api", package = "survey")
# stratified sample
cv.svy(apistrat, c("api00~ell",
                  "api00~ell+meals",
                  "api00~ell+meals+mobility"),
       nfolds = 5, strataID = "stype", weightsID = "pw", fpcID = "fpc")
# one-stage cluster sample
cv.svy(apiclus1, c("api00~ell",
                  "api00~ell+meals",
                  "api00~ell+meals+mobility"),
       nfolds = 5, clusterID = "dnum", weightsID = "pw", fpcID = "fpc")

# Compare CV MSEs and their SEs under 3 linear models
# for a stratified cluster sample with clusters nested within strata
data(NSFG_data)
library(splines)
cv.svy(NSFG_data, c("income ~ ns(age, df = 2)",
                  "income ~ ns(age, df = 3)",
                  "income ~ ns(age, df = 4)"),
       nfolds = 4,
       strataID = "strata", clusterID = "SECU",
       nest = TRUE, weightsID = "wgt")

# Logistic regression example, using the same stratified cluster sample;
# instead of CV MSE, we calculate CV binary cross-entropy loss,
# where (as with MSE) lower values indicate better fitting models
# (NOTE: na.rm=TRUE is not usually ideal;
# it's used below purely for convenience, to keep the example short,
# but a thorough analysis would look for better ways to handle the missing data)
cv.svy(NSFG_data, c("KnowPreg ~ ns(age, df = 1)",
                  "KnowPreg ~ ns(age, df = 2)",
                  "KnowPreg ~ ns(age, df = 3)"),
       method = "logistic", nfolds = 4,
       strataID = "strata", clusterID = "SECU",
       nest = TRUE, weightsID = "wgt",
       na.rm = TRUE)

```

## Description

Wrapper function which takes a [svydesign](#) object and a vector of model formulas (as strings), and passes it into [cv.svy](#). Returns survey CV estimates of the mean loss for each model (MSE for linear models, or binary cross-entropy for logistic models).

## Usage

```
cv.svydesign(  
  design_object,  
  formulae,  
  nfolds = 5,  
  method = c("linear", "logistic"),  
  na.rm = FALSE  
)
```

## Arguments

design_object	Name of a svydesign object created using the survey package. We do not yet support use of probs or pps.
formulae	Vector of formulas (as strings) for the GLMs to be compared in cross validation
nfolds	Number of folds to be used during cross validation, defaults to 5
method	String, must be either "linear" or "logistic", determines type of model fit during cross validation, defaults to linear
na.rm	Whether to drop cases with missing values when taking 'svymean' of test losses

## Details

If you have already fitted a `svyglm`, you may prefer the convenience wrapper function `cv.svyglm`. For models other than linear or logistic regression, you can use `folds.svy` or `folds.svydesign` to generate CV fold IDs that respect any stratification or clustering in the survey design. You can then carry out K-fold CV as usual, taking care to also use the survey design features and survey weights when fitting models in each training set and also when evaluating models against each test set.

## Value

Object of class `svyestat`, which is a named vector of survey CV estimates of the mean loss (MSE for linear models, or binary cross-entropy for logistic models) for each model, with names `".Model_1"`, `".Model_2"`, etc. corresponding to the models provided in `formulae`; and with a `var` attribute giving the variances. See [surveysummary](#) for details.

## See Also

[surveysummary](#), [svydesign](#)  
[cv.svyglm](#) for a wrapper to use with a `svyglm` object

## Examples

```
# Compare CV MSEs and their SEs under 3 linear models  
# for a stratified sample and a one-stage cluster sample,  
# using data from the `survey` package  
library(survey)  
data("api", package = "survey")  
# stratified sample  
dstrat <- svydesign(id = ~1, strata = ~stype, weights = ~pw, data = apistrat,
```

```

      fpc = ~fpc)
cv.svydesign(formulae = c("api00~ell",
                        "api00~ell+meals",
                        "api00~ell+meals+mobility"),
            design_object = dstrat, nfolds = 5)
# one-stage cluster sample
dclus1 <- svydesign(id = ~dnum, weights = ~pw, data = apiclus1, fpc = ~fpc)
cv.svydesign(formulae = c("api00~ell",
                        "api00~ell+meals",
                        "api00~ell+meals+mobility"),
            design_object = dclus1, nfolds = 5)

