# STATA SURVEY DATA REFERENCE MANUAL

## RELEASE 19

A Stata Press Publication
StataCorp LLC
College Station, Texas


Version 19

Published by Stata Press, 4905 Lakeway Drive, College Station, Texas 77845

ISBN-10: 1-59718-446-2
ISBN-13: 978-1-59718-446-5



The suggested citation for this software is

> StataCorp. 2025. *Stata 19*. Statistical software. StataCorp LLC.

The suggested citation for this manual is

> StataCorp. 2025. *Stata 19 Survey Data Reference Manual*. College Station, TX: Stata Press.

# Contents

# Cross-referencing the documentation

When reading this manual, you will find references to other Stata manuals, for example, **[U] 27 Overview of Stata estimation commands**; [R] **regress**; and [D] **reshape**. The first example is a reference to chapter 27, *Overview of Stata estimation commands*, in the *User's Guide*; the second is a reference to the `regress` entry in the *Base Reference Manual*; and the third is a reference to the `reshape` entry in the *Data Management Reference Manual*.

All the manuals in the Stata Documentation have a shorthand notation:

| | |
|---|---|
| [GSM] | *Getting Started with Stata for Mac* |
| [GSU] | *Getting Started with Stata for Unix* |
| [GSW] | *Getting Started with Stata for Windows* |
| [U] | *Stata User's Guide* |
| [R] | *Stata Base Reference Manual* |
| [ADAPT] | *Stata Adaptive Designs: Group Sequential Trials Reference Manual* |
| [BAYES] | *Stata Bayesian Analysis Reference Manual* |
| [BMA] | *Stata Bayesian Model Averaging Reference Manual* |
| [CAUSAL] | *Stata Causal Inference and Treatment-Effects Estimation Reference Manual* |
| [CM] | *Stata Choice Models Reference Manual* |
| [D] | *Stata Data Management Reference Manual* |
| [DSGE] | *Stata Dynamic Stochastic General Equilibrium Models Reference Manual* |
| [ERM] | *Stata Extended Regression Models Reference Manual* |
| [FMM] | *Stata Finite Mixture Models Reference Manual* |
| [FN] | *Stata Functions Reference Manual* |
| [G] | *Stata Graphics Reference Manual* |
| [H2OML] | *Machine Learning in Stata Using H2O: Ensemble Decision Trees Reference Manual* |
| [IRT] | *Stata Item Response Theory Reference Manual* |
| [LASSO] | *Stata Lasso Reference Manual* |
| [XT] | *Stata Longitudinal-Data/Panel-Data Reference Manual* |
| [META] | *Stata Meta-Analysis Reference Manual* |
| [ME] | *Stata Multilevel Mixed-Effects Reference Manual* |
| [MI] | *Stata Multiple-Imputation Reference Manual* |
| [MV] | *Stata Multivariate Statistics Reference Manual* |
| [PSS] | *Stata Power, Precision, and Sample-Size Reference Manual* |
| [P] | *Stata Programming Reference Manual* |
| [RPT] | *Stata Reporting Reference Manual* |
| [SP] | *Stata Spatial Autoregressive Models Reference Manual* |
| [SEM] | *Stata Structural Equation Modeling Reference Manual* |
| [SVY] | *Stata Survey Data Reference Manual* |
| [ST] | *Stata Survival Analysis Reference Manual* |
| [TABLES] | *Stata Customizable Tables and Collected Results Reference Manual* |
| [TS] | *Stata Time-Series Reference Manual* |
| [I] | *Stata Index* |
| [M] | *Mata Reference Manual* |

## Description

This manual documents the survey data commands and is referred to as [SVY] in references.

After this entry, [SVY] **Survey** provides an overview of the survey commands. This manual is arranged alphabetically. If you are new to Stata's survey data commands, we recommend that you read the following sections first:

| | |
|---|---|
| [SVY] **Survey** | Introduction to survey commands |
| [SVY] **svyset** | Declare survey design for dataset |
| [SVY] **svydescribe** | Describe survey data |
| [SVY] **svy estimation** | Estimation commands for survey data |
| [SVY] **svy postestimation** | Postestimation tools for svy |

Stata is continually being updated, and Stata users are continually writing new commands. To find out about the latest survey data features, type `search survey` after installing the latest official updates; see [R] **update**.

## Also see

**[U] 1.3 What's new**

[R] **Intro** — Introduction to base reference manual

**Survey** — Introduction to survey commands

Description Remarks and examples Acknowledgments References Also see

# Description

The *Survey Data Reference Manual* is organized alphabetically, making it easy to find an individual entry if you know the name of a command. This overview organizes and presents the commands conceptually, that is, according to the similarities in the functions they perform.

### Survey design tools

| | |
|---|---|
| [SVY] **svyset** | Declare survey design for dataset |
| [SVY] **svydescribe** | Describe survey data |

### Survey data analysis tools

| | |
|---|---|
| [SVY] **svy** | The survey prefix command |
| [SVY] **svy estimation** | Estimation commands for survey data |
| [SVY] **svy: tabulate oneway** | One-way tables for survey data |
| [SVY] **svy: tabulate twoway** | Two-way tables for survey data |
| [SVY] **svy postestimation** | Postestimation tools for svy |
| [SVY] **estat** | Postestimation statistics for survey data, such as design effects |
| [SVY] **svy bootstrap** | Bootstrap for survey data |
| [SVY] ***bootstrap_options*** | More options for bootstrap variance estimation |
| [SVY] **svy brr** | Balanced repeated replication for survey data |
| [SVY] ***brr_options*** | More options for BRR variance estimation |
| [SVY] **svy jackknife** | Jackknife estimation for survey data |
| [SVY] ***jackknife_options*** | More options for jackknife variance estimation |
| [SVY] **svy sdr** | Successive difference replication for survey data |
| [SVY] ***sdr_options*** | More options for SDR variance estimation |

### Survey data concepts

| | |
|---|---|
| [SVY] **Variance estimation** | Variance estimation for survey data |
| [SVY] **Subpopulation estimation** | Subpopulation estimation for survey data |
| [SVY] **Calibration** | Calibration for survey data |
| [SVY] **Direct standardization** | Direct standardization of means, proportions, and ratios |
| [SVY] **Poststratification** | Poststratification for survey data |

### Tools for programmers of new survey commands

| | |
|---|---|
| [SVY] **ml for svy** | Maximum pseudolikelihood estimation for survey data |
| [SVY] **svymarkout** | Mark observations for exclusion on the basis of survey characteristics |

# Remarks and examples

Remarks are presented under the following headings:



## Introduction

Stata's facilities for survey data analysis are centered around the `svy` prefix command. After you identify the survey design characteristics with the `svyset` command, prefix the estimation commands in your data analysis with "`svy:`". For example, where you would normally use the `regress` command to fit a linear regression model for nonsurvey data, use `svy: regress` to fit a linear regression model for your survey data.

Why should you use the `svy` prefix command when you have survey data? To answer this question, we need to discuss some of the characteristics of survey design and survey data collection because these characteristics affect how we must perform our analysis if we want to get it right.

Survey data are characterized by the following:

- Sampling weights, also called probability weights—`pweights` in Stata's terminology
- Cluster sampling
- Stratification

These features arise from the design and details of the data collection procedure. Here's a brief description of how these design features affect the analysis of the data:

- *Sampling weights*. In sample surveys, observations are selected through a random process, but different observations may have different probabilities of selection. Weights are equal to (or proportional to) the inverse of the probability of being sampled. Various postsampling adjustments to the weights are sometimes made, as well. A weight of $w_j$ for the $j$th observation means, roughly speaking, that the $j$th observation represents $w_j$ elements in the population from which the sample was drawn.

  Omitting weights from the analysis results in estimates that may be biased, sometimes seriously so. Sampling weights also play a role in estimating standard errors.

- *Clustering*. Individuals are not sampled independently in most survey designs. Collections of individuals (for example, counties, city blocks, or households) are typically sampled as a group, known as a *cluster*.

  There may also be further subsampling within the clusters. For example, counties may be sampled, then city blocks within counties, then households within city blocks, and then finally persons within households. The clusters at the first level of sampling are called *primary sampling units* (PSUs)—in this example, counties are the PSUs. In the absence of clustering, the PSUs are defined to be the individuals, or, equivalently, clusters, each of size one.

  Cluster sampling typically results in larger sample-to-sample variability than sampling individuals directly. This increased variability must be accounted for in standard error estimates, hypothesis testing, and other forms of inference.

- *Stratification.* In surveys, different groups of clusters are often sampled separately. These groups are called *strata*. For example, the 254 counties of a state might be divided into two strata, say, urban counties and rural counties. Then 10 counties might be sampled from the urban stratum, and 15 from the rural stratum.

  Sampling is done independently across strata; the stratum divisions are fixed in advance. Thus strata are statistically independent and can be analyzed as such. When the individual strata are more homogeneous than the population as a whole, the homogeneity can be exploited to produce smaller (and honestly so) estimates of standard errors.

To put it succinctly: using sampling weights is important to get the point estimates right. We must consider the weighting, clustering, and stratification of the survey design to get the standard errors right. If our analysis ignores the clustering in our design, we would probably produce standard errors that are smaller than they should be. Stratification can be used to get smaller standard errors for a given overall sample size.

For more detailed introductions to complex survey data analysis, see Cochran (1977); Heeringa, West, and Berglund (2017); Kish (1965); Levy and Lemeshow (2008); Scheaffer et al.; (2012); Skinner, Holt, and Smith (1989); Stuart (1984); Thompson (2012); and Williams (1978).

## Survey design tools

Before using `svy`, first take a quick look at [SVY] **svyset**. Use the `svyset` command to specify the variables that identify the survey design characteristics and default method for estimating standard errors. Once set, `svy` will automatically use these design specifications until they are cleared or changed or a new dataset is loaded into memory.

As the following two examples illustrate, `svyset` allows you to identify a wide range of complex sampling designs. First, we show a simple single-stage design and then a complex multistage design.

### ▷ Example 1: Survey data from a one-stage design

A commonly used single-stage survey design uses clustered sampling across several strata, where the clusters are sampled without replacement. In a Stata dataset composed of survey data from this design, the survey design variables identify information about the strata, PSUs (clusters), sampling weights, and finite population correction. Here we use `svyset` to specify these variables, respectively named `strata`, `su1`, `pw`, and `fpc1`.

```
. use https://www.stata-press.com/data/r19/stage5a
. svyset su1 [pweight=pw], strata(strata) fpc(fpc1)
Sampling weights: pw
             VCE: linearized
     Single unit: missing
        Strata 1: strata
 Sampling unit 1: su1
           FPC 1: fpc1
```

In addition to the variables we specified, `svyset` reports that the default method for estimating standard errors is Taylor linearization and that `svy` will report missing values for the standard errors when it encounters a stratum with one sampling unit (also called singleton strata).

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## ▷ Example 2: Multistage survey data

We have (fictional) data on American high school seniors (12th graders), and the data were collected according to the following multistage design. In the first stage, counties were independently selected within each state. In the second stage, schools were selected within each chosen county. Within each chosen school, a questionnaire was filled out by every attending high school senior. We have entered all the information into a Stata dataset called `multistage.dta`.

The survey design variables are as follows:

- `state` contains the stratum identifiers.
- `county` contains the first-stage sampling units.
- `ncounties` contains the total number of counties within each state.
- `school` contains the second-stage sampling units.
- `nschools` contains the total number of schools within each county.
- `sampwgt` contains the sampling weight for each sampled individual.

Here we load the dataset into memory and use `svyset` with the above variables to declare that these data are survey data.

```
. use https://www.stata-press.com/data/r19/multistage
. svyset county [pw=sampwgt], strata(state) fpc(ncounties) || school,
> fpc(nschools)
Sampling weights: sampwgt
             VCE: linearized
     Single unit: missing
        Strata 1: state
 Sampling unit 1: county
           FPC 1: ncounties
        Strata 2: <one>
 Sampling unit 2: school
           FPC 2: nschools
. save highschool
file highschool.dta saved
```

We saved the `svyset` dataset to `highschool.dta`. We can now `use` this new dataset without having to worry about respecifying the design characteristics.

```
. clear
. describe
Contains data
 Observations:             0
    Variables:             0
Sorted by:
. use highschool
. svyset
Sampling weights: sampwgt
             VCE: linearized
     Single unit: missing
        Strata 1: state
 Sampling unit 1: county
           FPC 1: ncounties
        Strata 2: <one>
 Sampling unit 2: school
           FPC 2: nschools
```

◁

After the design characteristics have been svyset, you should also look at [SVY] **svydescribe**. Use svydescribe to browse each stage of your survey data; svydescribe reports useful information on sampling unit counts, missing data, and singleton strata.

### ▷ Example 3: Survey describe

Here we use svydescribe to describe the first stage of our survey dataset of sampled high school seniors. We specified the weight variable to get svydescribe to report on where it contains missing values and how this affects the estimation sample.

```
. svydescribe weight

Survey: Describing stage 1 sampling units

Sampling weights: sampwgt
             VCE: linearized
     Single unit: missing
        Strata 1: state
 Sampling unit 1: county
           FPC 1: ncounties
        Strata 2: <one>
 Sampling unit 2: school
           FPC 2: nschools
```

| | Number of units | | Number of obs with complete | missing | # obs per included unit | | |
|---|---|---|---|---|---|---|---|
| Stratum | included | omitted | data | data | Min | Mean | Max |
| 1 | 2 | 0 | 92 | 0 | 34 | 46.0 | 58 |
| 2 | 2 | 0 | 112 | 0 | 51 | 56.0 | 61 |
| 3 | 2 | 0 | 43 | 0 | 18 | 21.5 | 25 |
| 4 | 2 | 0 | 37 | 0 | 14 | 18.5 | 23 |
| 5 | 2 | 0 | 96 | 0 | 38 | 48.0 | 58 |
| (*output omitted*) | | | | | | | |
| 46 | 2 | 0 | 115 | 0 | 56 | 57.5 | 59 |
| 47 | 2 | 0 | 67 | 0 | 28 | 33.5 | 39 |
| 48 | 2 | 0 | 56 | 0 | 23 | 28.0 | 33 |
| 49 | 2 | 0 | 78 | 0 | 39 | 39.0 | 39 |
| 50 | 2 | 0 | 64 | 0 | 31 | 32.0 | 33 |
| 50 | 100 | 0 | 4,071 | 0 | 14 | 40.7 | 81 |
| | | | 4,071 | | | | |

From the output, we gather that there are 50 strata, each stratum contains two PSUs, the PSUs vary in size, and the total sample size is 4,071 students. We can also see that there are no missing data in the weight variable.

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## Survey data analysis tools

Stata's suite of survey data commands is governed by the svy prefix command; see [SVY] **svy** and [SVY] **svy estimation**. svy runs the supplied estimation command while accounting for the survey design characteristics in the point estimates and variance estimation method. The available variance estimation methods are balanced repeated replication (BRR), the bootstrap, the jackknife, successive difference replication, and first-order Taylor linearization. By default, svy computes standard errors by using the linearized variance estimator—so called because it is based on a first-order Taylor series linear approximation (Wolter 2007). In the nonsurvey context, we refer to this variance estimator as the *robust* variance estimator, otherwise known in Stata as the Huber/White/sandwich estimator; see [P] **_robust**.

## ▷ Example 4: Estimating a population mean

Here we use the svy prefix with the mean command to estimate the average weight of high school seniors in our population.

```
. svy: mean weight
(running mean on estimation sample)

Survey: Mean estimation

Number of strata =  50                  Number of obs   =     4,071
Number of PSUs   = 100                  Population size = 8,000,000
                                        Design df       =        50

--------------------------------------------------------------------
                    |             Linearized
                    |       Mean   std. err.      [95% conf. interval]
--------------------+-----------------------------------------------
             weight |   160.2863   .7412512       158.7974    161.7751
--------------------------------------------------------------------
```

In its header, svy reports the number of strata and PSUs from the first stage, the sample size, an estimate of population size, and the design degrees of freedom. Just like the standard output from the mean command, the table of estimation results contains the estimated mean and its standard error as well as a confidence interval.

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## ▷ Example 5: Survey regression

Here we use the svy prefix with the regress command to model the association between weight and height in our population of high school seniors.

```
. svy: regress weight height
(running regress on estimation sample)

Survey: Linear regression

Number of strata =  50                        Number of obs   =     4,071
Number of PSUs   = 100                        Population size = 8,000,000
                                              Design df       =        50
                                              F(1, 50)        =    593.99
                                              Prob > F        =    0.0000
                                              R-squared       =    0.2787

------------------------------------------------------------------------------
             |             Linearized
      weight | Coefficient  std. err.      t    P>|t|     [95% conf. interval]
-------------+----------------------------------------------------------------
      height |   .7163115   .0293908    24.37   0.000     .6572784    .7753447
       _cons |  -149.6183   12.57265   -11.90   0.000    -174.8712   -124.3654
------------------------------------------------------------------------------
```

In addition to the header elements we saw in the previous example using svy: mean, the command svy: regress also reports a model $F$ test and estimated $R^2$. Although many of Stata's model-fitting commands report $Z$ statistics for testing coefficients against zero, svy always reports $t$ statistics and uses the design degrees of freedom to compute $p$-values.

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The svy prefix can be used with many estimation commands in Stata; see [SVY] **svy estimation** for a list of estimation commands that support the svy prefix.

## ▷ Example 6: Cox's proportional hazards model

Suppose that we want to model the incidence of lung cancer by using three risk factors: smoking status, sex, and place of residence. Our dataset comes from a longitudinal health survey: the First National Health and Nutrition Examination Survey (NHANES I) (Miller 1973; Engel et al. 1978) and its 1992 Epidemiologic Follow-up Study (NHEFS) (Cox et al. 1997); see the National Center for Health Statistics website at https://www.cdc.gov/nchs/. We will be using data from the samples identified by NHANES I examination locations 1–65 and 66–100; thus we will `svyset` the revised pseudo-PSU and strata variables associated with these locations. Similarly, our `pweight` variable was generated using the sampling weights for the nutrition and detailed samples for locations 1–65 and the weights for the detailed sample for locations 66–100.

```
. use https://www.stata-press.com/data/r19/nhefs
. svyset psu2 [pw=swgt2], strata(strata2)
Sampling weights: swgt2
             VCE: linearized
     Single unit: missing
        Strata 1: strata2
 Sampling unit 1: psu2
           FPC 1: <zero>
```

The lung cancer information was taken from the 1992 NHEFS interview data. We use the participants' ages for the time scale. Participants who never had lung cancer and were alive for the 1992 interview were considered censored. Participants who never had lung cancer and died before the 1992 interview were also considered censored at their age of death.

```
. stset age_lung_cancer [pw=swgt2], fail(lung_cancer)
Survival-time data settings
         Failure event: lung_cancer!=0 & lung_cancer<.
Observed time interval: (0, age_lung_cancer]
     Exit on or before: failure
               Weight: [pweight=swgt2]
--------------------------------------------------------------------------
     14,407  total observations
      5,126  event time missing (age_lung_cancer>=.)        PROBABLE ERROR
--------------------------------------------------------------------------
      9,281  observations remaining, representing
         83  failures in single-record/single-failure data
    599,691  total analysis time at risk and under observation
                                                At risk from t =         0
                                     Earliest observed entry t =         0
                                          Last observed exit t =        97
```

Although `stset` warns us that it is a "probable error" to have 5,126 observations with missing event times, we can verify from the 1992 NHEFS documentation that there were indeed 9,281 participants with complete information.

For our proportional hazards model, we pulled the risk factor information from the NHANES I and 1992 NHEFS datasets. Smoking status was taken from the 1992 NHEFS interview data, but we filled in all but 132 missing values by using the general medical history supplement data in NHANES I. Smoking status is represented by separate indicator variables for former smokers and current smokers; the base comparison group is nonsmokers. Sex was determined using the 1992 NHEFS vitality data and is represented by an indicator variable for males. Place-of-residence information was taken from the medical history questionnaire in NHANES I and is represented by separate indicator variables for rural and heavily populated (more than 1 million people) urban residences; the base comparison group is urban residences with populations of fewer than 1 million people.

```
. svy: stcox former_smoker smoker male urban1 rural
(running stcox on estimation sample)

Survey: Cox regression

Number of strata =  35                        Number of obs    =       9,149
Number of PSUs   = 105                        Population size = 151,327,827
                                              Design df        =          70
                                              F(5, 66)         =       14.07
                                              Prob > F         =      0.0000
```

| _t | Haz. ratio | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| former_smoker | 2.788113 | .6205102 | 4.61 | 0.000 | 1.788705 | 4.345923 |
| smoker | 7.849483 | 2.593249 | 6.24 | 0.000 | 4.061457 | 15.17051 |
| male | 1.187611 | .3445315 | 0.59 | 0.555 | .6658757 | 2.118142 |
| urban1 | .8035074 | .3285144 | -0.54 | 0.594 | .3555123 | 1.816039 |
| rural | 1.581674 | .5281859 | 1.37 | 0.174 | .8125799 | 3.078702 |

From the above results, we can see that both former and current smokers have a significantly higher risk for developing lung cancer than do nonsmokers.

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`svy: tabulate` can be used to produce one-way and two-way tables with survey data and can produce survey-adjusted tests of independence for two-way contingency tables; see [SVY] **svy: tabulate oneway** and [SVY] **svy: tabulate twoway**.

## ▷ Example 7: Two-way tables for survey data

With data from the Second National Health and Nutrition Examination Survey (NHANES II) (McDowell et al. 1981), we use `svy: tabulate` to produce a two-way table of cell proportions along with their standard errors and confidence intervals (the survey design characteristics have already been `svyset`). We also use the `format()` option to get `svy: tabulate` to report the cell values and marginals to four decimal places.

```
. use https://www.stata-press.com/data/r19/nhanes2b
. svy: tabulate race diabetes, row se ci format(%7.4f)
(running tabulate on estimation sample)
Number of strata = 31                        Number of obs   =      10,349
Number of PSUs   = 62                        Population size = 117,131,111
                                             Design df       =          31
```

| Race | Diabetes status: Not diab | Diabetic | Total |
|---|---|---|---|
| White | 0.9680 | 0.0320 | 1.0000 |
| | (0.0020) | (0.0020) | |
| | [0.9638,0.9718] | [0.0282,0.0362] | |
| Black | 0.9410 | 0.0590 | 1.0000 |
| | (0.0061) | (0.0061) | |
| | [0.9271,0.9523] | [0.0477,0.0729] | |
| Other | 0.9797 | 0.0203 | 1.0000 |
| | (0.0076) | (0.0076) | |
| | [0.9566,0.9906] | [0.0094,0.0434] | |
| Total | 0.9658 | 0.0342 | 1.0000 |
| | (0.0018) | (0.0018) | |
| | [0.9619,0.9693] | [0.0307,0.0381] | |

```
Key: Row proportion
     (Linearized standard error of row proportion)
     [95% confidence interval for row proportion]

  Pearson:
    Uncorrected   chi2(2)         =   21.3483
    Design-based  F(1.52, 47.26)  =   15.0056     P = 0.0000
```

`svy: tabulate` has many options, such as the `format()` option, for controlling how the table looks. See [SVY] **svy: tabulate twoway** for a discussion of the different design-based and unadjusted tests of association.

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All the standard postestimation commands (for example, `estimates`, `lincom`, `margins`, `nlcom`, `test`, `testnl`) are also available after `svy`.

## ▷ Example 8: Comparing means

Going back to our high school survey data in example 2, we estimate the mean of `weight` (in pounds) for each subpopulation identified by the categories of the `sex` variable (male and female).

```
. use https://www.stata-press.com/data/r19/highschool
. svy: mean weight, over(sex)
(running mean on estimation sample)
Survey: Mean estimation
Number of strata =  50              Number of obs    =     4,071
Number of PSUs   = 100              Population size = 8,000,000
                                    Design df       =        50
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| c.weight@sex | | | | |
| Male | 175.4809 | 1.116802 | 173.2377 | 177.7241 |
| Female | 146.204 | .9004157 | 144.3955 | 148.0125 |

Here we use the `test` command to test the hypothesis that the average male is 30 pounds heavier than the average female; from the results, we cannot reject this hypothesis at the 5% level.

```
. test weight#1.sex - weight#2.sex = 30
Adjusted Wald test
 ( 1)  c.weight@1bn.sex - c.weight@2.sex = 30
       F(  1,    50) =    0.23
            Prob > F =    0.6353
```

◁

`estat` has specific subroutines for use after `svy`; see [SVY] **estat**.

- `estat svyset` reports the survey design settings used to produce the current estimation results.
- `estat effects` and `estat lceffects` report a table of design and misspecification effects for point estimates and linear combinations of point estimates, respectively.
- `estat size` reports a table of sample and subpopulation sizes after `svy: mean`, `svy: proportion`, `svy: ratio`, and `svy: total`.
- `estat sd` reports subpopulation standard deviations on the basis of the estimation results from `mean` and `svy: mean`.
- `estat strata` reports the number of singleton and certainty strata within each sampling stage.
- `estat cv` reports the coefficient of variation for each coefficient in the current estimation results.
- `estat gof` reports a goodness-of-fit test for binary response models using survey data.

## ▷ Example 9: Design effects

Here we use `estat effects` to report the design effects DEFF and DEFT for the mean estimates from the previous example.

```
. estat effects
```

| Over | Mean | Linearized std. err. | DEFF | DEFT |
|---|---|---|---|---|
| c.weight@sex | | | | |
| Male | 175.4809 | 1.116802 | 2.61016 | 1.61519 |
| Female | 146.204 | .9004157 | 1.7328 | 1.31603 |

```
Note: Weights must represent population totals for DEFF to
      be correct when using an FPC; however, DEFT is
      invariant to the scale of weights.
```

Now we use `estat lceffects` to report the design effects DEFF and DEFT for the difference of the mean estimates from the previous example.

```
. estat lceffects weight#1.sex - weight#2.sex
 ( 1)  c.weight@1bn.sex - c.weight@2.sex = 0
```

| Mean | Coefficient | Std. err. | DEFF | DEFT |
|---|---|---|---|---|
| (1) | 29.27691 | 1.515201 | 2.42759 | 1.55768 |

```
Note: Weights must represent population totals for DEFF to
      be correct when using an FPC; however, DEFT is
      invariant to the scale of weights.
```

◁

The `svy brr` prefix command produces point and variance estimates by using the BRR method; see [SVY] **svy brr**. BRR was first introduced by McCarthy (1966, 1969a, and 1969b) as a method of variance estimation for designs with two PSUs in every stratum. The BRR variance estimator tends to give more reasonable variance estimates for this design than the linearized variance estimator, which can result in large values and undesirably wide confidence intervals.

The `svy jackknife` prefix command produces point and variance estimates by using the jackknife replication method; see [SVY] **svy jackknife**. The jackknife is a data-driven variance estimation method that can be used with model-fitting procedures for which the linearized variance estimator is not implemented, even though a linearized variance estimator is theoretically possible to derive (Shao and Tu 1995).

To protect the privacy of survey participants, public survey datasets may contain replicate-weight variables instead of variables that identify the PSUs and strata. These replicate-weight variables can be used with the appropriate replication method for variance estimation instead of the linearized variance estimator; see [SVY] **svyset**.

The `svy brr` and `svy jackknife` prefix commands can be used with those commands that may not be fully supported by `svy` but are compatible with the BRR and the jackknife replication methods. They can also be used to produce point estimates for expressions of estimation results from a prefixed command.

The `svy bootstrap` and `svy sdr` prefix commands work only with replicate weights. Both assume that you have obtained these weight variables externally.

The svy bootstrap prefix command produces variance estimates that have been adjusted for bootstrap sampling. Bootstrap sampling of complex survey has become more popular in recent years and is the variance-estimation method used in the National Population Health Survey conducted by Statistics Canada; see [SVY] **svy bootstrap** and [SVY] **Variance estimation** for more details.

The svy sdr prefix command produces variance estimates that implement successive difference replication (SDR), first introduced by Fay and Train (1995) as a method for annual demographic supplements to the Current Population Survey. This method is typically applied to systematic samples where the observed sampling units follow a natural order; see [SVY] **svy sdr** and [SVY] **Variance estimation** for more details.

## ▷ Example 10: BRR and replicate-weight variables

The survey design for the NHANES II data (McDowell et al. 1981) is specifically suited to BRR: there are two PSUs in every stratum.

```
. use https://www.stata-press.com/data/r19/nhanes2
. svydescribe
Survey: Describing stage 1 sampling units
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: strata
 Sampling unit 1: psu
           FPC 1: <zero>
```

| | | | Number of obs per unit | | |
|---|---|---|---|---|---|
| Stratum | # units | # obs | Min | Mean | Max |
| 1 | 2 | 380 | 165 | 190.0 | 215 |
| 2 | 2 | 185 | 67 | 92.5 | 118 |
| 3 | 2 | 348 | 149 | 174.0 | 199 |
| 4 | 2 | 460 | 229 | 230.0 | 231 |
| 5 | 2 | 252 | 105 | 126.0 | 147 |
| (*output omitted*) | | | | | |
| 29 | 2 | 503 | 215 | 251.5 | 288 |
| 30 | 2 | 365 | 166 | 182.5 | 199 |
| 31 | 2 | 308 | 143 | 154.0 | 165 |
| 32 | 2 | 450 | 211 | 225.0 | 239 |
| 31 | 62 | 10,351 | 67 | 167.0 | 288 |

Here is a privacy-conscious dataset equivalent to the one above; all the variables and values remain, except that strata and psu are replaced with BRR replicate-weight variables. The BRR replicate-weight variables are already svyset, and the default method for variance estimation is vce(brr).

```
. use https://www.stata-press.com/data/r19/nhanes2brr
. svyset
Sampling weights: finalwgt
             VCE: brr
             MSE: off
     BRR weights: brr_1 .. brr_32
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: <observations>
           FPC 1: <zero>
```

Suppose that we were interested in the population ratio of weight to height. Here we use `total` to estimate the population totals of weight and height and the `svy brr` prefix to estimate their ratio and variance; we use `total` instead of `ratio` (which is otherwise preferable here) to show how to specify an expression when using `svy: brr`.

```
. svy brr WtoH = (_b[weight]/_b[height]): total weight height
(running total on estimation sample)
BRR replications (32): .........10.........20.........30.. done
BRR results                                     Number of obs    =      10,351
                                                Population size  = 117,157,513
                                                Replications     =          32
                                                Design df        =          31

      Command: total weight height
         WtoH: _b[weight]/_b[height]
```

| | BRR | | | | | |
|---|---|---|---|---|---|---|
| | Coefficient | std. err. | t | P>\|t\| | [95% conf. | interval] |
| WtoH | .4268116 | .0008904 | 479.36 | 0.000 | .4249957 | .4286276 |

## Survey data concepts

The variance estimation methods that Stata uses are discussed in [SVY] **Variance estimation**.

Subpopulation estimation involves computing point and variance estimates for part of the population. This method is not the same as restricting the estimation sample to the collection of observations within the subpopulation because variance estimation for survey data measures sample-to-sample variability, assuming that the same survey design is used to collect the data. Use the `subpop()` option of the `svy` prefix to perform subpopulation estimation, and use `if` and `in` only when you need to make restrictions on the estimation sample; see [SVY] **Subpopulation estimation**.

### Example 11: Subpopulation estimation

Here we will use our `svyset` high school data to model the association between `weight` and `height` in the subpopulation of male high school seniors. First, we `describe` the `sex` variable to determine how to identify the males in the dataset. We then use `label list` to verify that the variable label agrees with the value labels.

```
. use https://www.stata-press.com/data/r19/highschool
. describe sex
Variable      Storage   Display    Value
    name         type    format    label      Variable label
------------------------------------------------------------------------------
sex             byte    %9.0g      sex        Sex
. label list sex
sex:
           1 Male
           2 Female
```

Here we generate a variable named `male` so that we can easily identify the male high school seniors. We specified `if !missing(sex)`; doing so will cause the generated `male` variable to contain a missing value at each observation where the `sex` variable does. This is done on purpose (although it is not necessary if `sex` is free of missing values) because missing values should not be misinterpreted to imply female.

```
. generate male = sex == 1 if !missing(sex)
```

Now we specify `subpop(male)` as an option to the `svy` prefix in our model fit.

```
. svy, subpop(male): regress weight height
(running regress on estimation sample)

Survey: Linear regression

Number of strata =  50                        Number of obs   =     4,071
Number of PSUs   = 100                        Population size = 8,000,000
                                              Subpop. no. obs =     1,938
                                              Subpop. size    = 3,848,021
                                              Design df       =        50
                                              F(1, 50)        =    225.38
                                              Prob > F        =    0.0000
                                              R-squared       =    0.2347

------------------------------------------------------------------------------
             |             Linearized
      weight | Coefficient  std. err.      t    P>|t|     [95% conf. interval]
-------------+----------------------------------------------------------------
      height |   .7632911   .0508432    15.01   0.000     .6611696    .8654127
       _cons |  -168.6532    22.5708    -7.47   0.000     -213.988   -123.3184
------------------------------------------------------------------------------
```

Although the table of estimation results contains the same columns as earlier, `svy` reports some extra subpopulation information in the header. Here the extra header information tells us that 1,938 of the 4,071 sampled high school seniors are male, and the estimated number of male high school seniors in the population is 3,848,021.

◁

Direct standardization is an estimation method that allows comparing rates that come from different frequency distributions; see [SVY] **Direct standardization**. In direct standardization, estimated rates (means, proportions, and ratios) are adjusted according to the frequency distribution of a standard population. The standard population is partitioned into categories, called standard strata. The stratum frequencies for the standard population are called standard weights. In the standardizing frequency distribution, the standard strata are most commonly identified by demographic information such as age, sex, and ethnicity. The standardized rate estimate is the weighted sum of unadjusted rates, where the weights are the relative frequencies taken from the standardizing frequency distribution. Direct standardization is available with `svy: mean`, `svy: proportion`, and `svy: ratio`.

## Example 12: Standardized rates

Table 3.12-6 of Korn and Graubard (1999, 156) contains enumerated data for two districts of London for the years 1840–1841. The age variable identifies the age groups in 5-year increments, bgliving contains the number of people living in the Bethnal Green district at the beginning of 1840, bgdeaths contains the number of people who died in Bethnal Green that year, hsliving contains the number of people living in St. George's Hanover Square at the beginning of 1840, and hsdeaths contains the number of people who died in Hanover Square that year.

```
. use https://www.stata-press.com/data/r19/stdize, clear
. list, noobs sep(0) sum
```

| | age | bgliving | bgdeaths | hsliving | hsdeaths |
|---|---|---|---|---|---|
| | 0-5 | 10739 | 850 | 5738 | 463 |
| | 5-10 | 9180 | 76 | 4591 | 55 |
| | 10-15 | 8006 | 38 | 4148 | 28 |
| | 15-20 | 7096 | 37 | 6168 | 36 |
| | 20-25 | 6579 | 38 | 9440 | 68 |
| | 25-30 | 5829 | 51 | 8675 | 78 |
| | 30-35 | 5749 | 51 | 7513 | 64 |
| | 35-40 | 4490 | 56 | 5091 | 78 |
| | 40-45 | 4385 | 47 | 4930 | 85 |
| | 45-50 | 2955 | 66 | 2883 | 66 |
| | 50-55 | 2995 | 74 | 2711 | 77 |
| | 55-60 | 1644 | 67 | 1275 | 55 |
| | 60-65 | 1835 | 64 | 1469 | 61 |
| | 65-70 | 1042 | 64 | 649 | 55 |
| | 70-75 | 879 | 68 | 619 | 58 |
| | 75-80 | 366 | 47 | 233 | 51 |
| | 80-85 | 173 | 39 | 136 | 20 |
| | 85-90 | 71 | 22 | 48 | 15 |
| | 90-95 | 21 | 6 | 10 | 4 |
| | 95-100 | 4 | 2 | 2 | 1 |
| | unknown | 50 | 1 | 124 | 0 |
| Sum | | 74088 | 1764 | 66453 | 1418 |

We can use svy: ratio to compute the deathrates for each district in 1840. Because this dataset is identified as census data, we will create an FPC variable that will contain a sampling rate of 100%. This method will result in zero standard errors, which are interpreted to mean no variability—appropriate because our point estimates came from the entire population.

```
. generate fpc = 1
. svyset, fpc(fpc)
Sampling weights: <none>
             VCE: linearized
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: <observations>
           FPC 1: fpc
. svy: ratio (Bethnal: bgdeaths/bgliving) (Hanover: hsdeaths/hsliving)
(running ratio on estimation sample)
Survey: Ratio estimation
Number of strata =  1                     Number of obs   = 21
Number of PSUs   = 21                     Population size = 21
                                          Design df       = 20
      Bethnal: bgdeaths/bgliving
      Hanover: hsdeaths/hsliving
------------------------------------------------------------------------------
             |             Linearized
             |      Ratio   std. err.      [95% conf. interval]
-------------+----------------------------------------------------------------
     Bethnal |   .0238095          0            .           .
     Hanover |   .0213384          0            .           .
------------------------------------------------------------------------------
Note: Zero standard errors because of 100% sampling rate
      detected for FPC in the first stage.
```

The deathrates are 2.38% for Bethnal Green and 2.13% for St. George's Hanover Square. These observed deathrates are not really comparable because they come from two different age distributions. We can standardize based on the age distribution from Bethnal Green. Here `age` identifies our standard strata and `bgliving` contains the associated population sizes.

```
. svy: ratio (Bethnal: bgdeaths/bgliving) (Hanover: hsdeaths/hsliving),
> stdize(age) stdweight(bgliving)
(running ratio on estimation sample)

Survey: Ratio estimation

Number of strata =  1                    Number of obs    = 21
Number of PSUs   = 21                    Population size = 21
N. of std strata = 21                    Design df       = 20

      Bethnal: bgdeaths/bgliving
      Hanover: hsdeaths/hsliving
```

| | Ratio | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| Bethnal | .0238095 | 0 | . | . |
| Hanover | .0266409 | 0 | . | . |

```
Note: Zero standard errors because of 100% sampling rate
      detected for FPC in the first stage.
```

The standardized deathrate for St. George's Hanover Square, 2.66%, is larger than the deathrate for Bethnal Green.

◁

Calibration and poststratification are methods for adjusting the sampling weights, usually to account for underrepresented groups in the population; see [SVY] **Calibration** and [SVY] **Poststratification**. These methods usually result in decreasing bias that is due to nonresponse and underrepresented groups in the population. They also tend to result in smaller variance estimates. Calibration and poststratification are available for all survey estimation commands and are specified using `svyset`; see [SVY] **svyset**.

## Example 13: Poststratified mean

Levy and Lemeshow (2008, sec. 6.6) give an example of poststratification by using simple survey data from a veterinarian's client list. The data in `poststrata.dta` were collected using simple random sampling (SRS) without replacement. The `totexp` variable contains the total expenses to the client, `type` identifies the cats and dogs, `postwgt` contains the poststratum sizes (450 for cats and 850 for dogs), and `fpc` contains the total number of clients ($850 + 450 = 1300$).

```
. use https://www.stata-press.com/data/r19/poststrata, clear
. svyset, poststrata(type) postweight(postwgt) fpc(fpc)
Sampling weights: <none>
             VCE: linearized
      Poststrata: type
Post. pop. sizes: postwgt
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: <observations>
           FPC 1: fpc
. svy: mean totexp
(running mean on estimation sample)
Survey: Mean estimation
Number of strata =  1                  Number of obs   =     50
Number of PSUs   = 50                  Population size = 1,300
N. of poststrata =  2                  Design df       =     49
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| totexp | 40.11513 | 1.163498 | 37.77699 | 42.45327 |

The mean total expenses is \$40.12 with a standard error of \$1.16. In the following, we omit the poststratification information from `svyset`, resulting in mean total expenses of \$39.73 with standard error \$2.22. The difference between the mean estimates is explained by the facts that expenses tend to be larger for dogs than for cats and that the dogs were slightly underrepresented in the sample ($850/1{,}300 \approx 0.65$ for the population; $32/50 = 0.64$ for the sample). This reasoning also explains why the variance estimate from the poststratified mean is smaller than the one that was not poststratified.

```
. svyset, fpc(fpc)
Sampling weights: <none>
             VCE: linearized
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: <observations>
           FPC 1: fpc
. svy: mean totexp
(running mean on estimation sample)
Survey: Mean estimation
Number of strata =  1                     Number of obs   = 50
Number of PSUs   = 50                     Population size = 50
                                          Design df       = 49
--------------------------------------------------------------
                    |             Linearized
                    |       Mean   std. err.     [95% conf. interval]
--------------------+-----------------------------------------------
             totexp |    39.7254   2.221747      35.26063    44.19017
--------------------------------------------------------------
```

◁

## Tools for programmers of new survey commands

The `ml` command can be used to fit a model by the method of maximum likelihood. When the `svy` option is specified, `ml` performs maximum pseudolikelihood, applying sampling weights and design-based linearization automatically; see [R] **ml** and Pitblado, Poi, and Gould (2024).

### ▷ Example 14

The `ml` command requires a program that computes likelihood values to perform maximum likelihood. Here is a likelihood evaluator used in Pitblado, Poi, and Gould (2024) to fit linear regression models using the likelihood from the normal distribution.

```
program mynormal_lf
        version 19.5      // (or version 19 if you do not have StataNow)
        args lnf mu lnsigma
        quietly replace `lnf' = ln(normalden($ML_y1,`mu',exp(`lnsigma')))
end
```

Back in example 5, we fit a linear regression model using the high school survey data. Here we use `ml` and `mynormal_lf` to fit the same survey regression model.

```
. use https://www.stata-press.com/data/r19/highschool
. ml model lf mynormal_lf (mu: weight = height) /lnsigma, svy
. ml max
Initial:      Log pseudolikelihood =     -<inf>  (could not be evaluated)
Feasible:     Log pseudolikelihood = -7.301e+08
Rescale:      Log pseudolikelihood =  -51944380
Rescale eq:   Log pseudolikelihood =  -47565331
Iteration 0:  Log pseudolikelihood =  -47565331
Iteration 1:  Log pseudolikelihood =  -41225560  (not concave)
Iteration 2:  Log pseudolikelihood =  -41221017  (not concave)
Iteration 3:  Log pseudolikelihood =  -41170786  (not concave)
Iteration 4:  Log pseudolikelihood =  -41151252  (not concave)
Iteration 5:  Log pseudolikelihood =  -41132554  (not concave)
Iteration 6:  Log pseudolikelihood =  -41107910  (not concave)
Iteration 7:  Log pseudolikelihood =  -41077230
Iteration 8:  Log pseudolikelihood =  -39815341  (backed up)
Iteration 9:  Log pseudolikelihood =  -38344045
Iteration 10: Log pseudolikelihood =  -38328784
Iteration 11: Log pseudolikelihood =  -38328739
Iteration 12: Log pseudolikelihood =  -38328739
Number of strata =  50                          Number of obs   =     4,071
Number of PSUs   = 100                          Population size = 8,000,000
                                                Design df       =        50
                                                F(1, 50)        =    593.99
                                                Prob > F        =    0.0000
```

| weight | Coefficient | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| height | .7163115 | .0293908 | 24.37 | 0.000 | .6572784 | .7753447 |
| _cons | -149.6183 | 12.57265 | -11.90 | 0.000 | -174.8712 | -124.3654 |
| /lnsigma | 3.372154 | .0180777 | 186.54 | 0.000 | 3.335844 | 3.408464 |

◁

`svymarkout` is a programmer's command that resets the values in a variable that identifies the estimation sample, dropping observations for which any of the survey characteristic variables contain missing values. This tool is most helpful for developing estimation commands that use `ml` to fit models using maximum pseudolikelihood directly, instead of relying on the `svy` prefix.

### Video examples

Basic introduction to the analysis of complex survey data in Stata

How to download, import, and merge multiple datasets from the NHANES website

How to download, import, and prepare data from the NHANES website

## Acknowledgments

Many of the `svy` commands were developed in collaboration with John L. Eltinge of the US Census Bureau. We thank him for his invaluable assistance.

We thank Wayne Johnson of the National Center for Health Statistics for providing the NHANES II dataset.

We thank Nicholas Winter of the Politics Department at the University of Virginia for his diligent efforts to keep Stata up to date with mainstream variance estimation methods for survey data, as well as for providing versions of `svy brr` and `svy jackknife`.

William Gemmell Cochran (1909–1980) was born in Rutherglen, Scotland, and educated at the Universities of Glasgow and Cambridge. He accepted a post at Rothamsted before finishing his doctorate. Cochran emigrated to the United States in 1939 and worked at Iowa State, North Carolina State, Johns Hopkins, and Harvard. He made many major contributions across several fields of statistics, including experimental design, the analysis of counted data, sample surveys, and observational studies, and was author or coauthor (with Gertrude M. Cox and George W. Snedecor) of various widely used texts.

Leslie Kish (1910–2000) was born in Poprad, Hungary, and entered the United States with his family in 1926. He worked as a lab assistant at the Rockefeller Institute for Medical Research and studied at the College of the City of New York, fighting in the Spanish Civil War before receiving his first degree in mathematics. Kish worked for the Bureau of the Census, the Department of Agriculture, the Army Air Corps, and the University of Michigan. He carried out pioneering work in the theory and practice of survey sampling, including design effects, BRR, response errors, rolling samples and censuses, controlled selection, multipurpose designs, and small-area estimation.

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## Also see

[SVY] **svy** — The survey prefix command

[SVY] **svy estimation** — Estimation commands for survey data

[SVY] **svyset** — Declare survey design for dataset

[P] **_robust** — Robust variance estimates

**bootstrap_options** — More options for bootstrap variance estimation

Description Syntax Options Also see

## Description

svy accepts more options when performing bootstrap variance estimation. See [SVY] **svy bootstrap** for a complete discussion.

## Syntax

| *bootstrap_options* | Description |
|---|---|
| SE | |
| mse | use MSE formula for variance |
| nodots | suppress replication dots |
| dots(#) | display dots every # replications |
| bsn(#) | bootstrap mean-weight adjustment |
| saving(*filename*, ...) | save results to *filename* |
| verbose | display the full table legend |
| noisily | display any output from *command* |
| trace | trace *command* |
| title(*text*) | use *text* as the title for results |
| nodrop | do not drop observations |
| reject(*exp*) | identify invalid results |

saving, verbose, noisily, trace, title(), nodrop, and reject() are not shown in the dialog boxes for estimation commands.

## Options

SE

mse specifies that svy compute the variance by using deviations of the replicates from the observed value of the statistics based on the entire dataset. By default, svy computes the variance by using deviations of the replicates from their mean.

nodots and dots(#) specify whether to display replication dots. By default, one dot character is displayed for each successful replication. An "x" is displayed if *command* returns an error, and an "e" is displayed if at least one value in *exp_list* is missing. You can also control whether dots are displayed using set dots; see [R] **set**.

nodots suppresses display of the replication dots.

dots(#) displays dots every # replications. dots(0) is a synonym for nodots.

bsn(#) specifies that # bootstrap replicate-weight variables were used to generate each bootstrap mean-weight variable specified in the bsrweight() option of svyset. The bsn() option of bootstrap overrides the bsn() option of svyset; see [SVY] **svyset**.

saving(), verbose, noisily, trace, title(), nodrop, reject(); see [SVY] **svy bootstrap**.

## Also see

[SVY] **svy** — The survey prefix command

[SVY] **svy bootstrap** — Bootstrap for survey data

**brr_options** — More options for BRR variance estimation

Description Syntax Options Also see

## Description

svy accepts more options when performing BRR variance estimation. See [SVY] **svy brr** for a complete discussion.

## Syntax

| *brr_options* | Description |
|---|---|
| SE | |
| mse | use MSE formula for variance |
| nodots | suppress replication dots |
| dots(#) | display dots every # replications |
| hadamard(*matrix*) | Hadamard matrix |
| fay(#) | Fay's adjustment |
| saving(*filename*, ...) | save results to *filename* |
| verbose | display the full table legend |
| noisily | display any output from *command* |
| trace | trace *command* |
| title(*text*) | use *text* as the title for results |
| nodrop | do not drop observations |
| reject(*exp*) | identify invalid results |

saving(), verbose, noisily, trace, title(), nodrop, and reject() are not shown in the dialog boxes for estimation commands.

## Options

SE

mse specifies that svy compute the variance by using deviations of the replicates from the observed value of the statistics based on the entire dataset. By default, svy computes the variance by using deviations of the replicates from their mean.

nodots and dots(#) specify whether to display replication dots. By default, one dot character is displayed for each successful replication. An "x" is displayed if *command* returns an error, and an "e" is displayed if at least one value in *exp_list* is missing. You can also control whether dots are displayed using set dots; see [R] **set**.

nodots suppresses display of the replication dots.

dots(#) displays dots every # replications. dots(0) is a synonym for nodots.

hadamard(*matrix*) specifies the Hadamard matrix to be used to determine which PSUs are chosen for each replicate.

fay(#) specifies Fay's adjustment. This option overrides the fay(#) option of svyset; see [SVY] **svyset**.

saving(), verbose, noisily, trace, title(), nodrop, reject(); see [SVY] **svy brr**.