# Compare CV MSEs and their SEs under 3 linear models
# for a stratified cluster sample with clusters nested within strata
data(NSFG_data)
library(splines)
NSFG.svydes <- svydesign(id = ~SECU, strata = ~strata, nest = TRUE,
                      weights = ~wgt, data = NSFG_data)
cv.svydesign(formulae = c("income ~ ns(age, df = 2)",
                        "income ~ ns(age, df = 3)",
                        "income ~ ns(age, df = 4)"),
            design_object = NSFG.svydes, nfolds = 4)

# Logistic regression example, using the same stratified cluster sample;
# instead of CV MSE, we calculate CV binary cross-entropy loss,
# where (as with MSE) lower values indicate better fitting models
# (NOTE: na.rm=TRUE is not usually ideal;
# it's used below purely for convenience, to keep the example short,
# but a thorough analysis would look for better ways to handle the missing data)
cv.svydesign(formulae = c("KnowPreg ~ ns(age, df = 1)",
                        "KnowPreg ~ ns(age, df = 2)",
                        "KnowPreg ~ ns(age, df = 3)"),
            design_object = NSFG.svydes, nfolds = 4,
            method = "logistic", na.rm = TRUE)

```

---

cv.svyglm

*CV for svyglm objects*


---

## Description

Wrapper function which takes a [svyglm](#) object (which itself contains a [svydesign](#) object) and passes it through [cv.svydesign](#) to [cv.svy](#). Chooses linear or logistic regression based on the [svyglm](#) object's value of family. Returns survey CV estimates of the mean loss for each model (MSE for linear models, or binary cross-entropy for logistic models).

## Usage

```
cv.svyglm(glm_object, nfolds = 5, na.rm = FALSE)
```



```

NSFG.svyglm <- svyglm(income ~ ns(age, df = 3), design = NSFG.svydes)
cv.svyglm(glm_object = NSFG.svyglm, nfolds = 4)

# Logistic regression example, using the same stratified cluster sample;
# instead of CV MSE, we calculate CV binary cross-entropy loss,
# where (as with MSE) lower values indicate better fitting models
# (NOTE: na.rm=TRUE is not usually ideal;
# it's used below purely for convenience, to keep the example short,
# but a thorough analysis would look for better ways to handle the missing data)
NSFG.svyglm.logreg <- svyglm(KnowPreg ~ ns(age, df = 2),
                             design = NSFG.svydes, family = quasibinomial())
cv.svyglm(glm_object = NSFG.svyglm.logreg, nfolds = 4, na.rm = TRUE)

```

---

folds.svy

*Creating CV folds based on the survey design*


---

## Description

This function creates a fold ID for each row in the dataset, to be used for carrying out cross validation on survey samples taken using a SRS, stratified, clustered, or clustered-and-stratified sampling design. Returns a vector of fold IDs, which in most cases you will want to append to your dataset using `cbind` or similar (see Examples below). These fold IDs respect any stratification or clustering in the survey design. You can then carry out K-fold CV as usual, taking care to also use the survey design features and survey weights when fitting models in each training set and also when evaluating models against each test set.

## Usage

```
folds.svy(Data, nfolds, strataID = NULL, clusterID = NULL)
```

## Arguments

<code>Data</code>	Dataframe of dataset
<code>nfolds</code>	Number of folds to be used during cross validation
<code>strataID</code>	String of the variable name used to stratify during sampling, must be the same as in the dataset used
<code>clusterID</code>	String of the variable name used to cluster during sampling, must be the same as in the dataset used

## Details

If you have already created a `svydesign` object, you will probably prefer the convenience wrapper function [folds.svydesign](#).

For the special cases of linear or logistic GLMs, use instead [cv.svy](#), [cv.svydesign](#), or [cv.svyglm](#) which will automate the whole CV process for you.



**Value**

Integer vector of fold IDs with length `nrow(Data)`. Most likely you will want to append the returned vector to your dataset, for instance with `cbind` (see Examples below).

**See Also**

[folds.svydesign](#) for a wrapper to use with a `svydesign` object

[cv.svy](#), [cv.svydesign](#), or [cv.svyglm](#) to carry out the whole CV process (not just forming folds but also training and testing your models) for linear or logistic regression models

**Examples**