## Also see

[SVY] **svy** — The survey prefix command

[SVY] **svy brr** — Balanced repeated replication for survey data

**Calibration** — Calibration for survey data



## Description

Calibration is a method for adjusting the sampling weights, often to account for nonresponse and underrepresented groups in the population.

See [SVY] **Poststratification** for a discussion of a weight adjustment method that is a special case of the calibration methods discussed here.

See [SVY] **Direct standardization** for a similar method of adjustment that allows the comparison of rates that come from different frequency distributions.

## Remarks and examples

The standard application of calibration uses population totals to adjust the sampling weights. Population totals are typically taken from a census or other source separate from the survey. In a business survey, the frame might have the number of employees from an earlier time period for each establishment. In a household survey, counts of persons in groups defined by age, race or ethnicity, and gender may be published from a census, population projections, or a separate survey.

Calibration involves adjusting the sampling weights so that they more closely estimate known population totals. Calibration is more general than poststratification because the weight adjustments can be made across multiple group-identifier variables simultaneously and also includes population totals other than simple counts. Calibration usually results in decreasing bias because of nonresponse and underrepresented groups in the population. Much like poststratification, calibration also tends to result in smaller variance estimates.

The `svyset` command has the options `rake()` and `regress()` for applying calibration adjustments to the sampling weights. `rake()` specifies that the weights be adjusted via the raking-ratio method. `regress()` specifies that the weights be adjusted via linear regression. `rake()` and `regress()` produce the same weight adjustment as poststratification when they are used to adjust the sampling weights across the levels of a single group-identifier variable.

In the following example, we use a version of the data that Valliant and Dever (2018) resampled from the Survey of Mental Health Organizations (SMHO) (Manderscheid and Henderson 2002).

### ▷ Example 1: Population mean, using calibrated weights

Valliant and Dever (2018, sec. 4.3) give an example of calibration by using a stratified simple random sample of 120 hospitals from the SMHO. The sample is stratified by four hospital types, identified in the variable `hosptype`. The four levels of `hosptype` are 1–Psychiatric, 2–Residential or veterans, 3–General, and 5–Multi-service, substance abuse. Within each hospital type, a simple random sample of 30 hospitals was selected without replacement.

For each sampled hospital, the eoycnt variable contains the end-of-year patient counts, and the beds variable contains the number of beds. Our separate source for the auxiliary information about the population is the full SMHO. The population total for eoycnt is 505,345. For beds, the population totals within each of the four hospital types is given in the following table:

| hosptype | beds |
|---|---|
| 1 | 37,978 |
| 2 | 13,066 |
| 3 | 9,573 |
| 5 | 10,077 |

We can use this information to adjust the original sampling weights that are stored in wt. In the calibration model specification, we use the interaction between the categorical variable hosptype and the continuous variable beds to specify regressors for the number of beds for each hospital type. See **[U] 11.4.3 Factor variables** for details of the interaction specification.

```
. use https://www.stata-press.com/data/r19/smho
(Resampled SMHO data from Valliant & Dever, 2018)
. svyset [pw=wt], strata(hosptype)
>        regress(eoycnt i.hosptype#c.beds, noconstant
>                totals(eoycnt=505345
>                       1.hosptype#c.beds=37978
>                       2.hosptype#c.beds=13066
>                       3.hosptype#c.beds=9573
>                       5.hosptype#c.beds=10077))
Sampling weights: wt
             VCE: linearized
     Calibration: regress
     Single unit: missing
        Strata 1: hosptype
 Sampling unit 1: <observations>
           FPC 1: <zero>
```

The goal of the analysis is to estimate the mean expenditures per hospital in the population. The variable exptotal contains the expenditures for each of the sampled hospitals, measured in millions of dollars.

```
. svy: mean exptotal
(running mean on estimation sample)
Survey: Mean estimation
Number of strata =   4            Number of obs   =        120
Number of PSUs   = 120            Population size = 889.062959
Calibration: regress              Design df       =        116
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| exptotal | 10.40552 | .8560101 | 8.710082 | 12.10095 |

The estimated mean expenditures per hospital are $10.41 (in millions) with a standard error of 0.86.

In the following, we re-estimate the mean expenditures per hospital using just the original survey design characteristics.

```
. svyset [pw=wt], strata(hosptype)
Sampling weights: wt
             VCE: linearized
     Single unit: missing
        Strata 1: hosptype
 Sampling unit 1: <observations>
           FPC 1: <zero>
. svy: mean exptotal
(running mean on estimation sample)
Survey: Mean estimation
Number of strata =   4                  Number of obs    = 120
Number of PSUs   = 120                  Population size = 725
                                        Design df       = 116
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| exptotal | 9.939402 | .9487877 | 8.060209 | 11.8186 |

The result is a mean expenditure per hospital of \$9.94 (in millions) with a standard error of 0.95. The difference between the mean estimates is explained by the fact that end-of-year patient counts and number of beds are strong predictors of hospital expenditures.

◁

## Methods and formulas

The following discussion assumes that you are already familiar with the topics discussed in [SVY] **Variance estimation**.

Calibration methods adjust the sampling weights to minimize the difference between known population totals and their weighted estimates. For a full discussion on the motivation and derivation of the methods described here, see Deville and Särndal (1992); Deville, Särndal, and Sautory (1993); and Valliant (2002).

Suppose that you used a complex survey design to sample $m$ individuals from a population of size $M$. Let $\mathbf{T}_a$ be a collection of population totals corresponding to a collection of auxiliary variables denoted by $\mathbf{a}$. The adjusted weights take on the form

$$w_j^* = w_j F(\mathbf{a}_j'\boldsymbol{\lambda})$$

where $w_j$ are the original sampling weights, $F(z)$ is derived from a chosen calibration method, and $\boldsymbol{\lambda}$ is a vector of Lagrange multipliers computed by solving the calibration equations

$$\sum_{j=1}^{m} w_j F(\mathbf{a}_j'\boldsymbol{\lambda})\mathbf{a}_j = \mathbf{T}_a$$

The linear regression method uses

$$F(z) = \begin{cases} 1+z & \text{if } z \in [L-1, U-1] \\ L & \text{if } z < L-1 \\ U & \text{if } z > U-1 \end{cases}$$

and corresponds to `svyset`'s option `regress()` with suboptions `ll(`$L$`)` and `ul(`$U$`)`. By default, $L = -\infty$ and $U = \infty$; otherwise, the only restriction is that $L < 1 < U$.

The raking-ratio method uses

$$F(z) = e^z$$

and corresponds to `svyset`'s option `rake()` specified without limits on the weight ratios. With limits on the weight ratios, the restrictions are $0 \leq L < 1 < U$. By default, $L = 0$; otherwise, $U$ must be specified if a different value of $L$ is specified. Therefore,

$$F(z) = \frac{L(U-1) + U(1-L)\exp(Az)}{U - 1 + (1-L)\exp(Az)}$$

where

$$A = \frac{U-L}{(1-L)(U-1)}$$

Point estimates are computed using the adjusted weights $w_j^*$. For example, the calibrated total estimator is

$$\hat{Y}^C = \sum_{j=1}^{m} w_j^* y_j$$

where $y_j$ is an item from the $j$th sampled individual.

For replication-based variance estimation, the replicate-weight variables are similarly adjusted to produce the replicate values used in the respective variance formulas.

The score variable for the linearized variance estimator of a calibrated total is taken directly from the residuals of a weighted linear regression of $y_j$ on $\mathbf{a}_j$ using the adjusted weights $w_j^*$. Let these residuals be denoted by $z_j(\hat{Y}^C)$. For the calibrated ratio estimator, the score variable is

$$z_j(\widehat{R}^C) = \frac{\widehat{X}^C z_j(\hat{Y}^C) - \hat{Y}^C z_j(\widehat{X}^C)}{(\widehat{X}^C)^2}$$

where $\widehat{X}^C$ is the calibrated total estimator for item $x_j$. For regression models, the equation-level scores are computed similarly to those of the calibrated total; that is, the adjusted scores are taken directly from the residuals of a weighted linear regression of each original score on $\mathbf{a}_j$ using the adjusted weights $w_j^*$.

## References


Deville, J.-C., and C.-E. Särndal. 1992. Calibration estimators in survey sampling. *Journal of the American Statistical Association* 87: 376–382. https://doi.org/10.1080/01621459.1992.10475217.

Deville, J.-C., C.-E. Särndal, and O. Sautory. 1993. Generalized raking procedures in survey sampling. *Journal of the American Statistical Association* 88: 1013–1020. https://doi.org/10.2307/2290793.

Manderscheid, R. W., and M. J. Henderson, eds. 2002. *Mental Health, United States, 2002.* DHHS Publication No. SMA04-3938. Rockville, MD: Substance Abuse and Mental Health Services Administration.

Valliant, R. 2002. Variance estimation for the general regression estimator. *Survey Methodology* 28: 103–114.

Valliant, R., and J. Dever. 2018. *Survey Weights: A Step-by-Step Guide to Calculation*. College Station, TX: Stata Press.

## Also see

[SVY] **Survey** — Introduction to survey commands

[SVY] **svy** — The survey prefix command

[SVY] **svyset** — Declare survey design for dataset

[SVY] **Direct standardization** — Direct standardization of means, proportions, and ratios

[SVY] **Poststratification** — Poststratification for survey data

**Direct standardization** — Direct standardization of means, proportions, and ratios



## Description

Direct standardization is an estimation method that allows comparing rates that come from different frequency distributions. The `mean`, `proportion`, and `ratio` commands can estimate means, proportions, and ratios by using direct standardization.

See [SVY] **Calibration** and [SVY] **Poststratification** for similar estimation methods when some population totals are known.

## Remarks and examples

In direct standardization, estimated rates (means, proportions, and ratios) are adjusted according to the frequency distribution of a standard population. The standard population is partitioned into categories, called standard strata. The stratum frequencies for the standard population are called standard weights. In the standardizing frequency distribution, the standard strata are most commonly identified by demographic information such as age, sex, and ethnicity.

Stata's `mean`, `proportion`, and `ratio` estimation commands have options for estimating means, proportions, and ratios by using direct standardization. The `stdize()` option takes a variable that identifies the standard strata, and the `stdweight()` option takes a variable that contains the standard weights.

The standard strata (specified using `stdize()`) from the standardizing population are not the same as the strata (specified using `svyset`'s `strata()` option) from the sampling design. In the output header, "Number of strata" is the number of strata in the first stage of the sampling design, and "N. of std strata" is the number of standard strata.

In the following example, we use direct standardization to compare the death rates between two districts of London in 1840.

## Example 1: Standardized rates

Table 3.12-6 of Korn and Graubard (1999, 156) contains enumerated data for two districts of London for the years 1840–1841. The age variable identifies the age groups in 5-year increments, bgliving contains the number of people living in the Bethnal Green district at the beginning of 1840, bgdeaths contains the number of people who died in Bethnal Green that year, hsliving contains the number of people living in St. George's Hanover Square at the beginning of 1840, and hsdeaths contains the number of people who died in Hanover Square that year.

```
. use https://www.stata-press.com/data/r19/stdize
. list, noobs sep(0) sum
```

| | age | bgliving | bgdeaths | hsliving | hsdeaths |
|---|---|---|---|---|---|
| | 0-5 | 10739 | 850 | 5738 | 463 |
| | 5-10 | 9180 | 76 | 4591 | 55 |
| | 10-15 | 8006 | 38 | 4148 | 28 |
| | 15-20 | 7096 | 37 | 6168 | 36 |
| | 20-25 | 6579 | 38 | 9440 | 68 |
| | 25-30 | 5829 | 51 | 8675 | 78 |
| | 30-35 | 5749 | 51 | 7513 | 64 |
| | 35-40 | 4490 | 56 | 5091 | 78 |
| | 40-45 | 4385 | 47 | 4930 | 85 |
| | 45-50 | 2955 | 66 | 2883 | 66 |
| | 50-55 | 2995 | 74 | 2711 | 77 |
| | 55-60 | 1644 | 67 | 1275 | 55 |
| | 60-65 | 1835 | 64 | 1469 | 61 |
| | 65-70 | 1042 | 64 | 649 | 55 |
| | 70-75 | 879 | 68 | 619 | 58 |
| | 75-80 | 366 | 47 | 233 | 51 |
| | 80-85 | 173 | 39 | 136 | 20 |
| | 85-90 | 71 | 22 | 48 | 15 |
| | 90-95 | 21 | 6 | 10 | 4 |
| | 95-100 | 4 | 2 | 2 | 1 |
| | unknown | 50 | 1 | 124 | 0 |
| Sum | | 74088 | 1764 | 66453 | 1418 |

We can use svy: ratio to compute the deathrates for each district in 1840. Because this dataset is identified as census data, we will create an FPC variable that will contain a sampling rate of 100%. This method will result in zero standard errors, which are interpreted to mean no variability—appropriate because our point estimates came from the entire population.

```
. generate fpc = 1
. svyset, fpc(fpc)
Sampling weights: <none>
             VCE: linearized
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: <observations>
           FPC 1: fpc
. svy: ratio (Bethnal: bgdeaths/bgliving) (Hanover: hsdeaths/hsliving)
(running ratio on estimation sample)
Survey: Ratio estimation
Number of strata =  1                     Number of obs   = 21
Number of PSUs   = 21                     Population size = 21
                                          Design df       = 20
      Bethnal: bgdeaths/bgliving
      Hanover: hsdeaths/hsliving
------------------------------------------------------------------------------
             |             Linearized
             |       Ratio   std. err.      [95% conf. interval]
-------------+----------------------------------------------------------------
     Bethnal |   .0238095          0            .           .
     Hanover |   .0213384          0            .           .
------------------------------------------------------------------------------
Note: Zero standard errors because of 100% sampling rate
      detected for FPC in the first stage.
```

The deathrates are 2.38% for Bethnal Green and 2.13% for St. George's Hanover Square. These observed deathrates are not really comparable because they come from two different age distributions. We can standardize based on the age distribution from Bethnal Green. Here age identifies our standard strata and bgliving contains the associated population sizes.

```
. svy: ratio (Bethnal: bgdeaths/bgliving) (Hanover: hsdeaths/hsliving),
> stdize(age) stdweight(bgliving)
(running ratio on estimation sample)
Survey: Ratio estimation
Number of strata =  1                     Number of obs   = 21
Number of PSUs   = 21                     Population size = 21
N. of std strata = 21                     Design df       = 20
      Bethnal: bgdeaths/bgliving
      Hanover: hsdeaths/hsliving
------------------------------------------------------------------------------
             |             Linearized
             |       Ratio   std. err.      [95% conf. interval]
-------------+----------------------------------------------------------------
     Bethnal |   .0238095          0            .           .
     Hanover |   .0266409          0            .           .
------------------------------------------------------------------------------
Note: Zero standard errors because of 100% sampling rate
      detected for FPC in the first stage.
```

The standardized deathrate for St. George's Hanover Square, 2.66%, is larger than the deathrate for Bethnal Green.

For this example, we could have used `dstdize` to compute the deathrates; however, `dstdize` will not compute the correct standard errors for survey data. Furthermore, `dstdize` is not an estimation command, so `test` and the other postestimation commands are not available.

◁

❑ Technical note

The values in the variable supplied to the `stdweight()` option are normalized so that (1) is true; see *Methods and formulas*. Thus the `stdweight()` variable can contain either population sizes or population proportions for the associated standard strata.

❑

## Methods and formulas

The following discussion assumes that you are already familiar with the topics discussed in [SVY] **Variance estimation**.

In direct standardization, a weighted sum of the point estimates from the standard strata is used to produce an overall point estimate for the population. This section will show how direct standardization affects the ratio estimator. The mean and proportion estimators are special cases of the ratio estimator.

Suppose that you used a complex survey design to sample $m$ individuals from a population of size $M$. Let $D_g$ be the set of individuals in the sample that belong to the $g$th standard stratum, and let $I_{D_g}(j)$ indicate if the $j$th individual is in standard stratum $g$, where

$$I_{D_g}(j) = \begin{cases} 1, & \text{if } j \in D_g \\ 0, & \text{otherwise} \end{cases}$$

Also let $L_D$ be the number of standard strata, and let $\pi_g$ be the proportion of the population that belongs to standard stratum $g$.

$$\sum_{g=1}^{L_D} \pi_g = 1 \tag{1}$$

In subpopulation estimation, $\pi_g$ is set to zero if none of the individuals in standard stratum $g$ are in the subpopulation. Then the standard stratum proportions are renormalized.

Let $y_j$ and $x_j$ be the items of interest and $w_j$ be the sampling weight for the $j$th sampled individual. The estimator for the standardized ratio of $R = Y/X$ is

$$\widehat{R}^D = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{Y}_g}{\widehat{X}_g}$$

where

$$\widehat{Y}_g = \sum_{j=1}^{m} I_{D_g}(j)\, w_j y_j$$

with $\widehat{X}_g$ similarly defined.

For replication-based variance estimation, replicates of the standardized values are used in the variance formulas.

The score variable for the linearized variance estimator of the standardized ratio is

$$z_j(\widehat{R}^D) = \sum_{g=1}^{L_D} \pi_g I_{D_g}(j) \frac{\widehat{X}_g y_j - \widehat{Y}_g x_j}{\widehat{X}_g^2}$$

This score variable was derived using the method described in [SVY] **Variance estimation** and is a direct result of the methods described in Deville (1999), Demnati and Rao (2004), and Shah (2004).

For the `mean` and `proportion` commands, the mean estimator is a ratio estimator with the denominator variable equal to one ($x_j = 1$) and the proportion estimator is the mean estimator with an indicator variable in the numerator ($y_j \in \{0, 1\}$).

## References

Demnati, A., and J. N. K. Rao. 2004. Linearization variance estimators for survey data. *Survey Methodology* 30: 17–26.

Deville, J.-C. 1999. Variance estimation for complex statistics and estimators: Linearization and residual techniques. *Survey Methodology* 25: 193–203.

Korn, E. L., and B. I. Graubard. 1999. *Analysis of Health Surveys*. New York: Wiley.

Shah, B. V. 2004. Comment [on Demnati and Rao (2004)]. *Survey Methodology* 30: 29.

## Also see

[SVY] **Survey** — Introduction to survey commands

[SVY] **svy** — The survey prefix command

[SVY] **svyset** — Declare survey design for dataset

[SVY] **Calibration** — Calibration for survey data

[SVY] **Poststratification** — Poststratification for survey data

**estat** — Postestimation statistics for survey data



## Description

`estat svyset` reports the survey design characteristics associated with the current estimation results.

`estat effects` displays a table of design and misspecification effects for each estimated parameter.

`estat lceffects` displays a table of design and misspecification effects for a user-specified linear combination of the parameter estimates.

`estat size` displays a table of sample and subpopulation sizes for each estimated subpopulation mean, proportion, ratio, or total. This command is available only after `svy: mean`, `svy: proportion`, `svy: ratio`, and `svy: total`; see [R] **mean**, [R] **proportion**, [R] **ratio**, and [R] **total**.

`estat sd` reports subpopulation standard deviations based on the estimation results from `mean` and `svy: mean`; see [R] **mean**. `estat sd` is not appropriate with estimation results that used direct standardization or poststratification.

`estat strata` displays a table of the number of singleton and certainty strata within each sampling stage. The variance scaling factors are also displayed for estimation results where `singleunit(scaled)` was `svyset`.

`estat cv` reports the coefficient of variation (CV) for each coefficient in the current estimation results. The CV for coefficient $b$ is

$$\mathrm{CV}(b) = \frac{\mathrm{SE}(b)}{|b|} \times 100\%$$

`estat gof` reports a goodness-of-fit test for binary response models using survey data. This command is available only after `svy: logistic`, `svy: logit`, and `svy: probit`; see [R] **logistic**, [R] **logit**, and [R] **probit**.

`estat vce` displays the covariance or correlation matrix of the parameter estimates of the previous model. See [R] **estat vce** for examples.

## Quick start

Design effects for each parameter in current estimation results after a command using the `svy:` prefix

```
estat effects
```

Design effects for the sum of parameter estimates for variables `v1` and `v2`

```
estat lceffects v1 + v2
```

Same as above, but add misspecification effects

```
estat lceffects v1 + v2, deff deft meff meft
```

Number of observations used and subpopulation size for each parameter

```
estat size
```

Estimate of subpopulation standard deviation based on estimation results from `svy: mean`

```
estat sd
```

Compute standard deviation using an estimate of SRS variance for sampling within a subpopulation

```
estat sd, srssubpop
```

Display the number of singleton and certainty strata within each sampling stage

```
estat strata
```

Coefficient of variation for each parameter in current estimation results

```
estat cv
```

Goodness-of-fit test for binary response models using survey data and grouping data into quintiles

```
estat gof, group(5)
```

Variance–covariance matrix of parameter estimates from the most recent model

```
estat vce
```

Same as above, but display a correlation matrix

```
estat vce, correlation
```

## Menu

Statistics > Survey data analysis > DEFF, MEFF, and other statistics

# Syntax

*Survey design characteristics*

```
estat svyset
```

*Design and misspecification effects for point estimates*

```
estat effects [ , estat_effects_options ]
```

*Design and misspecification effects for linear combinations of point estimates*

```
estat lceffects exp [ , estat_lceffects_options ]
```

*Subpopulation sizes*

```
estat size [ , estat_size_options ]
```

*Subpopulation standard-deviation estimates*

```
estat sd [ , estat_sd_options ]
```

*Singleton and certainty strata*

```
estat strata
```

*Coefficient of variation for survey data*

```
estat cv [ , estat_cv_options ]
```

*Goodness-of-fit test for binary response models using survey data*

```
estat gof [ if ] [ in ] [ , estat_gof_options ]
```

*Display covariance matrix estimates*

```
estat vce [ , estat_vce_options ]
```

| *estat_effects_options* | Description |
|---|---|
| `deff` | report DEFF design effects |
| `deft` | report DEFT design effects |
| `srssubpop` | report design effects, assuming SRS within subpopulation |
| `meff` | report MEFF design effects |
| `meft` | report MEFT design effects |
| *display_options* | control spacing and display of omitted variables and base and empty cells |

| *estat_lceffects_options* | Description |
|---|---|
| deff | report DEFF design effects |
| deft | report DEFT design effects |
| srssubpop | report design effects, assuming SRS within subpopulation |
| meff | report MEFF design effects |
| meft | report MEFT design effects |

| *estat_size_options* | Description |
|---|---|
| obs | report number of observations (within subpopulation) |
| size | report subpopulation sizes |

| *estat_sd_options* | Description |
|---|---|
| variance | report subpopulation variances instead of standard deviations |
| srssubpop | report standard deviation, assuming SRS within subpopulation |

| *estat_cv_options* | Description |
|---|---|
| nolegend | suppress the table legend |
| *display_options* | control spacing and display of omitted variables and base and empty cells |

| *estat_gof_options* | Description |
|---|---|
| group(#) | compute test statistic using # quantiles |
| total | compute test statistic using the total estimator instead of the mean estimator |
| all | execute test for all observations in the data |

| *estat_vce_options* | Description |
|---|---|
| covariance | display as covariance matrix; the default |
| correlation | display as correlation matrix |
| equation(*spec*) | display only specified equations |
| block | display submatrices by equation |
| diag | display submatrices by equation; diagonal blocks only |
| format(%*fmt*) | display format for covariances and correlations |
| nolines | suppress lines between equations |
| *display_options* | control display of omitted variables and base and empty cells |

collect is allowed with all estat commands; see **[U] 11.1.10 Prefix commands**.

# Options

Options are presented under the following headings:



## Options for estat effects

`deff` and `deft` request that the design-effect measures DEFF and DEFT be displayed. This is the default, unless direct standardization or poststratification was used.

The `deff` and `deft` options are not allowed with estimation results that used direct standardization or poststratification. These methods obscure the measure of design effect because they adjust the frequency distribution of the target population.

`srssubpop` requests that DEFF and DEFT be computed using an estimate of simple random sampling (SRS) variance for sampling within a subpopulation. By default, DEFF and DEFT are computed using an estimate of the SRS variance for sampling from the entire population. Typically, `srssubpop` is used when computing subpopulation estimates by strata or by groups of strata.

`meff` and `meft` request that the misspecification-effect measures MEFF and MEFT be displayed.

*display_options*: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`; see [R] **Estimation options**.

## Options for estat lceffects

`deff` and `deft` request that the design-effect measures DEFF and DEFT be displayed. This is the default, unless direct standardization or poststratification was used.

The `deff` and `deft` options are not allowed with estimation results that used direct standardization or poststratification. These methods obscure the measure of design effect because they adjust the frequency distribution of the target population.

`srssubpop` requests that DEFF and DEFT be computed using an estimate of simple random sampling (SRS) variance for sampling within a subpopulation. By default, DEFF and DEFT are computed using an estimate of the SRS variance for sampling from the entire population. Typically, `srssubpop` is used when computing subpopulation estimates by strata or by groups of strata.

`meff` and `meft` request that the misspecification-effect measures MEFF and MEFT be displayed.

## Options for estat size

`obs` requests that the number of observations used to compute the estimate be displayed for each row of estimates.

`size` requests that the estimate of the subpopulation size be displayed for each row of estimates. The subpopulation size estimate equals the sum of the weights for those observations in the estimation sample that are also in the specified subpopulation. The estimated population size is reported when a subpopulation is not specified.

## Options for estat sd

variance requests that the subpopulation variance be displayed instead of the standard deviation.

srssubpop requests that the standard deviation be computed using an estimate of SRS variance for sampling within a subpopulation. By default, the standard deviation is computed using an estimate of the SRS variance for sampling from the entire population. Typically, srssubpop is given when computing subpopulation estimates by strata or by groups of strata.

## Options for estat cv

nolegend prevents the table legend identifying the subpopulations from being displayed.

*display_options*: noomitted, vsquish, noemptycells, baselevels, allbaselevels; see [R] **Estimation options**.

## Options for estat gof

group(#) specifies the number of quantiles to be used to group the data for the goodness-of-fit test. The minimum allowed value is group(2). The maximum allowed value is group(*df*), where *df* is the design degrees of freedom (e(df_r)). The default is group(10).

total requests that the goodness-of-fit test statistic be computed using the total estimator instead of the mean estimator.

all requests that the goodness-of-fit test statistic be computed for all observations in the data, ignoring any if or in restrictions specified with the model fit.

## Options for estat vce

covariance displays the matrix as a variance–covariance matrix; this is the default.

correlation displays the matrix as a correlation matrix rather than a variance–covariance matrix. rho is a synonym.

equation(*spec*) selects the part of the VCE to be displayed. If *spec* is *eqlist*, the VCE for the listed equations is displayed. If *spec* is *eqlist1* \ *eqlist2*, the part of the VCE associated with the equations in *eqlist1* (rowwise) and *eqlist2* (columnwise) is displayed. If *spec* is *, all equations are displayed. equation() implies block if diag is not specified.

block displays the submatrices pertaining to distinct equations separately.

diag displays the diagonal submatrices pertaining to distinct equations separately.

format(%*fmt*) specifies the number format for displaying the elements of the matrix. The default is format(%10.0g) for covariances and format(%8.4f) for correlations. See **[U] 12.5 Formats: Controlling how data are displayed** for more information.

nolines suppresses lines between equations.

*display_options*: noomitted, noemptycells, baselevels, allbaselevels; see [R] **Estimation options**.

# Remarks and examples

## ▷ Example 1

Using data from the Second National Health and Nutrition Examination Survey (NHANES II) (McDowell et al. 1981), let's estimate the population means for total serum cholesterol (`tcresult`) and for serum triglycerides (`tgresult`).

```
. use https://www.stata-press.com/data/r19/nhanes2
. svy: mean tcresult tgresult
(running mean on estimation sample)
Survey: Mean estimation
Number of strata = 31             Number of obs    =      5,050
Number of PSUs   = 62             Population size = 56,820,832
                                  Design df       =         31
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| tcresult | 211.3975 | 1.252274 | 208.8435 | 213.9515 |
| tgresult | 138.576 | 2.071934 | 134.3503 | 142.8018 |

We can use `estat svyset` to remind us of the survey design characteristics that were used to produce these results.

```
. estat svyset
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: strata
 Sampling unit 1: psu
           FPC 1: <zero>
```

`estat effects` reports a table of design and misspecification effects for each mean we estimated.

```
. estat effects, deff deft meff meft
```

| | Mean | Linearized std. err. | DEFF | DEFT | MEFF | MEFT |
|---|---|---|---|---|---|---|
| tcresult | 211.3975 | 1.252274 | 3.57141 | 1.88982 | 3.46105 | 1.86039 |
| tgresult | 138.576 | 2.071934 | 2.35697 | 1.53524 | 2.32821 | 1.52585 |

`estat size` reports a table that contains sample and population sizes.

```
. estat size
```

| | Mean | Linearized std. err. | Obs | Size |
|---|---|---|---|---|
| tcresult | 211.3975 | 1.252274 | 5,050 | 56,820,832 |
| tgresult | 138.576 | 2.071934 | 5,050 | 56,820,832 |

estat size can also report a table of subpopulation sizes.

```
. svy: mean tcresult, over(sex)
 (output omitted)
. estat size
```

| Over | Mean | Linearized std. err. | Obs | Size |
|---|---|---|---|---|
| c.tcresult@ sex | | | | |
| Male | 210.7937 | 1.312967 | 4,915 | 56,159,480 |
| Female | 215.2188 | 1.193853 | 5,436 | 60,998,033 |

estat sd reports a table of subpopulation standard deviations.

```
. estat sd
```

| Over | Mean | Std. dev. |
|---|---|---|
| c.tcresult@ sex | | |
| Male | 210.7937 | 45.79065 |
| Female | 215.2188 | 50.72563 |

estat cv reports a table of coefficients of variations for the estimates.

```
. estat cv
```

| Over | Mean | Linearized std. err. | CV (%) |
|---|---|---|---|
| c.tcresult@ sex | | | |
| Male | 210.7937 | 1.312967 | .622868 |
| Female | 215.2188 | 1.193853 | .554716 |

◁

## ▷ Example 2: Design effects with subpopulations

When there are subpopulations, estat effects can compute design effects with respect to one of two different hypothetical SRS designs. The default design is one in which SRS is conducted across the full population. The alternate design is one in which SRS is conducted entirely within the subpopulation of interest. This alternate design is used when the srssubpop option is specified.

Deciding which design is preferable depends on the nature of the subpopulations. If we can imagine identifying members of the subpopulations before sampling them, the alternate design is preferable. This case arises primarily when the subpopulations are strata or groups of strata. Otherwise, we may prefer to use the default.

Here is an example using the default with the NHANES II data.

```
. use https://www.stata-press.com/data/r19/nhanes2b
. svy: mean iron, over(sex)
  (output omitted)
. estat effects
```

| Over | Mean | Linearized std. err. | DEFF | DEFT |
|---|---|---|---|---|
| c.iron@sex | | | | |
| Male | 104.7969 | .557267 | 1.36097 | 1.16661 |
| Female | 97.16247 | .6743344 | 2.01403 | 1.41916 |

Thus the design-based variance estimate is about 36% larger than the estimate from the hypothetical SRS design including the full population. We can get DEFF and DEFT for the alternate SRS design by using the `srssubpop` option.

```
. estat effects, srssubpop
```

| Over | Mean | Linearized std. err. | DEFF | DEFT |
|---|---|---|---|---|
| c.iron@sex | | | | |
| Male | 104.7969 | .557267 | 1.348 | 1.16104 |
| Female | 97.16247 | .6743344 | 2.03132 | 1.42524 |

Because the NHANES II did not stratify on sex, we think it problematic to consider design effects with respect to SRS of the female (or male) subpopulation. Consequently, we would prefer to use the default here, although the values of DEFF differ little between the two in this case.

For other examples (generally involving heavy oversampling or undersampling of specified subpopulations), the differences in DEFF for the two schemes can be much more dramatic.

Consider the NMIHS data (Gonzalez, Krauss, and Scott 1992), and compute the mean of `birthwgt` over `race`:

```
. use https://www.stata-press.com/data/r19/nmihs
. svy: mean birthwgt, over(race)
  (output omitted)
. estat effects
```

| Over | Mean | Linearized std. err. | DEFF | DEFT |
|---|---|---|---|---|
| c.birthwgt@race | | | | |
| nonblack | 3402.32 | 7.609532 | 1.44376 | 1.20157 |
| black | 3127.834 | 6.529814 | .172041 | .414778 |

```
. estat effects, srssubpop
```

| Over | Mean | Linearized std. err. | DEFF | DEFT |
|---|---|---|---|---|
| c.birthwgt@race | | | | |
| nonblack | 3402.32 | 7.609532 | .826842 | .909308 |
| black | 3127.834 | 6.529814 | .528963 | .727298 |

Because the NMIHS survey was stratified on race, marital status, age, and birthweight, we believe it reasonable to consider design effects computed with respect to SRS within an individual race group. Consequently, we would recommend here the alternative hypothetical design for computing design effects; that is, we would use the `srssubpop` option.

◁

## ▷ Example 3: Misspecification effects

Misspecification effects assess biases in variance estimators that are computed under the wrong assumptions. The survey literature (for example, Scott and Holt 1982 , 850; Skinner 1989 ) defines misspecification effects with respect to a general set of "wrong" variance estimators. `estat effects` considers only one specific form: variance estimators computed under the incorrect assumption that our *observed* sample was selected through SRS.

The resulting "misspecification effect" measure is informative primarily when an unweighted point estimator is approximately unbiased for the parameter of interest. See Eltinge and Sribney (1996a) for a detailed discussion of extensions of misspecification effects that are appropriate for *biased* point estimators.

Note the difference between a misspecification effect and a design effect. For a design effect, we compare our complex-design–based variance estimate with an estimate of the true variance that we would have obtained under a hypothetical true simple random sample. For a misspecification effect, we compare our complex-design–based variance estimate with an estimate of the variance from fitting the same model without weighting, clustering, or stratification.

estat effects defines MEFF and MEFT as

$$\text{MEFF} = \hat{V}/\hat{V}_{\text{msp}}$$

$$\text{MEFT} = \sqrt{\text{MEFF}}$$

where $\hat{V}$ is the appropriate design-based estimate of variance and $\hat{V}_{\text{msp}}$ is the variance estimate computed with a misspecified design—ignoring the sampling weights, stratification, and clustering.

Here we request that the misspecification effects be displayed for the estimation of mean zinc levels from our NHANES II data.

```
. use https://www.stata-press.com/data/r19/nhanes2b
. svy: mean zinc, over(sex)
  (output omitted)
. estat effects, meff meft
```

| Over | Mean | Linearized std. err. | MEFF | MEFT |
|---|---|---|---|---|
| c.zinc@sex | | | | |
| Male | 90.74543 | .5850741 | 6.28254 | 2.5065 |
| Female | 83.8635 | .4689532 | 6.32648 | 2.51525 |

If we run ci means without weights, we get the standard errors that are $(\hat{V}_{\text{msp}})^{1/2}$.

```
. sort sex
. ci means zinc if sex == "Male":sex
```

| Variable | Obs | Mean | Std. err. | [95% conf. | interval] |
|---|---|---|---|---|---|
| zinc | 4,375 | 89.53143 | .2334228 | 89.0738 | 89.98906 |

```
. display _se[zinc#1.sex]/r(se)
2.5064994
. display (_se[zinc#1.sex]/r(se))^2
6.2825393
. ci means zinc if sex == "Female":sex
```

| Variable | Obs | Mean | Std. err. | [95% conf. | interval] |
|---|---|---|---|---|---|
| zinc | 4,827 | 83.76652 | .186444 | 83.40101 | 84.13204 |

```
. display _se[zinc#2.sex]/r(se)
2.515249
. display (_se[zinc#2.sex]/r(se))^2
6.3264774
```

◁

## ▷ Example 4: Design and misspecification effects for linear combinations

Let's compare the mean of total serum cholesterol (tcresult) between men and women in the NHANES II dataset.

```
. use https://www.stata-press.com/data/r19/nhanes2
. svy: mean tcresult, over(sex)
(running mean on estimation sample)
Survey: Mean estimation
Number of strata = 31              Number of obs    =      10,351
Number of PSUs   = 62              Population size = 117,157,513
                                   Design df       =          31
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| c.tcresult@sex | | | | |
| Male | 210.7937 | 1.312967 | 208.1159 | 213.4715 |
| Female | 215.2188 | 1.193853 | 212.784 | 217.6537 |

We can use estat lceffects to report the standard error, design effects, and misspecification effects of the difference between the above means.

```
. estat lceffects tcresult#1.sex - tcresult#2.sex, deff deft meff meft
 ( 1)  c.tcresult@1bn.sex - c.tcresult@2.sex = 0
```

| Mean | Coefficient | Std. err. | DEFF | DEFT | MEFF | MEFT |
|---|---|---|---|---|---|---|
| (1) | -4.425109 | 1.086786 | 1.31241 | 1.1456 | 1.27473 | 1.12904 |

◁

## ▷ Example 5: Using survey data to determine Neyman allocation

Suppose that we have partitioned our population into $L$ strata and stratum $h$ contains $N_h$ individuals. Also let $\sigma_h$ represent the standard deviation of a quantity we wish to sample from the population. According to Cochran (1977, sec. 5.5), we can minimize the variance of the stratified mean estimator, for a fixed sample size $n$, if we choose the stratum sample sizes according to Neyman allocation:

$$n_h = n\frac{N_h\sigma_h}{\sum_{i=1}^{L} N_i\sigma_i} \tag{1}$$

We can use estat sd with our current survey data to produce a table of subpopulation standard-deviation estimates. Then we could plug these estimates into (1) to improve our survey design for the next time we sample from our population.

Here is an example using birthweight from the NMIHS data. First, we need estimation results from `svy: mean` over the strata.

```
. use https://www.stata-press.com/data/r19/nmihs
. svyset [pw=finwgt], strata(stratan)
Sampling weights: finwgt
             VCE: linearized
     Single unit: missing
        Strata 1: stratan
 Sampling unit 1: <observations>
           FPC 1: <zero>
. svy: mean birthwgt, over(stratan)
  (output omitted)
```

Next we will use `estat size` to report the table of stratum sizes. We will also generate matrix `p_obs` to contain the observed percent allocations for each stratum. In the matrix expression, `r(_N)` is a row vector of stratum sample sizes and `e(N)` contains the total sample size. `r(_N_subp)` is a row vector of the estimated population stratum sizes.

```
. estat size
```

| Over | Mean | Linearized std. err. | Obs | Size |
|---|---|---|---|---|
| c.birthwgt@ stratan | | | | |
| 1 | 1049.434 | 19.00149 | 841 | 18,402.98161 |
| 2 | 2189.561 | 9.162736 | 803 | 67,650.95932 |
| 3 | 3303.492 | 7.38429 | 3,578 | 579,104.6188 |
| 4 | 1036.626 | 12.32294 | 710 | 29,814.93215 |
| 5 | 2211.217 | 9.864682 | 714 | 153,379.07445 |
| 6 | 3485.42 | 8.057648 | 3,300 | 3,047,209.105 |

```
. matrix p_obs = 100 * r(_N)/e(N)
. matrix nsubp = r(_N_subp)
```

Now we call `estat sd` to report the stratum standard-deviation estimates and generate matrix `p_neyman` to contain the percent allocations according to (1). In the matrix expression, `r(sd)` is a vector of the stratum standard deviations.

```
. estat sd
```

| Over | Mean | Std. dev. |
|---|---|---|
| c.birthwgt@ stratan | | |
| 1 | 1049.434 | 2305.931 |
| 2 | 2189.561 | 555.7971 |
| 3 | 3303.492 | 687.3575 |
| 4 | 1036.626 | 999.0867 |
| 5 | 2211.217 | 349.8068 |
| 6 | 3485.42 | 300.6945 |

```
. matrix p_neyman = 100 * hadamard(nsubp,r(sd))/el(nsubp*r(sd)',1,1)
. matrix list p_obs, format(%4.1f)
p_obs[1,6]
     c.birthwgt@  c.birthwgt@  c.birthwgt@  c.birthwgt@  c.birthwgt@
      1.stratan    2.stratan    3.stratan    4.stratan    5.stratan
r1          8.5          8.1         36.0          7.1          7.2
     c.birthwgt@
      6.stratan
r1         33.2
. matrix list p_neyman, format(%4.1f)
p_neyman[1,6]
     c.birthwgt@  c.birthwgt@  c.birthwgt@  c.birthwgt@  c.birthwgt@
      1.stratan    2.stratan    3.stratan    4.stratan    5.stratan
r1          2.9          2.5         26.9          2.0          3.6
     c.birthwgt@
      6.stratan
r1         62.0
```

We can see that strata 3 and 6 each contain about one-third of the observed data, with the rest of the observations spread out roughly equally to the remaining strata. However, plugging our sample estimates into (1) indicates that stratum 6 should get 62% of the sampling units, stratum 3 should get about 27%, and the remaining strata should get a roughly equal distribution of sampling units.

◁

## ▷ Example 6: Summarizing singleton and certainty strata

Use `estat strata` with `svy` estimation results to produce a table that reports the number of singleton and certainty strata in each sampling stage. Here is an example using (fictional) data from a complex survey with five sampling stages (the dataset is already `svyset`). If singleton strata are present, `estat strata` will report their effect on the standard errors.

```
. use https://www.stata-press.com/data/r19/strata5
. svy: total y
  (output omitted)
. estat strata
```

| Stage | Singleton strata | Certainty strata | Total strata |
|---|---|---|---|
| 1 | 0 | 1 | 4 |
| 2 | 1 | 0 | 10 |
| 3 | 0 | 3 | 29 |
| 4 | 2 | 0 | 110 |
| 5 | 204 | 311 | 865 |

```
Note: Missing standard error because of
      stratum with single sampling unit.
```

`estat strata` also reports the scale factor used when the `singleunit(scaled)` option is `svyset`. Of the 865 strata in the last stage, 204 are singleton strata and 311 are certainty strata. Thus the scaling factor for the last stage is

$$\frac{865-311}{865-311-204} \approx 1.58$$

```
. svyset, singleunit(scaled) noclear
  (output omitted)
. svy: total y
  (output omitted)
. estat strata
```

| Stage | Singleton strata | Certainty strata | Total strata | Scale factor |
|---|---|---|---|---|
| 1 | 0 | 1 | 4 | 1 |
| 2 | 1 | 0 | 10 | 1.11 |
| 3 | 0 | 3 | 29 | 1 |
| 4 | 2 | 0 | 110 | 1.02 |
| 5 | 204 | 311 | 865 | 1.58 |

```
Note: Variances scaled within each stage to handle
      strata with a single sampling unit.
```

The `singleunit(scaled)` option of `svyset` is one of three methods in which Stata's `svy` commands can automatically handle singleton strata when performing variance estimation; see [SVY] **Variance estimation** for a brief discussion of these methods.

◁

### ▷ Example 7: Goodness-of-fit test for svy: logistic

From example 2 in [SVY] **svy estimation**, we modeled the incidence of high blood pressure as a function of height, weight, age, and sex (using the `female` indicator variable).

```
. use https://www.stata-press.com/data/r19/nhanes2d
. svyset
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: strata
 Sampling unit 1: psu
           FPC 1: <zero>
. svy: logistic highbp height weight age female
(running logistic on estimation sample)
Survey: Logistic regression
Number of strata = 31                         Number of obs    =      10,351
Number of PSUs   = 62                         Population size = 117,157,513
                                              Design df        =          31
                                              F(4, 28)         =      368.33
                                              Prob > F         =      0.0000
```

| highbp | Odds ratio | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| height | .9657022 | .0051511 | -6.54 | 0.000 | .9552534 | .9762654 |
| weight | 1.053023 | .0026902 | 20.22 | 0.000 | 1.047551 | 1.058524 |
| age | 1.050059 | .0019761 | 25.96 | 0.000 | 1.046037 | 1.054097 |
| female | .6272129 | .0368195 | -7.95 | 0.000 | .5564402 | .706987 |
| _cons | .716868 | .6106878 | -0.39 | 0.699 | .1261491 | 4.073749 |

```
Note: _cons estimates baseline odds.
```

We can use `estat gof` to perform a goodness-of-fit test for this model.

```
. estat gof
Logistic model for highbp, goodness-of-fit test
                     F(9,23) =          5.32
                   Prob > F =          0.0006
```

The $F$ statistic is significant at the 5% level, indicating that the model is not a good fit for these data. ◁

## Stored results

`estat svyset` stores the following in `r()`:

Scalars

| | |
|---|---|
| `r(stages)` | number of sampling stages |
| `r(stages_wt)` | last stage containing stage-level weights |
| `r(bsn)` | bootstrap mean-weight adjustment |
| `r(fay)` | Fay's adjustment |
| `r(dof)` | `dof()` value |

Macros

| | |
|---|---|
| `r(wtype)` | weight type |
| `r(wexp)` | weight expression |
| `r(wvar)` | weight variable name |

| | |
|---|---|
| r(weight#) | variable identifying weight for stage # |
| r(su#) | variable identifying sampling units for stage # |
| r(strata#) | variable identifying strata for stage # |
| r(fpc#) | FPC for stage # |
| r(bsrweight) | bsrweight() variable list |
| r(brrweight) | brrweight() variable list |
| r(jkrweight) | jkrweight() variable list |
| r(sdrweight) | sdrweight() variable list |
| r(sdrfpc) | fpc() value from within sdrweight() |
| r(vce) | *vcetype* specified in vce() |
| r(mse) | mse, if specified |
| r(poststrata) | poststrata() variable |
| r(postweight) | postweight() variable |
| r(rake) | rake() specification |
| r(regress) | regress() specification |
| r(settings) | svyset arguments to reproduce the current settings |
| r(singleunit) | singleunit() setting |

estat strata stores the following in r():

Matrices

| | |
|---|---|
| r(_N_strata_single) | number of strata with one sampling unit |
| r(_N_strata_certain) | number of certainty strata |
| r(_N_strata) | number of strata |
| r(scale) | variance scale factors used when singleunit(scaled) is svyset |

estat effects stores the following in r():

Matrices

| | |
|---|---|
| r(deff) | vector of DEFF estimates |
| r(deft) | vector of DEFT estimates |
| r(deffsub) | vector of DEFF estimates for srssubpop |
| r(deftsub) | vector of DEFT estimates for srssubpop |
| r(meff) | vector of MEFF estimates |
| r(meft) | vector of MEFT estimates |

estat lceffects stores the following in r():

Scalars

| | |
|---|---|
| r(estimate) | point estimate |
| r(se) | estimate of standard error |
| r(df) | degrees of freedom |
| r(deff) | DEFF estimate |
| r(deft) | DEFT estimate |
| r(deffsub) | DEFF estimate for srssubpop |
| r(deftsub) | DEFT estimate for srssubpop |
| r(meff) | MEFF estimate |
| r(meft) | MEFT estimate |

estat size stores the following in r():

Matrices

| | |
|---|---|
| r(_N) | vector of numbers of nonmissing observations |
| r(_N_subp) | vector of subpopulation size estimates |

estat sd stores the following in r():

Macros
- r(srssubpop) — srssubpop, if specified

Matrices
- r(mean) — vector of subpopulation mean estimates
- r(sd) — vector of subpopulation standard-deviation estimates
- r(variance) — vector of subpopulation variance estimates

estat cv stores the following in r():

Matrices
- r(b) — estimates
- r(se) — standard errors of the estimates
- r(cv) — coefficients of variation of the estimates

estat gof stores the following in r():

Scalars
- r(p) — $p$-value associated with the test statistic
- r(F) — $F$ statistic, if e(df_r) was stored by estimation command
- r(df1) — numerator degrees of freedom for $F$ statistic
- r(df2) — denominator degrees of freedom for $F$ statistic
- r(chi2) — $\chi^2$ statistic, if e(df_r) was not stored by estimation command
- r(df) — degrees of freedom for $\chi^2$ statistic

estat vce stores the following in r():

Matrices
- r(V) — VCE or correlation matrix

# Methods and formulas

Methods and formulas are presented under the following headings:

## Design effects

`estat effects` produces two estimators of design effect, DEFF and DEFT.

DEFF is estimated as described in Kish (1965) as

$$\text{DEFF} = \frac{\hat{V}(\hat{\theta})}{\hat{V}_{\text{srswor}}(\tilde{\theta}_{\text{srs}})}$$

where $\hat{V}(\hat{\theta})$ is the design-based estimate of variance for a parameter, $\theta$, and $\hat{V}_{\text{srswor}}(\tilde{\theta}_{\text{srs}})$ is an estimate of the variance for an estimator, $\tilde{\theta}_{\text{srs}}$, that would be obtained from a similar hypothetical survey conducted using SRS without replacement (wor) and with the same number of sample elements, $m$, as in the actual survey. For example, if $\theta$ is a total $Y$, then

$$\hat{V}_{\text{srswor}}(\tilde{\theta}_{\text{srs}}) = (1-f)\frac{\widehat{M}}{m-1}\sum_{j=1}^{m} w_j(y_j - \hat{\bar{Y}})^2 \tag{1}$$

where $\hat{\bar{Y}} = \hat{Y}/\widehat{M}$. The factor $(1-f)$ is a finite population correction. If the user sets an FPC for the first stage, $f = m/\widehat{M}$ is used; otherwise, $f = 0$.

DEFT is estimated as described in Kish (1987, 41) as

$$\text{DEFT} = \sqrt{\frac{\hat{V}(\hat{\theta})}{\hat{V}_{\text{srswr}}(\tilde{\theta}_{\text{srs}})}}$$

where $\hat{V}_{\text{srswr}}(\tilde{\theta}_{\text{srs}})$ is an estimate of the variance for an estimator, $\tilde{\theta}_{\text{srs}}$, obtained from a similar survey conducted using SRS with replacement (wr). $\hat{V}_{\text{srswr}}(\tilde{\theta}_{\text{srs}})$ is computed using (1) with $f = 0$.

When computing estimates for a subpopulation, $\mathcal{S}$, and the `srssubpop` option is *not* specified (that is, the default), (1) is used with $w_{\mathcal{S}j} = I_{\mathcal{S}}(j)\, w_j$ in place of $w_j$, where

$$I_{\mathcal{S}}(j) = \begin{cases} 1, \text{if } j \in \mathcal{S} \\ 0, \text{otherwise} \end{cases}$$

The sums in (1) are still calculated over all elements in the sample, regardless of whether they belong to the subpopulation: by default, the SRS is assumed to be done across the full population.

When the `srssubpop` option is specified, the SRS is carried out within subpopulation $\mathcal{S}$. Here (1) is used with the sums restricted to those elements belonging to the subpopulation; $m$ is replaced with $m_{\mathcal{S}}$, the number of sample elements from the subpopulation; $\widehat{M}$ is replaced with $\widehat{M}_{\mathcal{S}}$, the sum of the weights from the subpopulation; and $\hat{\bar{Y}}$ is replaced with $\hat{\bar{Y}}_{\mathcal{S}} = \hat{Y}_{\mathcal{S}}/\widehat{M}_{\mathcal{S}}$, the weighted mean across the subpopulation.

## Linear combinations

`estat lceffects` estimates $\eta = C\theta$, where $\theta$ is a $q \times 1$ vector of parameters (for example, population means or population regression coefficients) and $C$ is any $1 \times q$ vector of constants. The estimate of $\eta$ is $\hat{\eta} = C\hat{\theta}$, and its variance estimate is

$$\hat{V}(\hat{\eta}) = C\hat{V}(\hat{\theta})C'$$

Similarly, the SRS without replacement (srswor) variance estimator used in the computation of DEFF is

$$\hat{V}_{\text{srswor}}(\tilde{\eta}_{\text{srs}}) = C\hat{V}_{\text{srswor}}(\hat{\theta}_{\text{srs}})C'$$

and the SRS with replacement (srswr) variance estimator used in the computation of DEFT is

$$\hat{V}_{\text{srswr}}(\tilde{\eta}_{\text{srs}}) = C\hat{V}_{\text{srswr}}(\hat{\theta}_{\text{srs}})C'$$

The variance estimator used in computing MEFF and MEFT is

$$\hat{V}_{\text{msp}}(\tilde{\eta}_{\text{msp}}) = C\hat{V}_{\text{msp}}(\hat{\theta}_{\text{msp}})C'$$

`estat lceffects` was originally developed under a different command name; see Eltinge and Sribney (1996b).

## Misspecification effects

`estat effects` produces two estimators of misspecification effect, MEFF and MEFT.

$$\text{MEFF} = \frac{\hat{V}(\hat{\theta})}{\hat{V}_{\text{msp}}(\hat{\theta}_{\text{msp}})}$$

$$\text{MEFT} = \sqrt{\text{MEFF}}$$

where $\hat{V}(\hat{\theta})$ is the design-based estimate of variance for a parameter, $\theta$, and $\hat{V}_{\text{msp}}(\hat{\theta}_{\text{msp}})$ is the variance estimate for $\hat{\theta}_{\text{msp}}$. These estimators, $\hat{\theta}_{\text{msp}}$ and $\hat{V}_{\text{msp}}(\hat{\theta}_{\text{msp}})$, are based on the incorrect assumption that the observations were obtained through SRS with replacement: they are the estimators obtained by simply ignoring weights, stratification, and clustering. When $\theta$ is a total $Y$, the estimator and its variance estimate are computed using the standard formulas for an unweighted total:

$$\hat{Y}_{\text{msp}} = \widehat{M}\,\overline{y} = \frac{\widehat{M}}{m}\sum_{j=1}^{m} y_j$$

$$\hat{V}_{\text{msp}}(\hat{Y}_{\text{msp}}) = \frac{\widehat{M}^2}{m(m-1)}\sum_{j=1}^{m}(y_j - \overline{y})^2$$

When computing MEFF and MEFT for a subpopulation, sums are restricted to those elements belonging to the subpopulation, and $m_{\mathcal{S}}$ and $\widehat{M}_{\mathcal{S}}$ are used in place of $m$ and $\widehat{M}$.

## Population and subpopulation standard deviations

For srswr designs, the variance of the mean estimator is

$$V_{\text{srswr}}(\overline{y}) = \sigma^2/n$$

where $n$ is the sample size and $\sigma$ is the population standard deviation. `estat sd` uses this formula and the results from `mean` and `svy: mean` to estimate the population standard deviation via

$$\hat{\sigma} = \sqrt{n\,\hat{V}_{\text{srswr}}(\overline{y})}$$

Subpopulation standard deviations are computed similarly, using the corresponding variance estimate and sample size.

## Coefficient of variation

The coefficient of variation (CV) for estimate $\hat{\theta}$ is

$$\text{CV}(\hat{\theta}) = \frac{\sqrt{\hat{V}(\hat{\theta})}}{|\hat{\theta}|} \times 100\%$$

A missing value is reported when $\hat{\theta}$ is zero.

## Goodness of fit for binary response models

Let $y_j$ be the $j$th observed value of the dependent variable, $\hat{p}_j$ be the predicted probability of a positive outcome, and $\hat{r}_j = y_j - \hat{p}_j$. Let $g$ be the requested number of groups from the `group()` option; then the $\hat{r}_j$ are placed in $g$ quantile groups as described in *Methods and formulas* for the `xtile` command in [D] **pctile**. Let $\overline{r} = (\overline{r}_1, \ldots, \overline{r}_g)$, where $\overline{r}_i$ is the subpopulation mean of the $\hat{r}_j$ for the $i$th quantile group. The standard Wald statistic for testing $H_0 : \overline{r} = \mathbf{0}$ is

$$\widehat{X}^2 = \overline{r}\{\hat{V}(\overline{r})\}^{-1}\overline{r}'$$

where $\hat{V}(\overline{r})$ is the design-based variance estimate for $\overline{r}$. Here $\widehat{X}^2$ is approximately distributed as a $\chi^2$ with $g-1$ degrees of freedom. This Wald statistic is one of the three goodness-of-fit statistics discussed in Graubard, Korn, and Midthune (1997). `estat gof` reports this statistic when the design degrees of freedom is missing, such as with `svy bootstrap` results.

According to Archer and Lemeshow (2006), the $F$-adjusted mean residual test is given by

$$\hat{F} = \widehat{X}^2(d - g + 2)/(dg)$$

where $d$ is the design degrees of freedom. Here $\hat{F}$ is approximately distributed as an $F$ with $g-1$ numerator and $d-g+2$ denominator degrees of freedom.

With the `total` option, `estat gof` uses the subpopulation total estimator instead of the subpopulation mean estimator.

## References

Archer, K. J., and S. A. Lemeshow. 2006. Goodness-of-fit test for a logistic regression model fitted using survey sample data. *Stata Journal* 6: 97–105.

Cochran, W. G. 1977. *Sampling Techniques.* 3rd ed. New York: Wiley.

Eltinge, J. L., and W. M. Sribney. 1996a. Accounting for point-estimation bias in assessment of misspecification effects, confidence-set coverage rates and test sizes. Unpublished manuscript, Department of Statistics, Texas A&M University.

———. 1996b. svy5: Estimates of linear combinations and hypothesis tests for survey data. *Stata Technical Bulletin* 31: 31–42. Reprinted in *Stata Technical Bulletin Reprints*, vol. 6, pp. 246–259. College Station, TX: Stata Press.

Gonzalez, J. F., Jr., N. Krauss, and C. Scott. 1992. Estimation in the 1988 National Maternal and Infant Health Survey. *Proceedings of the Section on Statistics Education, American Statistical Association* 343–348.

Graubard, B. I., E. L. Korn, and D. Midthune. 1997. "Testing goodness-of-fit for logistic regression with survey data". In *Proceedings of the Section on Survey Research Methods, Joint Statistical Meetings*, 170–174. Alexandria, VA: American Statistical Association.

Kish, L. 1965. *Survey Sampling.* New York: Wiley.

———. 1987. *Statistical Design for Research.* New York: Wiley.

McDowell, A., A. Engel, J. T. Massey, and K. Maurer. 1981. "Plan and operation of the Second National Health and Nutrition Examination Survey, 1976–1980". In *Vital and Health Statistics*, ser. 1, no. 15. Hyattsville, MD: National Center for Health Statistics.

Scott, A. J., and D. Holt. 1982. The effect of two-stage sampling on ordinary least squares methods. *Journal of the American Statistical Association* 77: 848–854. https://doi.org/10.2307/2287317.

Skinner, C. J. 1989. "Introduction to part A". In *Analysis of Complex Surveys*, edited by C. J. Skinner, D. Holt, and T. M. F. Smith, 23–58. New York: Wiley.

West, B. T., and S. E. McCabe. 2012. Incorporating complex sample design effects when only final survey weights are available. *Stata Journal* 12: 718–725.

## Also see

[SVY] **svy postestimation** — Postestimation tools for svy

[SVY] **svy estimation** — Estimation commands for survey data

[SVY] **Subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **Variance estimation** — Variance estimation for survey data

**jackknife_options** — More options for jackknife variance estimation

## Description

svy accepts more options when performing jackknife variance estimation.

## Syntax

| *jackknife_options* | Description |
|---|---|
| SE | |
| mse | use MSE formula for variance |
| nodots | suppress replication dots |
| dots(#) | display dots every # replications |
| saving(*filename*, ...) | save results to *filename* |
| keep | keep pseudovalues |
| verbose | display the full table legend |
| noisily | display any output from *command* |
| trace | trace *command* |
| title(*text*) | use *text* as the title for results |
| nodrop | do not drop observations |
| reject(*exp*) | identify invalid results |

saving(), keep, verbose, noisily, trace, title(), nodrop, and reject() are not shown in the dialog boxes for estimation commands.

## Options

SE

mse specifies that svy compute the variance by using deviations of the replicates from the observed value of the statistic based on the entire dataset. By default, svy computes the variance by using deviations of the pseudovalues from their mean.

nodots and dots(#) specify whether to display replication dots. By default, one dot character is printed for each successful replication. An "x" is displayed if *command* returns an error, "e" is displayed if at least one value in *exp_list* is missing, "n" is displayed if the sample size is not correct, and a yellow "s" is displayed if the dropped sampling unit is outside the subpopulation sample.

nodots suppresses display of the replication dots.

dots(#) displays dots every # replications. dots(0) is a synonym for nodots.

saving(), keep, verbose, noisily, trace, title(), nodrop, reject(); see [SVY] **svy jackknife**.

## Also see

[SVY] **svy** — The survey prefix command

[SVY] **svy jackknife** — Jackknife estimation for survey data

Remarks and examples Reference Also see

## Remarks and examples

Stata's `ml` command can fit maximum likelihood–based models for survey data. Many `ml`-based estimators can now be modified to handle one or more stages of clustering, stratification, sampling weights, finite population correction, calibration, poststratification, and subpopulation estimation. See [R] **ml** for details.

See [P] **program properties** for a discussion of the programming requirements for an estimation command to work with the `svy` prefix. See Pitblado, Poi, and Gould (2024) for examples of community-contributed estimation commands that support the `svy` prefix.

### Example 1: User-written survey regression

The `ml` command requires a program that computes likelihood values to perform maximum likelihood. Here is a likelihood evaluator used in Pitblado, Poi, and Gould (2024) to fit linear regression models using likelihood from the normal distribution.

```
program mynormal_lf
        version 19.5      // (or version 19 if you do not have StataNow)
        args lnf mu lnsigma
        quietly replace `lnf' = ln(normalden($ML_y1,`mu',exp(`lnsigma')))
end
```

Here we fit a survey regression model using a multistage survey dataset with `ml` and the above likelihood evaluator.

```
. use https://www.stata-press.com/data/r19/multistage
. svyset county [pw=sampwgt], strata(state) fpc(ncounties) || school,
> fpc(nschools)
Sampling weights: sampwgt
             VCE: linearized
     Single unit: missing
        Strata 1: state
 Sampling unit 1: county
           FPC 1: ncounties
        Strata 2: <one>
 Sampling unit 2: school
           FPC 2: nschools
. ml model lf mynormal_lf (mu: weight = height) /lnsigma, svy
. ml max
Initial:      Log pseudolikelihood =     -<inf>  (could not be evaluated)
Feasible:     Log pseudolikelihood = -7.301e+08
Rescale:      Log pseudolikelihood =  -51944380
Rescale eq:   Log pseudolikelihood =  -47565331
Iteration 0:  Log pseudolikelihood =  -47565331
Iteration 1:  Log pseudolikelihood =  -41225560  (not concave)
Iteration 2:  Log pseudolikelihood =  -41221017  (not concave)
Iteration 3:  Log pseudolikelihood =  -41170786  (not concave)
Iteration 4:  Log pseudolikelihood =  -41151252  (not concave)
Iteration 5:  Log pseudolikelihood =  -41132554  (not concave)
Iteration 6:  Log pseudolikelihood =  -41107910  (not concave)
Iteration 7:  Log pseudolikelihood =  -41077230
Iteration 8:  Log pseudolikelihood =  -39815341  (backed up)
Iteration 9:  Log pseudolikelihood =  -38344045
Iteration 10: Log pseudolikelihood =  -38328784
Iteration 11: Log pseudolikelihood =  -38328739
Iteration 12: Log pseudolikelihood =  -38328739
Number of strata =  50                          Number of obs   =     4,071
Number of PSUs   = 100                          Population size = 8,000,000
                                                Design df       =        50
                                                F(1, 50)        =    593.99
                                                Prob > F        =    0.0000
```

| weight | Coefficient | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| height | .7163115 | .0293908 | 24.37 | 0.000 | .6572784 | .7753447 |
| _cons | -149.6183 | 12.57265 | -11.90 | 0.000 | -174.8712 | -124.3654 |
| /lnsigma | 3.372154 | .0180777 | 186.54 | 0.000 | 3.335844 | 3.408464 |

◁

# Reference

Pitblado, J. S., B. P. Poi, and W. W. Gould. 2024. *Maximum Likelihood Estimation with Stata*. 5th ed. College Station, TX: Stata Press.

## Also see

[SVY] **Survey** — Introduction to survey commands

[P] **program properties** — Properties of user-defined programs

[R] **Maximize** — Details of iterative maximization

[R] **ml** — Maximum likelihood estimation

**Poststratification** — Poststratification for survey data



## Description

Poststratification is a method for adjusting the sampling weights, usually to account for underrepresented groups in the population.

See [SVY] **Direct standardization** for a similar method of adjustment that allows the comparison of rates that come from different frequency distributions.

## Remarks and examples

Poststratification involves adjusting the sampling weights so that they sum to the population sizes within each poststratum. This usually results in decreasing bias because of nonresponse and underrepresented groups in the population. Poststratification also tends to result in smaller variance estimates.

The `svyset` command has options to set variables for applying poststratification adjustments to the sampling weights. The `poststrata()` option takes a variable that contains poststratum identifiers, and the `postweight()` option takes a variable that contains the poststratum population sizes.

In the following example, we use an example from Levy and Lemeshow (2008) to show how poststratification affects the point estimates and their variance.

### ▷ Example 1: Poststratified mean

Levy and Lemeshow (2008, sec. 6.6) give an example of poststratification by using simple survey data from a veterinarian's client list. The data in `poststrata.dta` were collected using simple random sampling without replacement. The `totexp` variable contains the total expenses to the client, `type` identifies the cats and dogs, `postwgt` contains the poststratum sizes (450 for cats and 850 for dogs), and `fpc` contains the total number of clients ($850 + 450 = 1300$).

```
. use https://www.stata-press.com/data/r19/poststrata
. svyset, poststrata(type) postweight(postwgt) fpc(fpc)
Sampling weights: <none>
             VCE: linearized
      Poststrata: type
Post. pop. sizes: postwgt
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: <observations>
           FPC 1: fpc
. svy: mean totexp
(running mean on estimation sample)
Survey: Mean estimation
Number of strata =  1                  Number of obs   =    50
Number of PSUs   = 50                  Population size = 1,300
N. of poststrata =  2                  Design df       =    49
------------------------------------------------------------------------------
             |             Linearized
             |      Mean   std. err.      [95% conf. interval]
-------------+----------------------------------------------------------------
      totexp |   40.11513   1.163498      37.77699    42.45327
------------------------------------------------------------------------------
```

The mean total expenses is \$40.12 with a standard error of \$1.16. In the following, we omit the poststratification information from `svyset`, resulting in mean total expenses of \$39.73 with standard error \$2.22. The difference between the mean estimates is explained by the facts that expenses tend to be larger for dogs than for cats and that the dogs were slightly underrepresented in the sample ($850/1{,}300 \approx 0.65$ for the population; $32/50 = 0.64$ for the sample). This reasoning also explains why the variance estimate from the poststratified mean is smaller than the one that was not poststratified.

```
. svyset, fpc(fpc)
Sampling weights: <none>
             VCE: linearized
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: <observations>
           FPC 1: fpc
. svy: mean totexp
(running mean on estimation sample)
Survey: Mean estimation
Number of strata =  1                  Number of obs   = 50
Number of PSUs   = 50                  Population size = 50
                                       Design df       = 49
------------------------------------------------------------------------------
             |             Linearized
             |      Mean   std. err.      [95% conf. interval]
-------------+----------------------------------------------------------------
      totexp |    39.7254   2.221747      35.26063    44.19017
------------------------------------------------------------------------------
```

◁

## Methods and formulas

The following discussion assumes that you are already familiar with the topics discussed in [SVY] **Variance estimation**.

Suppose that you used a complex survey design to sample $m$ individuals from a population of size $M$. Let $P_k$ be the set of individuals in the sample that belong to poststratum $k$, and let $I_{P_k}(j)$ indicate if the $j$th individual is in poststratum $k$, where

$$I_{P_k}(j) = \begin{cases} 1, \text{if } j \in P_k \\ 0, \text{otherwise} \end{cases}$$

Also let $L_P$ be the number of poststrata and $M_k$ be the population size for poststratum $k$.

If $w_j$ is the unadjusted sampling weight for the $j$th sampled individual, the poststratification adjusted sampling weight is

$$w_j^* = \sum_{k=1}^{L_P} I_{P_k}(j) \frac{M_k}{\widehat{M}_k} w_j$$

where $\widehat{M}_k$ is

$$\widehat{M}_k = \sum_{j=1}^{m} I_{P_k}(j) w_j$$

The point estimates are computed using these adjusted weights. For example, the poststratified total estimator is

$$\hat{Y}^P = \sum_{j=1}^{m} w_j^* y_j$$

where $y_j$ is an item from the $j$th sampled individual.

For replication-based variance estimation, the replicate-weight variables are similarly adjusted to produce the replicate values used in the respective variance formulas.

The score variable for the linearized variance estimator of a poststratified total is

$$z_j(\hat{Y}^P) = \sum_{k=1}^{L_P} I_{P_k}(j) \frac{M_k}{\widehat{M}_k} \left( y_j - \frac{\hat{Y}_k}{\widehat{M}_k} \right) \tag{1}$$

where $\hat{Y}_k$ is the total estimator for the $k$th poststratum,

$$\hat{Y}_k = \sum_{j=1}^{m} I_{P_k}(j) w_j y_j$$

For the poststratified ratio estimator, the score variable is

$$z_j(\widehat{R}^P) = \frac{\widehat{X}^P z_j(\hat{Y}^P) - \hat{Y}^P z_j(\widehat{X}^P)}{(\widehat{X}^P)^2} \tag{2}$$

where $\widehat{X}^P$ is the poststratified total estimator for item $x_j$. For regression models, the equation-level scores are adjusted as in (1). These score variables were derived using the method described in [SVY] **Variance estimation** for the ratio estimator and are a direct result of the methods described in Deville (1999), Demnati and Rao (2004), and Shah (2004).

## References

Demnati, A., and J. N. K. Rao. 2004. Linearization variance estimators for survey data. *Survey Methodology* 30: 17–26.

Deville, J.-C. 1999. Variance estimation for complex statistics and estimators: Linearization and residual techniques. *Survey Methodology* 25: 193–203.

Levy, P. S., and S. A. Lemeshow. 2008. *Sampling of Populations: Methods and Applications*. 4th ed. Hoboken, NJ: Wiley.

Shah, B. V. 2004. Comment [on Demnati and Rao (2004)]. *Survey Methodology* 30: 29.

## Also see

[SVY] **Survey** — Introduction to survey commands

[SVY] **svy** — The survey prefix command

[SVY] **svyset** — Declare survey design for dataset

[SVY] **Calibration** — Calibration for survey data

[SVY] **Direct standardization** — Direct standardization of means, proportions, and ratios

**sdr_options** — More options for SDR variance estimation

## Description

svy accepts more options when performing successive difference replication (SDR) variance estimation. See [SVY] **svy sdr** for a complete discussion.

## Syntax

| *sdr_options* | Description |
|---|---|
| SE | |
| mse | use MSE formula for variance |
| nodots | suppress replication dots |
| dots(#) | display dots every # replications |
| saving(*filename*, ...) | save results to *filename* |
| verbose | display the full table legend |
| noisily | display any output from *command* |
| trace | trace *command* |
| title(*text*) | use *text* as the title for results |
| nodrop | do not drop observations |
| reject(*exp*) | identify invalid results |

saving(), verbose, noisily, trace, title(), nodrop, and reject() are not shown in the dialog boxes for estimation commands.

## Options

SE

mse specifies that svy compute the variance by using deviations of the replicates from the observed value of the statistics based on the entire dataset. By default, svy computes the variance by using deviations of the replicates from their mean.

nodots and dots(#) specify whether to display replication dots. By default, one dot character is displayed for each successful replication. An "x" is displayed if *command* returns an error, and an "e" is displayed if at least one value in *exp_list* is missing. You can also control whether dots are displayed using set dots; see [R] **set**.

nodots suppresses display of the replication dots.

dots(#) displays dots every # replications. dots(0) is a synonym for nodots.

saving(), verbose, noisily, trace, title(), nodrop, reject(); see [SVY] **svy sdr**.

## Also see

[SVY] **svy** — The survey prefix command

[SVY] **svy sdr** — Successive difference replication for survey data

## Description

Subpopulation estimation focuses on part of the population. This entry discusses subpopulation estimation and explains why you should use the `subpop()` option instead of `if` and `in` for your survey data analysis.

## Remarks and examples

Subpopulation estimation involves computing point and variance estimates for part of the population. This is not the same as restricting the estimation sample to the collection of observations within the subpopulation because variance estimation for survey data measures sample-to-sample variability, assuming that the same survey design is used to collect the data; see *Methods and formulas* for a detailed explanation. West, Berglund, and Heeringa (2008) provides further information on subpopulation analysis.

The `svy` prefix command's `subpop()` option performs subpopulation estimation. The `svy: mean`, `svy: proportion`, `svy: ratio`, and `svy: total` commands also have the `over()` option to perform estimation for multiple subpopulations.

The following examples illustrate how to use the `subpop()` and `over()` options.

### ▷ Example 1

Suppose that we are interested in estimating the proportion of women in our population who have had a heart attack. In our NHANES II dataset (McDowell et al. 1981), the female participants can be identified using the `female` variable, and the `heartatk` variable indicates whether an individual has ever had a heart attack. Below we use `svy: mean` with the `heartatk` variable to estimate the proportion of individuals who have had a heart attack, and we use `subpop(female)` to identify our subpopulation of interest.

```
. use https://www.stata-press.com/data/r19/nhanes2d
. svy, subpop(female): mean heartatk
(running mean on estimation sample)
Survey: Mean estimation
Number of strata = 31            Number of obs    =      10,349
Number of PSUs   = 62            Population size = 117,131,111
                                 Subpop. no. obs =       5,434
                                 Subpop. size    =  60,971,631
                                 Design df       =          31
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| heartatk | .0193276 | .0017021 | .0158562 | .0227991 |

The `subpop(`*varname*`)` option takes a 0/1 variable, and the subpopulation of interest is defined by *varname* $= 1$. All other members of the sample not in the subpopulation are indicated by *varname* $= 0$.

If a person's subpopulation status is unknown, *varname* should be set to missing (.), so those observations will be omitted from the analysis. For instance, in the preceding analysis, if a person's sex was not recorded, `female` should be coded as missing rather than as male (`female` = 0).

◁

### ❑ Technical note

Actually, the `subpop(`*varname*`)` option takes a zero/nonzero variable, and the subpopulation is defined by *varname* $\neq 0$ and not missing. All other members of the sample not in the subpopulation are indicated by *varname* $= 0$, but 0, 1, and missing are typically the only values used for the `subpop()` variable.

Furthermore, you can specify an `if` qualifier within `subpop()` to identify a subpopulation. The result is the same as generating a variable equal to the conditional expression and supplying it as the `subpop()` variable. If a *varname* and an `if` qualifier are specified within the `subpop()` option, the subpopulation is identified by their logical conjunction (logical *and*), and observations with missing values in either are dropped from the estimation sample.

❑

### ▷ Example 2: Multiple subpopulation estimation

Means, proportions, ratios, and totals for multiple subpopulations can be estimated using the `over()` option with `svy: mean`, `svy: proportion`, `svy: ratio`, and `svy: total`, respectively. Here is an example using the NMIHS data (Gonzalez, Krauss, and Scott 1992), estimating mean birthweight over the categories of the `race` variable.

```
. use https://www.stata-press.com/data/r19/nmihs
. svy: mean birthwgt, over(race)
(running mean on estimation sample)
Survey: Mean estimation
Number of strata =     6              Number of obs   =     9,946
Number of PSUs   = 9,946              Population size = 3,895,562
                                      Design df       =     9,940
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| c.birthwgt@race | | | | |
| nonblack | 3402.32 | 7.609532 | 3387.404 | 3417.236 |
| black | 3127.834 | 6.529814 | 3115.035 | 3140.634 |

More than one variable can be used in the over() option.

```
. svy: mean birthwgt, over(race marital)
(running mean on estimation sample)

Survey: Mean estimation

Number of strata =     6                  Number of obs    =     9,946
Number of PSUs   = 9,946                  Population size = 3,895,562
                                          Design df        =     9,940
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| c.birthwgt@race#marital | | | | |
| nonblack#single | 3291.045 | 20.18795 | 3251.472 | 3330.617 |
| nonblack#married | 3426.407 | 8.379497 | 3409.982 | 3442.833 |
| black#single | 3073.122 | 8.752553 | 3055.965 | 3090.279 |
| black#married | 3221.616 | 12.42687 | 3197.257 | 3245.975 |

Here the race and marital variables have value labels. race has the value 0 labeled "nonblack" (that is, white and other) and 1 labeled "black"; marital has the value 0 labeled "single" and 1 labeled "married". Value labels on the over() variables make for a more informative legend above the table of point estimates. See [U] 12.6.3 Value labels for information on creating value labels.

We can also combine the subpop() option with the over() option.

```
. generate nonblack = (race == 0) if !missing(race)

. svy, subpop(nonblack): mean birthwgt, over(marital age20)
(running mean on estimation sample)

Survey: Mean estimation

Number of strata =     3                  Number of obs    =     4,724
Number of PSUs   = 4,724                  Population size = 3,230,403
                                          Subpop. no. obs =     4,724
                                          Subpop. size    = 3,230,403
                                          Design df        =     4,721
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| c.birthwgt@marital#age20 | | | | |
| single#age20+ | 3312.012 | 24.2869 | 3264.398 | 3359.625 |
| single#age<20 | 3244.709 | 36.85934 | 3172.448 | 3316.971 |
| married#age20+ | 3434.923 | 8.674633 | 3417.916 | 3451.929 |
| married#age<20 | 3287.301 | 34.15988 | 3220.332 | 3354.271 |

```
Note: 3 strata omitted because they contain no subpopulation members.
```

This time, we estimated means for the marital status and age ($<20$ or $\geq 20$) subpopulations for race == 0 (nonblack) only. We carefully define nonblack so that it is missing when race is missing. If we omitted the if !missing(race) in our generate statement, then nonblack would be 0 when race was missing. This would improperly assume that all individuals with a missing value for race were black and could cause our results to have incorrect standard errors. The standard errors could be incorrect because those observations for which race is missing would be counted as part of the estimation sample, potentially inflating the number of PSUs used in the formula for the variance estimator. For this reason, observations with missing values for any of the over() variables are omitted from the analysis.

◁

# Methods and formulas

The following discussion assumes that you are already familiar with the topics discussed in [SVY] **Variance estimation**.

Cochran (1977, sec. 2.13) discusses a method by which you can derive estimates for subpopulation totals. This section uses this method to derive the formulas for a subpopulation total from a simple random sample (without replacement) to explain how the `subpop()` option works, shows why this method will often produce different results from those produced using an equivalent `if` (or `in`) qualifier (outside the `subpop()` option), and discusses how this method applies to subpopulation means, proportions, ratios, and regression models.

Methods and formulas are presented under the following headings:



## Subpopulation totals

Let $Y_j$ be a survey item for individual $j$ in the population, where $j = 1, \ldots, N$ and $N$ is the population size. Let $S$ be a subset of individuals in the population and $I_S(j)$ indicate if the $j$th individual is in $S$, where

$$I_S(j) = \begin{cases} 1, & \text{if } j \in S \\ 0, & \text{otherwise} \end{cases}$$

The subpopulation total is

$$Y_S = \sum_{j=1}^{N} I_S(j) Y_j$$

and the subpopulation size is

$$N_S = \sum_{j=1}^{N} I_S(j)$$

Let $y_j$ be the items for those individuals selected in the sample, where $j = 1, \ldots, n$ and $n$ is the sample size. The number of individuals sampled from the subpopulation is

$$n_S = \sum_{j=1}^{n} I_S(j)$$

The estimator for the subpopulation total is

$$\hat{Y}_S = \sum_{j=1}^{n} I_S(j) w_j y_j \tag{1}$$

where $w_j = N/n$ is the unadjusted sampling weight for this design. The estimator for $N_S$ is

$$\widehat{N}_S = \sum_{j=1}^{n} I_S(j) w_j$$

The replicate values for the BRR and jackknife variance estimators are computed using the same method.

The linearized variance estimator for $\hat{Y}_S$ is

$$\hat{V}(\hat{Y}_S) = \left(1 - \frac{n}{N}\right) \frac{n}{n-1} \sum_{j=1}^{n} \left\{ I_S(j) w_j y_j - \frac{1}{n} \hat{Y}_S \right\}^2 \tag{2}$$

The covariance estimator for the subpopulation totals $\hat{Y}_S$ and $\widehat{X}_S$ (notation for $X_S$ is defined similarly to that of $Y_S$) is

$$\widehat{\mathrm{Cov}}(\hat{Y}_S, \widehat{X}_S) = \left(1 - \frac{n}{N}\right) \frac{n}{n-1} \sum_{j=1}^{n} \left\{ I_S(j) w_j y_j - \frac{1}{n} \hat{Y}_S \right\} \left\{ I_S(j) w_j x_j - \frac{1}{n} \widehat{X}_S \right\} \tag{3}$$

Equation (2) is not the same formula that results from restricting the estimation sample to the observations within $S$. The formula using this restricted sample (assuming a `svyset` with the corresponding FPC) is

$$\tilde{V}(\hat{Y}_S) = \left(1 - \frac{n_S}{\widehat{N}_S}\right) \frac{n_S}{n_S - 1} \sum_{j=1}^{n} I_S(j) \left\{ w_j y_j - \frac{1}{n_S} \hat{Y}_S \right\}^2 \tag{4}$$

These variance estimators, (2) and (4), assume two different survey designs. In (2), $n$ individuals are sampled without replacement from the population comprising the $N_S$ values from the subpopulation with $N - N_S$ additional zeros. In (4), $n_S$ individuals are sampled without replacement from the subpopulation of $N_S$ values. We discourage using (4) by warning against using the `if` and `in` qualifiers for subpopulation estimation because this variance estimator does not accurately measure the sample-to-sample variability of the subpopulation estimates for the survey design that was used to collect the data.

For survey data, there are only a few circumstances that require using the `if` qualifier. For example, if you suspected laboratory error for a certain set of measurements, then using the `if` qualifier to omit these observations from the analysis might be proper.

## Subpopulation estimates other than the total

To generalize the above results, note that the other point estimators—such as means, proportions, ratios, and regression coefficients—yield a linearized variance estimator based on one or more (equation level) score variables. For example, the weighted sample estimation equations of a regression model for a given subpopulation (see (3) from [SVY] **Variance estimation**) is

$$\widehat{G}(\boldsymbol{\beta}_S) = \sum_{j=1}^{n} I_S(j) w_j S(\boldsymbol{\beta}_S; y_j, \mathbf{x}_j) = 0 \tag{5}$$

You can write $\widehat{G}(\boldsymbol{\beta}_S)$ as

$$\widehat{G}(\boldsymbol{\beta}_S) = \sum_{j=1}^{n} I_S(j) w_j \mathbf{d}_j$$

which is an estimator for the subpopulation total $G(\boldsymbol{\beta}_S)$, so its variance estimator can be computed using the design-based variance estimator for a subpopulation total.

## Subpopulation with replication methods

The above comparison between the variance estimator from the `subpop()` option and the variance estimator from the `if` and `in` qualifiers is also true for the replication methods.

For the BRR method, the same number of replicates is produced with or without the `subpop()` option. The difference is how the replicate values are computed. Using the `if` and `in` qualifiers may cause an error because `svy brr` checks that there are two PSUs in every stratum within the restricted sample.

For the jackknife method, every PSU produces a replicate, even if it does not contain an observation within the subpopulation specified using the `subpop()` option. When the `if` and `in` qualifiers are used, only the PSUs that have at least 1 observation within the restricted sample will produce a replicate.

For methods using replicate weight variables, every weight variable produces a replicate, even if it does not contain an observation within the subpopulation specified using the `subpop()` option. When the `if` and `in` qualifiers are used, only the PSUs that have at least 1 observation within the restricted sample will produce a replicate.

## References

Cochran, W. G. 1977. *Sampling Techniques.* 3rd ed. New York: Wiley.

Gonzalez, J. F., Jr., N. Krauss, and C. Scott. 1992. Estimation in the 1988 National Maternal and Infant Health Survey. *Proceedings of the Section on Statistics Education, American Statistical Association* 343–348.

McDowell, A., A. Engel, J. T. Massey, and K. Maurer. 1981. "Plan and operation of the Second National Health and Nutrition Examination Survey, 1976–1980". In *Vital and Health Statistics*, ser. 1, no. 15. Hyattsville, MD: National Center for Health Statistics.

West, B. T., P. A. Berglund, and S. G. Heeringa. 2008. A closer examination of subpopulation analysis of complex-sample survey data. *Stata Journal* 8: 520–531.

## Also see

[SVY] **Survey** — Introduction to survey commands

[SVY] **svy** — The survey prefix command

[SVY] **svy postestimation** — Postestimation tools for svy

[SVY] **svyset** — Declare survey design for dataset

**svy** — The survey prefix command



## Description

svy fits statistical models for complex survey data by adjusting the results of a command for survey settings identified by svyset. Any Stata estimation command listed in [SVY] **svy estimation** may be used with svy. User-written programs that meet the requirements in [P] **program properties** may also be used.

## Quick start

Data for a two-stage design with sampling weight wvar1, strata defined by levels of svar, sampling units are identified by su1, and second-stage clustering is defined by su2

```
svyset su1 [pweight=wvar1], strata(svar) || su2
```

Adjust linear regression for complex survey design settings specified in svyset

```
svy: regress ...
```

Same as above, but restrict estimation to the subpopulation where group equals 4

```
svy, subpop(if group==4): regress ...
```

Same as above, but use new binary variable insample to indicate the subpopulation

```
generate insample = (group==4)
svy, subpop(insample): regress ...
```

Specify that the design degrees of freedom is 135 instead of the difference between the number of unique values of su1 and the number of levels of svar

```
svy, dof(135): regress ...
```

Note: Any estimation command meeting the requirements specified in the *Description* may be substituted for regress in the examples above.

# Syntax

```
svy [vcetype] [ , svy_options eform_option ] : command
```

| *vcetype* | Description |
|---|---|
| SE | |
| linearized | Taylor-linearized variance estimation |
| bootstrap | bootstrap variance estimation; see [SVY] **svy bootstrap** |
| brr | BRR variance estimation; see [SVY] **svy brr** |
| jackknife | jackknife variance estimation; see [SVY] **svy jackknife** |
| sdr | SDR variance estimation; see [SVY] **svy sdr** |

Specifying a *vcetype* overrides the default from `svyset`.

| *svy_options* | Description |
|---|---|
| if/in | |
| subpop([*varname*] [*if*]) | identify a subpopulation |
| SE | |
| dof(#) | design degrees of freedom |
| *bootstrap_options* | more options allowed with bootstrap variance estimation; see [SVY] ***bootstrap_options*** |
| *brr_options* | more options allowed with BRR variance estimation; see [SVY] ***brr_options*** |
| *jackknife_options* | more options allowed with jackknife variance estimation; see [SVY] ***jackknife_options*** |
| *sdr_options* | more options allowed with SDR variance estimation; see [SVY] ***sdr_options*** |
| Reporting | |
| level(#) | set confidence level; default is level(95) |
| nocnsreport | do not display constraints |
| *display_options* | control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling |
| noheader | suppress table header |
| nolegend | suppress table legend |
| noadjust | do not adjust model Wald statistic |
| noisily | display any output from *command* |
| trace | trace *command* |
| coeflegend | display legend instead of statistics |

`svy` requires that the survey design variables be identified using `svyset`; see [SVY] **svyset**.

*command* defines the estimation command to be executed. The `by` prefix cannot be part of *command*.

`collect` is allowed; see **[U] 11.1.10 Prefix commands**. `mi estimate` may be used with `svy linearized` if the estimation command allows `mi estimate`; it may not be used with `svy bootstrap`, `svy brr`, `svy jackknife`, or `svy sdr`.

`noheader`, `nolegend`, `noadjust`, `noisily`, `trace`, and `coeflegend` are not shown in the dialog boxes for estimation commands.

Warning: Using `if` or `in` restrictions will often not produce correct variance estimates for subpopulations. To compute estimates for subpopulations, use the `subpop()` option.

See **[U] 20 Estimation and postestimation commands** for more capabilities of estimation commands.

# Options

if/in

`subpop(`*subpop*`)` specifies that estimates be computed for the single subpopulation identified by *subpop*, which is

[ *varname* ] [ *if* ]

Thus the subpopulation is defined by the observations for which *varname* $\neq 0$ that also meet the `if` conditions. Typically, *varname* $= 1$ defines the subpopulation, and *varname* $= 0$ indicates observations not belonging to the subpopulation. For observations whose subpopulation status is uncertain, *varname* should be set to a missing value; such observations are dropped from the estimation sample.

See [SVY] **Subpopulation estimation** and [SVY] **estat**.

SE

`dof(`#`)` specifies the design degrees of freedom, overriding the default calculation, df $= N_{\text{psu}} - N_{\text{strata}}$.

*bootstrap_options* are other options that are allowed with bootstrap variance estimation specified by `svy bootstrap` or specified as `svyset` using the `vce(bootstrap)` option; see [SVY] ***bootstrap_options***.

*brr_options* are other options that are allowed with BRR variance estimation specified by `svy brr` or specified as `svyset` using the `vce(brr)` option; see [SVY] ***brr_options***.

*jackknife_options* are other options that are allowed with jackknife variance estimation specified by `svy jackknife` or specified as `svyset` using the `vce(jackknife)` option; see [SVY] ***jackknife_options***.

*sdr_options* are other options that are allowed with SDR variance estimation specified by `svy sdr` or specified as `svyset` using the `vce(sdr)` option; see [SVY] ***sdr_options***.

Reporting

`level(`#`)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see **[U] 20.8 Specifying the width of confidence intervals**.

`nocnsreport`; see [R] **Estimation options**.

*display_options*: `noci`, `nopvalues`, `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(`#`)`, `fvwrapon(`*style*`)`, `cformat(`%*fmt*`)`, `pformat(`%*fmt*`)`, `sformat(`%*fmt*`)`, and `nolstretch`; see [R] **Estimation options**.

The following options are available with `svy` but are not shown in the dialog boxes:

`noheader` prevents the table header from being displayed. This option implies `nolegend`.

`nolegend` prevents the table legend identifying the subpopulations from being displayed.

`noadjust` specifies that the model Wald test be carried out as $W/k \sim F(k,d)$, where $W$ is the Wald test statistic, $k$ is the number of terms in the model excluding the constant term, $d$ is the total number of sampled PSUs minus the total number of strata, and $F(k,d)$ is an $F$ distribution with $k$ numerator degrees of freedom and $d$ denominator degrees of freedom. By default, an adjusted Wald test is conducted: $(d-k+1)W/(kd) \sim F(k, d-k+1)$.

See Korn and Graubard (1990) for a discussion of the Wald test and the adjustments thereof. Using the `noadjust` option is not recommended.

`noisily` requests that any output from *command* be displayed.

`trace` causes a trace of the execution of *command* to be displayed.

`coeflegend`; see [R] **Estimation options**.

The following option is usually available with `svy` at the time of estimation or on replay but is not shown in all dialog boxes:

*eform_option*; see [R] ***eform_option***.

## Remarks and examples

The `svy` prefix is designed for use with complex survey data. Typical survey design characteristics include sampling weights, one or more stages of clustered sampling, and stratification. For a general discussion of various aspects of survey designs, including multistage designs, see [SVY] **svyset**.

Below we present an example of the effects of weights, clustering, and stratification. This is a typical case, but drawing general rules from any one example is still dangerous. You could find particular analyses from other surveys that are counterexamples for each of the trends for standard errors exhibited here.

### ▷ Example 1: The effects of weights, clustering, and stratification

We use data from the Second National Health and Nutrition Examination Survey (NHANES II) (McDowell et al. 1981) as our example. This is a national survey, and the dataset has sampling weights, strata, and clustering. In this example, we will consider the estimation of the mean serum zinc level of all adults in the United States.

First, consider a proper design-based analysis, which accounts for weighting, clustering, and stratification. Before we issue our `svy` estimation command, we set the weight, strata, and PSU identifier variables:

```
. use https://www.stata-press.com/data/r19/nhanes2f
. svyset psuid [pweight=finalwgt], strata(stratid)
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: stratid
 Sampling unit 1: psuid
           FPC 1: <zero>
```

We now estimate the mean by using the proper design-based analysis:

```
. svy: mean zinc
(running mean on estimation sample)
Survey: Mean estimation
Number of strata = 31            Number of obs    =       9,189
Number of PSUs   = 62            Population size = 104,176,071
                                 Design df       =          31
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| zinc | 87.18207 | .4944827 | 86.17356 | 88.19057 |

If we ignore the survey design and use `mean` to estimate the mean, we get

```
. mean zinc
Mean estimation                          Number of obs = 9,189
```

| | Mean | Std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| zinc | 86.51518 | .1510744 | 86.21904 | 86.81132 |

The point estimate from the unweighted analysis is smaller by more than one standard error than the proper design-based estimate. Also, design-based analysis produced a standard error that is 3.27 times larger than the standard error produced by our incorrect analysis.

◁

## ▷ Example 2: Halfway is not enough—the importance of stratification and clustering

When some people analyze survey data, they say, "I know I have to use my survey weights, but I will just ignore the stratification and clustering information." If we follow this strategy, we will obtain the proper design-based point estimates, but our standard errors, confidence intervals, and test statistics will usually be wrong.

To illustrate this effect, suppose that we used the `svy: mean` procedure with `pweights` only.