```
# Set up CV folds for a stratified sample and a one-stage cluster sample,
# using data from the `survey` package
library(survey)
data("api", package = "survey")
# stratified sample
apistrat <- cbind(apistrat,
                  .foldID = folds.svy(apistrat, nfolds = 5, strataID = "stype"))
# Each fold will have observations from every stratum
with(apistrat, table(stype, .foldID))
# Fold sizes should be roughly equal
table(apistrat$.foldID)
#
# one-stage cluster sample
apiclus1 <- cbind(apiclus1,
                  .foldID = folds.svy(apiclus1, nfolds = 5, clusterID = "dnum"))
# For any given cluster, all its observations will be in the same fold;
# and each fold should contain roughly the same number of clusters
with(apiclus1, table(dnum, .foldID))
# But if cluster sizes are unequal,
# the number of individuals per fold will also vary
table(apiclus1$.foldID)
# See the end of `intro` vignette for an example of using such folds
# as part of a custom loop over CV folds
# to tune parameters in a design-consistent random forest model
```

---

folds.svydesign

*Creating CV folds based on the svydesign object*


---

**Description**

Wrapper function which takes a [svydesign](#) object and desired number of CV folds, and passes it into [folds.svy](#). Returns a vector of fold IDs, which in most cases you will want to append to your `svydesign` object using `update.svydesign` (see Examples below). These fold IDs respect any stratification or clustering in the survey design. You can then carry out K-fold CV as usual, taking care to also use the survey design features and survey weights when fitting models in each training set and also when evaluating models against each test set.

**Usage**

```
folds.svydesign(design_object, nfolders)
```

**Arguments**

`design_object` Name of a `svydesign` object created using the `survey` package. The arguments `id` and `strata` (if used) must be specified as formulas, e.g. `svydesign(ids = ~MyPSUs, ...)`.

`nfolders` Number of folds to be used during cross validation

**Details**

For the special cases of linear or logistic GLMs, use instead `cv.svydesign` or `cv.svyglm` which will automate the whole CV process for you.

**Value**

Integer vector of fold IDs with length `nrow(Data)`. Most likely you will want to append the returned vector to the `svydesign` object, for instance with `update.svydesign` (see Examples below).

**See Also**

[folds.svy](#)

[cv.svy](#), [cv.svydesign](#), or [cv.svyglm](#) to carry out the whole CV process (not just forming folds but also training and testing your models) for linear or logistic regression models

**Examples**

```
# Set up CV folds for a stratified sample and a one-stage cluster sample,
# using data from the `survey` package
library(survey)
data("api", package = "survey")
# stratified sample
dstrat <- svydesign(id = ~1, strata = ~stype, weights = ~pw, data = apistrat,
                  fpc = ~fpc)
dstrat <- update(dstrat, .foldID = folds.svydesign(dstrat, nfolders = 5))
# Each fold will have observations from every stratum
with(dstrat$variables, table(stype, .foldID))
# Fold sizes should be roughly equal
table(dstrat$variables$.foldID)
#
# one-stage cluster sample
dclus1 <- svydesign(id = ~dnum, weights = ~pw, data = apiclus1, fpc = ~fpc)
dclus1 <- update(dclus1, .foldID = folds.svydesign(dclus1, nfolders = 5))
# For any given cluster, all its observations will be in the same fold;
# and each fold should contain roughly the same number of clusters
with(dclus1$variables, table(dnum, .foldID))
# But if cluster sizes are unequal,
# the number of individuals per fold will also vary
table(dclus1$variables$.foldID)
```

```
# See the end of `intro` vignette for an example of using such folds
# as part of a custom loop over CV folds
# to tune parameters in a design-consistent random forest model
```

---

NSFG_data	<i>Subset of the 2015-2017 National Survey of Family Growth (NSFG): one birth per respondent.</i>
-----------	---

---

## Description

We downloaded this data from the NSFG website and cleaned it following an approach posted to RPosts by Hunter Ratliff.

## Usage