```
. svyset [pweight=finalwgt]
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: <observations>
           FPC 1: <zero>
. svy: mean zinc
(running mean on estimation sample)
Survey: Mean estimation
Number of strata =     1         Number of obs    =       9,189
Number of PSUs   = 9,189         Population size = 104,176,071
                                 Design df       =       9,188
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| zinc | 87.18207 | .1828747 | 86.82359 | 87.54054 |

This approach gives us the same point estimate as our design-based analysis, but the reported standard error is less than one-half the design-based standard error. If we accounted only for clustering and weights and ignored stratification in NHANES II, we would obtain the following analysis:

```
. svyset psuid [pweight=finalwgt]

Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: psuid
           FPC 1: <zero>

. svy: mean zinc
(running mean on estimation sample)

Survey: Mean estimation

Number of strata = 1              Number of obs   =       9,189
Number of PSUs   = 2              Population size = 104,176,071
                                  Design df       =           1
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| zinc | 87.18207 | .7426221 | 77.74616 | 96.61798 |

Here our standard error is about 50% larger than what we obtained in our proper design-based analysis. ◁

## ▷ Example 3

Let's look at a regression. We model zinc on the basis of age, weight, sex, race, and rural or urban residence. We compare a proper design-based analysis with an ordinary regression (which assumes independent and identically distributed error).

Here is our design-based analysis:

```
. svyset psuid [pweight=finalwgt], strata(stratid)

Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: stratid
 Sampling unit 1: psuid
           FPC 1: <zero>

. svy: regress zinc age c.age#c.age weight female black orace rural
(running regress on estimation sample)

Survey: Linear regression

Number of strata = 31                         Number of obs    =       9,189
Number of PSUs   = 62                         Population size  = 104,176,071
                                              Design df        =          31
                                              F(7, 25)         =       62.50
                                              Prob > F         =      0.0000
                                              R-squared        =      0.0698
```

| zinc | Coefficient | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| age | -.1701161 | .0844192 | -2.02 | 0.053 | -.3422901 | .002058 |
| c.age#c.age | .0008744 | .0008655 | 1.01 | 0.320 | -.0008907 | .0026396 |
| weight | .0535225 | .0139115 | 3.85 | 0.001 | .0251499 | .0818951 |
| female | -6.134161 | .4403625 | -13.93 | 0.000 | -7.032286 | -5.236035 |
| black | -2.881813 | 1.075958 | -2.68 | 0.012 | -5.076244 | -.687381 |
| orace | -4.118051 | 1.621121 | -2.54 | 0.016 | -7.424349 | -.8117528 |
| rural | -.5386327 | .6171836 | -0.87 | 0.390 | -1.797387 | .7201216 |
| _cons | 92.47495 | 2.228263 | 41.50 | 0.000 | 87.93038 | 97.01952 |

If we had improperly ignored our survey weights, stratification, and clustering (that is, if we had used the usual Stata `regress` command), we would have obtained the following results:

```
. regress zinc age c.age#c.age weight female black orace rural
```

| Source | SS | df | MS | | |
|---|---|---|---|---|---|
| Model | 110417.827 | 7 | 15773.9753 | Number of obs | = 9,189 |
| Residual | 1816535.3 | 9,181 | 197.85811 | F(7, 9181) | = 79.72 |
| | | | | Prob > F | = 0.0000 |
| | | | | R-squared | = 0.0573 |
| | | | | Adj R-squared | = 0.0566 |
| Total | 1926953.13 | 9,188 | 209.724982 | Root MSE | = 14.066 |

| zinc | Coefficient | Std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| age | -.090298 | .0638452 | -1.41 | 0.157 | -.2154488 | .0348528 |
| c.age#c.age | -.0000324 | .0006788 | -0.05 | 0.962 | -.0013631 | .0012983 |
| weight | .0606481 | .0105986 | 5.72 | 0.000 | .0398725 | .0814237 |
| female | -5.021949 | .3194705 | -15.72 | 0.000 | -5.648182 | -4.395716 |
| black | -2.311753 | .5073536 | -4.56 | 0.000 | -3.306279 | -1.317227 |
| orace | -3.390879 | 1.060981 | -3.20 | 0.001 | -5.470637 | -1.311121 |
| rural | -.0966462 | .3098948 | -0.31 | 0.755 | -.7041089 | .5108166 |
| _cons | 89.49465 | 1.477528 | 60.57 | 0.000 | 86.59836 | 92.39093 |

The point estimates differ by 3%–100%, and the standard errors for the proper designed-based analysis are 30%–110% larger. The differences are not as dramatic as we saw with the estimation of the mean, but they are still substantial.

◁

## Stored results

svy stores the following in e():

Scalars

| | |
|---|---|
| e(N) | number of observations |
| e(N_sub) | subpopulation observations |
| e(N_strata) | number of strata |
| e(N_strata_omit) | number of strata omitted |
| e(singleton) | 1 if singleton strata, 0 otherwise |
| e(census) | 1 if census data, 0 otherwise |
| e(F) | model *F* statistic |
| e(df_m) | model degrees of freedom |
| e(df_r) | variance degrees of freedom |
| e(N_pop) | estimate of population size |
| e(N_subpop) | estimate of subpopulation size |
| e(N_psu) | number of sampled PSUs |
| e(stages) | number of sampling stages |
| e(k_eq) | number of equations in e(b) |
| e(k_aux) | number of ancillary parameters |
| e(p) | *p*-value |
| e(rank) | rank of e(V) |

Macros

| | |
|---|---|
| e(prefix) | svy |
| e(cmdname) | command name from *command* |
| e(cmd) | same as e(cmdname) or e(vce) |
| e(command) | *command* |
| e(cmdline) | command as typed |
| e(wtype) | weight type |
| e(wexp) | weight expression |
| e(weight#) | variable identifying weight for stage # |
| e(wvar) | weight variable name |
| e(singleunit) | singleunit() setting |
| e(strata) | strata() variable |
| e(strata#) | variable identifying strata for stage # |
| e(psu) | psu() variable |
| e(su#) | variable identifying sampling units for stage # |
| e(fpc) | fpc() variable |
| e(fpc#) | FPC for stage # |
| e(title) | title in estimation output |
| e(poststrata) | poststrata() variable |
| e(postweight) | postweight() variable |
| e(vce) | *vcetype* specified in vce() |
| e(vcetype) | title used to label Std. err. |
| e(mse) | mse, if specified |
| e(subpop) | *subpop* from subpop() |
| e(adjust) | noadjust, if specified |
| e(properties) | b V |
| e(estat_cmd) | program used to implement estat |
| e(predict) | program used to implement predict |
| e(marginsnotok) | predictions disallowed by margins |
| e(marginswtype) | weight type for margins |

Matrices

| | |
|---|---|
| e(b) | estimates |
| e(V) | design-based variance |
| e(V_srs) | simple-random-sampling-without-replacement variance, $\widehat{V}_{\text{srswor}}$ |
| e(V_srssub) | subpopulation simple-random-sampling-without-replacement variance, $\widehat{V}_{\text{srswor}}$ (created only when subpop() is specified) |
| e(V_srswr) | simple-random-sampling-with-replacement variance, $\widehat{V}_{\text{srswr}}$ (created only when fpc() option is svyset) |
| e(V_srssubwr) | subpopulation simple-random-sampling-with-replacement variance, $\widehat{V}_{\text{srswr}}$ (created only when subpop() is specified) |
| e(V_modelbased) | model-based variance |
| e(V_msp) | variance from misspecified model fit, $\widehat{V}_{\text{msp}}$ |
| e(_N_strata_single) | number of strata with one sampling unit |
| e(_N_strata_certain) | number of certainty strata |
| e(_N_strata) | number of strata |
| e(_N_subp) | estimate of subpopulation sizes within over() groups |

Functions

| | |
|---|---|
| e(sample) | marks estimation sample |

svy also carries forward most of the results already in e() from *command*.

In addition to the above, the following is stored in r():

Matrices

| | |
|---|---|
| r(table) | matrix containing the coefficients with their standard errors, test statistics, $p$-values, and confidence intervals |

Note that results stored in r() are updated when the command is replayed and will be replaced when any r-class command is run after the estimation command.

## Methods and formulas

See [SVY] **Variance estimation** for all the details behind the point estimate and variance calculations made by svy.

## References

Korn, E. L., and B. I. Graubard. 1990. Simultaneous testing of regression coefficients with complex survey data: Use of Bonferroni $t$ statistics. *American Statistician* 44: 270–276. https://doi.org/10.2307/2684345.

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## Also see

[SVY] **svy estimation** — Estimation commands for survey data

[SVY] **svy postestimation** — Postestimation tools for svy

[SVY] **svy bootstrap** — Bootstrap for survey data

[SVY] **svy brr** — Balanced repeated replication for survey data

[SVY] **svy jackknife** — Jackknife estimation for survey data

[SVY] **svy sdr** — Successive difference replication for survey data

[SVY] **svyset** — Declare survey design for dataset

[SVY] **Calibration** — Calibration for survey data

[SVY] **Poststratification** — Poststratification for survey data

[SVY] **Subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **Variance estimation** — Variance estimation for survey data

[P] **program properties** — Properties of user-defined programs

[P] **_robust** — Robust variance estimates

**[U] 20 Estimation and postestimation commands**

**svy bootstrap** — Bootstrap for survey data



## Description

`svy bootstrap` performs nonparametric bootstrap estimation of specified statistics (or expressions) for a Stata command or a user-written program. The command is executed once for each replicate using sampling weights that are adjusted according to the bootstrap methodology. Any Stata estimation command listed in [SVY] **svy estimation** may be used with `svy bootstrap`. User-written programs that meet the requirements in [P] **program properties** may also be used.

## Quick start

Estimate population mean of `v1` using bootstrap standard-error estimates and variables with prefix `rwvar` as the bootstrap replicate weights

```
svyset [pweight=wvar1], bsrweight(rwvar*)
svy bootstrap _b: mean v1
```

Same as above

```
svyset [pweight=wvar1], bsrweight(rwvar*) vce(bootstrap)
svy: mean v1
```

Same as above, and specify that 3 replicates were used to calculate each bootstrap replicate weight

```
svy, bsn(3): mean v1
```

Bootstrap standard error of the difference between the means of `v2` and `v3` using either `svyset` command above

```
svy bootstrap (_b[v2]-_b[v3]): mean v2 v3
```

Same as above, but name the result `diff` and save results from each replication to `mydata.dta`

```
svy bootstrap diff=(_b[v2]-_b[v3]), saving(mydata): mean v2 v3
```

Note: Any estimation command meeting the requirements specified in the *Description* may be substituted for `mean` in the examples above.

## Menu

Statistics > Survey data analysis > Resampling > Bootstrap estimation

# Syntax

svy bootstrap *exp_list* [ , *svy_options bootstrap_options eform_option* ] : *command*

| *svy_options* | Description |
|---|---|
| **if/in** | |
| subpop([ *varname* ] [ *if* ]) | identify a subpopulation |
| **Reporting** | |
| level(#) | set confidence level; default is level(95) |
| noheader | suppress table header |
| nolegend | suppress table legend |
| noadjust | do not adjust model Wald statistic |
| nocnsreport | do not display constraints |
| *display_options* | control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling |
| coeflegend | display legend instead of statistics |

coeflegend is not shown in the dialog boxes for estimation commands.

| *bootstrap_options* | Description |
|---|---|
| **Main** | |
| bsn(#) | bootstrap mean-weight adjustment |
| **Options** | |
| saving(*filename*[ , ... ]) | save results to *filename*; save statistics in double precision; save results to *filename* every # replications |
| mse | use MSE formula for variance |
| **Reporting** | |
| verbose | display the full table legend |
| nodots | suppress replication dots |
| dots(#) | display dots every # replications |
| noisily | display any output from *command* |
| trace | trace *command* |
| title(*text*) | use *text* as title for bootstrap results |
| **Advanced** | |
| nodrop | do not drop observations |
| reject(*exp*) | identify invalid results |
| dof(#) | design degrees of freedom |

svy requires that the survey design variables be identified using svyset; see [SVY] **svyset**.

*command* defines the statistical command to be executed. The by prefix cannot be part of *command*.

collect is allowed; see **[U] 11.1.10 Prefix commands**.

See **[U] 20 Estimation and postestimation commands** for more capabilities of estimation commands.

Warning: Using if or in restrictions will often not produce correct variance estimates for subpopulations. To compute estimates for subpopulations, use the subpop() option.

svy bootstrap requires that the bootstrap replicate weights be identified using svyset.

*exp_list* specifies the statistics to be collected from the execution of *command*. *exp_list* is required unless *command* has the `svyb` program property, in which case *exp_list* defaults to `_b`; see [P] **program properties**. The expressions in *exp_list* are assumed to conform to the following:

| | |
|---|---|
| *exp_list* contains | (*name*: *elist*) |
| | *elist* |
| | *eexp* |
| *elist* contains | *newvarname* = (*exp*) |
| | (*exp*) |
| *eexp* is | *specname* |
| | [*eqno*]*specname* |
| *specname* is | `_b` |
| | `_b[]` |
| | `_se` |
| | `_se[]` |
| *eqno* is | `#` # |
| | *name* |

*exp* is a standard Stata expression; see **[U] 13 Functions and expressions**.

Distinguish between `[]`, which are to be typed, and [ ], which indicate optional arguments.

## Options

*svy_options*; see [SVY] **svy**.

### Main

`bsn(#)` specifies that # bootstrap replicate-weight variables were used to generate each bootstrap mean-weight variable specified in the `bsrweight()` option of `svyset`. The default is `bsn(1)`. The `bsn()` option of `svy bootstrap` overrides the `bsn()` option of `svyset`; see [SVY] **svyset**.

### Options

`saving(`*filename*[ , *suboptions* ]`)` creates a Stata data file (`.dta` file) consisting of (for each statistic in *exp_list*) a variable containing the replicates.

`double` specifies that the results for each replication be saved as `doubles`, meaning 8-byte reals. By default, they are saved as `floats`, meaning 4-byte reals. This option may be used without the `saving()` option to compute the variance estimates by using double precision.

`every(#)` specifies that results be written to disk every #th replication. `every()` should be specified in conjunction with `saving()` only when *command* takes a long time for each replication. This will allow recovery of partial results should some other software crash your computer. See [P] **postfile**.

`replace` specifies that *filename* be overwritten if it exists. This option does not appear in the dialog box.

`mse` specifies that `svy bootstrap` compute the variance by using deviations of the replicates from the observed value of the statistics based on the entire dataset. By default, `svy bootstrap` computes the variance by using deviations of the replicates from their mean.

### Reporting

`verbose` requests that the full table legend be displayed.

`nodots` and `dots(#)` specify whether to display replication dots. By default, one dot character is displayed for each successful replication. An "x" is displayed if *command* returns an error, and an "e" is displayed if at least one value in *exp_list* is missing. You can also control whether dots are displayed using `set dots`; see [R] **set**.

`nodots` suppresses display of the replication dots.

`dots(#)` displays dots every # replications. `dots(0)` is a synonym for `nodots`.

`noisily` requests that any output from *command* be displayed. This option implies the `nodots` option.

`trace` causes a trace of the execution of *command* to be displayed. This option implies the `noisily` option.

`title(`*text*`)` specifies a title to be displayed above the table of bootstrap results; the default title is "Bootstrap results".

*eform_option*; see [R] ***eform_option***. This option is ignored if *exp_list* is not `_b`.

Advanced

`nodrop` prevents observations outside `e(sample)` and the `if` and `in` qualifiers from being dropped before the data are resampled.

`reject(`*exp*`)` identifies an expression that indicates when results should be rejected. When *exp* is true, the resulting values are reset to missing values.

`dof(#)` specifies the design degrees of freedom, overriding the default calculation, $\text{df} = N_{\text{psu}} - N_{\text{strata}}$.

## Remarks and examples

The bootstrap methods for survey data used in recent years are largely due to McCarthy and Snowden (1985), Rao and Wu (1988), and Rao, Wu, and Yue (1992). For example, Yeo, Mantel, and Liu (1999) cites Rao, Wu, and Yue (1992) as the method for variance estimation used in the National Population Health Survey conducted by Statistics Canada.

In the survey bootstrap, the model is fit multiple times, once for each of a set of adjusted sampling weights. The variance is estimated using the resulting replicated point estimates.

### ▷ Example 1

Suppose that we need to estimate the average birthweight for the population represented by the National Maternal and Infant Health Survey (NMIHS) (Gonzalez, Krauss, and Scott 1992).

In [SVY] **svy estimation**, the dataset `nmihs.dta` contained the following design information:

- Primary sampling units are mothers; that is, PSUs are individual observations—there is no separate PSU variable.
- The `finalwgt` variable contains the sampling weights.
- The `stratan` variable identifies strata.
- There is no variable for the finite population correction.

nmihs_bs.dta is equivalent to nmihs.dta except that the stratum identifier variable stratan is replaced by bootstrap replicate-weight variables. The replicate-weight variables are already svyset, and the default method for variance estimation is vce(bootstrap).

```
. use https://www.stata-press.com/data/r19/nmihs_bs
. svyset
 Sampling weights: finwgt
              VCE: bootstrap
              MSE: off
Bootstrap weights: bsrw1 .. bsrw1000
      Single unit: missing
         Strata 1: <one>
  Sampling unit 1: <observations>
            FPC 1: <zero>
```

Now we can use svy: mean to estimate the average birthweight for our population, and the standard errors will be estimated using the survey bootstrap.

```
. svy, nodots: mean birthwgt
Survey: Mean estimation            Number of obs    =     9,946
                                   Population size = 3,895,562
                                   Replications     =     1,000
```

| | Observed mean | Bootstrap std. err. | Normal-based [95% conf. | interval] |
|---|---|---|---|---|
| birthwgt | 3355.452 | 6.520637 | 3342.672 | 3368.233 |

From these results, we are 95% confident that the mean birthweight for our population is between 3,343 and 3,368 grams.

◁

To accommodate privacy concerns, many public-use datasets contain replicate-weight variables derived from the "mean bootstrap" described by Yung (1997). In the mean bootstrap, each adjusted weight is derived from more than one bootstrap sample. When replicate-weight variables for the mean bootstrap are svyset, the bsn() option identifying the number of bootstrap samples used to generate the adjusted-weight variables should also be specified. This number is used in the variance calculation; see [SVY] **Variance estimation**.

## ▷ Example 2

nmihs_mbs.dta is equivalent to nmihs.dta except that the strata identifier variable stratan is replaced by mean bootstrap replicate-weight variables. The replicate-weight variables and variance adjustment are already svyset, and the default method for variance estimation is vce(bootstrap).

```
. use https://www.stata-press.com/data/r19/nmihs_mbs
. svyset
 Sampling weights: finwgt
              VCE: bootstrap
              MSE: off
Bootstrap weights: mbsrw1 .. mbsrw200
Bootstrap samples: 5
      Single unit: missing
         Strata 1: <one>
  Sampling unit 1: <observations>
              FPC 1: <zero>
```

Notice that the 200 mean bootstrap replicate-weight variables were generated from 5 bootstrap samples; in fact, the mean bootstrap weight variables in nmihs_mbs.dta were generated from the bootstrap weight variables in nmihs_bs.dta.

Here we use svy: mean to estimate the average birthweight for our population.

```
. svy, nodots: mean birthwgt
Survey: Mean estimation            Number of obs    =     9,946
                                   Population size = 3,895,562
                                   Replications     =       200
```

| | Observed mean | Bootstrap std. err. | Normal-based [95% conf. | interval] |
|---|---|---|---|---|
| birthwgt | 3355.452 | 5.712574 | 3344.256 | 3366.649 |

The standard error and confidence limits differ from the previous example. This merely illustrates that the mean bootstrap is not numerically equivalent to the standard bootstrap, even when the replicate-weight variables are generated from the same resampled datasets.

◁

## ❑ Technical note

When the svy bootstrap prefix is used with a user-defined program and when the expression list is _b, svy bootstrap calls

```
set coeftabresults off
```

before entering the replication loop to prevent Stata from performing unnecessary calculations. This means that, provided option noisily is not specified, estimation commands will not build or post the coefficient table matrix r(table).

If your program calls an estimation command and needs r(table) to exist to perform properly, then your program will need to call

```
set coeftabresults on
```

before calling other estimation commands.

❑

## Stored results

In addition to the results documented in [SVY] **svy**, `svy bootstrap` stores the following in `e()`:

Scalars

| | |
|---|---|
| `e(N_reps)` | number of replications |
| `e(N_misreps)` | number of replications with missing values |
| `e(k_exp)` | number of standard expressions |
| `e(k_eexp)` | number of _b/_se expressions |
| `e(k_extra)` | number of extra estimates added to _b |
| `e(bsn)` | bootstrap mean-weight adjustment |

Macros

| | |
|---|---|
| `e(cmdname)` | command name from *command* |
| `e(cmd)` | same as `e(cmdname)` or `bootstrap` |
| `e(vce)` | `bootstrap` |
| `e(exp#)` | #th expression |
| `e(bsrweight)` | `bsrweight()` variable list |

Matrices

| | |
|---|---|
| `e(b_bs)` | bootstrap means |
| `e(V)` | bootstrap variance estimates |

When *exp_list* is _b, `svy bootstrap` will also carry forward most of the results already in `e()` from *command*.

## Methods and formulas

See [SVY] **Variance estimation** for details regarding bootstrap variance estimation.

## References


Gonzalez, J. F., Jr., N. Krauss, and C. Scott. 1992. Estimation in the 1988 National Maternal and Infant Health Survey. *Proceedings of the Section on Statistics Education, American Statistical Association* 343–348.

Kolenikov, S. 2010. Resampling variance estimation for complex survey data. *Stata Journal* 10: 165–199.

McCarthy, P. J., and C. B. Snowden. 1985. "The bootstrap and finite population sampling". In *Vital and Health Statistics*, ser. 2, no. 95. Hyattsville, MD: National Center for Health Statistics.

Rao, J. N. K., and C. F. J. Wu. 1988. Resampling inference with complex survey data. *Journal of the American Statistical Association* 83: 231–241. https://doi.org/10.2307/2288945.

Rao, J. N. K., C. F. J. Wu, and K. Yue. 1992. Some recent work on resampling methods for complex surveys. *Survey Methodology* 18: 209–217.

Yeo, D., H. Mantel, and T.-P. Liu. 1999. "Bootstrap variance estimation for the National Population Health Survey". In *Proceedings of the Survey Research Methods Section*, 778–785. American Statistical Association.

Yung, W. 1997. "Variance estimation for public use files under confidentiality constraints". In *Proceedings of the Survey Research Methods Section*, 434–439. American Statistical Association.

## Also see

[SVY] **svy postestimation** — Postestimation tools for svy

[SVY] **svy brr** — Balanced repeated replication for survey data

[SVY] **svy jackknife** — Jackknife estimation for survey data

[SVY] **svy sdr** — Successive difference replication for survey data

[SVY] **Calibration** — Calibration for survey data

[SVY] **Poststratification** — Poststratification for survey data

[SVY] **Subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **Variance estimation** — Variance estimation for survey data

[R] **bootstrap** — Bootstrap sampling and estimation

**[U] 20 Estimation and postestimation commands**

**svy brr** — Balanced repeated replication for survey data



## Description

`svy brr` performs balanced repeated replication (BRR) estimation of specified statistics (or expressions) for a Stata command or a user-written program. The command is executed once for each replicate using sampling weights that are adjusted according to the BRR methodology. Any Stata estimation command listed in [SVY] **svy estimation** may be used with `svy brr`. User-written programs that meet the requirements in [P] **program properties** may also be used.

## Quick start

Estimate population mean of `v1` using BRR standard-error estimates with sampling weight `wvar1` and replicate weights in variables with prefix `rwvar`

```
svyset [pweight = wvar1], brrweight(rwvar*)
svy brr _b: mean v1
```

BRR estimate of the standard error of the difference between the means of `v2` and `v3`

```
svy brr (_b[v2]-_b[v3]): mean v2 v3
```

Same as above, but name the result `diff` and save results from each replication to `mydata.dta`

```
svy brr diff=(_b[v2]-_b[v3]), saving(mydata): mean v2 v3
```

Same as above

```
brr diff=(_b[v2]-_b[v3]), saving(mydata): mean v2 v3
```

Note: Any estimation command meeting the requirements specified in the *Description* may be substituted for `mean` in the examples above.

## Menu

Statistics > Survey data analysis > Resampling > Balanced repeated replications estimation

# Syntax

[ svy ] brr *exp_list* [ , *svy_options brr_options eform_option* ] : *command*

| *svy_options* | Description |
|---|---|
| **if/in** | |
| subpop( [ *varname* ] [ *if* ] ) | identify a subpopulation |
| **Reporting** | |
| level(#) | set confidence level; default is level(95) |
| noheader | suppress table header |
| nolegend | suppress table legend |
| noadjust | do not adjust model Wald statistic |
| nocnsreport | do not display constraints |
| *display_options* | control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling |
| coeflegend | display legend instead of statistics |

coeflegend is not shown in the dialog boxes for estimation commands.

| *brr_options* | Description |
|---|---|
| **Main** | |
| hadamard(*matrix*) | Hadamard matrix |
| fay(#) | Fay's adjustment |
| **Options** | |
| saving(*filename* [ , ... ]) | save results to *filename*; save statistics in double precision; save results to *filename* every # replications |
| mse | use MSE formula for variance |
| **Reporting** | |
| verbose | display the full table legend |
| nodots | suppress replication dots |
| dots(#) | display dots every # replications |
| noisily | display any output from *command* |
| trace | trace *command* |
| title(*text*) | use *text* as title for BRR results |
| **Advanced** | |
| nodrop | do not drop observations |
| reject(*exp*) | identify invalid results |
| dof(#) | design degrees of freedom |

svy requires that the survey design variables be identified using svyset; see [SVY] **svyset**.

*command* defines the statistical command to be executed. The by prefix cannot be part of *command*.

collect is allowed; see **[U] 11.1.10 Prefix commands**.

See **[U] 20 Estimation and postestimation commands** for more capabilities of estimation commands.

Warning: Using if or in restrictions will often not produce correct variance estimates for subpopulations. To compute estimates for subpopulations, use the subpop() option.

*exp_list* specifies the statistics to be collected from the execution of *command*. *exp_list* is required unless *command* has the `svyb` program property, in which case *exp_list* defaults to `_b`; see [P] **program properties**. The expressions in *exp_list* are assumed to conform to the following:

| | |
|---|---|
| *exp_list* contains | (*name*: *elist*) |
| | *elist* |
| | *eexp* |
| *elist* contains | *newvarname* = (*exp*) |
| | (*exp*) |
| *eexp* is | *specname* |
| | [*eqno*]*specname* |
| *specname* is | `_b` |
| | `_b[]` |
| | `_se` |
| | `_se[]` |
| *eqno* is | `#` # |
| | *name* |

*exp* is a standard Stata expression; see **[U] 13 Functions and expressions**.

Distinguish between `[]`, which are to be typed, and [ ], which indicate optional arguments.

## Options

*svy_options*; see [SVY] **svy**.

### Main

`hadamard(`*matrix*`)` specifies the Hadamard matrix to be used to determine which PSUs are chosen for each replicate.

`fay(`#`)` specifies Fay's adjustment (Judkins 1990), where $0 \leq \# \leq 2$, but excluding 1. This option overrides the `fay(`#`)` option of `svyset`; see [SVY] **svyset**.

### Options

`saving(`*filename*[ , *suboptions* ]`)` creates a Stata data file (`.dta` file) consisting of (for each statistic in *exp_list*) a variable containing the replicates.

`double` specifies that the results for each replication be saved as `doubles`, meaning 8-byte reals. By default, they are saved as `floats`, meaning 4-byte reals. This option may be used without the `saving()` option to compute the variance estimates by using double precision.

`every(`#`)` specifies that results be written to disk every #th replication. `every()` should be specified in conjunction with `saving()` only when *command* takes a long time for each replication. This will allow recovery of partial results should some other software crash your computer. See [P] **postfile**.

`replace` specifies that *filename* be overwritten if it exists. This option does not appear in the dialog box.

`mse` specifies that `svy brr` compute the variance by using deviations of the replicates from the observed value of the statistics based on the entire dataset. By default, `svy brr` computes the variance by using deviations of the replicates from their mean.

Reporting

`verbose` requests that the full table legend be displayed.

`nodots` and `dots(#)` specify whether to display replication dots. By default, one dot character is displayed for each successful replication. An "x" is displayed if *command* returns an error, and an "e" is displayed if at least one value in *exp_list* is missing. You can also control whether dots are displayed using `set dots`; see [R] **set**.

`nodots` suppresses display of the replication dots.

`dots(#)` displays dots every # replications. `dots(0)` is a synonym for `nodots`.

`noisily` requests that any output from *command* be displayed. This option implies the `nodots` option.

`trace` causes a trace of the execution of *command* to be displayed. This option implies the `noisily` option.

`title(`*text*`)` specifies a title to be displayed above the table of BRR results; the default title is "BRR results".

*eform_option*; see [R] ***eform_option***. This option is ignored if *exp_list* is not `_b`.

Advanced

`nodrop` prevents observations outside `e(sample)` and the `if` and `in` qualifiers from being dropped before the data are resampled.

`reject(`*exp*`)` identifies an expression that indicates when results should be rejected. When *exp* is true, the resulting values are reset to missing values.

`dof(#)` specifies the design degrees of freedom, overriding the default calculation, $\text{df} = N_{\text{psu}} - N_{\text{strata}}$.

## Remarks and examples

BRR was first introduced by McCarthy (1966, 1969a, 1969b) as a method of variance estimation for designs with two PSUs in every stratum. The BRR variance estimator tends to give more reasonable variance estimates for this design than the linearized variance estimator, which can result in large values and undesirably wide confidence intervals.

In BRR, the model is fit multiple times, once for each of a balanced set of combinations where one PSU is dropped from each stratum. The variance is estimated using the resulting replicated point estimates. Although the BRR method has since been generalized to include other designs, Stata's implementation of BRR requires two PSUs per stratum.

To protect the privacy of survey participants, public survey datasets may contain replicate-weight variables instead of variables that identify the PSUs and strata. These replicate-weight variables are adjusted copies of the sampling weights. For BRR, the sampling weights are adjusted for dropping one PSU from each stratum; see [SVY] **Variance estimation** for more details.

## Example 1: BRR replicate-weight variables

The survey design for the NHANES II data (McDowell et al. 1981) is specifically suited to BRR; there are two PSUs in every stratum.

```
. use https://www.stata-press.com/data/r19/nhanes2
. svydescribe
Survey: Describing stage 1 sampling units
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: strata
 Sampling unit 1: psu
           FPC 1: <zero>
```

| Stratum | # units | # obs | Number of obs per unit Min | Mean | Max |
|---|---|---|---|---|---|
| 1 | 2 | 380 | 165 | 190.0 | 215 |
| 2 | 2 | 185 | 67 | 92.5 | 118 |
| 3 | 2 | 348 | 149 | 174.0 | 199 |
| 4 | 2 | 460 | 229 | 230.0 | 231 |
| 5 | 2 | 252 | 105 | 126.0 | 147 |
| (*output omitted*) | | | | | |
| 29 | 2 | 503 | 215 | 251.5 | 288 |
| 30 | 2 | 365 | 166 | 182.5 | 199 |
| 31 | 2 | 308 | 143 | 154.0 | 165 |
| 32 | 2 | 450 | 211 | 225.0 | 239 |
| 31 | 62 | 10,351 | 67 | 167.0 | 288 |

Here is a privacy-conscious dataset equivalent to the one above; all the variables and values remain, except `strata` and `psu` are replaced with BRR replicate-weight variables. The BRR replicate-weight variables are already `svyset`, and the default method for variance estimation is `vce(brr)`.

```
. use https://www.stata-press.com/data/r19/nhanes2brr
. svyset
Sampling weights: finalwgt
             VCE: brr
             MSE: off
     BRR weights: brr_1 .. brr_32
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: <observations>
           FPC 1: <zero>
```

Suppose that we were interested in the population ratio of weight to height. Here we use `total` to estimate the population totals of `weight` and `height` and the `svy brr` prefix to estimate their ratio and variance; we use `total` instead of `ratio` (which is otherwise preferable here) to illustrate how to specify an *exp_list*.

```
. svy brr WtoH = (_b[weight]/_b[height]): total weight height
(running total on estimation sample)
BRR replications (32): .........10.........20.........30.. done
BRR results                                     Number of obs    =      10,351
                                                Population size = 117,157,513
                                                Replications     =           32
                                                Design df        =           31

      Command: total weight height
         WtoH: _b[weight]/_b[height]
```

| | BRR | | | | | |
|---|---|---|---|---|---|---|
| | Coefficient | std. err. | t | P>\|t\| | [95% conf. | interval] |
| WtoH | .4268116 | .0008904 | 479.36 | 0.000 | .4249957 | .4286276 |

The `mse` option causes `svy brr` to use the MSE form of the BRR variance estimator. This variance estimator will tend to be larger than the previous because of the addition of the familiar squared bias term in the MSE; see [SVY] **Variance estimation** for more details. The header for the column of standard errors in the table of results is `BRR *` for the BRR variance estimator using the MSE formula.

```
. svy brr WtoH = (_b[weight]/_b[height]), mse: total weight height
(running total on estimation sample)
BRR replications (32): .........10.........20.........30.. done
BRR results                                     Number of obs    =      10,351
                                                Population size = 117,157,513
                                                Replications     =           32
                                                Design df        =           31

      Command: total weight height
         WtoH: _b[weight]/_b[height]
```

| | BRR * | | | | | |
|---|---|---|---|---|---|---|
| | Coefficient | std. err. | t | P>\|t\| | [95% conf. | interval] |
| WtoH | .4268116 | .0008904 | 479.36 | 0.000 | .4249957 | .4286276 |

The bias term here is too small to see any difference in the standard errors.

◁

## ▷ Example 2: Survey data without replicate-weight variables

For survey data with the PSU and strata variables but no replication weights, `svy brr` can compute adjusted sampling weights within its replication loop. Here the `hadamard()` option must be supplied with the name of a Stata matrix that is a Hadamard matrix of appropriate order for the number of strata in your dataset (see the following technical note for a quick introduction to Hadamard matrices).

There are 31 strata in nhanes2.dta, so we need a Hadamard matrix of order 32 (or more) to use svy brr with this dataset. Here we use h32 (from the following technical note) to estimate the population ratio of weight to height by using the BRR variance estimator.

```
. use https://www.stata-press.com/data/r19/nhanes2
. svy brr, hadamard(h32): ratio (WtoH: weight/height)
(running ratio on estimation sample)
BRR replications (32): .........10.........20.........30.. done
Survey: Ratio estimation
Number of strata = 31            Number of obs    =      10,351
Number of PSUs   = 62            Population size  = 117,157,513
                                 Replications     =          32
                                 Design df        =          31
          WtoH: weight/height
```

| | BRR | | | |
|---|---|---|---|---|
| | Ratio | std. err. | [95% conf. | interval] |
| WtoH | .4268116 | .0008904 | .4249957 | .4286276 |

◁

## ❑ Technical note

A Hadamard matrix is a square matrix with $r$ rows and columns that has the property

$$H_r' H_r = r I_r$$

where $I_r$ is the identity matrix of order $r$. Generating a Hadamard matrix with order $r = 2^p$ is easily accomplished. Start with a Hadamard matrix of order 2 ($H_2$), and build your $H_r$ by repeatedly applying Kronecker products with $H_2$. Here is the Stata code to generate the Hadamard matrix for the previous example.

```
matrix h2 = (-1, 1 \ 1, 1)
matrix h32 = h2
forvalues i = 1/4 {
        matrix h32 = h2 # h32
}
```

svy brr consumes Hadamard matrices from left to right, so it is best to make sure that $r$ is greater than the number of strata and that the last column is the one consisting of all 1s. This will ensure full orthogonal balance according to Wolter (2007).

❑

## ❑ Technical note

When the svy brr prefix is used with a user-defined program and when the expression list is _b, svy brr calls

```
set coeftabresults off
```

before entering the replication loop to prevent Stata from performing unnecessary calculations. This means that, provided option noisily is not specified, estimation commands will not build or post the coefficient table matrix r(table).

If your program calls an estimation command and needs `r(table)` to exist to perform properly, then your program will need to call

```
set coeftabresults on
```

before calling other estimation commands.

❑

## Stored results

In addition to the results documented in [SVY] **svy**, `svy brr` stores the following in `e()`:

Scalars

| | |
|---|---|
| `e(N_reps)` | number of replications |
| `e(N_misreps)` | number of replications with missing values |
| `e(k_exp)` | number of standard expressions |
| `e(k_eexp)` | number of _b/_se expressions |
| `e(k_extra)` | number of extra estimates added to _b |
| `e(fay)` | Fay's adjustment |

Macros

| | |
|---|---|
| `e(cmdname)` | command name from *command* |
| `e(cmd)` | same as `e(cmdname)` or `brr` |
| `e(vce)` | `brr` |
| `e(brrweight)` | `brrweight()` variable list |

Matrices

| | |
|---|---|
| `e(b_brr)` | BRR means |
| `e(V)` | BRR variance estimates |

When *exp_list* is _b, `svy brr` will also carry forward most of the results already in `e()` from *command*.

## Methods and formulas

See [SVY] **Variance estimation** for details regarding BRR variance estimation.

## References

Judkins, D. R. 1990. Fay's method for variance estimation. *Journal of Official Statistics* 6: 223–239.

McCarthy, P. J. 1966. "Replication: An approach to the analysis of data from complex surveys". In *Vital and Health Statistics*, ser. 2, no. 14. Hyattsville, MD: National Center for Health Statistics.

———. 1969a. "Pseudoreplication: Further evaluation and application of the balanced half-sample technique". In *Vital and Health Statistics*, ser. 2, no. 31. Hyattsville, MD: National Center for Health Statistics.

———. 1969b. Pseudo-replication: Half-samples. *Revue de l'Institut International de Statistique* 37: 239–264. https://doi.org/10.2307/1402116.

McDowell, A., A. Engel, J. T. Massey, and K. Maurer. 1981. "Plan and operation of the Second National Health and Nutrition Examination Survey, 1976–1980". In *Vital and Health Statistics*, ser. 1, no. 15. Hyattsville, MD: National Center for Health Statistics.

Wolter, K. M. 2007. *Introduction to Variance Estimation*. 2nd ed. New York: Springer. https://doi.org/10.1007/978-0-387-35099-8.

## Also see

[SVY] **svy postestimation** — Postestimation tools for svy

[SVY] **svy bootstrap** — Bootstrap for survey data

[SVY] **svy jackknife** — Jackknife estimation for survey data

[SVY] **svy sdr** — Successive difference replication for survey data

[SVY] **Calibration** — Calibration for survey data

[SVY] **Poststratification** — Poststratification for survey data

[SVY] **Subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **Variance estimation** — Variance estimation for survey data

**[U] 20 Estimation and postestimation commands**

**svy estimation** — Estimation commands for survey data

Description Menu Remarks and examples References Also see

## Description

Survey data analysis in Stata is essentially the same as standard data analysis. The standard syntax applies; you just need to also remember the following:

- Use `svyset` to identify the survey design characteristics.
- Prefix the estimation commands with `svy:`.

For example,

```
. use https://www.stata-press.com/data/r19/nhanes2f
. svyset psuid [pweight=finalwgt], strata(stratid)
. svy: regress zinc age c.age#c.age weight female black orace rural
```

See [SVY] **svyset** and [SVY] **svy**.

The following estimation commands support the `svy` prefix:

**Descriptive statistics**

| | |
|---|---|
| `mean` | [R] **mean** — Estimate means |
| `proportion` | [R] **proportion** — Estimate proportions |
| `ratio` | [R] **ratio** — Estimate ratios |
| `tabulate` (one-way) | [SVY] **svy: tabulate oneway** — One-way tables for survey data |
| `tabulate` (two–way) | [SVY] **svy: tabulate twoway** — Two-way tables for survey data |
| `total` | [R] **total** — Estimate totals |

**Linear regression models**

| | |
|---|---|
| `churdle` | [R] **churdle** — Cragg hurdle regression |
| `cnsreg` | [R] **cnsreg** — Constrained linear regression |
| `eintreg` | [ERM] **eintreg** — Extended interval regression |
| `eregress` | [ERM] **eregress** — Extended linear regression |
| `etregress` | [CAUSAL] **etregress** — Linear regression with endogenous treatment effects |
| `glm` | [R] **glm** — Generalized linear models |
| `hetregress` | [R] **hetregress** — Heteroskedastic linear regression |
| `intreg` | [R] **intreg** — Interval regression |
| `nl` | [R] **nl** — Nonlinear least-squares estimation |
| `regress` | [R] **regress** — Linear regression |
| `tobit` | [R] **tobit** — Tobit regression |
| `truncreg` | [R] **truncreg** — Truncated regression |

**Structural equation models**

| | |
|---|---|
| `sem` | [SEM] **sem** — Structural equation model estimation command |
| `gsem` | [SEM] **gsem** — Generalized structural equation model estimation command |

**Survival-data regression models**

| | |
|---|---|
| `stcox` | [ST] **stcox** — Cox proportional hazards model |
| `stintreg` | [ST] **stintreg** — Parametric models for interval-censored survival-time data |
| `streg` | [ST] **streg** — Parametric survival models |

**Binary-response regression models**

| | |
|---|---|
| `biprobit` | [R] **biprobit** — Bivariate probit regression |
| `cloglog` | [R] **cloglog** — Complementary log–log regression |
| `eprobit` | [ERM] **eprobit** — Extended probit regression |
| `hetprobit` | [R] **hetprobit** — Heteroskedastic probit model |
| `logistic` | [R] **logistic** — Logistic regression, reporting odds ratios |
| `logit` | [R] **logit** — Logistic regression, reporting coefficients |
| `probit` | [R] **probit** — Probit regression |
| `scobit` | [R] **scobit** — Skewed logistic regression |

**Discrete-response regression models**

| | |
|---|---|
| `clogit` | [R] **clogit** — Conditional (fixed-effects) logistic regression |
| `cmmixlogit` | [CM] **cmmixlogit** — Mixed logit choice model |
| `cmxtmixlogit` | [CM] **cmxtmixlogit** — Panel-data mixed logit choice model |
| `eoprobit` | [ERM] **eoprobit** — Extended ordered probit regression |
| `hetoprobit` | [R] **hetoprobit** — Heteroskedastic ordered probit regression |
| `mlogit` | [R] **mlogit** — Multinomial (polytomous) logistic regression |
| `mprobit` | [R] **mprobit** — Multinomial probit regression |
| `ologit` | [R] **ologit** — Ordered logistic regression |
| `oprobit` | [R] **oprobit** — Ordered probit regression |
| `slogit` | [R] **slogit** — Stereotype logistic regression |
| `ziologit` | [R] **ziologit** — Zero-inflated ordered logit regression |
| `zioprobit` | [R] **zioprobit** — Zero-inflated ordered probit regression |

**Fractional-response regression models**

| | |
|---|---|
| `betareg` | [R] **betareg** — Beta regression |
| `fracreg` | [R] **fracreg** — Fractional response regression |

**Poisson regression models**

| | |
|---|---|
| `cpoisson` | [R] **cpoisson** — Censored Poisson regression |
| `etpoisson` | [CAUSAL] **etpoisson** — Poisson regression with endogenous treatment effects |
| `gnbreg` | Generalized negative binomial regression in [R] **nbreg** |
| `nbreg` | [R] **nbreg** — Negative binomial regression |
| `poisson` | [R] **poisson** — Poisson regression |
| `tnbreg` | [R] **tnbreg** — Truncated negative binomial regression |
| `tpoisson` | [R] **tpoisson** — Truncated Poisson regression |
| `zinb` | [R] **zinb** — Zero-inflated negative binomial regression |
| `zip` | [R] **zip** — Zero-inflated Poisson regression |

**Instrumental-variables regression models**

| | |
|---|---|
| `ivfprobit` | [R] **ivfprobit** — Fractional probit model with continuous endogenous covariates |
| `ivprobit` | [R] **ivprobit** — Probit model with continuous endogenous covariates |
| `ivregress` | [R] **ivregress** — Single-equation instrumental-variables regression |
| `ivtobit` | [R] **ivtobit** — Tobit model with continuous endogenous covariates |

**Regression models with selection**

| | |
|---|---|
| `heckman` | [R] **heckman** — Heckman selection model |
| `heckoprobit` | [R] **heckoprobit** — Ordered probit model with sample selection |
| `heckpoisson` | [R] **heckpoisson** — Poisson regression with sample selection |
| `heckprobit` | [R] **heckprobit** — Probit model with sample selection |

**Longitudinal/panel-data regression models**

| | |
|---|---|
| `xtmlogit` | [XT] **xtmlogit** — Fixed-effects and random-effects multinomial logit models |

**Multilevel mixed-effects models**

| | |
|---|---|
| `mecloglog` | [ME] **mecloglog** — Multilevel mixed-effects complementary log–log regression |
| `meglm` | [ME] **meglm** — Multilevel mixed-effects generalized linear models |
| `meintreg` | [ME] **meintreg** — Multilevel mixed-effects interval regression |
| `melogit` | [ME] **melogit** — Multilevel mixed-effects logistic regression |
| `menbreg` | [ME] **menbreg** — Multilevel mixed-effects negative binomial regression |
| `meologit` | [ME] **meologit** — Multilevel mixed-effects ordered logistic regression |
| `meoprobit` | [ME] **meoprobit** — Multilevel mixed-effects ordered probit regression |
| `mepoisson` | [ME] **mepoisson** — Multilevel mixed-effects Poisson regression |
| `meprobit` | [ME] **meprobit** — Multilevel mixed-effects probit regression |
| `mestreg` | [ME] **mestreg** — Multilevel mixed-effects parametric survival models |
| `metobit` | [ME] **metobit** — Multilevel mixed-effects tobit regression |

**Finite mixture models**

| | |
|---|---|
| `fmm: betareg` | [FMM] **fmm: betareg** — Finite mixtures of beta regression models |
| `fmm: cloglog` | [FMM] **fmm: cloglog** — Finite mixtures of complementary log–log regression models |
| `fmm: glm` | [FMM] **fmm: glm** — Finite mixtures of generalized linear regression models |
| `fmm: intreg` | [FMM] **fmm: intreg** — Finite mixtures of interval regression models |
| `fmm: ivregress` | [FMM] **fmm: ivregress** — Finite mixtures of linear regression models with endogenous covariates |
| `fmm: logit` | [FMM] **fmm: logit** — Finite mixtures of logistic regression models |
| `fmm: mlogit` | [FMM] **fmm: mlogit** — Finite mixtures of multinomial (polytomous) logistic regression models |
| `fmm: nbreg` | [FMM] **fmm: nbreg** — Finite mixtures of negative binomial regression models |
| `fmm: ologit` | [FMM] **fmm: ologit** — Finite mixtures of ordered logistic regression models |
| `fmm: oprobit` | [FMM] **fmm: oprobit** — Finite mixtures of ordered probit regression models |
| `fmm: pointmass` | [FMM] **fmm: pointmass** — Finite mixtures models with a density mass at a single point |
| `fmm: poisson` | [FMM] **fmm: poisson** — Finite mixtures of Poisson regression models |

| | |
|---|---|
| fmm: probit | [FMM] **fmm: probit** — Finite mixtures of probit regression models |
| fmm: regress | [FMM] **fmm: regress** — Finite mixtures of linear regression models |
| fmm: streg | [FMM] **fmm: streg** — Finite mixtures of parametric survival models |
| fmm: tobit | [FMM] **fmm: tobit** — Finite mixtures of tobit regression models |
| fmm: tpoisson | [FMM] **fmm: tpoisson** — Finite mixtures of truncated Poisson regression models |
| fmm: truncreg | [FMM] **fmm: truncreg** — Finite mixtures of truncated linear regression models |

**Item response theory**

| | |
|---|---|
| irt 1pl | [IRT] **irt 1pl** — One-parameter logistic model |
| irt 2pl | [IRT] **irt 2pl** — Two-parameter logistic model |
| irt 3pl | [IRT] **irt 3pl** — Three-parameter logistic model |
| irt grm | [IRT] **irt grm** — Graded response model |
| irt nrm | [IRT] **irt nrm** — Nominal response model |
| irt pcm | [IRT] **irt pcm** — Partial credit model |
| irt rsm | [IRT] **irt rsm** — Rating scale model |
| irt hybrid | [IRT] **irt hybrid** — Hybrid IRT models |

# Menu

Statistics > Survey data analysis > ...

Dialog boxes for all statistical estimators that support svy can be found on the above menu path. In addition, you can access survey data estimation from standard dialog boxes on the **SE/Robust** or **SE/Cluster** tab.

# Remarks and examples

Remarks are presented under the following headings:



## Overview of survey analysis in Stata

Many Stata commands estimate the parameters of a process or population by using sample data. For example, mean estimates means, ratio estimates ratios, regress fits linear regression models, poisson fits Poisson regression models, and logistic fits logistic regression models. Some of these *estimation commands* support the svy prefix, that is, they may be prefixed by svy: to produce results appropriate for complex survey data. Whereas poisson is used with standard, nonsurvey data, svy: poisson is used with survey data. In what follows, we refer to any estimation command not prefixed by svy: as the standard command. A standard command prefixed by svy: is referred to as a svy command.

Most standard commands (and all standard commands supported by svy) allow pweights and the vce(cluster *clustvar*) option, where *clustvar* corresponds to the PSU variable that you svyset. If your survey data exhibit only sampling weights or first-stage clusters (or both), you can get by with using the standard command with pweights, vce(cluster *clustvar*), or both. Your parameter estimates will

always be identical to those you would have obtained from the svy command, and the standard command uses the same robust (linearization) variance estimator as the svy command with a similarly svyset design.

Most standard commands are also fit using maximum likelihood. When used with independently distributed, nonweighted data, the likelihood to be maximized reflects the joint probability distribution of the data given the chosen model. With complex survey data, however, this interpretation of the likelihood is no longer valid, because survey data are weighted, not independently distributed, or both. Yet for survey data, (valid) parameter estimates for a given model can be obtained using the associated likelihood function with appropriate weighting. Because the probabilistic interpretation no longer holds, the likelihood here is instead called a *pseudolikelihood*, but likelihood-ratio tests are no longer valid. See Skinner (1989, sec. 3.4.4) for a discussion of maximum pseudolikelihood estimators.

Here we highlight the other features of svy commands:

- svy commands handle stratified sampling, but none of the standard commands do. Because stratification usually makes standard errors smaller, ignoring stratification is usually conservative. So not using svy with stratified sample data is not a terrible thing to do. However, to get the smallest possible "honest" standard-error estimates for stratified sampling, use svy.

- svy commands use $t$ statistics with $n-L$ degrees of freedom to test the significance of coefficients, where $n$ is the total number of sampled PSUs (clusters) and $L$ is the number of strata in the first stage. Some of the standard commands use $t$ statistics, but most use $z$ statistics. If the standard command uses $z$ statistics for its standard variance estimator, then it also uses $z$ statistics with the robust (linearization) variance estimator. Strictly speaking, $t$ statistics are appropriate with the robust (linearization) variance estimator; see [P] **_robust** for the theoretical rationale. But, using $z$ rather than $t$ statistics yields a nontrivial difference only when there is a small number of clusters ($< 50$). If a regression model command uses $t$ statistics and the vce(cluster *clustvar*) option is specified, then the degrees of freedom used is the same as that of the svy command (in the absence of stratification).

- svy commands produce an adjusted Wald test for the model test, and test can be used to produce adjusted Wald tests for other hypotheses after svy commands. Only unadjusted Wald tests are available if the svy prefix is not used. The adjustment can be important when the degrees of freedom, $n - L$, is small relative to the dimension of the test. (If the dimension is one, then the adjusted and unadjusted Wald tests are identical.) This fact along with the point made in the second bullet make using the svy command important if the number of sampled PSUs (clusters) is small ($< 50$).

- svy: regress differs slightly from regress and svy: ivregress differs slightly from ivregress in that they use different multipliers for the variance estimator. regress and ivregress (when the small option is specified) use a multiplier of $\{(N-1)/(N-k)\}\{n/(n-1)\}$, where $N$ is the number of observations, $n$ is the number of clusters (PSUs), and $k$ is the number of regressors including the constant. svy: regress and svy: ivregress use $n/(n-1)$ instead. Thus they produce slightly different standard errors. The $(N-1)/(N-k)$ is ad hoc and has no rigorous theoretical justification; hence, the purist svy commands do not use it. The svy commands tacitly assume that $N \gg k$. If $(N-1)/(N-k)$ is not close to 1, you may be well advised to use regress or ivregress so that some punishment is inflicted on your variance estimates. Maximum likelihood estimators in Stata (for example, logit) do no such adjustment but rely on the sensibilities of the analyst to ensure that $N$ is reasonably larger than $k$. Thus the maximum

pseudolikelihood estimators (for example, `svy: logit`) produce the same standard errors as the corresponding maximum likelihood commands (for example, `logit`), but $p$-values are slightly different because of the point made in the second bullet.

- `svy` commands can produce proper estimates for subpopulations by using the `subpop()` option. Using an `if` restriction with `svy` or standard commands can yield incorrect standard-error estimates for subpopulations. Often an `if` restriction will yield the same standard error as `subpop()`; most other times, the two standard errors will be slightly different; but sometimes—usually for thinly sampled subpopulations—the standard errors can be appreciably different. Hence, the `svy` command with the `subpop()` option should be used to obtain estimates for thinly sampled subpopulations. See [SVY] **Subpopulation estimation** for more information.
- `svy` commands handle zero sampling weights properly. Standard commands ignore any observation with a weight of zero. Usually, this will yield the same standard errors, but sometimes they will differ. Sampling weights of zero can arise from various postsampling adjustment procedures. If the sum of weights for one or more PSUs is zero, `svy` and standard commands will produce different standard errors, but usually this difference is very small.
- You can `svyset iweights` and let these weights be negative. Negative sampling weights can arise from various postsampling adjustment procedures. If you want to use negative sampling weights, then you must `svyset iweights` instead of `pweights`; no standard command will allow negative sampling weights.
- The `svy` commands compute finite population corrections (FPCs).
- After a `svy` command, `estat effects` will compute the design effects DEFF and DEFT and the misspecification effects MEFF and MEFT.
- `svy` commands can perform variance estimation that accounts for multiple stages of clustered sampling.
- `svy` commands can perform variance estimation that accounts for poststratification adjustments to the sampling weights.
- Some standard options are not allowed with the `svy` prefix. For example, `vce()` and weights cannot be specified when using the `svy` prefix because `svy` is already using the variance estimation and sampling weights identified by `svyset`. Some options are not allowed with survey data because they would be statistically invalid, such as `noskip` for producing optional likelihood-ratio tests. Other options are not allowed because they change how estimation results are reported (for example, `nodisplay`, `first`, `plus`) or are not compatible with `svy`'s variance estimation methods (for example, `irls`, `mse1`, `hc2`, `hc3`).
- Estimation results are presented in the standard way, except that `svy` has its own table header: In addition to the sample size, model test, and $R^2$ (if present in the output from the standard command), `svy` will also report the following information in the header:
    a. number of strata and PSUs
    b. number of poststrata, if specified to `svyset`
    c. population size estimate
    d. subpopulation sizes, if the `subpop()` option was specified
    e. design degrees of freedom

## Descriptive statistics

Use `svy: mean`, `svy: ratio`, `svy: proportion`, and `svy: total` to estimate finite population and subpopulation means, ratios, proportions, and totals, respectively. You can also estimate standardized means, ratios, and proportions for survey data; see [SVY] **Direct standardization**. Estimates for multiple subpopulations can be obtained using the `over()` option; see [SVY] **Subpopulation estimation**.

### ▷ Example 1

Suppose that we need to estimate the average birthweight for the population represented by the National Maternal and Infant Health Survey (NMIHS) (Gonzalez, Krauss, and Scott 1992).

First, we gather the survey design information.

- Primary sampling units are mothers; that is, PSUs are individual observations—there is no separate PSU variable.
- The `finalwgt` variable contains the sampling weights.
- The `stratan` variable identifies strata.
- There is no variable for the finite population correction.

Then we use `svyset` to identify the variables for sampling weights and stratification.

```
. use https://www.stata-press.com/data/r19/nmihs
. svyset [pweight=finwgt], strata(stratan)
Sampling weights: finwgt
             VCE: linearized
     Single unit: missing
        Strata 1: stratan
 Sampling unit 1: <observations>
           FPC 1: <zero>
```

Now we can use `svy: mean` to estimate the average birthweight for our population.

```
. svy: mean birthwgt
(running mean on estimation sample)
Survey: Mean estimation
Number of strata =     6           Number of obs   =     9,946
Number of PSUs   = 9,946           Population size = 3,895,562
                                   Design df       =     9,940
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| birthwgt | 3355.452 | 6.402741 | 3342.902 | 3368.003 |

From these results, we are 95% confident that the mean birthweight for our population is between 3,343 and 3,368 grams.

◁

## Regression models

As exhibited in the table at the beginning of this manual entry, many of Stata's regression model commands support the svy prefix. If you know how to use one of these commands with standard data, then you can also use the corresponding svy command with your survey data.

### ▷ Example 2

Let's model the incidence of high blood pressure with a dataset from the Second National Health and Nutrition Examination Survey (NHANES II) (McDowell et al. 1981). The survey design characteristics are already svyset, so we will just replay them.

```
. use https://www.stata-press.com/data/r19/nhanes2d
. svyset
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: strata
 Sampling unit 1: psu
           FPC 1: <zero>
```

Now we can use svy: logistic to model the incidence of high blood pressure as a function of height, weight, age, and sex (using the female indicator variable).

```
. svy: logistic highbp height weight age female
(running logistic on estimation sample)
Survey: Logistic regression
Number of strata = 31                         Number of obs    =      10,351
Number of PSUs   = 62                         Population size = 117,157,513
                                              Design df        =          31
                                              F(4, 28)         =      368.33
                                              Prob > F         =      0.0000
```

| highbp | Odds ratio | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| height | .9657022 | .0051511 | -6.54 | 0.000 | .9552534 | .9762654 |
| weight | 1.053023 | .0026902 | 20.22 | 0.000 | 1.047551 | 1.058524 |
| age | 1.050059 | .0019761 | 25.96 | 0.000 | 1.046037 | 1.054097 |
| female | .6272129 | .0368195 | -7.95 | 0.000 | .5564402 | .706987 |
| _cons | .716868 | .6106878 | -0.39 | 0.699 | .1261491 | 4.073749 |

```
Note: _cons estimates baseline odds.
```

The odds ratio for the female predictor is 0.63 (rounded to two decimal places) and is significantly less than 1. This finding implies that females have a lower incidence of high blood pressure than do males.

Here we use the subpop() option to model the incidence of high blood pressure in the subpopulation identified by the female variable.

```
. svy, subpop(female): logistic highbp height weight age
(running logistic on estimation sample)

Survey: Logistic regression

Number of strata = 31                        Number of obs    =      10,351
Number of PSUs   = 62                        Population size  = 117,157,513
                                             Subpop. no. obs  =       5,436
                                             Subpop. size     =  60,998,033
                                             Design df        =          31
                                             F(3, 29)         =      227.53
                                             Prob > F         =      0.0000

------------------------------------------------------------------------------
             |             Linearized
      highbp | Odds ratio   std. err.      t    P>|t|     [95% conf. interval]
-------------+----------------------------------------------------------------
      height |   .9630557   .0074892    -4.84   0.000     .9479018    .9784518
      weight |   1.053197    .003579    15.25   0.000     1.045923    1.060522
         age |   1.066112   .0034457    19.81   0.000     1.059107    1.073163
       _cons |   .3372393   .4045108    -0.91   0.372      .029208    3.893807
------------------------------------------------------------------------------
Note: _cons estimates baseline odds.
```

Because the odds ratio for the age predictor is significantly greater than 1, we can conclude that older females are more likely to have high blood pressure than are younger females.

◁

## Health surveys

There are many sources of bias when modeling the association between a disease and its risk factors (Korn, Graubard, and Midthune 1997; Korn and Graubard 1999, sec. 3.7). In cross-sectional health surveys, inference is typically restricted to the target population as it stood when the data were collected. This type of survey cannot capture the fact that participants may change their habits over time. Some health surveys collect data retrospectively, relying on the participants to recall the status of risk factors as they stood in the past. This type of survey is vulnerable to recall bias.

Longitudinal surveys collect data over time, monitoring the survey participants over several years. Although the above biases are minimized, analysts are still faced with some tough choices/situations when modeling time-to-event data. For example:

- Time scale. When studying cancer, should we measure the time scale by using the participant's age or the initial date from which data were collected?
- Time-varying covariates. Were all relevant risk factors sampled over time, or do we have only the baseline measurement?
- Competing risks. When studying mortality, do we have the data specific to cause of death?

Binder (1983) provides the foundation for fitting most of the common parametric models by using survey data. Similarly, Lin and Wei (1989) provide the foundational theory for robust inference by using the proportional hazards model. Binder (1992) describes how to estimate standard errors for the proportional hazards model from survey data, and Lin (2000) provides a rigorous justification for Binder's method. Korn and Graubard (1999) discuss many aspects of model fitting by using data from health surveys. O'Donnell et al. (2008, chap. 10) use Stata survey commands to perform multivariate analysis using health survey data.

## ▷ Example 3: Cox's proportional hazards model

Suppose that we want to model the incidence of lung cancer by using three risk factors: smoking status, sex, and place of residence. Our dataset comes from a longitudinal health survey: the First National Health and Nutrition Examination Survey (NHANES I) (Miller 1973; Engel et al. 1978) and its 1992 Epidemiologic Follow-up Study (NHEFS) (Cox et al. 1997); see the National Center for Health Statistics website at https://www.cdc.gov/nchs/. We will be using data from the samples identified by NHANES I examination locations 1–65 and 66–100; thus we will `svyset` the revised pseudo-PSU and strata variables associated with these locations. Similarly, our `pweight` variable was generated using the sampling weights for the nutrition and detailed samples for locations 1–65 and the weights for the detailed sample for locations 66–100.

```
. use https://www.stata-press.com/data/r19/nhefs
. svyset psu2 [pw=swgt2], strata(strata2)
Sampling weights: swgt2
             VCE: linearized
     Single unit: missing
        Strata 1: strata2
 Sampling unit 1: psu2
           FPC 1: <zero>
```

The lung cancer information was taken from the 1992 NHEFS interview data. We use the participants' ages for the time scale. Participants who never had lung cancer and were alive for the 1992 interview were considered censored. Participants who never had lung cancer and died before the 1992 interview were also considered censored at their age of death.

```
. stset age_lung_cancer [pw=swgt2], fail(lung_cancer)
Survival-time data settings
         Failure event: lung_cancer!=0 & lung_cancer<.
Observed time interval: (0, age_lung_cancer]
     Exit on or before: failure
               Weight: [pweight=swgt2]
--------------------------------------------------------------------------
     14,407  total observations
      5,126  event time missing (age_lung_cancer>=.)        PROBABLE ERROR
--------------------------------------------------------------------------
      9,281  observations remaining, representing
         83  failures in single-record/single-failure data
    599,691  total analysis time at risk and under observation
                                                At risk from t =         0
                                     Earliest observed entry t =         0
                                          Last observed exit t =        97
```

Although `stset` warns us that it is a "probable error" to have 5,126 observations with missing event times, we can verify from the 1992 NHEFS documentation that there were indeed 9,281 participants with complete information.

For our proportional hazards model, we pulled the risk factor information from the NHANES I and 1992 NHEFS datasets. Smoking status was taken from the 1992 NHEFS interview data, but we filled in all but 132 missing values by using the general medical history supplement data in NHANES I. Smoking status is represented by separate indicator variables for former smokers and current smokers; the base comparison group is nonsmokers. Sex was determined using the 1992 NHEFS vitality data and is represented by an indicator variable for males. Place-of-residence information was taken from the medical history questionnaire in NHANES I and is represented by separate indicator variables for rural and heavily populated (more than 1 million people) urban residences; the base comparison group is urban residences with populations of fewer than 1 million people.

```
. svy: stcox former_smoker smoker male urban1 rural
(running stcox on estimation sample)

Survey: Cox regression

Number of strata =  35                        Number of obs    =       9,149
Number of PSUs   = 105                        Population size = 151,327,827
                                              Design df        =          70
                                              F(5, 66)         =       14.07
                                              Prob > F         =      0.0000
```

| _t | Haz. ratio | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| former_smoker | 2.788113 | .6205102 | 4.61 | 0.000 | 1.788705 | 4.345923 |
| smoker | 7.849483 | 2.593249 | 6.24 | 0.000 | 4.061457 | 15.17051 |
| male | 1.187611 | .3445315 | 0.59 | 0.555 | .6658757 | 2.118142 |
| urban1 | .8035074 | .3285144 | −0.54 | 0.594 | .3555123 | 1.816039 |
| rural | 1.581674 | .5281859 | 1.37 | 0.174 | .8125799 | 3.078702 |

From the above results, we can see that both former and current smokers have a significantly higher risk for developing lung cancer than do nonsmokers.

◁

## ❑ Technical note

In the previous example, we specified a sampling weight variable in the calls to both `svyset` and `stset`. When the `svy` prefix is used with `stcox` and `streg`, it identifies the sampling weight variable by using the data characteristics from both `svyset` and `stset`. `svy` will report an error if the `svyset pweight` variable is different from the `stset pweight` variable. The `svy` prefix will use the specified `pweight` variable, even if it is `svyset` but not `stset`. If a `pweight` variable is `stset` but not `svyset`, `svy` will note that it will be using the `stset pweight` variable and then `svyset` it.

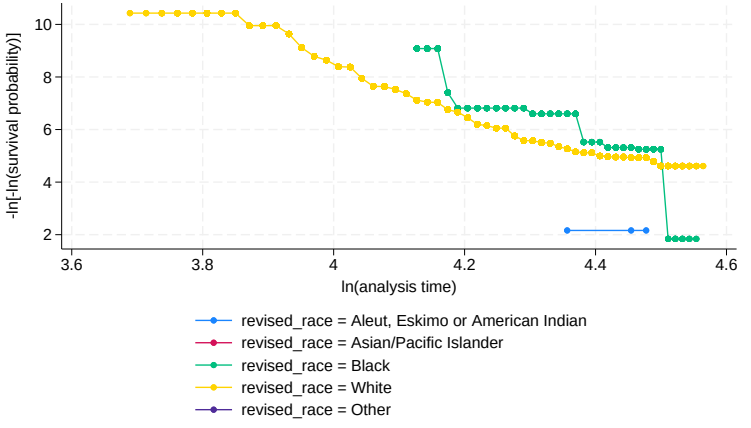
The standard st commands will not use the `svyset pweight` variable if it is not also `stset`.

❑

## ▷ Example 4: Multiple baseline hazards

We can assess the proportional-hazards assumption across the observed race categories for the model fit in the previous example. The race information in our 1992 NHEFS dataset is contained in the `revised_race` variable. We will use `stphplot` to produce a log–log plot for each category of `revised_race`. As described in [ST] **PH plots (right-censored)**, if the plotted lines are reasonably parallel, the proportional-hazards assumption has not been violated. We will use the `zero` option to reset the risk factors to their base comparison group.

```
. stphplot, strata(revised_race) adjust(former_smoker smoker male urban1 rural)
> zero legend(pos(6))
       Failure _d: lung_cancer
  Analysis time _t: age_lung_cancer
          Weight: [pweight=swgt2]
```




As we can see from the graph produced above, the lines for the black and white race categories intersect. This indicates a violation of the proportional-hazards assumption, so we should consider using separate baseline hazard functions for each race category in our model fit. We do this next, by specifying `strata(revised_race)` in our call to `svy: stcox`.

```
. svy: stcox former_smoker smoker male urban1 rural, strata(revised_race)
(running stcox on estimation sample)

Survey: Cox regression

Number of strata =  35                        Number of obs    =       9,149
Number of PSUs   = 105                        Population size  = 151,327,827
                                              Design df        =          70
                                              F(5, 66)         =       13.95
                                              Prob > F         =      0.0000
```

| _t | Haz. ratio | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| former_smoker | 2.801797 | .6280352 | 4.60 | 0.000 | 1.791761 | 4.381201 |
| smoker | 7.954921 | 2.640022 | 6.25 | 0.000 | 4.103709 | 15.42038 |
| male | 1.165724 | .3390339 | 0.53 | 0.600 | .6526527 | 2.082139 |
| urban1 | .784031 | .3120525 | -0.61 | 0.543 | .3544764 | 1.73412 |
| rural | 1.490269 | .5048569 | 1.18 | 0.243 | .7582848 | 2.928851 |

## References

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## Also see

[SVY] **svy postestimation** — Postestimation tools for svy

[SVY] **estat** — Postestimation statistics for survey data

[SVY] **svy** — The survey prefix command

[SVY] **svyset** — Declare survey design for dataset

[SVY] **Calibration** — Calibration for survey data

[SVY] **Direct standardization** — Direct standardization of means, proportions, and ratios

[SVY] **Poststratification** — Poststratification for survey data

[SVY] **Subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **Variance estimation** — Variance estimation for survey data

[U] **20 Estimation and postestimation commands**

**svy jackknife** — Jackknife estimation for survey data



## Description

`svy jackknife` performs jackknife estimation of specified statistics (or expressions) for a Stata command or a user-written program. The command is executed once for each replicate using sampling weights that are adjusted according to the jackknife methodology. Any Stata estimation command listed in [SVY] **svy estimation** may be used with `svy jackknife`. User-written programs that meet the requirements in [P] **program properties** may also be used.

## Quick start

Estimate population mean of `v1` using jackknife standard-error estimates with sampling weight `wvar1` and sampling units identified by `su1`

```
svyset su1 [pweight = wvar1]
svy jackknife _b: mean v1
```

Same as above, but with jackknife replication weights in variables with prefix `rwvar`

```
svyset [pweight = wvar1], vce(jackknife) jkrweight(rwvar*)
svy: mean v1
```

Jackknife standard error of the difference between the means of `v2` and `v3` using either `svyset` command above

```
svy jackknife (_b[v2]-_b[v3]): mean v2 v3
```

Same as above, but name the result `diff` and save results from each replication to `mydata.dta`

```
svy jackknife diff=(_b[v2]-_b[v3]), saving(mydata): mean v2 v3
```

Note: Any estimation command meeting the requirements specified in the *Description* may be substituted for `mean` in the examples above.

## Menu

Statistics > Survey data analysis > Resampling > Jackknife estimation

# Syntax

svy jackknife *exp_list* [ , *svy_options jackknife_options eform_option* ] : *command*

| *svy_options* | Description |
|---|---|
| **if/in** | |
| subpop([ *varname* ] [ *if* ]) | identify a subpopulation |
| **Reporting** | |
| level(#) | set confidence level; default is level(95) |
| noheader | suppress table header |
| nolegend | suppress table legend |
| noadjust | do not adjust model Wald statistic |
| nocnsreport | do not display constraints |
| *display_options* | control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling |
| coeflegend | display legend instead of statistics |

coeflegend is not shown in the dialog boxes for estimation commands.

| *jackknife_options* | Description |
|---|---|
| **Main** | |
| eclass | number of observations is in e(N) |
| rclass | number of observations is in r(N) |
| n(*exp*) | specify *exp* that evaluates to number of observations used |
| **Options** | |
| saving(*filename*[ , ... ]) | save results to *filename*; save statistics in double precision; save results to *filename* every # replications |
| keep | keep pseudovalues |
| mse | use MSE formula for variance |
| **Reporting** | |
| verbose | display the full table legend |
| nodots | suppress replication dots |
| dots(#) | display dots every # replications |
| noisily | display any output from *command* |
| trace | trace *command* |
| title(*text*) | use *text* as title for jackknife results |
| **Advanced** | |
| nodrop | do not drop observations |
| reject(*exp*) | identify invalid results |
| dof(#) | design degrees of freedom |

svy requires that the survey design variables be identified using svyset; see [SVY] **svyset**.

*command* defines the statistical command to be executed. The by prefix cannot be part of *command*.

collect is allowed; see **[U] 11.1.10 Prefix commands**.

See **[U] 20 Estimation and postestimation commands** for more capabilities of estimation commands.

Warning: Using if or in restrictions will often not produce correct variance estimates for subpopulations. To compute estimates for subpopulations, use the subpop() option.

*exp_list* specifies the statistics to be collected from the execution of *command*. *exp_list* is required unless *command* has the `svyj` program property, in which case *exp_list* defaults to `_b`; see [P] **program properties**. The expressions in *exp_list* are assumed to conform to the following:

| | |
|---|---|
| *exp_list* contains | (*name*: *elist*) |
| | *elist* |
| | *eexp* |
| *elist* contains | *newvarname* = (*exp*) |
| | (*exp*) |
| *eexp* is | *specname* |
| | [*eqno*]*specname* |
| *specname* is | `_b` |
| | `_b[]` |
| | `_se` |
| | `_se[]` |
| *eqno* is | `#` # |
| | *name* |

*exp* is a standard Stata expression; see [U] **13 Functions and expressions**.

Distinguish between `[]`, which are to be typed, and [ ], which indicate optional arguments.

## Options

*svy_options*; see [SVY] **svy**.

### Main

`eclass`, `rclass`, and `n(`*exp*`)` specify where *command* stores the number of observations on which it based the calculated results. We strongly advise you to specify one of these options.

`eclass` specifies that *command* store the number of observations in `e(N)`.

`rclass` specifies that *command* store the number of observations in `r(N)`.

`n(`*exp*`)` allows you to specify an expression that evaluates to the number of observations used. Specifying `n(r(N))` is equivalent to specifying the `rclass` option. Specifying `n(e(N))` is equivalent to specifying the `eclass` option. If *command* stores the number of observations in `r(N1)`, specify `n(r(N1))`.

If you specify none of these options, `svy jackknife` will assume `eclass` or `rclass` depending upon which of `e(N)` and `r(N)` is not missing (in that order). If both `e(N)` and `r(N)` are missing, `svy jackknife` assumes that all observations in the dataset contribute to the calculated result. If that assumption is incorrect, then the reported standard errors will be incorrect. For instance, say that you specify

```
. svy jackknife coef=_b[x2]: myreg y x1 x2 x3
```

where `myreg` uses `e(n)` instead of `e(N)` to identify the number of observations used in calculations. Further assume that observation 42 in the dataset has `x3` equal to missing. The 42nd observation plays no role in obtaining the estimates, but `svy jackknife` has no way of knowing that and will use the wrong *N*. If, on the other hand, you specify

```
. svy jackknife coef=_b[x2], n(e(n)): myreg y x1 x2 x3
```

Then svy jackknife will notice that observation 42 plays no role. The n(e(n)) option is specified because myreg is an estimation command, but it stores the number of observations used in e(n) (instead of the standard e(N)). When svy jackknife runs the regression omitting the 42nd observation, svy jackknife will observe that e(n) has the same value as when svy jackknife previously ran the regression by using all the observations. Thus svy jackknife will know that myreg did not use the observation.

## Options

saving(*filename*[ , *suboptions* ]) creates a Stata data file (.dta file) consisting of (for each statistic in *exp_list*) a variable containing the replicates.

double specifies that the results for each replication be saved as doubles, meaning 8-byte reals. By default, they are saved as floats, meaning 4-byte reals. This option may be used without the saving() option to compute the variance estimates by using double precision.

every(#) specifies that results be written to disk every #th replication. every() should be specified in conjunction with saving() only when *command* takes a long time for each replication. This will allow recovery of partial results should some other software crash your computer. See [P] **postfile**.

replace specifies that *filename* be overwritten if it exists. This option does not appear in the dialog box.

keep specifies that new variables be added to the dataset containing the pseudovalues of the requested statistics. For instance, if you typed

```
. svy jackknife coef=_b[x2], eclass keep: regress y x1 x2 x3
```

Then the new variable coef would be added to the dataset containing the pseudovalues for _b[x2]. Let $b$ be defined as the value of _b[x2] when all observations are used to fit the model, and let $b(j)$ be the value when the $j$th observation is omitted. The pseudovalues are defined as

$$\text{pseudovalue}_j = N \times \{b - b(j)\} + b(j)$$

where $N$ is the number of observations used to produce $b$.

keep implies the nodrop option.

mse specifies that svy jackknife compute the variance by using deviations of the replicates from the observed value of the statistics based on the entire dataset. By default, svy jackknife computes the variance by using deviations of the pseudovalues from their mean.

## Reporting

verbose requests that the full table legend be displayed.

nodots and dots(#) specify whether to display replication dots. By default, one dot character is printed for each successful replication. An "x" is displayed if *command* returns an error, "e" is displayed if at least one value in *exp_list* is missing, "n" is displayed if the sample size is not correct, and a yellow "s" is displayed if the dropped sampling unit is outside the subpopulation sample.

nodots suppresses display of the replication dots.

dots(#) displays dots every # replications. dots(0) is a synonym for nodots.

noisily requests that any output from *command* be displayed. This option implies the nodots option.

trace causes a trace of the execution of *command* to be displayed. This option implies the noisily option.

`title(`*text*`)` specifies a title to be displayed above the table of jackknife results; the default title is "Jackknife results".

*eform_option*; see [R] ***eform_option***. This option is ignored if *exp_list* is not `_b`.

Advanced

`nodrop` prevents observations outside `e(sample)` and the `if` and `in` qualifiers from being dropped before the data are resampled.

`reject(`*exp*`)` identifies an expression that indicates when results should be rejected. When *exp* is true, the resulting values are reset to missing values.

`dof(#)` specifies the design degrees of freedom, overriding the default calculation, $\text{df} = N_{\text{psu}} - N_{\text{strata}}$.

## Remarks and examples

The jackknife is

- an alternative, first-order unbiased estimator for a statistic;
- a data-dependent way to calculate the standard error of the statistic and to obtain significance levels and confidence intervals; and
- a way of producing measures called pseudovalues for each observation, reflecting the observation's influence on the overall statistic.

The idea behind the simplest form of the jackknife—the one implemented in [R] **jackknife**—is to repeatedly calculate the statistic in question, each time omitting just one of the dataset's observations. Assume that our statistic of interest is the sample mean. Let $y_j$ be the $j$th observation of our data on some measurement $y$, where $j = 1, \ldots, N$ and $N$ is the sample size. If $\overline{y}$ is the sample mean of $y$ using the entire dataset and $\overline{y}_{(j)}$ is the mean when the $j$th observation is omitted, then

$$\overline{y} = \frac{(N-1)\,\overline{y}_{(j)} + y_j}{N}$$

Solving for $y_j$, we obtain

$$y_j = N\overline{y} - (N-1)\,\overline{y}_{(j)}$$

These are the pseudovalues that `svy: jackknife` calculates. To move this discussion beyond the sample mean, let $\hat{\theta}$ be the value of our statistic (not necessarily the sample mean) using the entire dataset, and let $\hat{\theta}_{(j)}$ be the computed value of our statistic with the $j$th observation omitted. The pseudovalue for the $j$th observation is

$$\hat{\theta}^*_j = N\hat{\theta} - (N-1)\,\hat{\theta}_{(j)}$$

The mean of the pseudovalues is the alternative, first-order unbiased estimator mentioned above, and the standard error of the mean of the pseudovalues is an estimator for the standard error of $\hat{\theta}$ (Tukey 1958 , Shao and Tu 1995 ).

When the jackknife is applied to survey data, primary sampling units (PSUs) are omitted instead of observations, $N$ is the number of PSUs instead of the sample size, and the sampling weights are adjusted owing to omitting PSUs; see [SVY] **Variance estimation** for more details.

Because of privacy concerns, many public survey datasets contain jackknife replication-weight variables instead of variables containing information on the PSUs and strata. These replication-weight variables are the adjusted sampling weights, and there is one replication-weight variable for each omitted PSU.

## Example 1: Jackknife with information on PSUs and strata

Suppose that we were interested in a measure of association between the weight and height of individuals in the population represented by the NHANES II data (McDowell et al. 1981). To measure the association, we will use the slope estimate from a linear regression of `weight` on `height`. We also use `svy jackknife` to estimate the variance of the slope.

```
. use https://www.stata-press.com/data/r19/nhanes2
. svyset
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: strata
 Sampling unit 1: psu
           FPC 1: <zero>
. svy jackknife slope = _b[height]: regress weight height
(running regress on estimation sample)
Jackknife replications (62): .........10.........20.........30.........40.......
> ..50.........60.. done
Linear regression
Number of strata = 31                              Number of obs   =      10,351
Number of PSUs   = 62                              Population size = 117,157,513
                                                   Replications    =          62
                                                   Design df       =          31
      Command: regress weight height
        slope: _b[height]
           n(): e(N)
```

| | Coefficient | Jackknife std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| slope | .8014753 | .0160281 | 50.00 | 0.000 | .7687858 | .8341648 |

## Example 2: Jackknife replicate-weight variables

nhanes2jknife.dta is a privacy-conscious dataset equivalent to nhanes2.dta; all the variables and values remain, except that strata and psu are replaced with jackknife replicate-weight variables. The replicate-weight variables are already svyset, and the default method for variance estimation is vce(jackknife).

```
. use https://www.stata-press.com/data/r19/nhanes2jknife
. svyset
 Sampling weights: finalwgt
              VCE: jackknife
              MSE: off
Jackknife weights: jkw_1 .. jkw_62
      Single unit: missing
         Strata 1: <one>
  Sampling unit 1: <observations>
              FPC 1: <zero>
```

Here we perform the same analysis as in the previous example, using jackknife replication weights.

```
. svy jackknife slope = _b[height], nodots: regress weight height
Linear regression
Number of strata = 31                              Number of obs    =      10,351
                                                   Population size = 117,157,513
                                                   Replications     =          62
                                                   Design df        =          31
      Command: regress weight height
        slope: _b[height]
```

| | Coefficient | Jackknife std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| slope | .8014753 | .0160281 | 50.00 | 0.000 | .7687858 | .8341648 |

The mse option causes svy jackknife to use the MSE form of the jackknife variance estimator. This variance estimator will tend to be larger than the previous because of the addition of the familiar squared bias term in the MSE; see [SVY] **Variance estimation** for more details. The header for the column of standard errors in the table of results is Jknife * for the jackknife variance estimator, which uses the MSE formula.

```
. svy jackknife slope = _b[height], mse nodots: regress weight height
Linear regression
Number of strata = 31                              Number of obs    =      10,351
                                                   Population size = 117,157,513
                                                   Replications     =          62
                                                   Design df        =          31
      Command: regress weight height
        slope: _b[height]
```

| | Coefficient | Jknife * std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| slope | .8014753 | .0160284 | 50.00 | 0.000 | .7687852 | .8341654 |

❑ Technical note

When the `svy jackknife` prefix is used with a user-defined program and when the expression list is `_b`, `svy jackknife` calls

```
set coeftabresults off
```

before entering the replication loop to prevent Stata from performing unnecessary calculations. This means that, provided option `noisily` is not specified, estimation commands will not build or post the coefficient table matrix `r(table)`.

If your program calls an estimation command and needs `r(table)` to exist to perform properly, then your program will need to call

```
set coeftabresults on
```

before calling other estimation commands.

❑

## Stored results

In addition to the results documented in [SVY] **svy**, `svy jackknife` stores the following in `e()`:

Scalars

| | |
|---|---|
| `e(N_reps)` | number of replications |
| `e(N_misreps)` | number of replications with missing values |
| `e(k_exp)` | number of standard expressions |
| `e(k_eexp)` | number of `_b`/`_se` expressions |
| `e(k_extra)` | number of extra estimates added to `_b` |

Macros

| | |
|---|---|
| `e(cmdname)` | command name from *command* |
| `e(cmd)` | same as `e(cmdname)` or `jackknife` |
| `e(vce)` | `jackknife` |
| `e(exp#)` | #th expression |
| `e(jkrweight)` | `jkrweight()` variable list |

Matrices

| | |
|---|---|
| `e(b_jk)` | jackknife means |
| `e(V)` | jackknife variance estimates |

When *exp_list* is `_b`, `svy jackknife` will also carry forward most of the results already in `e()` from *command*.

## Methods and formulas

See [SVY] **Variance estimation** for details regarding jackknife variance estimation.

## References

McDowell, A., A. Engel, J. T. Massey, and K. Maurer. 1981. "Plan and operation of the Second National Health and Nutrition Examination Survey, 1976–1980". In *Vital and Health Statistics*, ser. 1, no. 15. Hyattsville, MD: National Center for Health Statistics.

Shao, J., and D. Tu. 1995. *The Jackknife and Bootstrap*. New York: Springer. https://doi.org/10.1007/978-1-4612-0795-5.

Tukey, J. W. 1958. Bias and confidence in not-quite large samples. Abstract in *Annals of Mathematical Statistics* 29: 614. https://doi.org/10.1214/aoms/1177706647.

## Also see

[SVY] **svy postestimation** — Postestimation tools for svy

[SVY] **svy bootstrap** — Bootstrap for survey data

[SVY] **svy brr** — Balanced repeated replication for survey data

[SVY] **svy sdr** — Successive difference replication for survey data

[SVY] **Calibration** — Calibration for survey data

[SVY] **Poststratification** — Poststratification for survey data

[SVY] **Subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **Variance estimation** — Variance estimation for survey data

[R] **jackknife** — Jackknife estimation

**[U] 20 Estimation and postestimation commands**

**svy postestimation** — Postestimation tools for svy



## Postestimation commands

The following postestimation commands are available after svy:

| command | Description |
|---|---|
| contrast | contrasts and ANOVA-style joint tests of parameters |
| estat (svy) | postestimation statistics for survey data |
| estimates | cataloging estimation results |
| etable | table of estimation results |
| lincom | point estimates, standard errors, testing, and inference for linear combinations of parameters |
| margins | marginal means, predictive margins, marginal effects, and average marginal effects |
| marginsplot | graph the results from margins (profile plots, interaction plots, etc.) |
| nlcom | point estimates, standard errors, testing, and inference for nonlinear combinations of parame |
| predict | predictions, residuals, influence statistics, and other diagnostic measures |
| predictnl | point estimates, standard errors, testing, and inference for generalized predictions |
| pwcompare | pairwise comparisons of parameters |
| suest | seemingly unrelated estimation |
| test | Wald tests of simple and composite linear hypotheses |
| testnl | Wald tests of nonlinear hypotheses |

See [SVY] **estat**.

## predict

The syntax of predict (and even if predict is allowed) after svy depends on the command used with svy. Specifically, predict is not allowed after svy: mean, svy: proportion, svy: ratio, svy: tabulate, or svy: total.

## margins

The syntax of margins (and even if margins is allowed) after svy depends on the command used with svy. Specifically, margins is not allowed after svy: mean, svy: proportion, svy: ratio, svy: tabulate, or svy: total.

## Remarks and examples

What follows are some examples of applications of postestimation commands using survey data. The examples are meant only to introduce the commands in a survey context and explore a few of the possibilities for postestimation analysis. See the individual entries for each command in the *Base Reference Manual* for complete syntax and many more examples.

## Example 1: Linear and nonlinear combinations

`lincom` will display an estimate of a linear combination of parameters, along with its standard error, a confidence interval, and a test that the linear combination is zero. `nlcom` will do likewise for nonlinear combinations of parameters.

`lincom` is commonly used to compute the differences of two subpopulation means. For example, suppose that we wish to estimate the difference of zinc levels in white males versus black males in the population represented by the NHANES II data (McDowell et al. 1981). Because the survey design characteristics are already `svyset` in `nhanes2.dta`, we only need to generate a variable for identifying the male subpopulation before using `svy: mean`.

```
. use https://www.stata-press.com/data/r19/nhanes2
. generate male = (sex == 1)
. svy, subpop(male): mean zinc, over(race)
(running mean on estimation sample)
Survey: Mean estimation
Number of strata = 31                  Number of obs    =       9,811
Number of PSUs   = 62                  Population size  = 111,127,314
                                       Subpop. no. obs  =       4,375
                                       Subpop. size     =  50,129,281
                                       Design df        =          31
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| c.zinc@race | | | | |
| White | 91.15725 | .541625 | 90.0526 | 92.2619 |
| Black | 88.269 | 1.208336 | 85.80458 | 90.73342 |
| Other | 85.54716 | 2.608974 | 80.22612 | 90.8682 |

Then we run `lincom` to estimate the difference of zinc levels between the two subpopulations.

```
. lincom zinc#1.race - zinc#2.race
 ( 1)  c.zinc@1bn.race - c.zinc@2.race = 0
```

| Mean | Coefficient | Std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| (1) | 2.888249 | 1.103999 | 2.62 | 0.014 | .6366288 | 5.139868 |

The $t$ statistic and its $p$-value give a survey analysis equivalent of a two-sample $t$ test.

`lincom` and `nlcom` can be used after any of the estimation commands described in [SVY] **svy estimation**. `lincom` can, for example, display results as odds ratios after `svy: logit` and can be used to compute odds ratios for one covariate group relative to another. `nlcom` can display odds ratios, as well, and allows more general nonlinear combinations of the parameters. See [R] **lincom** and [R] **nlcom** for full details. Also see Eltinge and Sribney (1996) for an earlier implementation of `lincom` for survey data.

Finally, `lincom` and `nlcom` operate on the estimated parameters only. To obtain estimates and inference for functions of the parameters and of the data, such as for an exponentiated linear predictor or a predicted probability of success from a logit model, use `predictnl`; see [R] **predictnl**.

## ▷ Example 2: Quadratic terms

From example 2 in [SVY] **svy estimation**, we modeled the incidence of high blood pressure as a function of height, weight, age, and sex (using the `female` indicator variable). Here we also include `c.age#c.age`, a squared term for age.

```
. use https://www.stata-press.com/data/r19/nhanes2d, clear
. svy: logistic highbp height weight age c.age#c.age female
(running logistic on estimation sample)
Survey: Logistic regression
Number of strata = 31                        Number of obs    =      10,351
Number of PSUs   = 62                        Population size  = 117,157,513
                                             Design df        =          31
                                             F(5, 27)         =      284.33
                                             Prob > F         =      0.0000
```

| highbp | Odds ratio | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| height | .9656421 | .005163 | -6.54 | 0.000 | .9551693 | .9762298 |
| weight | 1.052911 | .0026433 | 20.54 | 0.000 | 1.047534 | 1.058316 |
| age | 1.055829 | .0133575 | 4.29 | 0.000 | 1.028935 | 1.083426 |
| c.age#c.age | .9999399 | .0001379 | -0.44 | 0.666 | .9996588 | 1.000221 |
| female | .6260988 | .0364945 | -8.03 | 0.000 | .5559217 | .7051347 |
| _cons | .653647 | .5744564 | -0.48 | 0.632 | .108869 | 3.924483 |

Note: **_cons** estimates baseline odds.

Because our model includes a quadratic in the `age` variable, the peak incidence of high blood pressure with respect to `age` will occur at `-_b[age]/(2*_b[c.age#c.age])`, which we can estimate, along with its standard error, using `nlcom`.

```
. nlcom peak: -_b[age]/(2*_b[c.age#c.age])
       peak: -_b[age]/(2*_b[c.age#c.age])
```

| highbp | Coefficient | Std. err. | z | P>\|z\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| peak | 452.0979 | 933.512 | 0.48 | 0.628 | -1377.552 | 2281.748 |

Or we can use `testnl` to test that the peak incidence of high blood pressure in the population is 70 years.

```
. testnl -_b[age]/(2*_b[c.age#c.age]) = 70
  (1)  -_b[age]/(2*_b[c.age#c.age]) = 70
               chi2(1) =        0.17
           Prob > chi2 =        0.6823
```

These data do not reject our theory. `testnl` allows multiple hypotheses to be tested jointly and applies the degrees-of-freedom adjustment for survey results; see [R] **testnl**.

◁

## Example 3: Predictive margins

Changing our logistic regression for high blood pressure slightly, we add a factor variable for the levels of `race`. Level 1 of `race` represents whites, level 2 represents blacks, and level 3 represents others. We also specify that `female` is a factor variable, which does not change its coefficient but does increase its functionality with some postestimation commands.

```
. svy: logistic highbp height weight age c.age#c.age i.female i.race, baselevels
(running logistic on estimation sample)

Survey: Logistic regression

Number of strata = 31                         Number of obs    =      10,351
Number of PSUs   = 62                         Population size  = 117,157,513
                                              Design df        =          31
                                              F(7, 25)         =      230.16
                                              Prob > F         =      0.0000
```

| highbp | Odds ratio | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| height | .9675961 | .0052361 | -6.09 | 0.000 | .9569758 | .9783343 |
| weight | 1.052683 | .0026091 | 20.72 | 0.000 | 1.047376 | 1.058018 |
| age | 1.056628 | .0134451 | 4.33 | 0.000 | 1.029559 | 1.084408 |
| c.age#c.age | .9999402 | .0001382 | -0.43 | 0.668 | .9996585 | 1.000222 |
| female | | | | | | |
| Male | 1 | (base) | | | | |
| Female | .6382331 | .0377648 | -7.59 | 0.000 | .5656774 | .720095 |
| race | | | | | | |
| White | 1 | (base) | | | | |
| Black | 1.422003 | .1556023 | 3.22 | 0.003 | 1.137569 | 1.777557 |
| Other | 1.63456 | .2929919 | 2.74 | 0.010 | 1.13405 | 2.355971 |
| _cons | .4312846 | .378572 | -0.96 | 0.345 | .0719901 | 2.583777 |

Note: **_cons** estimates baseline odds.

Our point estimates indicate that the odds of females having high blood pressure is about 64% of the odds for men and that the odds of blacks having high blood pressure is about 1.4 times that of whites. The odds ratios give us the relative effects of their covariates, but they do not give us any sense of the absolute size of the effects. The odds ratio comparing blacks with whites is clearly large and statistically significant, but does it represent a sizable change? One way to answer that question is to explore the probabilities of high blood pressure from our fitted model. Let's first look at the predictive margins of the probability of high blood pressure for the three levels of `race`.

```
. margins race, vce(unconditional)
Predictive margins
Number of strata = 31                             Number of obs   =      10,351
Number of PSUs   = 62                             Population size = 117,157,513
                                                  Design df       =          31
Expression: Pr(highbp), predict()
```

| | Margin | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| race | | | | | | |
| White | .3600722 | .0150121 | 23.99 | 0.000 | .3294548 | .3906895 |
| Black | .4256413 | .0211311 | 20.14 | 0.000 | .3825441 | .4687385 |
| Other | .4523404 | .0311137 | 14.54 | 0.000 | .3888836 | .5157972 |

Because our response is a probability, these margins are sometimes called predicted marginal proportions or model-adjusted risks. They let us compare the effect of our three racial groups while controlling for the distribution of other covariates in the groups. Computationally, these predictive margins are the weighted average of the predicted probabilities for each observation in the estimation sample. The marginal probability for whites is the average probability, assuming that everyone in the sample is white; the margin for blacks assumes that everyone is black; and the margin for others assumes that everyone is something other than black or white.

There is a sizable difference in blood pressure between whites and blacks, with the marginal probability of high blood pressure for whites being about 36% and that for blacks being almost 43%. These are the adjusted probability levels. A more direct answer to our question about whether the odds ratios represent a substantial effect requires looking at the differences of these marginal probabilities. Researchers in the health-related sciences call such differences risk differences, whereas researchers in the social sciences usually call them average marginal effects or average partial effects.

Regardless of terminology, we are interested in the difference in the probability of blacks having high blood pressure as compared with whites, while adjusting for all other covariates in the model. We request risk differences by specifying the variables of interest in a `dydx()` option.

```
. margins, vce(unconditional) dydx(race)
Average marginal effects
Number of strata = 31                             Number of obs   =      10,351
Number of PSUs   = 62                             Population size = 117,157,513
                                                  Design df       =          31
Expression: Pr(highbp), predict()
dy/dx wrt:  2.race 3.race
```

| | dy/dx | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| race | | | | | | |
| Black | .0655691 | .0204063 | 3.21 | 0.003 | .0239501 | .1071881 |
| Other | .0922682 | .0343809 | 2.68 | 0.012 | .0221478 | .1623886 |

```
Note: dy/dx for factor levels is the discrete change from the base level.
```

Looking in the column labeled `dy/dx`, we see that the risk difference between blacks and whites is about 6.6% (0.6557). That is a sizable as well as significant difference.

Because they are population-weighted averages over the whole sample, these margins are estimates of the population average risk differences. And because we specified the `vce(unconditional)` option, their standard errors and confidence intervals can be used to make inferences about the population average risk differences. See *Methods and formulas* in [R] **margins** for details.

We can also compute margins or risk differences for subpopulations. To compute risk differences for the four subpopulations that are the regions of the United States—Northeast, Midwest, South, and West—we add the `over(region)` option.

```
. margins, vce(unconditional) dydx(race) over(region)
Average marginal effects
Number of strata = 31                          Number of obs   =      10,351
Number of PSUs   = 62                          Population size = 117,157,513
                                               Design df       =          31
Expression: Pr(highbp), predict()
dy/dx wrt:  2.race 3.race
Over:       region
```

| | dy/dx | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| 1.race | (base outcome) | | | | | |
| 2.race | | | | | | |
| region | | | | | | |
| NE | .0662951 | .0207354 | 3.20 | 0.003 | .0240051 | .1085852 |
| MW | .065088 | .0204357 | 3.19 | 0.003 | .0234091 | .106767 |
| S | .0663448 | .0202173 | 3.28 | 0.003 | .0251112 | .1075783 |
| W | .0647221 | .0203523 | 3.18 | 0.003 | .0232134 | .1062308 |
| 3.race | | | | | | |
| region | | | | | | |
| NE | .093168 | .0343919 | 2.71 | 0.011 | .0230253 | .1633106 |
| MW | .091685 | .034247 | 2.68 | 0.012 | .0218379 | .1615322 |
| S | .0932303 | .0345933 | 2.70 | 0.011 | .0226769 | .1637837 |
| W | .0912062 | .034322 | 2.66 | 0.012 | .021206 | .1612063 |

```
Note: dy/dx for factor levels is the discrete change from the base level.
```

The differences in the covariate distributions across the regions have little effect on the risk differences between blacks and whites, or between other races and whites.

Rather than explore the probabilities after logistic regression, we might have explored the hazards or mean survival times after fitting a survival model. See [R] **margins** for many more applications of `margins`.

◁

## ▷ Example 4: Predictive means with replication-based variance estimators

When performing estimations with linearized standard errors, we use the `vce(unconditional)` option to compute marginal effects so that we can use the results to make inferences on the population. `margins` with `vce(unconditional)` uses linearization to compute the unconditional variance of the marginal means.

The vce(unconditional) option, therefore, cannot be used when a different variance estimation method has been specified for the model. If you are using a replication-based method to estimate the variance in your model, you may want to use this method to perform the variance estimation for your margins as well. To do that, you can write a program that performs both your main estimation and the computation of your margins and use the replication method with your program.

Continuing with the logistic example, we will see how to estimate the marginal means for race by using the jackknife variance estimator. The program below accepts an argument that contains the estimation command line. Notice that the program should accept the if qualifier and also weights. In addition, the set buildfvinfo on command is included so that margins checks for estimability. buildfvinfo is usually set on, but is set off because it increases the computation time when you use replication methods; thus you need to set it on. The option post of margins posts the results to e(b), so they can be used by svy jackknife.

```
program mymargins, eclass
    version 19.5      // (or version 19 if you do not have StataNow)
    syntax anything [if] [iw pw]
    if "‘weight’" != "" {
      local wgtexp "[‘weight’ ‘exp’]"
    }
    set buildfvinfo on
    ‘anything’ ‘if’ ‘wgtexp’
    margins race, post
end
```

We can now type

```
. local mycmdline logistic highbp height weight age c.age#c.age i.race i.female
. quietly mymargins ‘mycmdline’
. svy jackknife _b: mymargins ‘mycmdline’
(running mymargins on estimation sample)
Jackknife replications (62): .........10.........20.........30.........40.......
> ..50.........60.. done
Predictive margins
Number of strata = 31                          Number of obs    =      10,351
Number of PSUs   = 62                          Population size = 117,157,513
                                               Replications     =          62
                                               Design df        =          31
```

| | Coefficient | Jackknife std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| race | | | | | | |
| White | .3600722 | .0150128 | 23.98 | 0.000 | .3294534 | .390691 |
| Black | .4256413 | .0211504 | 20.12 | 0.000 | .3825048 | .4687778 |
| Other | .4523404 | .0322488 | 14.03 | 0.000 | .3865684 | .5181124 |

You can see that now the jackknife standard errors are being reported.

◁

## ▷ Example 5: Nonlinear predictions and their standard errors

Continuing with the NHANES II data, we fit a linear regression of log of blood lead level on age, age-squared, gender, race, and region.

```
. use https://www.stata-press.com/data/r19/nhanes2d
. svy: regress loglead age c.age#c.age i.female i.race i.region
(running regress on estimation sample)
Survey: Linear regression
Number of strata = 31                         Number of obs   =      4,948
Number of PSUs   = 62                         Population size = 56,405,414
                                              Design df       =         31
                                              F(8, 24)        =     156.24
                                              Prob > F        =     0.0000
                                              R-squared       =     0.2379
```

| loglead | Coefficient | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| age | .0158388 | .0027352 | 5.79 | 0.000 | .0102603 | .0214173 |
| c.age#c.age | -.0001464 | .0000295 | -4.96 | 0.000 | -.0002066 | -.0000862 |
| female | | | | | | |
| Female | -.3655338 | .0116157 | -31.47 | 0.000 | -.3892242 | -.3418434 |
| race | | | | | | |
| Black | .178402 | .0314173 | 5.68 | 0.000 | .114326 | .242478 |
| Other | -.0516952 | .0402381 | -1.28 | 0.208 | -.1337614 | .030371 |
| region | | | | | | |
| MW | -.02283 | .0389823 | -0.59 | 0.562 | -.1023349 | .0566749 |
| S | -.1685453 | .056004 | -3.01 | 0.005 | -.2827662 | -.0543244 |
| W | -.0362295 | .0387508 | -0.93 | 0.357 | -.1152623 | .0428032 |
| _cons | 2.440671 | .0627987 | 38.86 | 0.000 | 2.312592 | 2.568749 |

Given that we modeled the natural log of the lead measurement, we can use `predictnl` to compute the exponentiated linear prediction (in the original units of the `lead` variable), along with its standard error.