```
NSFG_data
```

## Format

A data frame with 2801 rows and 17 variables:

**CASEID** Respondent ID number (per respondent, not per pregnancy)

**LBW** (originally LBW1) Low birthweight (TRUE/FALSE) for the 1st baby from this pregnancy

**PreMe** (recode of WKSGEST) Whether gestational age was premature (below 37 weeks) or full term

**gotPNcare** (recode of BGNPRENA) Whether or not respondent got prenatal care in first trimester (before 13 weeks)

**KnowPreg** (recode of KNEWPREG) Whether or not respondent learned she was pregnant by 6 weeks

**age** (originally AGECON) Age at time of conception

**income** (originally POVERTY) Income as percent of poverty level, so that 100 = income is at the poverty line; topcoded at 500

**YrEdu** (originally EDUCAT) Education (number of years of schooling)

**race** (originally HISPRACE) Race & Hispanic origin of respondent

**BMI** Body Mass Index

**PregNum** (originally PREGNUM) Respondent's total number of pregnancies

**eduCat** (originally HIEDUC) Highest completed year of school or highest degree received

**GA** (originally WKSGEST) Gestational length of completed pregnancy (in weeks)

**Wanted** (recode of NEWWANTR) Whether or not pregnancy came at right time according to respondent (rather than too soon, too late, or unwanted)

**wgt** (originally WGT2015\_2017) Final weight for the 2015-2017 NSFG (at the respondent level, not pregnancy level)

**SECU** Randomized version of cluster ID, or "sampling error computational unit" – these are nested within strata

**strata** (originally SEST) Randomized version of stratum ID

**Details**

Note that these data were filtered down to include only:

- live births, - with gestational ages below 45 weeks, - born to mothers who were aged 20-40 years old at time of conception;

...then filtered further down to only the *\*first\** such birth per respondent.

Also note that SECUs = Sampling Error Computation Units are effectively pseudo-PSUs, nested within (pseudo-)strata. See page 35 of the NSFG 2011-2013 sample design documentation for details.

**Source**

[https://www.cdc.gov/nchs/nsfg/nsfg\\_2015\\_2017\\_puf.htm](https://www.cdc.gov/nchs/nsfg/nsfg_2015_2017_puf.htm)

[https://rpubs.com/HunterRatliff1/NSFG\\_Wrangle](https://rpubs.com/HunterRatliff1/NSFG_Wrangle)

[https://www.cdc.gov/nchs/data/nsfg/nsfg\\_2011\\_2013\\_sampledesign.pdf](https://www.cdc.gov/nchs/data/nsfg/nsfg_2011_2013_sampledesign.pdf)

---

NSFG_data_everypreg	<i>Subset of the 2015-2017 National Survey of Family Growth (NSFG): all live births per respondent.</i>
---------------------	---

---

**Description**

Same as 'NSFG\_data' but using *\*every\** birth, not just the *\*first\** birth, out of the initial subset there (live births with gestational age < 45 weeks for mothers aged 20 to 40 at time of conception).

**Usage**

NSFG\_data\_everypreg

**Format**

A data frame with 5089 rows and 17 variables

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surveyCV	<i>surveyCV: Cross Validation Based on Survey Design</i>
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**Description**

Functions to generate K-fold cross validation (CV) folds and CV test error estimates that take into account how a survey dataset's sampling design was constructed (SRS, clustering, stratification, and/or unequal sampling weights). You can input linear and logistic regression models, along with data and a type of survey design in order to get an output that can help you determine which model best fits the data using K-fold cross validation. Our paper on "K-Fold Cross-Validation for Complex Sample Surveys" by Wieczorek, Guerin, and McMahon (2022) <doi: [10.1002/sta4.454](https://doi.org/10.1002/sta4.454)> explains why differing how we take folds based on survey design is useful.

**Details**

The code for this package seeks to create an alternative for the [boot::cv.glm](#) function, so that results correctly account for survey designs during K-fold cross validation.

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