```
. predictnl leadhat = exp(xb()) if e(sample), se(leadhat_se)
(5,403 missing values generated)
. sort lead leadhat
. generate showobs = inrange(_n,1,5) + inrange(_n,2501,2505) +
> inrange(_n,4945,4948)
```

```
. list lead leadhat leadhat_se age c.age#c.age if showobs, abbrev(10)
```

| | lead | leadhat | leadhat_se | age | c.age# c.age |
|---|---|---|---|---|---|
| 1. | 2 | 9.419804 | .5433255 | 29 | 841 |
| 2. | 3 | 8.966098 | .5301117 | 23 | 529 |
| 3. | 3 | 9.046788 | .5298448 | 24 | 576 |
| 4. | 3 | 9.046788 | .5298448 | 24 | 576 |
| 5. | 3 | 9.27693 | .5347956 | 27 | 729 |
| 2501. | 13 | 16.88317 | .7728783 | 37 | 1369 |
| 2502. | 13 | 16.90057 | 2.296082 | 71 | 5041 |
| 2503. | 13 | 16.90057 | 2.296082 | 71 | 5041 |
| 2504. | 13 | 16.90237 | 1.501056 | 48 | 2304 |
| 2505. | 13 | 16.90852 | 2.018708 | 60 | 3600 |
| 4945. | 61 | 17.18581 | 2.052034 | 58 | 3364 |
| 4946. | 64 | 15.08437 | .647629 | 24 | 576 |
| 4947. | 66 | 17.78698 | 1.641349 | 56 | 3136 |
| 4948. | 80 | 16.85864 | 1.333927 | 42 | 1764 |

◁

## ▷ Example 6: Multiple-hypothesis testing

Joint-hypothesis tests can be performed after svy commands with the `test` command. Using the results from the regression model fit in the previous example, we can use `test` to test the joint significance of `2.region`, `3.region`, and `4.region`. (`1.region` is the Northeast, `2.region` is the Midwest, `3.region` is the South, and `4.region` is the West.) We test the hypothesis that `2.region` $= 0$, `3.region` $= 0$, and `4.region` $= 0$.

```
. test 2.region 3.region 4.region
Adjusted Wald test
 ( 1)  2.region = 0
 ( 2)  3.region = 0
 ( 3)  4.region = 0
       F(  3,    29) =    2.96
            Prob > F =    0.0486
```

The `nosvyadjust` option on `test` produces an unadjusted Wald test.

```
. test 2.region 3.region 4.region, nosvyadjust
Unadjusted Wald test
 ( 1)  2.region = 0
 ( 2)  3.region = 0
 ( 3)  4.region = 0
       F(  3,    31) =    3.17
            Prob > F =    0.0382
```

For one-dimensional tests, the adjusted and unadjusted $F$ statistics are identical, but they differ for higher-dimensional tests. Using the `nosvyadjust` option is not recommended because the unadjusted $F$ statistic can produce extremely anticonservative $p$-values (that is, $p$-values that are too small) when the variance degrees of freedom (equal to the number of sampled PSUs minus the number of strata) is not large relative to the dimension of the test.

Bonferroni-adjusted $p$-values can also be computed:

```
. test 2.region 3.region 4.region, mtest(bonferroni)
Adjusted Wald test
 ( 1)  2.region = 0
 ( 2)  3.region = 0
 ( 3)  4.region = 0
```

| | F(df,29) | df | p > F |
|---|---|---|---|
| (1) | 0.34 | 1 | 1.0000* |
| (2) | 9.06 | 1 | 0.0155* |
| (3) | 0.87 | 1 | 1.0000* |
| All | 2.96 | 3 | 0.0486 |

* Bonferroni-adjusted $p$-values

See Korn and Graubard (1990) for a discussion of these three different procedures for conducting joint-hypothesis tests. See Eltinge and Sribney (1996) for an earlier implementation of `test` for survey data.

◁

## ▷ Example 7: Contrasts

After svy commands, we can estimate contrasts and make pairwise comparisons with the `contrast` and `pwcompare` commands. First, we will fit a regression of serum zinc levels on health status:

```
. use https://www.stata-press.com/data/r19/nhanes2f, clear
. label list hlthgrp
hlthgrp:
           1 Poor
           2 Fair
           3 Average
           4 Good
           5 Excellent
. svy: regress zinc i.health
(running regress on estimation sample)
Survey: Linear regression
Number of strata = 31                        Number of obs   =       9,188
Number of PSUs   = 62                        Population size = 104,162,204
                                             Design df       =          31
                                             F(4, 28)        =       15.61
                                             Prob > F        =      0.0000
                                             R-squared       =      0.0098
```

| zinc | Coefficient | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| health | | | | | | |
| Fair | .9272308 | .7690396 | 1.21 | 0.237 | -.6412357 | 2.495697 |
| Average | 2.444004 | .6407097 | 3.81 | 0.001 | 1.137268 | 3.75074 |
| Good | 4.038285 | .6830349 | 5.91 | 0.000 | 2.645226 | 5.431344 |
| Excellent | 4.770911 | .7151641 | 6.67 | 0.000 | 3.312324 | 6.229498 |
| _cons | 83.94729 | .8523379 | 98.49 | 0.000 | 82.20893 | 85.68564 |

Higher levels of zinc are associated with better health. We can use reverse adjacent contrasts to compare each health status with the preceding status.

```
. contrast ar.health
Contrasts of marginal linear predictions
                                                        Design df = 31
Margins: asbalanced
```

| | df | F | P>F |
|---|---|---|---|
| health | | | |
| (Fair vs Poor) | 1 | 1.45 | 0.2371 |
| (Average vs Fair) | 1 | 5.49 | 0.0257 |
| (Good vs Average) | 1 | 10.92 | 0.0024 |
| (Excellent vs Good) | 1 | 1.93 | 0.1744 |
| Joint | 4 | 15.61 | 0.0000 |
| Design | 31 | | |

Note: F statistics are adjusted for the survey design.

| | Contrast | Std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| health | | | | |
| (Fair vs Poor) | .9272308 | .7690396 | -.6412357 | 2.495697 |
| (Average vs Fair) | 1.516773 | .6474771 | .1962347 | 2.837311 |
| (Good vs Average) | 1.594281 | .4824634 | .6102904 | 2.578271 |
| (Excellent vs Good) | .7326264 | .5270869 | -.3423744 | 1.807627 |

The first table reports significance tests for each contrast, along with a joint test of all the contrasts. The row labeled `(Fair vs Poor)`, for example, tests the null hypothesis that the first two health statuses have the same mean zinc level. The test statistics are automatically adjusted for the survey design.

The second table reports estimates, standard errors, and confidence limits for each contrast. The row labeled `(Good vs Average)`, for example, shows that those in good health have a mean zinc level about 1.6 units higher than those of average health. The standard errors and confidence intervals also account for the survey design.

If we would like to go further and make all possible pairwise comparisons of the health groups, we can use the pwcompare command. We will specify the mcompare(sidak) option to account for multiple comparisons and the cformat(%3.1f) option to reduce the number of decimal places in the output:

```
. pwcompare health, mcompare(sidak) cformat(%3.1f)
Pairwise comparisons of marginal linear predictions
                                                Design df = 31
Margins: asbalanced
```

| | Number of comparisons |
|---|---|
| health | 10 |

| | Contrast | Std. err. | Sidak [95% conf. | interval] |
|---|---|---|---|---|
| health | | | | |
| Fair vs Poor | 0.9 | 0.8 | -1.4 | 3.2 |
| Average vs Poor | 2.4 | 0.6 | 0.5 | 4.4 |
| Good vs Poor | 4.0 | 0.7 | 2.0 | 6.1 |
| Excellent vs Poor | 4.8 | 0.7 | 2.6 | 6.9 |
| Average vs Fair | 1.5 | 0.6 | -0.4 | 3.5 |
| Good vs Fair | 3.1 | 0.5 | 1.5 | 4.8 |
| Excellent vs Fair | 3.8 | 0.7 | 1.7 | 6.0 |
| Good vs Average | 1.6 | 0.5 | 0.1 | 3.0 |
| Excellent vs Average | 2.3 | 0.7 | 0.3 | 4.4 |
| Excellent vs Good | 0.7 | 0.5 | -0.9 | 2.3 |

Seven of the ten Šidák intervals exclude the null value of zero. See [R] **pwcompare** for more information on pairwise comparisons and multiple-comparison adjustments.

◁

## ▷ Example 8: Using suest with survey data, the svy prefix

suest can be used to obtain the variance estimates for a series of estimators that used the svy prefix. To use suest for this purpose, perform the following steps:

1. Be sure to set the survey design characteristics correctly by using svyset. Do not use the vce() option to change the default variance estimator from the linearized variance estimator. vce(brr) and vce(jackknife) are not supported by suest.
2. Fit the model or models by using the svy prefix command, optionally including subpopulation estimation with the subpop() option.
3. Store the estimation results with estimates store *name*.

In the following, we illustrate how to use suest to compare the parameter estimates between two ordered logistic regression models.

In the NHANES II dataset, we have the variable health containing self-reported health status, which takes on the values 1–5, with 1 being "poor" and 5 being "excellent". Because this is an ordered categorical variable, it makes sense to model it by using svy: ologit. We use some basic demographic variables as predictors: female (an indicator of female individuals), black (an indicator for black individuals), age in years, and c.age#c.age (age squared).

```
. use https://www.stata-press.com/data/r19/nhanes2f, clear
. svyset psuid [pw=finalwgt], strata(stratid)
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: stratid
 Sampling unit 1: psuid
           FPC 1: <zero>
. svy: ologit health female black age c.age#c.age
(running ologit on estimation sample)
Survey: Ordered logistic regression
Number of strata = 31                         Number of obs   =      10,335
Number of PSUs   = 62                         Population size = 116,997,257
                                              Design df       =          31
                                              F(4, 28)        =      223.27
                                              Prob > F        =      0.0000
```

| health | Coefficient | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| female | -.1615219 | .0523678 | -3.08 | 0.004 | -.2683267 | -.054717 |
| black | -.986568 | .0790277 | -12.48 | 0.000 | -1.147746 | -.8253899 |
| age | -.0119491 | .0082974 | -1.44 | 0.160 | -.0288717 | .0049736 |
| c.age#c.age | -.0003234 | .000091 | -3.55 | 0.001 | -.000509 | -.0001377 |
| /cut1 | -4.566229 | .1632561 | | | -4.899192 | -4.233266 |
| /cut2 | -3.057415 | .1699944 | | | -3.404121 | -2.710709 |
| /cut3 | -1.520596 | .1714342 | | | -1.870239 | -1.170954 |
| /cut4 | -.242785 | .1703965 | | | -.590311 | .104741 |

The self-reported health variable takes five categories. Categories 1 and 2 denote negative categories, whereas categories 4 and 5 denote positive categories. We wonder whether the distinctions between the two positive categories and between the two negative categories are produced in accordance with one latent dimension, which is an assumption of the ordered logistic model. To test one-dimensionality, we will collapse the five-point health measure into a three-point measure, refit the ordered logistic model, and compare the regression coefficients and cutpoints between the two analyses. If the single latent variable assumption is valid, the coefficients and cutpoints should match. This can be seen as a Hausman-style specification test. Estimation of the ordered logistic model parameters for survey data is by maximum pseudolikelihood. Neither estimator is fully efficient, and thus the assumptions for the classic Hausman test and for the hausman command are not satisfied. With suest, we can obtain an appropriate Hausman test for survey data.

To perform the Hausman test, we are already almost halfway there by following steps 1 and 2 for one of the models. We just need to store the current estimation results before moving on to the next model. Here we store the results with `estimates store` under the name `H5`, indicating that in this analysis, the dependent variable `health` has five categories.

```
. estimates store H5
```

We proceed by generating a new dependent variable `health3`, which maps values 1 and 2 into 2, 3 into 3, and 4 and 5 into 4. This transformation is conveniently accomplished with the `clip()` function. We then fit an `ologit` model with this new dependent variable and store the estimation results under the name `H3`.

```
. generate health3 = clip(health, 2, 4)
(2 missing values generated)

. svy: ologit health3 female black age c.age#c.age
(running ologit on estimation sample)

Survey: Ordered logistic regression

Number of strata = 31                     Number of obs   =      10,335
Number of PSUs   = 62                     Population size = 116,997,257
                                          Design df       =          31
                                          F(4, 28)        =      197.08
                                          Prob > F        =      0.0000
```

| health3 | Coefficient | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| female | -.1551238 | .0563809 | -2.75 | 0.010 | -.2701133 | -.0401342 |
| black | -1.046316 | .0728274 | -14.37 | 0.000 | -1.194849 | -.8977836 |
| age | -.0365408 | .0073653 | -4.96 | 0.000 | -.0515624 | -.0215192 |
| c.age#c.age | -.00009 | .0000791 | -1.14 | 0.264 | -.0002512 | .0000713 |
| /cut1 | -3.655498 | .1610211 | | | -3.983903 | -3.327093 |
| /cut2 | -2.109584 | .1597057 | | | -2.435306 | -1.783862 |

```
. estimates store H3
```

We can now obtain the combined estimation results of the two models stored under H5 and H3 with design-based standard errors.

```
. suest H5 H3

Simultaneous survey results for H5, H3

Number of strata = 31                             Number of obs   =      10,335
Number of PSUs   = 62                             Population size = 116,997,257
                                                  Design df       =          31
```

| | Coefficient | Linearized std. err. | t | P>\|t\| | [95% conf. | interval] |
|---|---|---|---|---|---|---|
| H5_health | | | | | | |
| female | -.1615219 | .0523678 | -3.08 | 0.004 | -.2683267 | -.054717 |
| black | -.986568 | .0790277 | -12.48 | 0.000 | -1.147746 | -.8253899 |
| age | -.0119491 | .0082974 | -1.44 | 0.160 | -.0288717 | .0049736 |
| c.age#c.age | -.0003234 | .000091 | -3.55 | 0.001 | -.000509 | -.0001377 |
| /H5 | | | | | | |
| cut1 | -4.566229 | .1632561 | | | -4.899192 | -4.233266 |
| cut2 | -3.057415 | .1699944 | | | -3.404121 | -2.710709 |
| cut3 | -1.520596 | .1714342 | | | -1.870239 | -1.170954 |
| cut4 | -.242785 | .1703965 | | | -.590311 | .104741 |
| H3_health3 | | | | | | |
| female | -.1551238 | .0563809 | -2.75 | 0.010 | -.2701133 | -.0401342 |
| black | -1.046316 | .0728274 | -14.37 | 0.000 | -1.194849 | -.8977836 |
| age | -.0365408 | .0073653 | -4.96 | 0.000 | -.0515624 | -.0215192 |
| c.age#c.age | -.00009 | .0000791 | -1.14 | 0.264 | -.0002512 | .0000713 |
| /H3 | | | | | | |
| cut1 | -3.655498 | .1610211 | | | -3.983903 | -3.327093 |
| cut2 | -2.109584 | .1597057 | | | -2.435306 | -1.783862 |

The coefficients of H3 and H5 look rather similar. We now use `test` to perform a formal Hausman-type test for the hypothesis that the regression coefficients are indeed the same, as we would expect if there is indeed a one-dimensional latent dimension for health. Thus we test that the coefficients in the equation H5_health are equal to those in H3_health3.

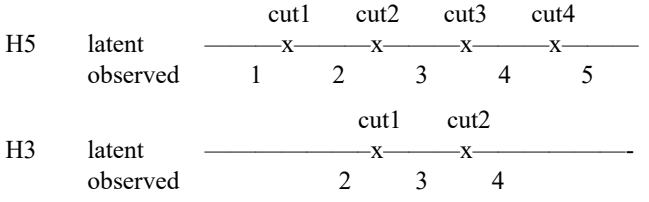
```
. test [H5_health=H3_health3]

Adjusted Wald test

 ( 1)  [H5_health]female - [H3_health3]female = 0
 ( 2)  [H5_health]black - [H3_health3]black = 0
 ( 3)  [H5_health]age - [H3_health3]age = 0
 ( 4)  [H5_health]c.age#c.age - [H3_health3]c.age#c.age = 0

       F(  4,    28) =   17.13
            Prob > F =    0.0000
```

We can reject the null hypothesis, which indicates that the ordered logistic regression model is indeed misspecified. Another specification test can be conducted with respect to the cutpoints. Variable `health3` was constructed from `health` by collapsing the two worst categories into value 2 and the two best categories into value 4. This action effectively has removed two cutpoints, but if the model fits the data, it should not affect the other two cutpoints. The comparison is hampered by a difference in the names of the cutpoints between the models, as illustrated in the figure below:




Cutpoint `/cut2` of model `H5` should be compared with cutpoint `/cut1` of `H3`, and similarly, `/cut3` of `H5` with `/cut2` of `H3`.

```
. test (/H5:cut2=/H3:cut1) (/H5:cut3=/H3:cut2)
Adjusted Wald test
 ( 1)  [/H5]cut2 - [/H3]cut1 = 0
 ( 2)  [/H5]cut3 - [/H3]cut2 = 0
       F(  2,    30) =   33.49
            Prob > F =    0.0000
```

We conclude that the invariance of the cutpoints under the collapse of categories is not supported by the data, again providing evidence against the reduced specification of the ordered logistic model in this case.

◁

## ▷ Example 9: Using suest with survey data, the svy option

Not all estimation commands support the `svy` prefix, but you can use the `svy` option with `suest` to get survey estimation results. If you can use `suest` after a command, you can use `suest, svy`. Here are the corresponding Stata commands to perform the analysis in the previous example, using the `svy` option instead of the `svy` prefix.

```
. use https://www.stata-press.com/data/r19/nhanes2f, clear
. svyset psuid [pw=finalwgt], strata(stratid)
. ologit health female black age c.age#c.age [iw=finalwgt]
. estimates store H5
. generate health3 = clip(health,2,4)
. ologit health3 female black age c.age#c.age [iw=finalwgt]
. estimates store H3
. suest H5 H3, svy
. test [H5_health=H3_health3]
. test (/H5:cut2=/H3:cut1) (/H5:cut3=/H3:cut2)
```

The calls to `ologit` now use `iweights` instead of the `svy` prefix, and the `svy` option was added to `suest`. No other changes are required.

◁

## References

Eltinge, J. L., and W. M. Sribney. 1996. svy5: Estimates of linear combinations and hypothesis tests for survey data. *Stata Technical Bulletin* 31: 31–42. Reprinted in *Stata Technical Bulletin Reprints*, vol. 6, pp. 246–259. College Station, TX: Stata Press.

Graubard, B. I., and E. L. Korn. 2004. Predictive margins with survey data. *Biometrics* 55: 652–659. https://doi.org/10.1111/j.0006-341X.1999.00652.x.

Korn, E. L., and B. I. Graubard. 1990. Simultaneous testing of regression coefficients with complex survey data: Use of Bonferroni $t$ statistics. *American Statistician* 44: 270–276. https://doi.org/10.2307/2684345.

McDowell, A., A. Engel, J. T. Massey, and K. Maurer. 1981. "Plan and operation of the Second National Health and Nutrition Examination Survey, 1976–1980". In *Vital and Health Statistics*, ser. 1, no. 15. Hyattsville, MD: National Center for Health Statistics.

## Also see

[SVY] **svy** — The survey prefix command

[SVY] **estat** — Postestimation statistics for survey data

[SVY] **svy bootstrap** — Bootstrap for survey data

[SVY] **svy brr** — Balanced repeated replication for survey data

[SVY] **svy estimation** — Estimation commands for survey data

[SVY] **svy jackknife** — Jackknife estimation for survey data

[SVY] **svy sdr** — Successive difference replication for survey data

**[U] 13.5 Accessing coefficients and standard errors**

**[U] 20 Estimation and postestimation commands**

**svy sdr** — Successive difference replication for survey data



## Description

`svy sdr` performs successive difference replication (SDR) estimation of specified statistics (or expressions) for a Stata command or a user-written program. The command is executed once for each replicate using sampling weights that are adjusted according to the SDR methodology. Any Stata estimation command listed in [SVY] **svy estimation** may be used with `svy sdr`. User-written programs that meet the requirements in [P] **program properties** may also be used.

## Quick start

Estimate population mean of `v1` using SDR standard-error estimates with sampling weight `wvar1` and replicate weights in variables with prefix `rwvar`

```
svyset [pweight=wvar1], sdrweight(rwvar*)
svy sdr _b: mean v1
```

Same as above

```
svyset [pweight=wvar1], sdrweight(rwvar*) vce(sdr)
svy: mean v1
```

SDR estimate of the standard error of the difference between the means of `v2` and `v3` using either `svyset` command above

```
svy sdr (_b[v2]-_b[v3]): mean v2 v3
```

Same as above, but name the result `diff` and save results from each replication to `mydata.dta`

```
svy sdr diff=(_b[v2]-_b[v3]), saving(mydata): mean v2 v3
```

Same as above

```
sdr diff=(_b[v2]-_b[v3]), saving(mydata): mean v2 v3
```

Note: Any estimation command meeting the requirements specified in the *Description* may be substituted for `mean` in the examples above.

## Menu

Statistics > Survey data analysis > Resampling > Successive difference replications estimation

# Syntax

[ svy ] sdr *exp_list* [ , *svy_options sdr_options eform_option* ] : *command*

| *svy_options* | Description |
|---|---|
| **if/in** | |
| subpop( [ *varname* ] [ *if* ] ) | identify a subpopulation |
| **Reporting** | |
| level(#) | set confidence level; default is level(95) |
| noheader | suppress table header |
| nolegend | suppress table legend |
| noadjust | do not adjust model Wald statistic |
| nocnsreport | do not display constraints |
| *display_options* | control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling |
| coeflegend | display legend instead of statistics |

coeflegend is not shown in the dialog boxes for estimation commands.

| *sdr_options* | Description |
|---|---|
| **Options** | |
| saving( *filename* [ , ... ] ) | save results to *filename*; save statistics in double precision; save results to *filename* every # replications |
| mse | use MSE formula for variance |
| **Reporting** | |
| verbose | display the full table legend |
| nodots | suppress replication dots |
| dots(#) | display dots every # replications |
| noisily | display any output from *command* |
| trace | trace *command* |
| title(*text*) | use *text* as title for SDR results |
| **Advanced** | |
| nodrop | do not drop observations |
| reject(*exp*) | identify invalid results |
| dof(#) | design degrees of freedom |

svy requires that the survey design variables be identified using svyset; see [SVY] **svyset**.

*command* defines the statistical command to be executed. The by prefix cannot be part of *command*.

collect is allowed; see **[U] 11.1.10 Prefix commands**.

See **[U] 20 Estimation and postestimation commands** for more capabilities of estimation commands.

Warning: Using if or in restrictions will often not produce correct variance estimates for subpopulations. To compute estimates for subpopulations, use the subpop() option.

svy sdr requires that the successive difference replicate weights be identified using svyset.

*exp_list* specifies the statistics to be collected from the execution of *command*. *exp_list* is required unless *command* has the `svyb` program property, in which case *exp_list* defaults to `_b`; see [P] **program properties**. The expressions in *exp_list* are assumed to conform to the following:

| | |
|---|---|
| *exp_list* contains | (*name*: *elist*) |
| | *elist* |
| | *eexp* |
| *elist* contains | *newvarname* = (*exp*) |
| | (*exp*) |
| *eexp* is | *specname* |
| | [*eqno*]*specname* |
| *specname* is | `_b` |
| | `_b[]` |
| | `_se` |
| | `_se[]` |
| *eqno* is | `#` # |
| | *name* |

*exp* is a standard Stata expression; see **[U] 13 Functions and expressions**.

Distinguish between `[]`, which are to be typed, and [ ], which indicate optional arguments.

## Options

*svy_options*; see [SVY] **svy**.

### Options

`saving(`*filename*[ , *suboptions* ]`)` creates a Stata data file (`.dta` file) consisting of (for each statistic in *exp_list*) a variable containing the replicates.

`double` specifies that the results for each replication be stored as `doubles`, meaning 8-byte reals. By default, they are stored as `floats`, meaning 4-byte reals. This option may be used without the `saving()` option to compute the variance estimates by using double precision.

`every(#)` specifies that results be written to disk every #th replication. `every()` should be specified in conjunction with `saving()` only when *command* takes a long time for each replication. This will allow recovery of partial results should some other software crash your computer. See [P] **postfile**.

`replace` specifies that *filename* be overwritten if it exists. This option does not appear in the dialog box.

`mse` specifies that `svy sdr` compute the variance by using deviations of the replicates from the observed value of the statistics based on the entire dataset. By default, `svy sdr` computes the variance by using deviations of the replicates from their mean.

### Reporting

`verbose` requests that the full table legend be displayed.

`nodots` and `dots(#)` specify whether to display replication dots. By default, one dot character is displayed for each successful replication. An "x" is displayed if *command* returns an error, and an "e" is displayed if at least one value in *exp_list* is missing. You can also control whether dots are displayed using `set dots`; see [R] **set**.

`nodots` suppresses display of the replication dots.

`dots(#)` displays dots every # replications. `dots(0)` is a synonym for `nodots`.

`noisily` requests that any output from *command* be displayed. This option implies the `nodots` option.

`trace` causes a trace of the execution of *command* to be displayed. This option implies the `noisily` option.

`title(`*text*`)` specifies a title to be displayed above the table of SDR results; the default title is "SDR results".

*eform_option*; see [R] ***eform_option***. This option is ignored if *exp_list* is not `_b`.

Advanced

`nodrop` prevents observations outside `e(sample)` and the `if` and `in` qualifiers from being dropped before the data are resampled.

`reject(`*exp*`)` identifies an expression that indicates when results should be rejected. When *exp* is true, the resulting values are reset to missing values.

`dof(#)` specifies the design degrees of freedom, overriding the default calculation, $\text{df} = N_{\text{psu}} - N_{\text{strata}}$.

## Remarks and examples

SDR was first introduced by Fay and Train (1995) as a method of variance estimation for annual demographic supplements to the Current Population Survey (CPS). In SDR, the model is fit multiple times, once for each of a set of adjusted sampling weights. The variance is estimated using the resulting replicated point estimates.

### ▷ Example 1

The US Census Bureau publishes public-use data from several of its surveys. These data can be downloaded from https://factfinder.census.gov. We downloaded the American Community Survey (ACS) Public Use Microdata Sample (PUMS) data collected in 2007. We extracted data for the state of Texas and kept the variables containing age, sex, and sampling weight for each person in the dataset. This sample dataset also contains 80 SDR weight variables.

```
. use https://www.stata-press.com/data/r19/ss07ptx
. svyset
Sampling weights: pwgtp
             VCE: sdr
             MSE: off
     SDR weights: pwgtp1 .. pwgtp80
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: <observations>
           FPC 1: <zero>
```

This dataset was already `svyset` as

```
. svyset [pw=pwgtp], sdrweight(pwgtp1-pwgtp80) vce(sdr)
```

Here we estimate the average age of the males and of the females for our Texas subpopulation. The standard errors are estimated using SDR.

```
. svy: mean agep, over(sex)
(running mean on estimation sample)
SDR replications (80): .........10.........20.........30.........40.........50..
> .......60.........70.........80 done
Survey: Mean estimation           Number of obs   =    230,817
                                  Population size = 23,904,380
                                  Replications    =         80
```

| | SDR | | | |
|---|---|---|---|---|
| | Mean | std. err. | [95% conf. | interval] |
| c.agep@sex | | | | |
| Male | 33.24486 | .0470986 | 33.15255 | 33.33717 |
| Female | 35.23908 | .0386393 | 35.16335 | 35.31481 |

◁

## ❑ Technical note

When the `svy sdr` prefix is used with a user-defined program and when the expression list is `_b`, `svy sdr` calls

```
set coeftabresults off
```

before entering the replication loop to prevent Stata from performing unnecessary calculations. This means that, provided option `noisily` is not specified, estimation commands will not build or post the coefficient table matrix `r(table)`.

If your program calls an estimation command and needs `r(table)` to exist to perform properly, then your program will need to call

```
set coeftabresults on
```

before calling other estimation commands.

❑

## Stored results

In addition to the results documented in [SVY] **svy**, `svy sdr` stores the following in `e()`:

Scalars

| | |
|---|---|
| `e(N_reps)` | number of replications |
| `e(N_misreps)` | number of replications with missing values |
| `e(k_exp)` | number of standard expressions |
| `e(k_eexp)` | number of `_b`/`_se` expressions |
| `e(k_extra)` | number of extra estimates added to `_b` |

Macros

| | |
|---|---|
| `e(cmdname)` | command name from *command* |
| `e(cmd)` | same as `e(cmdname)` or `sdr` |
| `e(vce)` | `sdr` |
| `e(exp#)` | #th expression |
| `e(sdrweight)` | `sdrweight()` variable list |

Matrices

| | |
|---|---|
| `e(b_sdr)` | SDR means |
| `e(V)` | SDR variance estimates |

When *exp_list* is `_b`, `svy sdr` will also carry forward most of the results already in `e()` from *command*.

## Methods and formulas

See [SVY] **Variance estimation** for details regarding SDR variance estimation.

## Reference

Fay, R. E., and G. F. Train. 1995. "Aspects of survey and model-based postcensal estimation of income and poverty characteristics for states and counties". In *Proceedings of the Government Statistics Section*, 154–159. American Statistical Association.

## Also see

[SVY] **svy postestimation** — Postestimation tools for svy

[SVY] **svy bootstrap** — Bootstrap for survey data

[SVY] **svy brr** — Balanced repeated replication for survey data

[SVY] **svy jackknife** — Jackknife estimation for survey data

[SVY] **Calibration** — Calibration for survey data

[SVY] **Poststratification** — Poststratification for survey data

[SVY] **Subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **Variance estimation** — Variance estimation for survey data

**[U] 20 Estimation and postestimation commands**

**svy: tabulate oneway** — One-way tables for survey data



## Description

`svy: tabulate` produces one-way tabulations for complex survey data. See [SVY] **svy: tabulate twoway** for two-way tabulations for complex survey data.

## Quick start

One-way table showing weighted proportions for categories of `v1` using `svyset` data

```
svy: tabulate v1
```

Add 95% confidence intervals and weighted counts

```
svy: tabulate v1, ci count
```

Same as above, and display large counts in a more readable format

```
svy: tabulate v1 ci count format(%11.3g)
```

Unweighted numbers of observations and weighted proportions for categories of `v2`

```
svy: tabulate v2, obs
```

Weighted proportions and CIs for categories of `v3` in the subpopulation defined by `v4` $>$ 40

```
svy, subpop(if v4>40): tabulate v3, ci
```

## Menu

Statistics > Survey data analysis > Tables > One-way tables

# Syntax

*Basic syntax*

```
svy: tabulate varname
```

*Full syntax*

```
svy [vcetype] [ , svy_options ] : tabulate varname [if] [in]
    [ , tabulate_options display_items display_options ]
```

*Syntax to report results*

```
svy [ , display_items display_options ]
```

| *vcetype* | Description |
|---|---|
| SE | |
| `linearized` | Taylor-linearized variance estimation |
| `bootstrap` | bootstrap variance estimation; see [SVY] **svy bootstrap** |
| `brr` | BRR variance estimation; see [SVY] **svy brr** |
| `jackknife` | jackknife variance estimation; see [SVY] **svy jackknife** |
| `sdr` | SDR variance estimation; see [SVY] **svy sdr** |

Specifying a *vcetype* overrides the default from `svyset`.

| *svy_options* | Description |
|---|---|
| if/in | |
| `subpop(`[*varname*] [*if*]`)` | identify a subpopulation |
| SE | |
| *bootstrap_options* | more options allowed with bootstrap variance estimation; see [SVY] ***bootstrap_options*** |
| *brr_options* | more options allowed with BRR variance estimation; see [SVY] ***brr_options*** |
| *jackknife_options* | more options allowed with jackknife variance estimation; see [SVY] ***jackknife_options*** |
| *sdr_options* | more options allowed with SDR variance estimation; see [SVY] ***sdr_options*** |

`svy` requires that the survey design variables be identified using `svyset`; see [SVY] **svyset**.

See **[U] 20 Estimation and postestimation commands** for more capabilities of estimation commands.

Warning: Using `if` or `in` restrictions will often not produce correct variance estimates for subpopulations. To compute estimates for subpopulations, use the `subpop()` option.

| *tabulate_options* | Description |
|---|---|
| Model | |
| `stdize(`*varname*`)` | variable identifying strata for standardization |
| `stdweight(`*varname*`)` | weight variable for standardization |
| `tab(`*varname*`)` | variable for which to compute cell totals/proportions |
| `missing` | treat missing values like other values |
| Collect | |
| `collect` | post results to collection `Tabulate` |
| `collect(`[ *cname* ][ , *collect_options* ]`)` | post results to a named collection |

| *collect_options* | Description |
|---|---|
| `append` | append results to an existing collection |
| `replace` | replace results of an existing collection |
| `label(`*filename*`)` | specify the collection labels |
| `style(`*filename*[ , `override` ]`)` | specify the collection style |

| *display_items* | Description |
|---|---|
| Table items | |
| `cell` | cell proportions |
| `count` | weighted cell counts |
| `se` | standard errors |
| `ci` | confidence intervals |
| `deff` | display the DEFF design effects |
| `deft` | display the DEFT design effects |
| `cv` | display the coefficient of variation |
| `srssubpop` | report design effects assuming SRS within subpopulation |
| `obs` | cell observations |

When any of `se`, `ci`, `deff`, `deft`, `cv`, or `srssubpop` is specified, only one of `cell` or `count` can be specified. If none of `se`, `ci`, `deff`, `deft`, `cv`, or `srssubpop` is specified, both `cell` and `count` can be specified.

| *display_options* | Description |
|---|---|
| Reporting | |
| `level(#)` | set confidence level; default is `level(95)` |
| `proportion` | display proportions; the default |
| `percent` | display percentages instead of proportions |
| `nomarginal` | suppress column marginal |
| `nolabel` | suppress displaying value labels |
| `cellwidth(#)` | cell width |
| `csepwidth(#)` | column-separation width |
| `stubwidth(#)` | stub width |
| `format(`*%fmt*`)` | cell format; default is `format(%6.0g)` |

`proportion` is not shown in the dialog box.

## Options

*svy_options*; see [SVY] **svy**.

Model

`stdize(`*varname*`)` specifies that the point estimates be adjusted by direct standardization across the strata identified by *varname*. This option requires the `stdweight()` option.

`stdweight(`*varname*`)` specifies the weight variable associated with the standard strata identified in the `stdize()` option. The standardization weights must be constant within the standard strata.

`tab(`*varname*`)` specifies that counts be cell totals of this variable and that proportions (or percentages) be relative to (that is, weighted by) this variable. For example, if this variable denotes income, then the cell "counts" are instead totals of income for each cell, and the cell proportions are proportions of income for each cell.

`missing` specifies that missing values of *varname* be treated as another row category rather than be omitted from the analysis (the default).

Collect

`collect` and `collect(`[ *cname* ][ `,` *collect_options* ]`)` specify that results be posted to a collection. This collection produces a table that you can customize and publish to Microsoft Word, Microsoft Excel, PDF, HTML, LaTeX, SMCL, or Markdown. Output does not change when these options are specified. Use `collect preview` to see the customizeable table.

`collect` is a shortcut for `collect(Tabulate)`.

*cname* specifies that a collection named *cname* be associated with the collected results. The default is `Tabulate`.

`append` specifies that results be appended to collection *cname*.

`replace` permits `tabulate` to overwrite an existing collection. This option is implied for collection `Tabulate` when `append` is not specified.

`label(`*filename*`)` specifies the *filename* containing the collection labels to use for your table. Labels in *filename* will be loaded into the collection, and any labels not specified in *filename* will be taken from the labels defined in `c(collect_label)`. The default is to use only the collection labels set in `c(collect_label)`; see [TABLES] **set collect_label**.

`style(`*filename*[ `, override` ]`)` specifies the *filename* containing the collection styles to use for your table. The default collection styles will be discarded, and only the collection styles in *filename* will be applied.

If you prefer the default collection styles but also want to apply any styles in *filename*, specify `override`. If there are conflicts between the default collection styles and those in *filename*, the ones in *filename* will take precedence.

The default is to use only the collection styles set in `c(tabulate_style)`; see [TABLES] **set tabulate_style**.

Table items

`cell` requests that cell proportions (or percentages) be displayed. This is the default if `count` is not specified.

`count` requests that weighted cell counts be displayed.

`se` requests that the standard errors of cell proportions (the default) or weighted counts be displayed. When `se` (or `ci`, `deff`, `deft`, or `cv`) is specified, only one of `cell` or `count` can be selected. The standard error computed is the standard error of the one selected.

`ci` requests confidence intervals for cell proportions or weighted counts.

`deff` and `deft` request that the design-effect measures DEFF and DEFT be displayed for each cell proportion or weighted count. See [SVY] **estat** for details.

The `deff` and `deft` options are not allowed with estimation results that used direct standardization or poststratification.

`cv` requests that the coefficient of variation be displayed for each cell proportion, count, or row or column proportion. See [SVY] **estat** for details.

`srssubpop` requests that DEFF and DEFT be computed using an estimate of SRS (simple random sampling) variance for sampling within a subpopulation. By default, DEFF and DEFT are computed using an estimate of the SRS variance for sampling from the entire population. Typically, `srssubpop` would be given when computing subpopulation estimates by strata or by groups of strata.

`obs` requests that the number of observations for each cell be displayed.

Reporting

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see **[U] 20.8 Specifying the width of confidence intervals**.

`proportion`, the default, requests that proportions be displayed.

`percent` requests that percentages be displayed instead of proportions.

`nomarginal` requests that the column marginal not be displayed.

`nolabel` requests that variable labels and value labels be ignored.

`cellwidth(#)`, `csepwidth(#)`, and `stubwidth(#)` specify widths of table elements in the output; see [P] **tabdisp**. Acceptable values for the `stubwidth()` option range from 4 to 32.

`format(%`*fmt*`)` specifies a format for the items in the table. The default is `format(%6.0g)`. See **[U] 12.5 Formats: Controlling how data are displayed**.

`svy: tabulate` uses the `tabdisp` command (see [P] **tabdisp**) to produce the table. Only five items can be displayed in the table at one time. The `ci` option implies two items. If too many items are selected, a warning will appear immediately. To view more items, redisplay the table while specifying different options.

# Remarks and examples

Remarks are presented under the following headings:



## Introduction

Despite the long list of options for `svy: tabulate`, it is a simple command to use. Using the `svy: tabulate` command is just like using `tabulate` to produce one-way tables for ordinary data. The main difference is that `svy: tabulate` computes standard errors appropriate for complex survey data.

Standard errors and confidence intervals can optionally be displayed for weighted counts or cell proportions. The confidence intervals for proportions are constructed using a logit transform so that their endpoints always lie between 0 and 1; see [SVY] **svy: tabulate twoway**. Associated design effects (DEFF and DEFT) can be viewed for the variance estimates.

### ▷ Example 1

Here we use `svy: tabulate` to estimate the distribution of the `race` category variable from our NHANES II dataset (McDowell et al. 1981). Before calling `svy: tabulate`, we use `svyset` to declare the survey structure of the data.

```
. use https://www.stata-press.com/data/r19/nhanes2b
. svyset psuid [pweight=finalwgt], strata(stratid)
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: stratid
 Sampling unit 1: psuid
           FPC 1: <zero>
. svy: tabulate race
(running tabulate on estimation sample)
Number of strata = 31                         Number of obs    =      10,351
Number of PSUs   = 62                         Population size = 117,157,513
                                              Design df       =          31

------------------------
     Race | proportion
----------+-------------
    White |       .8792
    Black |       .0955
    Other |       .0253
          |
    Total |          1
------------------------
Key: proportion = Cell proportion
```

Here we display weighted counts for each category of `race` along with the 95% confidence bounds, as well as the design effects DEFF and DEFT. We also use the `format()` option to improve the look of the table.

```
. svy: tabulate race, format(%11.3g) count ci deff deft
(running tabulate on estimation sample)
Number of strata = 31                         Number of obs   =      10,351
Number of PSUs   = 62                         Population size = 117,157,513
                                              Design df       =          31
```

| Race | count | lb | ub | deff | deft |
|---|---|---|---|---|---|
| White | 102999549 | 97060400 | 108938698 | 60.2 | 7.76 |
| Black | 11189236 | 8213964 | 14164508 | 18.6 | 4.31 |
| Other | 2968728 | 414930 | 5522526 | 47.9 | 6.92 |
| Total | 117157513 | | | | |

```
Key:    count = Weighted count
           lb = Lower 95% confidence bound for weighted count
           ub = Upper 95% confidence bound for weighted count
         deff = DEFF for variance of weighted count
         deft = DEFT for variance of weighted count
```

From the above results, we can conclude with 95% confidence that the number of people in the population that fall within the `White` category is between 97,060,400 and 108,938,698.

## Publish your tables

With the `collect` option, `svy: tabulate` posts the tabulated values to a collection named `Tabulate` and sets it as the current collection. With collections, you can customize the look of your table and then publish it to HTML, Word, LaTeX, PDF, Excel, or another format appropriate for your report.

If you are not familiar with collections, see [TABLES] **Intro**. The predefined styles for `svy: tabulate` are documented in [TABLES] **Predefined styles**.

## ▷ Example 2

Building on the table from the previous example, let's add the `collect` option to produce a collection with our tabulated values.

```
. svy: tabulate race, format(%11.3g) count ci deff deft collect
(running tabulate on estimation sample)
Number of strata = 31                         Number of obs   =      10,351
Number of PSUs   = 62                         Population size = 117,157,513
                                              Design df       =          31
```

| Race | count | lb | ub | deff | deft |
|---|---|---|---|---|---|
| White | 102999549 | 97060400 | 108938698 | 60.2 | 7.76 |
| Black | 11189236 | 8213964 | 14164508 | 18.6 | 4.31 |
| Other | 2968728 | 414930 | 5522526 | 47.9 | 6.92 |
| Total | 117157513 | | | | |

```
Key:    count = Weighted count
           lb = Lower 95% confidence bound for weighted count
           ub = Upper 95% confidence bound for weighted count
         deff = DEFF for variance of weighted count
         deft = DEFT for variance of weighted count
```

The output does not change; however, we can use the `collect dir` command to see that `svy: tabulate` created a collection named `Tabulate`.

```
. collect dir
Collections in memory
Current: Tabulate
```

| Name | No. items |
|---|---|
| Tabulate | 16 |

In this collection, weighted counts are tagged with `result[count]`; the confidence bounds are tagged with `result[_r_lb]` and `result[_r_ub]`; DEFF values are tagged with `result[deff]`; and DEFT values are tagged with `result[deft]`. Here we use `collect label list` to show the levels and labels of the `result` dimension.

```
. collect label list result
  Collection: Tabulate
   Dimension: result
       Label: Result
Level labels:
       _r_lb  Lower __LEVEL__% CI bound
       _r_ub  Upper __LEVEL__% CI bound
       count  Weighted count
        deff  DEFF
        deft  DEFT
```

When specified, the other table items are similarly tagged: proportions are tagged with `result[proportion]`, percentages with `result[percent]`, standard errors with `result[se]`, coefficients of variation with `result[cv]`, and the numbers of observations with `result[obs]`.

The tabulated variable (that is, race) is added to the collection as a dimension and is used to tag the collected results. In addition to the name, label, level values, and value labels of the tabulated variable, this dimension also has the __margCode__ level with the Total label for tagging the table items for the entire sample. Here we use collect label list to show the levels and labels of the dimension for the tabulated variable.

```
. collect label list race
  Collection: Tabulate
   Dimension: race
       Label: Race
Level labels:
           1  White
           2  Black
           3  Other
__margCode__  Total
```

svy: tabulate constructs a default layout, so you can view your customizable table with the collect preview command. Here we use the collect layout command to report the default layout specification and corresponding table.

```
. collect layout
Collection: Tabulate
      Rows: cmdset#race
   Columns: result
   Table 1: 5 x 5
```

| | Weighted count | Lower 95% CI bound | Upper 95% CI bound | DEFF | DEFT |
|---|---|---|---|---|---|
| Race | | | | | |
| White | 102,999,549 | 97,060,400 | 108,938,698 | 60.187 | 7.758 |
| Black | 11,189,236 | 8,213,964 | 14,164,508 | 18.577 | 4.310 |
| Other | 2,968,728 | 414,930 | 5,522,526 | 47.870 | 6.919 |
| Total | 117,157,513 | | | | |

We can make further changes to the table with the collect suite of commands. But we are happy with this layout and ready to publish the table to a PDF file with collect export. We simply specify the filename to which we want to export it.

```
. collect export table1.pdf
(collection Tabulate exported to file table1.pdf)
```

With collect export, you can publish the table to several formats, such as HTML, PDF, and LaTeX files, by specifying the appropriate file extension.

◁

## Stored results

In addition to the results documented in [SVY] **svy**, `svy: tabulate` stores the following in `e()`:

Scalars

| | |
|---|---|
| `e(r)` | number of rows |
| `e(total)` | weighted sum of `tab()` variable |

Macros

| | |
|---|---|
| `e(cmd)` | `tabulate` |
| `e(tab)` | `tab()` variable |
| `e(rowlab)` | `label` or empty |
| `e(rowvlab)` | row variable label |
| `e(rowvar)` | *varname*, the row variable |
| `e(setype)` | `cell` or `count` |

Matrices

| | |
|---|---|
| `e(Prop)` | matrix of cell proportion |
| `e(Obs)` | matrix of observation count |
| `e(Deff)` | DEFF vector for `e(setype)` items |
| `e(Deft)` | DEFT vector for `e(setype)` items |
| `e(Row)` | values for row variable |
| `e(V_row)` | variance for row totals |
| `e(V_srs_row)` | $V_{srs}$ for row totals |
| `e(Deff_row)` | DEFF for row totals |
| `e(Deft_row)` | DEFT for row totals |

## Methods and formulas

See *Methods and formulas* in [SVY] **svy: tabulate twoway** for a discussion of how table items and confidence intervals are computed. A one-way table is really just a two-way table that has one row or column.

Margaret E. Martin (1912–2012) is best known for her work developing the US Current Population Survey (CPS). Martin was born in New York City and had an early love for mathematics. She received a bachelor's degree in economics from Barnard College and went on to earn an MA and a PhD in economics from Columbia University. Martin began her career in the midst of the Great Depression, working for a New Deal agency in New York to classify employers covered by the unemployment insurance system. Despite having the third highest score on the qualifying civil service exam, she almost did not take the job because she "had been trained by economists primarily, and they had a very low opinion of government work".

Her work in New York allowed her to later move to the US Bureau of Budget (now the Office of Management and Budget), where she joined the team that developed the CPS. The majority of Martin's work focused on the CPS, a survey of employment and demographics among US households. She worked to explain differences in previous unemployment survey results derived from sampling businesses. She also oversaw an effort to improve the reliability of information from the CPS by adding questions that addressed labor-force participation and the use of paid and unpaid leave. Today, the CPS is a continuous monthly survey and the primary source of information about characteristics of the US labor force.

In 1973, Martin became the first executive director of the National Academy of Sciences' Committee on National Statistics. She was elected president of the American Statistical Association (ASA) in 1980 and was the first recipient of the ASA's Founders Award.

## Reference

McDowell, A., A. Engel, J. T. Massey, and K. Maurer. 1981. "Plan and operation of the Second National Health and Nutrition Examination Survey, 1976–1980". In *Vital and Health Statistics*, ser. 1, no. 15. Hyattsville, MD: National Center for Health Statistics.

## Also see

[SVY] **svy postestimation** — Postestimation tools for svy

[SVY] **svy** — The survey prefix command

[SVY] **svy: tabulate twoway** — Two-way tables for survey data

[SVY] **svydescribe** — Describe survey data

[SVY] **Calibration** — Calibration for survey data

[SVY] **Direct standardization** — Direct standardization of means, proportions, and ratios

[SVY] **Poststratification** — Poststratification for survey data

[SVY] **Subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **Variance estimation** — Variance estimation for survey data

[R] **tabulate oneway** — One-way table of frequencies

**[U] 20 Estimation and postestimation commands**

**svy: tabulate twoway** — Two-way tables for survey data



## Description

`svy: tabulate` produces two-way tabulations with tests of independence for complex survey data. See [SVY] **svy: tabulate oneway** for one-way tabulations for complex survey data.

## Quick start

Two-way table of weighted cell proportions for `v1` and `v2` using `svyset` data

```
svy: tabulate v1 v2
```

Same as above, but with a test of independence using Pearson's $\chi^2$ statistic with and without correction for the complex design

```
svy: tabulate v1 v2, pearson
```

Within-row and within-column proportions

```
svy: tabulate v1 v2, row column
```

95% confidence intervals for within-column proportions

```
svy: tabulate v1 v2, column ci
```

Unweighted numbers of observations and weighted counts

```
svy: tabulate v1 v2, obs count
```

Same as above, but display large counts in a more readable format

```
svy: tabulate v1 v2, obs count format(%11.0fc)
```

Weighted counts in the subpopulation defined by `v3` $> 0$

```
svy, subpop(v3): tabulate v1 v2, count
```

## Menu

Statistics > Survey data analysis > Tables > Two-way tables

# Syntax

*Basic syntax*

```
svy: tabulate varname1 varname2
```

*Full syntax*

```
svy [vcetype] [ , svy_options ] : tabulate varname1 varname2 [if] [in]
    [ , tabulate_options display_items display_options statistic_options ]
```

*Syntax to report results*

```
svy [ , display_items display_options statistic_options ]
```

| *vcetype* | Description |
|---|---|
| SE | |
| `linearized` | Taylor-linearized variance estimation |
| `bootstrap` | bootstrap variance estimation; see [SVY] **svy bootstrap** |
| `brr` | BRR variance estimation; see [SVY] **svy brr** |
| `jackknife` | jackknife variance estimation; see [SVY] **svy jackknife** |
| `sdr` | SDR variance estimation; see [SVY] **svy sdr** |

Specifying a *vcetype* overrides the default from `svyset`.

| *svy_options* | Description |
|---|---|
| if/in | |
| `subpop(`[ *varname* ] [ *if* ]`)` | identify a subpopulation |
| SE | |
| *bootstrap_options* | more options allowed with bootstrap variance estimation; see [SVY] ***bootstrap_options*** |
| *brr_options* | more options allowed with BRR variance estimation; see [SVY] ***brr_options*** |
| *jackknife_options* | more options allowed with jackknife variance estimation; see [SVY] ***jackknife_options*** |
| *sdr_options* | more options allowed with SDR variance estimation; see [SVY] ***sdr_options*** |

`svy` requires that the survey design variables be identified using `svyset`; see [SVY] **svyset**.

See **[U] 20 Estimation and postestimation commands** for more capabilities of estimation commands.

Warning: Using `if` or `in` restrictions will often not produce correct variance estimates for subpopulations. To compute estimates for subpopulations, use the `subpop()` option.

| *tabulate_options* | Description |
|---|---|
| Model | |
| stdize(*varname*) | variable identifying strata for standardization |
| stdweight(*varname*) | weight variable for standardization |
| tab(*varname*) | variable for which to compute cell totals/proportions |
| missing | treat missing values like other values |
| Collect | |
| collect | post results to collection Tabulate |
| collect([*cname*][, *collect_options*]) | post results to a named collection |

| *collect_options* | Description |
|---|---|
| append | append results to an existing collection |
| replace | replace results of an existing collection |
| label(*filename*) | specify the collection labels |
| style(*filename*[, override]) | specify the collection style |

| *display_items* | Description |
|---|---|
| Table items | |
| cell | cell proportions |
| count | weighted cell counts |
| column | within-column proportions |
| row | within-row proportions |
| se | standard errors |
| ci | confidence intervals |
| deff | display the DEFF design effects |
| deft | display the DEFT design effects |
| cv | display the coefficient of variation |
| srssubpop | report design effects assuming SRS within subpopulation |
| obs | cell observations |

When any of se, ci, deff, deft, cv, or srssubpop is specified, only one of cell, count, column, or row can be specified. If none of se, ci, deff, deft, cv, or srssubpop is specified, any of or all cell, count, column, and row can be specified.

| *display_options* | Description |
|---|---|
| Reporting | |
| level(#) | set confidence level; default is level(95) |
| proportion | display proportions; the default |
| percent | display percentages instead of proportions |
| vertical | stack confidence interval endpoints vertically |
| nomarginals | suppress row and column marginals |
| nolabel | suppress displaying value labels |
| notable | suppress displaying the table |
| cellwidth(#) | cell width |
| csepwidth(#) | column-separation width |
| stubwidth(#) | stub width |
| format(%*fmt*) | cell format; default is format(%6.0g) |

proportion and notable are not shown in the dialog box.

| *statistic_options* | Description |
|---|---|
| Test statistics | |
| pearson | Pearson's $\chi^2$ |
| lr | likelihood ratio |
| null | display null-based statistics |
| wald | adjusted Wald |
| llwald | adjusted log-linear Wald |
| noadjust | report unadjusted Wald statistics |

## Options

*svy_options*; see [SVY] **svy**.

Model

stdize(*varname*) specifies that the point estimates be adjusted by direct standardization across the strata identified by *varname*. This option requires the stdweight() option.

stdweight(*varname*) specifies the weight variable associated with the standard strata identified in the stdize() option. The standardization weights must be constant within the standard strata.

tab(*varname*) specifies that counts be cell totals of this variable and that proportions (or percentages) be relative to (that is, weighted by) this variable. For example, if this variable denotes income, the cell "counts" are instead totals of income for each cell, and the cell proportions are proportions of income for each cell.

missing specifies that missing values of $varname_1$ and $varname_2$ be treated as another row or column category rather than be omitted from the analysis (the default).

Collect

`collect` and `collect(`[ *cname* ][ `,` *collect_options* ]`)` specify that results be posted to a collection. This collection produces a table that you can customize and publish to Microsoft Word, Microsoft Excel, PDF, HTML, LaTeX, SMCL, or Markdown. Output does not change when these options are specified. Use `collect preview` to see the customizeable table.

`collect` is a shortcut for `collect(Tabulate)`.

*cname* specifies that a collection named *cname* be associated with the collected results. The default is `Tabulate`.

`append` specifies that results be appended to collection *cname*.

`replace` permits `tabulate` to overwrite an existing collection. This option is implied for collection `Tabulate` when `append` is not specified.

`label(`*filename*`)` specifies the *filename* containing the collection labels to use for your table. Labels in *filename* will be loaded into the collection, and any labels not specified in *filename* will be taken from the labels defined in `c(collect_label)`. The default is to use only the collection labels set in `c(collect_label)`; see [TABLES] **set collect_label**.

`style(`*filename*[ `, override` ]`)` specifies the *filename* containing the collection styles to use for your table. The default collection styles will be discarded, and only the collection styles in *filename* will be applied.

If you prefer the default collection styles but also want to apply any styles in *filename*, specify `override`. If there are conflicts between the default collection styles and those in *filename*, the ones in *filename* will take precedence.

The default is to use only the collection styles set in `c(tabulate_style)`; see [TABLES] **set tabulate_style**.

Table items

`cell` requests that cell proportions (or percentages) be displayed. This is the default if none of `count`, `row`, or `column` is specified.

`count` requests that weighted cell counts be displayed.

`column` or `row` requests that column or row proportions (or percentages) be displayed.

`se` requests that the standard errors of cell proportions (the default), weighted counts, or row or column proportions be displayed. When `se` (or `ci`, `deff`, `deft`, or `cv`) is specified, only one of `cell`, `count`, `row`, or `column` can be selected. The standard error computed is the standard error of the one selected.

`ci` requests confidence intervals for cell proportions, weighted counts, or row or column proportions. The confidence intervals are constructed using a logit transform so that their endpoints always lie between 0 and 1.

`deff` and `deft` request that the design-effect measures DEFF and DEFT be displayed for each cell proportion, count, or row or column proportion. See [SVY] **estat** for details. The mean generalized DEFF is also displayed when `deff`, `deft`, or `subpop` is requested; see *Methods and formulas* for an explanation.

The `deff` and `deft` options are not allowed with estimation results that used direct standardization or poststratification.

`cv` requests that the coefficient of variation be displayed for each cell proportion, count, or row or column proportion. See [SVY] **estat** for details.

`srssubpop` requests that DEFF and DEFT be computed using an estimate of SRS (simple random sampling) variance for sampling within a subpopulation. By default, DEFF and DEFT are computed using an estimate of the SRS variance for sampling from the entire population. Typically, `srssubpop` would be given when computing subpopulation estimates by strata or by groups of strata.

`obs` requests that the number of observations for each cell be displayed.

Reporting

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see **[U] 20.8 Specifying the width of confidence intervals**.

`proportion`, the default, requests that proportions be displayed.

`percent` requests that percentages be displayed instead of proportions.

`vertical` requests that the endpoints of confidence intervals be stacked vertically on display.

`nomarginals` requests that row and column marginals not be displayed.

`nolabel` requests that variable labels and value labels be ignored.

`notable` prevents the header and table from being displayed in the output. When specified, only the results of the requested test statistics are displayed. This option may not be specified with any other option in *display_options* except the `level()` option.

`cellwidth(#)`, `csepwidth(#)`, and `stubwidth(#)` specify widths of table elements in the output; see [P] **tabdisp**. Acceptable values for the `stubwidth()` option range from 4 to 32.

`format(%`*fmt*`)` specifies a format for the items in the table. The default is `format(%6.0g)`. See **[U] 12.5 Formats: Controlling how data are displayed**.

Test statistics

`pearson` requests that the Pearson $\chi^2$ statistic be computed. By default, this is the test of independence that is displayed. The Pearson $\chi^2$ statistic is corrected for the survey design with the second-order correction of Rao and Scott (1984) and is converted into an $F$ statistic. One term in the correction formula can be calculated using either observed cell proportions or proportions under the null hypothesis (that is, the product of the marginals). By default, observed cell proportions are used. If the `null` option is selected, then a statistic corrected using proportions under the null hypothesis is displayed as well.

`lr` requests that the likelihood-ratio test statistic for proportions be computed. This statistic is not defined when there are one or more zero cells in the table. The statistic is corrected for the survey design by using the same correction procedure that is used with the `pearson` statistic. Again either observed cell proportions or proportions under the null hypothesis can be used in the correction formula. By default, the former is used; specifying the `null` option gives both the former and the latter. Neither variant of this statistic is recommended for sparse tables. For nonsparse tables, the `lr` statistics are similar to the corresponding `pearson` statistics.

`null` modifies the `pearson` and `lr` options only. If `null` is specified, two corrected statistics are displayed. The statistic labeled "D-B (null)" ("D-B" stands for design-based) uses proportions under the null hypothesis (that is, the product of the marginals) in the Rao and Scott (1984) correction. The statistic labeled merely "Design-based" uses observed cell proportions. If `null` is not specified, only the correction that uses observed proportions is displayed.

`wald` requests a Wald test of whether observed weighted proportions equal the product of the marginals (Koch, Freeman, and Freeman 1975). By default, an adjusted $F$ statistic is produced; an unadjusted statistic can be produced by specifying `noadjust`. The unadjusted $F$ statistic can yield extremely anticonservative $p$-values (that is, $p$-values that are too small) when the degrees of freedom of the variance estimates (the number of sampled PSUs minus the number of strata) are small relative to the $(R-1)(C-1)$ degrees of freedom of the table (where $R$ is the number of rows and $C$ is the number of columns). Hence, the statistic produced by `wald` and `noadjust` should not be used for inference unless it is essentially identical to the adjusted statistic.

This option must be specified at run time to be used on subsequent calls to `svy` to report results.

`llwald` requests a Wald test of the log-linear model of independence (Koch, Freeman, and Freeman 1975). The statistic is not defined when there are one or more zero cells in the table. The adjusted statistic (the default) can produce anticonservative $p$-values, especially for sparse tables, when the degrees of freedom of the variance estimates are small relative to the degrees of freedom of the table. Specifying `noadjust` yields a statistic with more severe problems. Neither the adjusted nor the unadjusted statistic is recommended for inference; the statistics are made available only for pedagogical purposes.

`noadjust` modifies the `wald` and `llwald` options only. It requests that an unadjusted $F$ statistic be displayed in addition to the adjusted statistic.

`svy: tabulate` uses the `tabdisp` command (see [P] **tabdisp**) to produce the table. Only five items can be displayed in the table at one time. The `ci` option implies two items. If too many items are selected, a warning will appear immediately. To view more items, redisplay the table while specifying different options.

# Remarks and examples

Remarks are presented under the following headings:



## Introduction

Despite the long list of options for `svy: tabulate`, it is a simple command to use. Using the `svy: tabulate` command is just like using `tabulate` to produce two-way tables for ordinary data. The main difference is that `svy: tabulate` computes a test of independence that is appropriate for complex survey data.

The test of independence that is displayed by default is based on the usual Pearson $\chi^2$ statistic for two-way tables. To account for the survey design, the statistic is turned into an $F$ statistic with noninteger degrees of freedom by using a second-order Rao and Scott (1981, 1984) correction. Although the theory behind the Rao and Scott correction is complicated, the $p$-value for the corrected $F$ statistic can be interpreted in the same way as a $p$-value for the Pearson $\chi^2$ statistic for "ordinary" data (that is, data that are assumed independent and identically distributed [i.i.d.]).

svy: tabulate, in fact, computes four statistics for the test of independence with two variants of each, for a total of eight statistics. The option combination for each of the eight statistics are the following:

1. pearson (the default)
2. pearson null
3. lr
4. lr null
5. wald
6. wald noadjust
7. llwald
8. llwald noadjust

The wald and llwald options with noadjust yield the statistics developed by Koch, Freeman, and Freeman (1975), which have been implemented in the CROSSTAB procedure of the SUDAAN software (Research Triangle Institute 1997 , release 7.5).

These eight statistics, along with other variants, have been evaluated in simulations (Sribney 1998). On the basis of these simulations, we advise researchers to use the default statistic (the pearson option) in all situations. We recommend that the other statistics be used only for comparative or pedagogical purposes. Sribney (1998) gives a detailed comparison of the statistics; a summary of his conclusions is provided later in this entry.

Other than the test-statistic options (*statistic_options*) and the survey design options (*svy_options*), most of the other options of svy: tabulate simply relate to different choices for what can be displayed in the body of the table. By default, cell proportions are displayed, but viewing either row or column proportions or weighted counts usually makes more sense.

Standard errors and confidence intervals can optionally be displayed for weighted counts or cell, row, or column proportions. The confidence intervals for proportions are constructed using a logit transform so that their endpoints always lie between 0 and 1. Associated design effects (DEFF and DEFT) can be viewed for the variance estimates. The mean generalized DEFF (Rao and Scott 1984) is also displayed when option deff, deft, or srssubpop is specified. The mean generalized DEFF is essentially a design effect for the asymptotic distribution of the test statistic; see the *Methods and formulas* section at the end of this entry.

## Example 1

Using data from the Second National Health and Nutrition Examination Survey (NHANES II) (McDowell et al. 1981), we identify the survey design characteristics with `svyset` and then produce a two-way table of cell proportions with `svy: tabulate`.

```
. use https://www.stata-press.com/data/r19/nhanes2b
. svyset psuid [pweight=finalwgt], strata(stratid)
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: stratid
 Sampling unit 1: psuid
           FPC 1: <zero>
. svy: tabulate race diabetes
(running tabulate on estimation sample)
Number of strata = 31                         Number of obs    =      10,349
Number of PSUs   = 62                         Population size = 117,131,111
                                              Design df        =          31
```

| Race | Diabetes status: Not diab | Diabetic | Total |
|---|---|---|---|
| White | .851 | .0281 | .8791 |
| Black | .0899 | .0056 | .0955 |
| Other | .0248 | 5.2e-04 | .0253 |
| Total | .9658 | .0342 | 1 |

```
Key: Cell proportion
  Pearson:
    Uncorrected   chi2(2)         =   21.3483
    Design-based  F(1.52, 47.26)  =   15.0056     P = 0.0000
```

The default table displays only cell proportions, and this makes it difficult to compare the incidence of diabetes in white, black, and "other" racial groups. It would be better to look at row proportions. This can be done by redisplaying the results (that is, reissuing the command without specifying any variables) with the `row` option.

```
. svy: tabulate, row
Number of strata = 31                         Number of obs    =      10,349
Number of PSUs   = 62                         Population size = 117,131,111
                                              Design df        =          31
```

| Race | Diabetes status: Not diab | Diabetic | Total |
|---|---|---|---|
| White | .968 | .032 | 1 |
| Black | .941 | .059 | 1 |
| Other | .9797 | .0203 | 1 |
| Total | .9658 | .0342 | 1 |

```
Key: Row proportion
  Pearson:
    Uncorrected   chi2(2)         =   21.3483
    Design-based  F(1.52, 47.26)  =   15.0056     P = 0.0000
```

This table is much easier to interpret. A larger proportion of blacks have diabetes than do whites or persons in the "other" racial category. The test of independence for a two-way contingency table is equivalent to the test of homogeneity of row (or column) proportions. Hence, we can conclude that there is a highly significant difference between the incidence of diabetes among the three racial groups.

We may now wish to compute confidence intervals for the row proportions. If we try to redisplay, specifying `ci` along with `row`, we get the following result:

```
. svy: tabulate, row ci
confidence intervals are only available for cells
    To compute row confidence intervals, rerun command with row and ci options.
r(111);
```

There are limits to what `svy: tabulate` can redisplay. Basically, any of the options relating to variance estimation (that is, `se`, `ci`, `deff`, and `deft`) must be specified at run time along with the single item (that is, `count`, `cell`, `row`, or `column`) for which you want standard errors, confidence intervals, DEFF, or DEFT. So to get confidence intervals for row proportions, we must rerun the command. We do so below, requesting not only `ci` but also `se`.

```
. svy: tabulate race diabetes, row se ci format(%7.4f)
(running tabulate on estimation sample)
Number of strata = 31                          Number of obs    =      10,349
Number of PSUs   = 62                          Population size = 117,131,111
                                               Design df       =          31
```

| Race | Diabetes status: Not diab | Diabetic | Total |
|---|---|---|---|
| White | 0.9680 | 0.0320 | 1.0000 |
| | (0.0020) | (0.0020) | |
| | [0.9638,0.9718] | [0.0282,0.0362] | |
| Black | 0.9410 | 0.0590 | 1.0000 |
| | (0.0061) | (0.0061) | |
| | [0.9271,0.9523] | [0.0477,0.0729] | |
| Other | 0.9797 | 0.0203 | 1.0000 |
| | (0.0076) | (0.0076) | |
| | [0.9566,0.9906] | [0.0094,0.0434] | |
| Total | 0.9658 | 0.0342 | 1.0000 |
| | (0.0018) | (0.0018) | |
| | [0.9619,0.9693] | [0.0307,0.0381] | |

```
Key: Row proportion
     (Linearized standard error of row proportion)
     [95% confidence interval for row proportion]

  Pearson:
    Uncorrected   chi2(2)         =   21.3483
    Design-based  F(1.52, 47.26)  =   15.0056     P = 0.0000
```

In the above table, we specified a `%7.4f` format rather than using the default `%6.0g` format. The single format applies to every item in the table. We can omit the marginal totals by specifying `nomarginals`. If the above style for displaying the confidence intervals is obtrusive—and it can be in a wider table—we can use the `vertical` option to stack the endpoints of the confidence interval, one over the other, and omit the brackets (the parentheses around the standard errors are also omitted when `vertical` is specified). To express results as percentages, as with the `tabulate` command (see [R] **tabulate twoway**), we can

use the percent option. Or we can play around with these display options until we get a table that we are satisfied with, first making changes to the options on redisplay (that is, omitting the cross-tabulated variables when we issue the command).

◁

## ❑ Technical note

The standard errors computed by svy: tabulate are the same as those produced by svy: mean, svy: proportion, and svy: ratio. Indeed, svy: tabulate uses these commands as subroutines to produce its table.

In the previous example, the estimate of the proportion of African Americans with diabetes (the second proportion in the second row of the preceding table) is simply a ratio estimate; hence, we can also obtain the same estimates by using svy: ratio:

```
. drop black
. generate black = (race==2) if !missing(race)
. generate diablk = diabetes*black
(2 missing values generated)
. svy: ratio diablk/black
(running ratio on estimation sample)
Survey: Ratio estimation
Number of strata = 31            Number of obs    =      10,349
Number of PSUs   = 62            Population size = 117,131,111
                                 Design df       =          31
     _ratio_1: diablk/black
```

| | Ratio | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| _ratio_1 | .0590349 | .0061443 | .0465035 | .0715662 |

Although the standard errors are the same, the confidence intervals are slightly different. The svy: tabulate command produced the confidence interval $[0.0477, 0.0729]$, and svy: ratio gave $[0.0465, 0.0716]$. The difference is because svy: tabulate uses a logit transform to produce confidence intervals whose endpoints are always between 0 and 1. This transformation also shifts the confidence intervals slightly toward 0.5, which is beneficial because the untransformed confidence intervals tend to be, on average, biased away from 0.5. See *Methods and formulas* for details.

❑

### ▷ Example 2: The tab() option

The `tab()` option allows us to compute proportions relative to a certain variable. Suppose that we wish to compare the proportion of total income among different racial groups in males with that of females. We do so below with fictitious data:

```
. use https://www.stata-press.com/data/r19/svy_tabopt, clear
. svy: tabulate gender race, tab(income) row
(running tabulate on estimation sample)
Number of strata = 31                        Number of obs    =      10,351
Number of PSUs   = 62                        Population size = 117,157,513
                                             Design df       =          31
```

| Gender | Race: White | Black | Other | Total |
|---|---|---|---|---|
| Male | .8857 | .0875 | .0268 | 1 |
| Female | .884 | .094 | .022 | 1 |
| Total | .8848 | .0909 | .0243 | 1 |

```
  Tabulated variable:  income
Key: Row proportion
  Pearson:
    Uncorrected   chi2(2)         =    3.6241
    Design-based  F(1.91, 59.12)  =    0.8626     P = 0.4227
```

◁

## The Rao and Scott correction

`svy: tabulate` can produce eight different statistics for the test of independence. By default, `svy: tabulate` displays the Pearson $\chi^2$ statistic with the Rao and Scott (1981, 1984) second-order correction. On the basis of simulations Sribney (1998), we recommend that you use this statistic in all situations. The statistical literature, however, contains several alternatives, along with other possibilities for implementing the Rao and Scott correction. Hence, for comparative or pedagogical purposes, you may want to view some of the other statistics computed by `svy: tabulate`. This section briefly describes the differences among these statistics; for a more detailed discussion, see Sribney (1998).

Two statistics commonly used for i.i.d. data for the test of independence of $R \times C$ tables ($R$ rows and $C$ columns) are the Pearson $\chi^2$ statistic

$$X^2_{\text{P}} = m \sum_{r=1}^{R} \sum_{c=1}^{C} (\hat{p}_{rc} - \hat{p}_{0rc})^2 / \hat{p}_{0rc}$$

and the likelihood-ratio $\chi^2$ statistic

$$X^2_{\text{LR}} = 2m \sum_{r=1}^{R} \sum_{c=1}^{C} \hat{p}_{rc} \ln (\hat{p}_{rc}/\hat{p}_{0rc})$$

where $m$ is the total number of sampled individuals, $\hat{p}_{rc}$ is the estimated proportion for the cell in the $r$th row and $c$th column of the table, and $\hat{p}_{0rc}$ is the estimated proportion under the null hypothesis of independence; that is, $\hat{p}_{0rc} = \hat{p}_{r\cdot}\hat{p}_{\cdot c}$, the product of the row and column marginals: $\hat{p}_{r\cdot} = \sum_{c=1}^{C} \hat{p}_{rc}$ and $\hat{p}_{\cdot c} = \sum_{r=1}^{R} \hat{p}_{rc}$.

For i.i.d. data, both these statistics are distributed asymptotically as $\chi^2_{(R-1)(C-1)}$. The likelihood-ratio statistic is not defined when one or more of the cells in the table are empty. The Pearson statistic, however, can be calculated when one or more cells in the table are empty—the statistic may not have good properties in this case, but the statistic still has a computable value.

For survey data, $X^2_{\text{P}}$ and $X^2_{\text{LR}}$ can be computed using weighted estimates of $\hat{p}_{rc}$ and $\hat{p}_{0rc}$. However, for a complex sampling design, one can no longer claim that they are distributed as $\chi^2_{(R-1)(C-1)}$, but you can estimate the variance of $\hat{p}_{rc}$ under the sampling design. For instance, in Stata, this variance can be estimated via linearization methods by using `svy: mean` or `svy: ratio`.

Rao and Scott (1981, 1984) derived the asymptotic distribution of $X^2_{\text{P}}$ and $X^2_{\text{LR}}$ in terms of the variance of $\hat{p}_{rc}$. Unfortunately, the result (see (1) in *Methods and formulas*) is not computationally feasible, but it can be approximated using correction formulas. `svy: tabulate` uses the second-order correction developed by Rao and Scott (1984). By default, or when the `pearson` option is specified, `svy: tabulate` displays the second-order correction of the Pearson statistic. The `lr` option gives the second-order correction of the likelihood-ratio statistic. Because it is the default of `svy: tabulate`, the correction computed with $\hat{p}_{rc}$ is referred to as the default correction.

The Rao and Scott papers, however, left some details outstanding about the computation of the correction. One term in the correction formula can be computed using either $\hat{p}_{rc}$ or $\hat{p}_{0rc}$. Because under the null hypothesis both are asymptotically equivalent, theory offers no guidance about which is best. By default, `svy: tabulate` uses $\hat{p}_{rc}$ for the corrections of the Pearson and likelihood-ratio statistics. If the `null` option is specified, the correction is computed using $\hat{p}_{0rc}$. For nonsparse tables, these two correction methods yield almost identical results. However, in simulations of sparse tables, Sribney (1998) found that the null-corrected statistics were extremely anticonservative for $2 \times 2$ tables (that is, under the null, "significance" was declared too often) and were too conservative for other tables. The default correction, however, had better properties. Hence, we do not recommend using `null`.

For the computational details of the Rao and Scott–corrected statistics, see *Methods and formulas*.

## Wald statistics

Prior to the work by Rao and Scott (1981, 1984), Wald tests for the test of independence for two-way tables were developed by Koch, Freeman, and Freeman (1975). Two Wald statistics have been proposed. The first, similar to the Pearson statistic, is based on

$$\hat{Y}_{rc} = \widehat{N}_{rc} - \widehat{N}_{r\cdot}\widehat{N}_{\cdot c}/\widehat{N}_{\cdot\cdot}$$

where $\widehat{N}_{rc}$ is the estimated weighted count for the $r$, $c$th cell. The delta method can be used to approximate the variance of $\hat{Y}_{rc}$, and a Wald statistic can be calculated as usual. A second Wald statistic can be constructed based on a log-linear model for the table. Like the likelihood-ratio statistic, this statistic is undefined when there is a zero proportion in the table.

These Wald statistics are initially $\chi^2$ statistics, but they have better properties when converted into $F$ statistics with denominator degrees of freedom that account for the degrees of freedom of the variance estimator. They can be converted to $F$ statistics in two ways.

One method is the standard manner: divide by the $\chi^2$ degrees of freedom $d_0 = (R-1)(C-1)$ to get an $F$ statistic with $d_0$ numerator degrees of freedom and $\nu = n - L$ denominator degrees of freedom. This is the form of the $F$ statistic suggested by Koch, Freeman, and Freeman (1975) and implemented in the CROSSTAB procedure of the SUDAAN software (Research Triangle Institute 1997 , release 7.5), and it is the method used by `svy: tabulate` when the `noadjust` option is specified with `wald` or `llwald`.

Another technique is to adjust the $F$ statistic by using

$$F_{\text{adj}} = (\nu - d_0 + 1)W/(\nu d_0) \qquad \text{with} \qquad F_{\text{adj}} \sim F(d_0, \nu - d_0 + 1)$$

This is the default adjustment for `svy: tabulate. test` and the other `svy` estimation commands produce adjusted $F$ statistics by default, using the same adjustment procedure. See Korn and Graubard (1990) for a justification of the procedure.

The adjusted $F$ statistic is identical to the unadjusted $F$ statistic when $d_0 = 1$, that is, for $2 \times 2$ tables.

As Thomas and Rao (1987) point out (also see Korn and Graubard [1990]), the unadjusted $F$ statistics can become extremely anticonservative as $d_0$ increases when $\nu$ is small or moderate; that is, under the null, the statistics are "significant" far more often than they should be. Because the unadjusted statistics behave so poorly for larger tables when $\nu$ is not large, their use can be justified only for small tables or when $\nu$ is large. But when the table is small or when $\nu$ is large, the unadjusted statistic is essentially identical to the adjusted statistic. Hence, for statistical inference, looking at the unadjusted statistics has no point.

The adjusted "Pearson" Wald $F$ statistic usually behaves reasonably under the null. However, even the adjusted $F$ statistic for the log-linear Wald test tends to be moderately anticonservative when $\nu$ is not large (Thomas and Rao 1987 ; Sribney 1998 ).

## ▷ Example 3

With the NHANES II data, we tabulate, for the male subpopulation, high blood pressure (highbp) versus a variable (sizplace) that indicates the degree of urbanity/ruralness. We request that all eight statistics for the test of independence be displayed.

```
. use https://www.stata-press.com/data/r19/nhanes2b
. generate male = (sex==1) if !missing(sex)
. svy, subpop(male): tabulate highbp sizplace, col obs pearson lr null wald
> llwald noadj
(running tabulate on estimation sample)
Number of strata = 31                        Number of obs    =      10,351
Number of PSUs   = 62                        Population size = 117,157,513
                                             Subpop. no. obs =       4,915
                                             Subpop. size    =  56,159,480
                                             Design df       =          31
```

| High blood pressure | 1=urban, ..., 8=rural 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | Total |
|---|---|---|---|---|---|---|---|---|---|
| 0 | .4949 | .5884 | .6768 | .5308 | .5563 | .629 | .5502 | .5618 | .5724 |
| | 241 | 326 | 381 | 228 | 121 | 135 | 186 | 993 | 2611 |
| 1 | .5051 | .4116 | .3232 | .4692 | .4437 | .371 | .4498 | .4382 | .4276 |
| | 285 | 281 | 241 | 217 | 101 | 95 | 185 | 899 | 2304 |
| Total | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| | 526 | 607 | 622 | 445 | 222 | 230 | 371 | 1892 | 4915 |

```
Key: Column proportion
     Number of observations
  Pearson:
    Uncorrected   chi2(7)         =  114.9556
    D-B (null)    F(5.33, 165.13) =    2.1460     P = 0.0584
    Design-based  F(5.48, 169.80) =    2.4281     P = 0.0325
  Likelihood ratio:
    Uncorrected   chi2(7)         =  116.5144
    D-B (null)    F(5.33, 165.13) =    2.1751     P = 0.0552
    Design-based  F(5.48, 169.80) =    2.4610     P = 0.0305
  Wald (Pearson):
    Unadjusted    chi2(7)         =   11.1739
    Unadjusted    F(7, 31)        =    1.5963     P = 0.1735
    Adjusted      F(7, 25)        =    1.2873     P = 0.2967
  Wald (log-linear):
    Unadjusted    chi2(7)         =   14.9598
    Unadjusted    F(7, 31)        =    2.1371     P = 0.0688
    Adjusted      F(7, 25)        =    1.7235     P = 0.1490
```

The $p$-values from the null-corrected Pearson and likelihood-ratio statistics (lines labeled "D-B (null)"; "D-B" stands for "design-based") are bigger than the corresponding default-corrected statistics (lines labeled "Design-based"). Simulations (Sribney 1998) show that the null-corrected statistics are overly conservative for many sparse tables (except $2 \times 2$ tables); this appears to be the case here, although this table is hardly sparse. The default-corrected Pearson statistic has good properties under the null for both sparse and nonsparse tables; hence, the smaller $p$-value for it should be considered reliable.

The default-corrected likelihood-ratio statistic is usually similar to the default-corrected Pearson statistic except for sparse tables, when it tends to be anticonservative. This example follows this pattern, with its $p$-value being slightly smaller than that of the default-corrected Pearson statistic.

For tables of these dimensions ($2 \times 8$), the unadjusted "Pearson" Wald and log-linear Wald $F$ statistics are extremely anticonservative under the null when the variance degrees of freedom is small. Here the variance degrees of freedom is only 31 (62 PSUs minus 31 strata), so we expect that the unadjusted Wald $F$ statistics yield smaller $p$-values than the adjusted $F$ statistics. Because of their poor behavior under the null for small variance degrees of freedom, they cannot be trusted here. Simulations show that although the adjusted "Pearson" Wald $F$ statistic has good properties under the null, it is often less powerful than the default Rao and Scott–corrected statistics. That is probably the explanation for the larger $p$-value for the adjusted "Pearson" Wald $F$ statistic than that for the default-corrected Pearson and likelihood-ratio statistics.

The $p$-value for the adjusted log-linear Wald $F$ statistic is about the same as that for the trustworthy default-corrected Pearson statistic. However, that is probably because of the anticonservatism of the log-linear Wald under the null balancing out its lower power under alternative hypotheses.

The "uncorrected" $\chi^2$ Pearson and likelihood-ratio statistics displayed in the table are misspecified statistics; that is, they are based on an i.i.d. assumption, which is not valid for complex survey data. Hence, they are not correct, even asymptotically. The "unadjusted" Wald $\chi^2$ statistics, on the other hand, are completely different. They are valid asymptotically as the variance degrees of freedom becomes large.

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## Properties of the statistics

This section briefly summarizes the properties of the eight statistics computed by `svy: tabulate`. For details, see Sribney (1998), Rao and Thomas (1989), Thomas and Rao (1987), and Korn and Graubard (1990).

`pearson` is the Rao and Scott (1984) second-order corrected Pearson statistic, computed using $\hat{p}_{rc}$ in the correction (default correction). It is displayed by default. Simulations show it to have good properties under the null for both sparse and nonsparse tables. Its power is similar to that of the `lr` statistic in most situations. It often appears to be more powerful than the adjusted "Pearson" Wald $F$ statistic (`wald` option), especially for larger tables. We recommend using this statistic in all situations.

`pearson null` is the Rao and Scott second-order corrected Pearson statistic, computed using $\hat{p}_{0rc}$ in the correction. It is numerically similar to the `pearson` statistic for nonsparse tables. For sparse tables, it can be erratic. Under the null, it can be anticonservative for sparse $2 \times 2$ tables but conservative for larger sparse tables.

`lr` is the Rao and Scott second-order corrected likelihood-ratio statistic, computed using $\hat{p}_{rc}$ in the correction (default correction). The correction is identical to that for `pearson`. It is numerically similar to the `pearson` statistic for nonsparse tables. It can be anticonservative ($p$-values too small) in sparse tables. If there is a zero cell, it cannot be computed.

`lr null` is the Rao and Scott second-order corrected likelihood-ratio statistic, computed using $\hat{p}_{0rc}$ in the correction. The correction is identical to that for `pearson null`. It is numerically similar to the `lr` statistic for nonsparse tables. For sparse tables, it can be overly conservative. If there is a zero cell, it cannot be computed.

`wald` statistic is the adjusted "Pearson" Wald $F$ statistic. It has good properties under the null for nonsparse tables. It can be erratic for sparse $2 \times 2$ tables and some sparse large tables. The `pearson` statistic often appears to be more powerful.

`wald noadjust` is the unadjusted "Pearson" Wald $F$ statistic. It can be extremely anticonservative under the null when the table degrees of freedom (number of rows minus one times the number of columns minus one) approaches the variance degrees of freedom (number of sampled PSUs minus the number of strata). It is the same as the adjusted `wald` statistic for $2 \times 2$ tables. It is similar to the adjusted `wald` statistic for small tables, large variance degrees of freedom, or both.

`llwald` statistic is the adjusted log-linear Wald $F$ statistic. It can be anticonservative for both sparse and nonsparse tables. If there is a zero cell, it cannot be computed.

`llwald noadjust` statistic is the unadjusted log-linear Wald $F$ statistic. Like `wald noadjust`, it can be extremely anticonservative under the null when the table degrees of freedom approaches the variance degrees of freedom. It also suffers from the same general anticonservatism of the `llwald` statistic. If there is a zero cell, it cannot be computed.

## Publish your tables

With the `collect` option, `svy: tabulate` posts the tabulated values to a collection named `Tabulate` and sets it as the current collection. With collections, you can customize the look of your table and then publish it to HTML, Word, LaTeX, PDF, Excel, or another format appropriate for your report.

If you are not familiar with collections, see [TABLES] **Intro**. The predefined styles for `svy: tabulate` are documented in [TABLES] **Predefined styles**.

### ▷ Example 4

Recall the final table from example 1. Let's rerun that command but add the `collect` option to produce a collection with the reported values.

```
. svy: tabulate race diabetes, row se ci format(%7.4f) collect
(running tabulate on estimation sample)
Number of strata = 31                         Number of obs    =      10,349
Number of PSUs   = 62                         Population size = 117,131,111
                                              Design df        =          31
```

| Race | Diabetes status: Not diab | Diabetic | Total |
|---|---|---|---|
| White | 0.9680 | 0.0320 | 1.0000 |
| | (0.0020) | (0.0020) | |
| | [0.9638,0.9718] | [0.0282,0.0362] | |
| Black | 0.9410 | 0.0590 | 1.0000 |
| | (0.0061) | (0.0061) | |
| | [0.9271,0.9523] | [0.0477,0.0729] | |
| Other | 0.9797 | 0.0203 | 1.0000 |
| | (0.0076) | (0.0076) | |
| | [0.9566,0.9906] | [0.0094,0.0434] | |
| Total | 0.9658 | 0.0342 | 1.0000 |
| | (0.0018) | (0.0018) | |
| | [0.9619,0.9693] | [0.0307,0.0381] | |

```
Key: Row proportion
     (Linearized standard error of row proportion)
     [95% confidence interval for row proportion]

  Pearson:
    Uncorrected   chi2(2)         =   21.3483
    Design-based  F(1.52, 47.26)  =   15.0056     P = 0.0000
```

The output does not change; however, we can use the `collect dir` command to see that `svy: tabulate` created a collection named `Tabulate`.

```
. collect dir
Collections in memory
Current: Tabulate
──────────────────────
    Name   No. items
──────────────────────
Tabulate   42
 default   0
──────────────────────
```

In this collection, within-row proportions are tagged with `result[row_proportion]`, standard errors with `result[se]`, and confidence bounds with `result[_r_lb]` and `result[_r_ub]`. Here is a table of all *display_items* and their corresponding `result[`*level*`]` tag elements.

| *display_item* | *level* |
|---|---|
| cell proportion | proportion |
| cell percent | percent |
| weighted cell count | count |
| column proportion | column_proportion |
| column percent | column_percent |
| row proportion | row_proportion |
| row percent | row_percent |
| se | se |
| ci | _r_lb |
| | _r_ub |
| deff | deff |
| deft | deft |
| cv | cv |
| obs | obs |

The tabulated variables (that is, `race` and `diabetes`) are added to the collection as dimensions and are used to tag the collected results. In addition to the name, label, level values, and value labels of the tabulated variables, these dimensions also have the `__margCode__` level with the `Total` label for tagging the marginal values. Here we use `collect label list` to show the levels and labels of the dimension for each tabulated variable.

```
. collect label list race

  Collection: Tabulate
   Dimension: race
       Label: Race
Level labels:
           1  White
           2  Black
           3  Other
__margCode__  Total

. collect label list diabetes

  Collection: Tabulate
   Dimension: diabetes
       Label: Diabetes status
Level labels:
           0  Not diabetic
           1  Diabetic
__margCode__  Total
```

When tests of independence are reported, `svy: tabulate` uses a style that defines composite results for them. Each test of independence has a corresponding composite result that composes it in a single cell of a second table. Here is a table of all the tests and the corresponding name of the composite result.

| *statistic_options* | Description | Composite result |
|---|---|---|
| `pearson` | Uncorrected Pearson's $\chi^2$ | `UncorrectedPearson_ma` |
| `pearson` | Design-based Pearson's $F$ | `DesignbasedPearson_ma` |
| `pearson null` | Design-based (null) Pearson's $F$ | `DBnullPearson_ma` |
| `lr` | Uncorrected likelihood ratio $\chi^2$ | `UncorrectedLR_ma` |
| `lr` | Design-based likelihood ratio $F$ | `DesignbasedLR_ma` |
| `lr null` | Design-based (null) likelihood ratio $F$ | `DBnullLR_ma` |
| `wald` | Unadjusted Wald $\chi^2$ | `UnadjustedWaldX2_ma` |
| `wald` | Adjusted Wald $F$ | `AdjustedWaldF_ma` |
| `wald noadjust` | Unadjusted Wald $F$ | `UnadjustedWaldF_ma` |
| `llwald` | Unadjusted Wald (log-linear) $\chi^2$ | `UnadjustedLLWX2_ma` |
| `llwald` | Adjusted Wald (log-linear) $F$ | `AdjustedLLWF_ma` |
| `llwald noadjust` | Unadjusted Wald (log-linear) $F$ | `UnadjustedLLWF_ma` |

`svy: tabulate` constructs a default layout, so you can view your customizable table with the `collect preview` command. Here we use the `collect layout` command to report the default layout specification and corresponding table.

```
. collect layout

Collection: Tabulate
      Rows: race#result result
   Columns: diabetes _overall
    Tables: cmdset#item_type
   Table 1: 17 x 3
   Table 2: 2 x 1
```

| | Diabetes status | | |
|---|---|---|---|
| | Not diabetic | Diabetic | Total |
| Race | | | |
| White | | | |
| Row proportion | 0.9680 | 0.0320 | 1.0000 |
| Standard error | (0.0020) | (0.0020) | |
| 95% CI | [0.9638 0.9718] | [0.0282 0.0362] | |
| Black | | | |
| Row proportion | 0.9410 | 0.0590 | 1.0000 |
| Standard error | (0.0061) | (0.0061) | |
| 95% CI | [0.9271 0.9523] | [0.0477 0.0729] | |
| Other | | | |
| Row proportion | 0.9797 | 0.0203 | 1.0000 |
| Standard error | (0.0076) | (0.0076) | |
| 95% CI | [0.9566 0.9906] | [0.0094 0.0434] | |
| Total | | | |
| Row proportion | 0.9658 | 0.0342 | 1.0000 |
| Standard error | (0.0018) | (0.0018) | |
| 95% CI | [0.9619 0.9693] | [0.0307 0.0381] | |

```
                    Uncorrected Pearson χ²(2) = 21.3483
Design-based Pearson F(1.52, 47.26) = 15.0056 P = <0.0001
```

We can make further changes to the table with the `collect` suite of commands. But we are happy with this layout and ready to publish the table to an HTML file with `collect export`. We simply specify the filename to which we want to export it.

```
. collect export table2.html
(collection Tabulate exported to file table2.html)
```

With `collect export`, you can publish the table to several formats, such as HTML, PDF, and LaTeX files, by specifying the appropriate file extension.

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## Stored results

In addition to the results documented in [SVY] **svy**, `svy: tabulate` stores the following in `e()`:

Scalars

| | |
|---|---|
| `e(r)` | number of rows |
| `e(c)` | number of columns |
| `e(cvgdeff)` | coefficient of variation of generalized DEFF eigenvalues |
| `e(mgdeff)` | mean generalized DEFF |
| `e(total)` | weighted sum of `tab()` variable |
| `e(F_Pear)` | default-corrected Pearson $F$ |
| `e(F_Penl)` | null-corrected Pearson $F$ |
| `e(df1_Pear)` | numerator d.f. for `e(F_Pear)` |
| `e(df2_Pear)` | denominator d.f. for `e(F_Pear)` |
| `e(df1_Penl)` | numerator d.f. for `e(F_Penl)` |
| `e(df2_Penl)` | denominator d.f. for `e(F_Penl)` |
| `e(p_Pear)` | $p$-value for `e(F_Pear)` |
| `e(p_Penl)` | $p$-value for `e(F_Penl)` |
| `e(cun_Pear)` | uncorrected Pearson $\chi^2$ |
| `e(cun_Penl)` | null variant uncorrected Pearson $\chi^2$ |
| `e(F_LR)` | default-corrected likelihood-ratio $F$ |
| `e(F_LRnl)` | null-corrected likelihood-ratio $F$ |
| `e(df1_LR)` | numerator d.f. for `e(F_LR)` |
| `e(df2_LR)` | denominator d.f. for `e(F_LR)` |
| `e(df1_LRnl)` | numerator d.f. for `e(F_LRnl)` |
| `e(df2_LRnl)` | denominator d.f. for `e(F_LRnl)` |
| `e(p_LR)` | $p$-value for `e(F_LR)` |
| `e(p_LRnl)` | $p$-value for `e(F_LRnl)` |
| `e(cun_LR)` | uncorrected likelihood-ratio $\chi^2$ |
| `e(cun_LRnl)` | null variant uncorrected likelihood-ratio $\chi^2$ |
| `e(F_Wald)` | adjusted "Pearson" Wald $F$ |
| `e(F_LLW)` | adjusted log-linear Wald $F$ |
| `e(p_Wald)` | $p$-value for `e(F_Wald)` |
| `e(p_LLW)` | $p$-value for `e(F_LLW)` |
| `e(Fun_Wald)` | unadjusted "Pearson" Wald $F$ |
| `e(Fun_LLW)` | unadjusted log-linear Wald $F$ |
| `e(pun_Wald)` | $p$-value for `e(Fun_Wald)` |
| `e(pun_LLW)` | $p$-value for `e(Fun_LLW)` |
| `e(cun_Wald)` | unadjusted "Pearson" Wald $\chi^2$ |
| `e(cun_LLW)` | unadjusted log-linear Wald $\chi^2$ |

Macros

| | |
|---|---|
| `e(cmd)` | `tabulate` |
| `e(tab)` | `tab()` variable |
| `e(rowlab)` | label or empty |
| `e(collab)` | label or empty |
| `e(rowvlab)` | row variable label |

| | |
|---|---|
| `e(colvlab)` | column variable label |
| `e(rowvar)` | *varname*$_1$, the row variable |
| `e(colvar)` | *varname*$_2$, the column variable |
| `e(setype)` | `cell`, `count`, `column`, or `row` |

Matrices

| | |
|---|---|
| `e(Prop)` | matrix of cell proportions |
| `e(Obs)` | matrix of observation counts |
| `e(Deff)` | DEFF vector for `e(setype)` items |
| `e(Deft)` | DEFT vector for `e(setype)` items |
| `e(Row)` | values for row variable |
| `e(Col)` | values for column variable |
| `e(V_row)` | variance for row totals |
| `e(V_col)` | variance for column totals |
| `e(V_srs_row)` | $V_{srs}$ for row totals |
| `e(V_srs_col)` | $V_{srs}$ for column totals |
| `e(Deff_row)` | DEFF for row totals |
| `e(Deff_col)` | DEFF for column totals |
| `e(Deft_row)` | DEFT for row totals |
| `e(Deft_col)` | DEFT for column totals |

# Methods and formulas

Methods and formulas are presented under the following headings:



See *Coefficient of variation* under *Methods and formulas* of [SVY] **estat** for information on the coefficient of variation (the `cv` option).

## The table items

For a table of $R$ rows by $C$ columns with cells indexed by $r$, $c$, let

$$y_{(rc)j} = \begin{cases} 1 & \text{if the } j\text{th observation of the data is in the } r,c\text{th cell} \\ 0 & \text{otherwise} \end{cases}$$

where $j = 1, \ldots, m$ indexes individuals in the sample. Weighted cell counts (`count` option) are

$$\widehat{N}_{rc} = \sum_{j=1}^{m} w_j \, y_{(rc)j}$$

where $w_j$ is a sampling weight. If a variable, $x_j$, is specified with the `tab()` option, $\widehat{N}_{rc}$ becomes

$$\widehat{N}_{rc} = \sum_{j=1}^{m} w_j \, x_j \, y_{(rc)j}$$

Let

$$\widehat{N}_{r\cdot} = \sum_{c=1}^{C} \widehat{N}_{rc}\,, \qquad \widehat{N}_{\cdot c} = \sum_{r=1}^{R} \widehat{N}_{rc}\,, \qquad \text{and} \qquad \widehat{N}_{\cdot\cdot} = \sum_{r=1}^{R}\sum_{c=1}^{C} \widehat{N}_{rc}$$

Estimated cell proportions are $\hat{p}_{rc} = \widehat{N}_{rc}/\widehat{N}_{..}$; estimated row proportions (`row` option) are $\hat{p}_{\text{row}\,rc} = \widehat{N}_{rc}/\widehat{N}_{r.}$; estimated column proportions (`column` option) are $\hat{p}_{\text{col}\,rc} = \widehat{N}_{rc}/\widehat{N}_{.c}$; estimated row marginals are $\hat{p}_{r.} = \widehat{N}_{r.}/\widehat{N}_{..}$; and estimated column marginals are $\hat{p}_{.c} = \widehat{N}_{.c}/\widehat{N}_{..}$.

$\widehat{N}_{rc}$ is a total, the proportion estimators are ratios, and their variances can be estimated using linearization methods as outlined in [SVY] **Variance estimation**. `svy: tabulate` computes the variance estimates by using `svy: mean`, `svy: ratio`, and `svy: total`.

## Confidence intervals

Confidence intervals for proportions are calculated using a logit transform so that the endpoints lie between 0 and 1. Let $\hat{p}$ be an estimated proportion and $\hat{s}$ be an estimate of its standard error. Let

$$f(\hat{p}) = \ln\left(\frac{\hat{p}}{1-\hat{p}}\right)$$

be the logit transform of the proportion. In this metric, an estimate of the standard error is

$$\widehat{\text{SE}}\{f(\hat{p})\} = f'(\hat{p})\hat{s} = \frac{\hat{s}}{\hat{p}(1-\hat{p})}$$

Thus a $100(1-\alpha)\%$ confidence interval in this metric is

$$\ln\left(\frac{\hat{p}}{1-\hat{p}}\right) \pm \frac{t_{1-\alpha/2,\nu}\,\hat{s}}{\hat{p}(1-\hat{p})}$$

where $t_{1-\alpha/2,\nu}$ is the $(1-\alpha/2)$th quantile of Student's $t$ distribution with $\nu$ degrees of freedom. The endpoints of this confidence interval are transformed back to the proportion metric by using the inverse of the logit transform

$$f^{-1}(y) = \frac{e^y}{1+e^y}$$

Hence, the displayed confidence intervals for proportions are

$$f^{-1}\left\{\ln\left(\frac{\hat{p}}{1-\hat{p}}\right) \pm \frac{t_{1-\alpha/2,\nu}\,\hat{s}}{\hat{p}(1-\hat{p})}\right\}$$

Confidence intervals for weighted counts are untransformed and are identical to the intervals produced by `svy: total`.

## The test statistics

The uncorrected Pearson $\chi^2$ statistic is

$$X^2_{\text{P}} = m \sum_{r=1}^{R} \sum_{c=1}^{C} \left(\hat{p}_{rc} - \hat{p}_{0rc}\right)^2 / \hat{p}_{0rc}$$

and the uncorrected likelihood-ratio $\chi^2$ statistic is

$$X^2_{\text{LR}} = 2m \sum_{r=1}^{R} \sum_{c=1}^{C} \hat{p}_{rc} \ln\left(\hat{p}_{rc}/\hat{p}_{0rc}\right)$$

where $m$ is the total number of sampled individuals, $\hat{p}_{rc}$ is the estimated proportion for the cell in the $r$th row and $c$th column of the table as defined earlier, and $\hat{p}_{0rc}$ is the estimated proportion under the null hypothesis of independence; that is, $\hat{p}_{0rc} = \hat{p}_{r\cdot}\hat{p}_{\cdot c}$, the product of the row and column marginals.

Rao and Scott (1981, 1984) show that, asymptotically, $X^2_{\text{P}}$ and $X^2_{\text{LR}}$ are distributed as

$$X^2 \sim \sum_{k=1}^{(R-1)(C-1)} \delta_k W_k \tag{1}$$

where the $W_k$ are independent $\chi^2_1$ variables and the $\delta_k$ are the eigenvalues of

$$\Delta = (\widetilde{\mathbf{X}}_2' \mathbf{V}_{\text{srs}} \widetilde{\mathbf{X}}_2)^{-1} (\widetilde{\mathbf{X}}_2' \mathbf{V} \widetilde{\mathbf{X}}_2) \tag{2}$$

where $\mathbf{V}$ is the variance of the $\hat{p}_{rc}$ under the survey design and $\mathbf{V}_{\text{srs}}$ is the variance of the $\hat{p}_{rc}$ that you would have if the design were simple random sampling; namely, $\mathbf{V}_{\text{srs}}$ has diagonal elements $p_{rc}(1-p_{rc})/m$ and off-diagonal elements $-p_{rc}p_{st}/m$.

$\widetilde{\mathbf{X}}_2$ is calculated as follows. Rao and Scott do their development in a log-linear modeling context, so consider $[\,\mathbf{1} \mid \mathbf{X_1} \mid \mathbf{X_2}\,]$ as predictors for the cell counts of the $R \times C$ table in a log-linear model. The $\mathbf{X_1}$ matrix of dimension $RC \times (R + C - 2)$ contains the $R - 1$ "main effects" for the rows and the $C - 1$ "main effects" for the columns. The $\mathbf{X_2}$ matrix of dimension $RC \times (R-1)(C-1)$ contains the row and column "interactions". Hence, fitting $[\,\mathbf{1} \mid \mathbf{X}_1 \mid \mathbf{X}_2\,]$ gives the fully saturated model (that is, fits the observed values perfectly) and $[\,\mathbf{1} \mid \mathbf{X}_1\,]$ gives the independence model. The $\widetilde{\mathbf{X}}_2$ matrix is the projection of $\mathbf{X}_2$ onto the orthogonal complement of the space spanned by the columns of $\mathbf{X}_1$, where the orthogonality is defined with respect to $\mathbf{V}_{\text{srs}}$; that is, $\widetilde{\mathbf{X}}_2' \mathbf{V}_{\text{srs}} \mathbf{X}_1 = \mathbf{0}$.

See Rao and Scott (1984) for the proof justifying (1) and (2). However, even without a full understanding, you can get a feeling for $\Delta$. It is like a ratio (although remember that it is a matrix) of two variances. The variance in the numerator involves the variance under the true survey design, and the variance in the denominator involves the variance assuming that the design was simple random sampling. The design effect DEFF for an estimated proportion (see [SVY] **estat**) is defined as

$$\text{DEFF} = \frac{\hat{V}(\hat{p}_{rc})}{\tilde{V}_{\text{srsor}}(\tilde{p}_{rc})}$$

Hence, $\Delta$ can be regarded as a design-effects matrix, and Rao and Scott call its eigenvalues, the $\delta_k$s, the "generalized design effects".

Computing an estimate for $\Delta$ by using estimates for $\mathbf{V}$ and $\mathbf{V}_{\text{srs}}$ is easy. Rao and Scott (1984) derive a simpler formula for $\widehat{\Delta}$:

$$\widehat{\Delta} = (\mathbf{C}'\mathbf{D}_{\hat{\mathbf{p}}}^{-1}\hat{V}_{\text{srs}}\mathbf{D}_{\hat{\mathbf{p}}}^{-1}\mathbf{C})^{-1}(\mathbf{C}'\mathbf{D}_{\hat{\mathbf{p}}}^{-1}\hat{V}\mathbf{D}_{\hat{\mathbf{p}}}^{-1}\mathbf{C})$$

Here $\mathbf{C}$ is a contrast matrix that is any $RC \times (R-1)(C-1)$ full-rank matrix orthogonal to $[\mathbf{1} \,|\, \mathbf{X}_1]$; that is, $\mathbf{C}'\mathbf{1} = \mathbf{0}$ and $\mathbf{C}'\mathbf{X}_1 = \mathbf{0}$. $\mathbf{D}_{\hat{\mathbf{p}}}$ is a diagonal matrix with the estimated proportions $\hat{p}_{rc}$ on the diagonal. When one of the $\hat{p}_{rc}$ is zero, the corresponding variance estimate is also zero; hence, the corresponding element for $\mathbf{D}_{\hat{\mathbf{p}}}^{-1}$ is immaterial for computing $\widehat{\Delta}$.

Unfortunately, (1) is not practical for computing a $p$-value. However, you can compute simple first-order and second-order corrections based on it. A first-order correction is based on downweighting the i.i.d. statistics by the average eigenvalue of $\widehat{\Delta}$; namely, you compute

$$X^2_{\text{P}}(\hat{\delta}_{\cdot}) = X^2_{\text{P}}/\hat{\delta}_{\cdot} \qquad \text{and} \qquad X^2_{\text{LR}}(\hat{\delta}_{\cdot}) = X^2_{\text{LR}}/\hat{\delta}_{\cdot}$$

where $\hat{\delta}_{\cdot}$ is the mean-generalized DEFF

$$\hat{\delta}_{\cdot} = \frac{1}{(R-1)(C-1)} \sum_{k=1}^{(R-1)(C-1)} \delta_k$$

These corrected statistics are asymptotically distributed as $\chi^2_{(R-1)(C-1)}$. Thus, to first-order, you can view the i.i.d. statistics $X^2_{\text{P}}$ and $X^2_{\text{LR}}$ as being "too big" by a factor of $\hat{\delta}_{\cdot}$ for true survey design.

A better second-order correction can be obtained by using the Satterthwaite approximation to the distribution of a weighted sum of $\chi^2_1$ variables. Here the Pearson statistic becomes

$$X^2_{\text{P}}(\hat{\delta}_{\cdot}, \hat{a}) = \frac{X^2_{\text{P}}}{\hat{\delta}_{\cdot}(\hat{a}^2 + 1)} \tag{3}$$

where $\hat{a}$ is the coefficient of variation of the eigenvalues:

$$\hat{a}^2 = \frac{\sum \hat{\delta}_k^2}{(R-1)(C-1)\hat{\delta}_{\cdot}^2} - 1$$

Because $\sum \hat{\delta}_k = \operatorname{tr}\widehat{\Delta}$ and $\sum \hat{\delta}_k^2 = \operatorname{tr}\widehat{\Delta}^2$, (3) can be written in an easily computable form as

$$X^2_{\text{P}}(\hat{\delta}_{\cdot}, \hat{a}) = \frac{\operatorname{tr}\widehat{\Delta}}{\operatorname{tr}\widehat{\Delta}^2} X^2_{\text{P}}$$

These corrected statistics are asymptotically distributed as $\chi^2_d$, with

$$d = \frac{(R-1)(C-1)}{\hat{a}^2 + 1} = \frac{(\operatorname{tr}\widehat{\Delta})^2}{\operatorname{tr}\widehat{\Delta}^2}$$

that is, a $\chi^2$ with, in general, noninteger degrees of freedom. The likelihood-ratio statistic $X^2_{\text{LR}}$ can also be given this second-order correction in an identical manner.

Two issues remain. First, there are two possible ways to compute the variance estimate $\widehat{V}_{\text{srs}}$, which is used to compute $\widehat{\Delta}$. $\mathbf{V}_{\text{srs}}$ has diagonal elements $p_{rc}(1-p_{rc})/m$ and off-diagonal elements $-p_{rc}p_{st}/m$, but here $p_{rc}$ is the true, not estimated, proportion. Hence, the question is what to use to estimate $p_{rc}$: the observed proportions, $\hat{p}_{rc}$, or the proportions estimated under the null hypothesis of independence, $\hat{p}_{0rc} = \hat{p}_{r\cdot}\hat{p}_{\cdot c}$? Rao and Scott (1984, 53) leave this as an open question.

Because of the question of using $\hat{p}_{rc}$ or $\hat{p}_{0rc}$ to compute $\widehat{V}_{\text{srs}}$, `svy: tabulate` can compute both corrections. By default, when the `null` option is not specified, only the correction based on $\hat{p}_{rc}$ is displayed. If `null` is specified, two corrected statistics and corresponding $p$-values are displayed, one computed using $\hat{p}_{rc}$ and the other using $\hat{p}_{0rc}$.

The second outstanding issue concerns the degrees of freedom resulting from the variance estimate, $\widehat{V}$, of the cell proportions under the survey design. The customary degrees of freedom for $t$ statistics resulting from this variance estimate is $\nu = n - L$, where $n$ is the number of PSUs in the sample and $L$ is the number of strata.

Rao and Thomas (1989) suggest turning the corrected $\chi^2$ statistic into an $F$ statistic by dividing it by its degrees of freedom, $d_0 = (R-1)(C-1)$. The $F$ statistic is then taken to have numerator degrees of freedom equal to $d_0$ and denominator degrees of freedom equal to $\nu d_0$. Hence, the corrected Pearson $F$ statistic is

$$F_{\text{P}} = \frac{X^2_{\text{P}}}{\operatorname{tr}\widehat{\Delta}} \quad \text{with} \quad F_{\text{P}} \sim F(d, \nu d) \quad \text{where} \quad d = \frac{(\operatorname{tr}\widehat{\Delta})^2}{\operatorname{tr}\widehat{\Delta}^2} \quad \text{and} \quad \nu = n - L \tag{4}$$

This is the corrected statistic that `svy: tabulate` displays by default or when the `pearson` option is specified. When the `lr` option is specified, an identical correction is produced for the likelihood-ratio statistic $X^2_{\text{LR}}$. When `null` is specified, (4) is also used. For the statistic labeled "D-B (null)", $\widehat{\Delta}$ is computed using $\hat{p}_{0rc}$. For the statistic labeled "Design-based", $\widehat{\Delta}$ is computed using $\hat{p}_{rc}$.

The Wald statistics computed by `svy: tabulate` with the `wald` and `llwald` options were developed by Koch, Freeman, and Freeman (1975). The statistic given by the `wald` option is similar to the Pearson statistic because it is based on

$$\hat{Y}_{rc} = \widehat{N}_{rc} - \widehat{N}_{r\cdot}\widehat{N}_{\cdot c}/\widehat{N}_{\cdot\cdot}$$

where $r = 1, \ldots, R-1$ and $c = 1, \ldots, C-1$. The delta method can be used to estimate the variance of $\widehat{\mathbf{Y}}$ (which is $\hat{Y}_{rc}$ stacked into a vector), and a Wald statistic can be constructed in the usual manner:

$$W = \widehat{\mathbf{Y}}'\{\mathbf{J}_{\mathbf{N}}\hat{V}(\widehat{\mathbf{N}})\mathbf{J}_{\mathbf{N}}{}'\}^{-1}\widehat{\mathbf{Y}} \qquad \text{where} \qquad \mathbf{J}_{\mathbf{N}} = \partial\widehat{\mathbf{Y}}/\partial\widehat{\mathbf{N}}'$$

The statistic given by the `llwald` option is based on the log-linear model with predictors $[\,\mathbf{1}\,|\,\mathbf{X}_1\,|\,\mathbf{X}_2\,]$ that was mentioned earlier. This Wald statistic is

$$W_{\text{LL}} = (\mathbf{X}_2'\ln\hat{\mathbf{p}})'\{\mathbf{X}_2'\mathbf{J}_{\mathbf{p}}\hat{V}(\hat{\mathbf{p}})\mathbf{J}_{\mathbf{p}}{}'\mathbf{X}_2\}^{-1}(\mathbf{X}_2'\ln\hat{\mathbf{p}})$$

where $\mathbf{J}_{\mathbf{p}}$ is the matrix of first derivatives of $\ln\hat{\mathbf{p}}$ with respect to $\hat{\mathbf{p}}$, which is, of course, just a matrix with $\hat{p}_{rc}^{-1}$ on the diagonal and zero elsewhere. This log-linear Wald statistic is undefined when there is a zero cell in the table.

Unadjusted $F$ statistics (`noadjust` option) are produced using

$$F_{\text{unadj}} = W/d_0 \qquad \text{with} \qquad F_{\text{unadj}} \sim F(d_0, \nu)$$

Adjusted $F$ statistics are produced using

$$F_{\text{adj}} = (\nu - d_0 + 1)W/(\nu d_0) \qquad \text{with} \qquad F_{\text{adj}} \sim F(d_0, \nu - d_0 + 1)$$

The other `svy` estimators also use this adjustment procedure for $F$ statistics. See Korn and Graubard (1990) for a justification of the procedure.

## References


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## Also see

[SVY] **svy postestimation** — Postestimation tools for svy

[SVY] **svy** — The survey prefix command

[SVY] **svy: tabulate oneway** — One-way tables for survey data

[SVY] **svydescribe** — Describe survey data

[SVY] **Calibration** — Calibration for survey data

[SVY] **Direct standardization** — Direct standardization of means, proportions, and ratios

[SVY] **Poststratification** — Poststratification for survey data

[SVY] **Subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **Variance estimation** — Variance estimation for survey data

[R] **tabulate twoway** — Two-way table of frequencies

[R] **test** — Test linear hypotheses after estimation

**[U] 20 Estimation and postestimation commands**

**svydescribe** — Describe survey data



## Description

`svydescribe` displays a table that describes the strata and the sampling units for a given sampling stage in a survey dataset.

## Quick start

Describe the stage 1 strata and sampling units

```
svydescribe
```

Describe the stage 2 strata and sampling units

```
svydescribe, stage(2)
```

Describe the final stage strata and sampling units

```
svydescribe, finalstage
```

Describe stage 1 strata, and report on where `x` contains missing values

```
svydescribe x
```

Create variable `onepsu` that identifies strata containing one sampling unit

```
svydescribe, generate(onepsu)
```

Show which strata have only one PSU for observations with nonmissing values of `x`

```
svydescribe x, single
```

Show which strata have only one PSU for observations in the estimation sample

```
svydescribe if e(sample), single
```

## Menu

Statistics > Survey data analysis > Setup and utilities > Describe survey data

# Syntax

```
svydescribe [varlist] [if] [in] [, options]
```

| *options* | Description |
|---|---|
| Main | |
| `stage(#)` | sampling stage to describe; default is `stage(1)` |
| `finalstage` | display information per sampling unit in the final stage |
| `single` | display only the strata with one sampling unit |
| `generate(`*newvar*`)` | generate a variable identifying strata with one sampling unit |

`svydescribe` requires that the survey design variables be identified using `svyset`; see [SVY] **svyset**.

# Options

Main

`stage(#)` specifies the sampling stage to describe. The default is `stage(1)`.

`finalstage` specifies that results be displayed for each sampling unit in the final sampling stage; that is, a separate line of output is produced for every sampling unit in the final sampling stage. This option is not allowed with `stage()`, `single`, or `generate()`.

`single` specifies that only the strata containing one sampling unit be displayed in the table.

`generate(`*newvar*`)` stores a variable that identifies strata containing one sampling unit for a given sampling stage.

# Remarks and examples

Survey datasets are typically the result of a stratified survey design with cluster sampling in one or more stages. Within a stratum for a given sampling stage, there are sampling units, which may be either clusters of observations or individual observations.

`svydescribe` displays a table that describes the strata and sampling units for a given sampling stage. One row of the table is produced for each stratum. Each row contains the number of sampling units, the range and mean of the number of observations per sampling unit, and the total number of observations. If the `finalstage` option is specified, one row of the table is produced for each sampling unit of the final stage. Here each row contains the number of observations for the respective sampling unit.

If a varlist is specified, `svydescribe` reports the number of sampling units that contain at least one observation with complete data (that is, no missing values) for all variables in *varlist*. These are the sampling units that would be used to compute point estimates by using the variables in *varlist* with a given `svy` estimation command.

## Example 1: Strata with one sampling unit

We use data from the Second National Health and Nutrition Examination Survey (NHANES II) (McDowell et al. 1981) as our example. First, we set the PSU, `pweight`, and strata variables.

```
. use https://www.stata-press.com/data/r19/nhanes2b
. svyset psuid [pweight=finalwgt], strata(stratid)
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: stratid
 Sampling unit 1: psuid
           FPC 1: <zero>
```

`svydescribe` will display the strata and PSU arrangement of the dataset.

```
. svydescribe
Survey: Describing stage 1 sampling units
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: stratid
 Sampling unit 1: psuid
           FPC 1: <zero>
```

| | | | Number of obs per unit | | |
|---|---|---|---|---|---|
| Stratum | # units | # obs | Min | Mean | Max |
| 1 | 2 | 380 | 165 | 190.0 | 215 |
| 2 | 2 | 185 | 67 | 92.5 | 118 |
| 3 | 2 | 348 | 149 | 174.0 | 199 |
| (*output omitted*) | | | | | |
| 17 | 2 | 393 | 180 | 196.5 | 213 |
| 18 | 2 | 359 | 144 | 179.5 | 215 |
| 20 | 2 | 285 | 125 | 142.5 | 160 |
| 21 | 2 | 214 | 102 | 107.0 | 112 |
| (*output omitted*) | | | | | |
| 31 | 2 | 308 | 143 | 154.0 | 165 |
| 32 | 2 | 450 | 211 | 225.0 | 239 |
| 31 | 62 | 10,351 | 67 | 167.0 | 288 |

Our NHANES II dataset has 31 strata (stratum 19 is missing) and two PSUs per stratum.

The `hdresult` variable contains serum levels of high-density lipoprotein (HDL). If we try to estimate the mean of `hdresult`, we get a missing value for the standard error estimate and a note explaining why.

```
. svy: mean hdresult
(running mean on estimation sample)
Survey: Mean estimation
Number of strata = 31              Number of obs    =      8,720
Number of PSUs   = 60              Population size = 98,725,345
                                   Design df       =         29
```

| | Mean | Linearized std. err. | [95% conf. | interval] |
|---|---|---|---|---|
| hdresult | 49.67141 | . | . | . |

```
Note: Missing standard error because of stratum with single
      sampling unit.
```

Running svydescribe with hdresult and the single option will show which strata have only one PSU.

```
. svydescribe hdresult, single

Survey: Describing strata with a single sampling unit in stage 1

Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: stratid
 Sampling unit 1: psuid
           FPC 1: <zero>
```

| Stratum | Number of units included | Number of units omitted | Number of obs with complete data | Number of obs with missing data | # obs per included unit Min | # obs per included unit Mean | # obs per included unit Max |
|---|---|---|---|---|---|---|---|
| 1 | 1* | 1 | 114 | 266 | 114 | 114.0 | 114 |
| 2 | 1* | 1 | 98 | 87 | 98 | 98.0 | 98 |
| | 2 | | | | | | |

Both stratid = 1 and stratid = 2 have only one PSU with nonmissing values of hdresult. Because this dataset has only 62 PSUs, the finalstage option produces a manageable amount of output:

```
. svydescribe hdresult, finalstage

Survey: Describing final stage sampling units

Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: stratid
 Sampling unit 1: psuid
           FPC 1: <zero>
```

| Stratum | Unit | Number of obs with complete data | Number of obs with missing data |
|---|---|---|---|
| 1 | 1 | 0 | 215 |
| 1 | 2 | 114 | 51 |
| 2 | 1 | 98 | 20 |
| 2 | 2 | 0 | 67 |
| (*output omitted*) | | | |
| 32 | 2 | 203 | 8 |
| 31 | 62 | 8,720 | 1,631 |
| | | 10,351 | |

It is rather striking that there are two PSUs with no values for hdresult. All other PSUs have only a moderate number of missing values. Obviously, here a data analyst should first try to ascertain why these data are missing. The answer here (C. L. Johnson, 1995, pers. comm.) is that HDL measurements could not be collected until the third survey location. Thus there are no hdresult data for the first two locations: stratid = 1, psuid = 1 and stratid = 2, psuid = 2.

Assuming that we wish to go ahead and analyze the hdresult data, we must collapse strata—that is, merge them—so that every stratum has at least two PSUs with some nonmissing values. We can accomplish this by collapsing stratid = 1 into stratid = 2. To perform the stratum collapse, we create a new strata identifier, newstr, and a new PSU identifier, newpsu.

```
. generate newstr = stratid
. generate newpsu = psuid
. replace newpsu = psuid + 2 if stratid == 1
(380 real changes made)
. replace newstr = 2 if stratid == 1
(380 real changes made)
```

svyset the new PSU and strata variables.

```
. svyset newpsu [pweight=finalwgt], strata(newstr)
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: newstr
 Sampling unit 1: newpsu
           FPC 1: <zero>
```

Then use svydescribe to check what we have done.

```
. svydescribe hdresult, finalstage
Survey: Describing final stage sampling units
Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: newstr
 Sampling unit 1: newpsu
           FPC 1: <zero>
```

| Stratum | Unit | Number of obs with complete data | missing data |
|---|---|---|---|
| 2 | 1 | 98 | 20 |
| 2 | 2 | 0 | 67 |
| 2 | 3 | 0 | 215 |
| 2 | 4 | 114 | 51 |
| 3 | 1 | 161 | 38 |
| 3 | 2 | 116 | 33 |
| (*output omitted*) | | | |
| 32 | 1 | 180 | 59 |
| 32 | 2 | 203 | 8 |
| 30 | 62 | 8,720 | 1,631 |
| | | 10,351 | |

The new stratum, `newstr` = 2, has four PSUs, two of which contain some nonmissing values of `hdresult`. This is sufficient to allow us to estimate the mean of `hdresult` and get a nonmissing standard-error estimate.

```
. svy: mean hdresult
(running mean on estimation sample)

Survey: Mean estimation

Number of strata = 30              Number of obs    =      8,720
Number of PSUs   = 60              Population size = 98,725,345
                                   Design df       =         30

------------------------------------------------------------------
             |             Linearized
             |       Mean   std. err.     [95% conf. interval]
-------------+----------------------------------------------------
    hdresult |   49.67141   .3830147      48.88919    50.45364
------------------------------------------------------------------
```

## Example 2: Using e(sample) to find strata with one sampling unit

Some estimation commands drop observations from the estimation sample when they encounter collinear predictors or perfect predictors. Ascertaining which strata contain one sampling unit is therefore difficult. We can then use `if e(sample)` instead of *varlist* when faced with the problem of strata with one sampling unit. We revisit the previous analysis to illustrate.

```
. use https://www.stata-press.com/data/r19/nhanes2b, clear

. svy: mean hdresult
(running mean on estimation sample)

Survey: Mean estimation

Number of strata = 31              Number of obs    =      8,720
Number of PSUs   = 60              Population size = 98,725,345
                                   Design df       =         29

------------------------------------------------------------------
             |             Linearized
             |       Mean   std. err.     [95% conf. interval]
-------------+----------------------------------------------------
    hdresult |   49.67141          .             .           .
------------------------------------------------------------------

Note: Missing standard error because of stratum with single
      sampling unit.

. svydescribe if e(sample), single

Survey: Describing strata with a single sampling unit in stage 1

Sampling weights: finalwgt
             VCE: linearized
     Single unit: missing
        Strata 1: stratid
 Sampling unit 1: psuid
           FPC 1: <zero>

                                        Number of obs per unit
 Stratum   # units     # obs       Min       Mean        Max
-------------------------------------------------------------
       1         1*      114       114      114.0        114
       2         1*       98        98       98.0         98
-------------------------------------------------------------
                 2
```

## Methods and formulas

See Eltinge and Sribney (1996) for an earlier implementation of `svydescribe`.

## References

Eltinge, J. L., and W. M. Sribney. 1996. svy3: Describing survey data: Sampling design and missing data. *Stata Technical Bulletin* 31: 23–26. Reprinted in *Stata Technical Bulletin Reprints*, vol. 6, pp. 235–239. College Station, TX: Stata Press.

McDowell, A., A. Engel, J. T. Massey, and K. Maurer. 1981. "Plan and operation of the Second National Health and Nutrition Examination Survey, 1976–1980". In *Vital and Health Statistics*, ser. 1, no. 15. Hyattsville, MD: National Center for Health Statistics.

## Also see

[SVY] **svy** — The survey prefix command

[SVY] **svyset** — Declare survey design for dataset

[SVY] **Survey** — Introduction to survey commands

[SVY] **Variance estimation** — Variance estimation for survey data

**svymarkout** — Mark observations for exclusion on the basis of survey characteristics

Description Syntax Remarks and examples Stored results Also see

## Description

`svymarkout` is a programmer's command that resets the values of *markvar* to contain 0 wherever any of the survey-characteristic variables (previously set by `svyset`) contain missing values.

## Syntax

`svymarkout` [ *markvar* ]

## Remarks and examples

`svymarkout` assumes that *markvar* was created by `marksample` or `mark`; see [P] **mark**. This command is most helpful for developing estimation commands that use `ml` to fit models using maximum pseudolikelihood directly, instead of relying on the `svy` prefix; see [P] **program properties** for a discussion of how to write programs to be used with the `svy` prefix.

▷ Example 1

```
program mysvyprogram, ...
    ...
    syntax ...
    marksample touse
    svymarkout `touse'
    ...
end
```

◁

## Stored results

`svymarkout` stores the following in `s()`:

Macros

| | |
|---|---|
| `s(weight)` | weight variable set by `svyset` |

## Also see

[P] **mark** — Mark observations for inclusion

[P] **program properties** — Properties of user-defined programs

**svyset** — Declare survey design for dataset



## Description

`svyset` manages the survey analysis settings of a dataset. You use `svyset` to designate variables that contain information about the survey design, such as the sampling units and weights. `svyset` is also used to specify other design characteristics, such as the number of sampling stages and the sampling method, and analysis defaults, such as the method for variance estimation. You must `svyset` your data before using any `svy` command; see [SVY] **svy estimation**.

`svyset` without arguments reports the current settings. `svyset, clear` removes the current survey settings.

## Quick start

One-stage design with sampling weight `wvar1`, strata defined by levels of `svar`, and sampling units identified by `su1`

```
svyset su1 [pweight=wvar1], strata(svar)
```

Two-stage design with finite population correction `fpc` and `_n` indicating second-stage sampling units are the sampled individuals

```
svyset su1 [pweight=wvar1], strata(svar) fpc(fpc) || _n
```

Two-stage design with second-stage clustering defined by `su2`

```
svyset su1 [pweight=wvar1], strata(svar) fpc(fpc) || su2
```

Jackknife variance estimation as the default for `svy` commands, with sampling weight `wvar2`, and replicate-weight variables `rwvar*`

```
svyset [pweight=wvar2], vce(jackknife) jkrweight(rwvar*)
```

Same as above, but use the MSE formula

```
svyset [pweight=wvar2], vce(jackknife) jkrweight(rwvar*) mse
```

Display current survey settings

```
svyset
```

Clear current survey settings

```
svyset, clear
```

## Menu

Statistics > Survey data analysis > Setup and utilities > Declare survey design for dataset

# Syntax

*Single-stage design*

```
svyset [psu] [weight] [ , design_options options ]
```

*Multiple-stage design*

```
svyset psu [weight] [ , design_options ] [ || ssu , design_options ] ... [ options ]
```

*Clear the current settings*

```
svyset, clear
```

*Report the current settings*

```
svyset
```

*psu* identifies the primary sampling units and may be `_n` or *varname*. In the single-stage syntax, *psu* is optional and defaults to `_n`.

`_n` indicates that individuals were randomly sampled if the design does not involve clustered sampling.

*varname* contains identifiers for the clusters in a clustered sampling design.

*ssu* is `_n` or *varname* containing identifiers for sampling units (clusters) in subsequent stages of the survey design.

`_n` indicates that individuals were randomly sampled within the last sampling stage.

| *design_options* | Description |
|---|---|
| Main | |
| `strata(`*varname*`)` | variable identifying strata |
| `fpc(`*varname*`)` | finite population correction |
| `weight(`*varname*`)` | stage-level sampling weight |

| *options* | Description |
|---|---|
| **Weights** | |
| `brrweight(`*varlist*`)` | balanced repeated replicate (BRR) weights |
| `fay(`#`)` | Fay's adjustment |
| `bsrweight(`*varlist*`)` | bootstrap replicate weights |
| `bsn(`#`)` | bootstrap mean-weight adjustment |
| `jkrweight(`*varlist*`,` *jkropts*`)` | jackknife replicate weights |
| `sdrweight(`*varlist*`,` *sdropts*`)` | successive difference replicate (SDR) weights |
| **SE** | |
| `vce(linearized)` | Taylor linearized variance estimation |
| `vce(bootstrap)` | bootstrap variance estimation |
| `vce(brr)` | BRR variance estimation |
| `vce(jackknife)` | jackknife variance estimation |
| `vce(sdr)` | SDR variance estimation |
| `dof(`#`)` | design degrees of freedom |
| `mse` | use the MSE formula with `vce(bootstrap)`, `vce(brr)`, `vce(jackknife)`, or `vce(sdr)` |
| `singleunit(`*method*`)` | strata with a single sampling unit; *method* may be `missing`, `certainty`, `scaled`, or `centered` |
| **Poststratification** | |
| `poststrata(`*varname*`)` | variable identifying poststrata |
| `postweight(`*varname*`)` | poststratum population sizes |
| **Calibration** | |
| `rake(`*varlist*`,` *calopts*`)` | adjust weights using the raking-ratio method |
| `regress(`*varlist*`,` *calopts*`)` | adjust weights using linear regression calibration |
| `clear` | clear all settings from the data |
| `noclear` | change some of the settings without clearing the others |
| `clear(`*opnames*`)` | clear specified settings without clearing all others; *opnames* may be one or more of `weight`, `vce`, `dof`, `mse`, `bsrweight`, `brrweight`, `jkrweight`, `sdrweight`, `poststrata`, `rake`, or `regress` |

`collect` is allowed; see **[U] 11.1.10 Prefix commands**.
`pweights` and `iweights` are allowed; see **[U] 11.1.6 weight**.
`clear`, `noclear`, and `clear()` are not shown in the dialog box.

| *jkropts* | Description |
|---|---|
| `stratum(`#`[`#`...])` | stratum identifier for each jackknife replicate weight |
| `fpc(`#`[`#`...])` | finite population correction for each jackknife replicate weight |
| `multiplier(`#`[`#`...])` | variance multiplier for each jackknife replicate weight |
| `reset` | reset characteristics for each jackknife replicate weight |

| *sdropts* | Description |
|---|---|
| `fpc(`#`[`#`...])` | finite population correction for each SDR weight |

| *calopts* | Description |
|---|---|
| * totals(*spec*) | population totals |
| noconstant | suppress constant term |
| ll(#) | lower limit for weight ratios |
| ul(#) | upper limit for weight ratios |
| iterate(#) | maximum number of iterations |
| tolerance(#) | convergence tolerance |
| force | allow calibration adjustments that failed to converge |

*totals() is required.

## Options

### Main

strata(*varname*) specifies the name of a variable (numeric or string) that contains stratum identifiers.

fpc(*varname*) requests a finite population correction for the variance estimates. If *varname* has values less than or equal to 1, it is interpreted as a stratum sampling rate $f_h = n_h/N_h$, where $n_h$ = number of units sampled from stratum $h$ and $N_h$ = total number of units in the population belonging to stratum $h$. If *varname* has values greater than or equal to $n_h$, it is interpreted as containing $N_h$. It is an error for *varname* to have values between 1 and $n_h$ or to have a mixture of sampling rates and stratum sizes.

weight(*varname*) specifies a stage-level sampling weight variable. For most models, stage-level sampling weights are multiplied together to create a single observation-level sampling weight variable used for weighted estimation. For commands such as gsem and meglm, each stage-level weight variable is assumed to correspond with a hierarchical group level in the model and is used to compute the pseudolikelihood at that associated group level. Stage-level sampling weights are required to be constant within their corresponding group level. For examples of fitting a multilevel model with stage-level sampling weights, see example 5 and example 6 in [ME] **meglm**.

### Weights

brrweight(*varlist*) specifies the replicate-weight variables to be used with vce(brr) or with svy brr.

fay(#) specifies Fay's adjustment (Judkins 1990). The value specified in fay(#) is used to adjust the BRR weights and is present in the BRR variance formulas.

The sampling weight of the selected PSUs for a given replicate is multiplied by 2−#, where the sampling weight for the unselected PSUs is multiplied by #. When brrweight(*varlist)* is specified, the replicate-weight variables in *varlist* are assumed to be adjusted using #.

fay(0) is the default and is equivalent to the original BRR method. # must be between 0 and 2, inclusive, and excluding 1. fay(1) is not allowed because this results in unadjusted weights.

bsrweight(*varlist*) specifies the replicate-weight variables to be used with vce(bootstrap) or with svy bootstrap.

bsn(#) specifies that # bootstrap replicate-weight variables were used to generate each bootstrap mean-weight variable specified in the bsrweight() option. The default is bsn(1). The value specified in bsn(#) is used to adjust the variance estimate to account for mean bootstrap weights.

`jkrweight(`*varlist*`,` *jkropts*`)` specifies the replicate-weight variables to be used with `vce(jackknife)` or with `svy jackknife`.

The following *jkropts* set characteristics on the jackknife replicate-weight variables. If one value is specified, all the specified jackknife replicate-weight variables will be supplied with the same characteristic. If multiple values are specified, each replicate-weight variable will be supplied with the corresponding value according to the order specified. *jkropts* are not shown in the dialog box.

`stratum(`# [ # ... ]`)` specifies an identifier for the stratum in which the sampling weights have been adjusted.

`fpc(`# [ # ... ]`)` specifies the FPC value to be added as a characteristic of the jackknife replicate-weight variables. The values set by this suboption have the same interpretation as the `fpc(`*varname*`)` option.

`multiplier(`# [ # ... ]`)` specifies the value of a jackknife multiplier to be added as a characteristic of the jackknife replicate-weight variables.

`reset` indicates that the characteristics for the replicate-weight variables may be overwritten or reset to the default, if they exist.

`sdrweight(`*varlist*`,` *sdropts*`)` specifies the replicate-weight variables to be used with `vce(sdr)` or with `svy sdr`. The following *sdropts* is available:

`fpc(`#`)` specifies the FPC value associated with the SDR weights. The value set by this suboption has the same interpretation as the `fpc(`*varname*`)` option. This option is not shown in the dialog box.

SE

`vce(`*vcetype*`)` specifies the default method for variance estimation; see [SVY] **Variance estimation**.

`vce(linearized)` sets the default to Taylor linearization.

`vce(bootstrap)` sets the default to the bootstrap; also see [SVY] **svy bootstrap**.

`vce(brr)` sets the default to BRR; also see [SVY] **svy brr**.

`vce(jackknife)` sets the default to the jackknife; also see [SVY] **svy jackknife**.

`vce(sdr)` sets the default to the SDR; also see [SVY] **svy sdr**.

`dof(`#`)` specifies the design degrees of freedom, overriding the default calculation, $\text{df} = N_{\text{psu}} - N_{\text{strata}}$.

`mse` specifies that the MSE formula be used when `vce(bootstrap)`, `vce(brr)`, `vce(jackknife)`, or `vce(sdr)` is specified. This option requires `vce(bootstrap)`, `vce(brr)`, `vce(jackknife)`, or `vce(sdr)`.

`singleunit(`*method*`)` specifies how to handle strata with one sampling unit.

`singleunit(missing)` results in missing values for the standard errors and is the default.

`singleunit(certainty)` causes strata with single sampling units to be treated as certainty units. Certainty units contribute nothing to the standard error.

`singleunit(scaled)` results in a scaled version of `singleunit(certainty)`. The scaling factor comes from using the average of the variances from the strata with multiple sampling units for each stratum with one sampling unit.

`singleunit(centered)` specifies that strata with one sampling unit are centered at the grand mean instead of the stratum mean.

Poststratification

`poststrata(`*varname*`)` specifies the name of the variable (numeric or string) that contains poststratum identifiers. See [SVY] **Poststratification** for more information.

`postweight(`*varname*`)` specifies the name of the numeric variable that contains poststratum population totals (or sizes), that is, the number of elementary sampling units in the population within each poststratum. See [SVY] **Poststratification** for more information.

Calibration

`rake(`*varlist*`, `*calopts*`)` and `regress(`*varlist*`, `*calopts*`)` specify that the sampling weights be adjusted using a calibration adjustment. See [SVY] **Calibration** for more information.

`rake()` specifies that the weights be adjusted by the raking-ratio method.

`regress()` specifies that the weights be adjusted by linear regression.

The following *calopts* are available:

`totals(`*spec*`)` is required. It specifies the population totals corresponding to the variables specified in *varlist*. *spec* is one of

*matname* [ `, skip copy` ]

{ [ *eqname*: ] *name* = # | / *eqname* = # } [ ... ]

# [ # ... ] `, copy`

That is, *spec* may be a matrix name, for example, `totals(poptotals)`; a list of variable names in *varlist* with their population totals, for example, `totals(_cons=1300 dogs=850 cats=450)`; or a list of values, for example, `totals(850 450 1300)`.

`skip` specifies that any parameters found in the specified totals vector that are not also found in the model be ignored. The default action is to issue an error message.

`copy` specifies that the list of values or the totals vector be copied into the population-totals vector by position rather than by name.

`noconstant` suppresses the intercept in the linear regression adjustment.

`ll(#)` specifies a lower limit for the weight ratios for truncated linear calibration.

`ul(#)` specifies an upper limit for the weight ratios for truncated linear calibration.

`iterate(#)` specifies the maximum number of iterations. When the number of iterations equals `iterate()`, the calibration adjustment stops and presents a note. The default is `iterate(1000)`.

`tolerance(#)` specifies the tolerance for the Lagrange multiplier in the calibration equations. Convergence is achieved when the relative change in the Lagrange multiplier from one iteration to the next is less than or equal to `tolerance()`. The default is `tolerance(1e-7)`.

`force` prevents `svy` estimation from exiting with an error if the calibration adjustment fails to converge.

The following options are available with svyset but are not shown in the dialog box:

clear clears all the settings from the data. Typing

```
. svyset, clear
```

clears the survey design characteristics from the data in memory. Although this option may be specified with some of the other svyset options, it is redundant because svyset automatically clears the previous settings before setting new survey design characteristics.

noclear allows some of the options in *options* to be changed without clearing all the other settings. This option is not allowed with *psu*, *ssu*, *design_options*, or clear.

clear(*opnames*) allows some of the options in *options* to be cleared without clearing all the other settings. *opnames* refers to an option name and may be one or more of the following: weight, vce, dof, mse, brrweight, bsrweight, jkrweight, sdrweight, poststrata, rake, or regress.

This option implies the noclear option.

# Remarks and examples

Remarks are presented under the following headings:



## Introduction to survey design characteristics

Stata's suite of commands for survey data analysis relies on properly identified survey design characteristics for point estimation, model fitting, and variance estimation. In fact, the svy prefix will report an error if no survey design characteristics have been identified using svyset. Settings made by svyset are saved with a dataset. So, if a dataset is saved after it has been svyset, it does not have to be set again.

Typical survey design characteristics include sampling weights, one or more stages of clustered sampling, and stratification. O'Donnell et al. (2008, 26–27) show four survey sample designs with the corresponding svyset specification. Use svyset to declare your dataset to be complex survey data by specifying the survey design variables. We will use the following contrived dataset for the examples in this section.

```
. use https://www.stata-press.com/data/r19/stage5a
```

### ▷ Example 1: Simple random sampling with replacement

Use _n for *psu* to specify that the primary sampling units (PSUs) are the sampled individuals.

```
. svyset _n
Sampling weights: <none>
             VCE: linearized
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: <observations>
           FPC 1: <zero>
```

The output from svyset states that there are no sampling weights (each observation is given a sampling weight of 1), there is only one stratum (which is the same as no stratification), and the PSUs are the observed individuals.

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## ▷ Example 2: One-stage clustered design with stratification

The most commonly specified design, one-stage clustered design with stratification, can be used to approximate multiple-stage designs when only the first-stage information is available. In this design, the population is partitioned into strata and the PSUs are sampled independently within each stratum. A dataset from this design will have a variable that identifies the strata, another variable that identifies the PSUs, and a variable containing the sampling weights. Let's assume that these variables are, respectively, strata, su1, and pw.

```
. svyset su1 [pweight=pw], strata(strata)
Sampling weights: pw
             VCE: linearized
     Single unit: missing
        Strata 1: strata
 Sampling unit 1: su1
           FPC 1: <zero>
```

◁

## ▷ Example 3: Two-stage designs

In two-stage designs, the PSUs are sampled without replacement and then collections of individuals are sampled within the selected PSUs. svyset uses || (double "or" bars) to separate the stage-specific design specifications. The first-stage information is specified before ||, and the second-stage information is specified afterward. We will assume that the variables containing the finite population correction (FPC) information for the two stages are named fpc1 and fpc2; see *Finite population correction (FPC)* for a discussion about the FPC.

Use _n for *ssu* to specify that the second-stage sampling units are the sampled individuals.

```
. svyset su1 [pweight=pw], fpc(fpc1) || _n, fpc(fpc2)
Sampling weights: pw
             VCE: linearized
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: su1
           FPC 1: fpc1
        Strata 2: <one>
 Sampling unit 2: <observations>
           FPC 2: fpc2
```

Suppose that su2 identifies the clusters of individuals sampled in the second stage.

```
. svyset su1 [pweight=pw], fpc(fpc1) || su2, fpc(fpc2)
Sampling weights: pw
             VCE: linearized
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: su1
           FPC 1: fpc1
        Strata 2: <one>
 Sampling unit 2: su2
           FPC 2: fpc2
```

Stratification can take place in one or both of the sampling stages. Suppose that `strata` identifies the second-stage strata and the first stage was not stratified.

```
. svyset su1 [pweight=pw], fpc(fpc1) || su2, fpc(fpc2) strata(strata)

Sampling weights: pw
             VCE: linearized
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: su1
           FPC 1: fpc1
        Strata 2: strata
 Sampling unit 2: su2
           FPC 2: fpc2
```

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## ▷ Example 4: Multiple-stage designs

Specifying designs with three or more stages is not much more difficult than specifying two-stage designs. Each stage will have its own variables for identifying strata, sampling units, and the FPC. Not all stages will be stratified and some will be sampled with replacement; thus some stages may not have a variable for identifying strata or the FPC.

Suppose that we have a three-stage design with variables `su#` and `fpc#` for the sampling unit and FPC information in stage #. Also assume that the design called for stratification in the first stage only.

```
. svyset su1 [pweight=pw], fpc(fpc1) strata(strata)
>         || su2, fpc(fpc2)
>         || su3, fpc(fpc3)

Sampling weights: pw
             VCE: linearized
     Single unit: missing
        Strata 1: strata
 Sampling unit 1: su1
           FPC 1: fpc1
        Strata 2: <one>
 Sampling unit 2: su2
           FPC 2: fpc2
        Strata 3: <one>
 Sampling unit 3: su3
           FPC 3: fpc3
```

Use _n for *ssu* in the last stage if the individuals are sampled within the third stage of clustered sampling.

```
. svyset su1 [pweight=pw], fpc(fpc1) strata(strata)
>         || su2, fpc(fpc2)
>         || su3, fpc(fpc3)
>         || _n
Sampling weights: pw
             VCE: linearized
     Single unit: missing
        Strata 1: strata
 Sampling unit 1: su1
           FPC 1: fpc1
        Strata 2: <one>
 Sampling unit 2: su2
           FPC 2: fpc2
        Strata 3: <one>
 Sampling unit 3: su3
           FPC 3: fpc3
        Strata 4: <one>
 Sampling unit 4: <observations>
           FPC 4: <zero>
```

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## Finite population correction (FPC)

An FPC accounts for the reduction in variance that occurs when sampling *without* replacement from a finite population compared to sampling *with* replacement from the same population. Specifying an FPC variable for stage $i$ indicates that the sampling units in that stage were sampled without replacement. See Cochran (1977) for an introduction to variance estimation and sampling without replacement.

### ▷ Example 5

Consider the following dataset:

```
. use https://www.stata-press.com/data/r19/fpc
. list
```

| | stratid | psuid | weight | nh | Nh | x |
|---|---|---|---|---|---|---|
| 1. | 1 | 1 | 3 | 5 | 15 | 2.8 |
| 2. | 1 | 2 | 3 | 5 | 15 | 4.1 |
| 3. | 1 | 3 | 3 | 5 | 15 | 6.8 |
| 4. | 1 | 4 | 3 | 5 | 15 | 6.8 |
| 5. | 1 | 5 | 3 | 5 | 15 | 9.2 |
| 6. | 2 | 1 | 4 | 3 | 12 | 3.7 |
| 7. | 2 | 2 | 4 | 3 | 12 | 6.6 |
| 8. | 2 | 3 | 4 | 3 | 12 | 4.2 |

Here the variable nh is the number of PSUs per stratum that were sampled, Nh is the total number of PSUs per stratum in the sampling frame (that is, the population), and x is our survey item of interest.

If we wish to use a finite population correction in our computations, we must svyset an FPC variable when we specify the variables for sampling weights, PSUs, and strata. The FPC variable typically contains the number of sampling units per stratum in the population; Nh is our FPC variable. Here we estimate the population mean of x assuming sampling without replacement.

```
. svyset psuid [pweight=weight], strata(stratid) fpc(Nh)
Sampling weights: weight
             VCE: linearized
     Single unit: missing
        Strata 1: stratid
 Sampling unit 1: psuid
           FPC 1: Nh
. svy: mean x
(running mean on estimation sample)
Survey: Mean estimation
Number of strata = 2                     Number of obs   =  8
Number of PSUs   = 8                     Population size = 27
                                         Design df       =  6
--------------------------------------------------------------
                    |             Linearized
                    |       Mean   std. err.     [95% conf. interval]
--------------------+-----------------------------------------------
                  x |   5.448148   .6160407      3.940751    6.955545
--------------------------------------------------------------
```

We must respecify the survey design before estimating the population mean of x assuming sampling with replacement.

```
. svyset psuid [pweight=weight], strata(stratid)
Sampling weights: weight
             VCE: linearized
     Single unit: missing
        Strata 1: stratid
 Sampling unit 1: psuid
           FPC 1: <zero>
. svy: mean x
(running mean on estimation sample)
Survey: Mean estimation
Number of strata = 2                     Number of obs   =  8
Number of PSUs   = 8                     Population size = 27
                                         Design df       =  6
--------------------------------------------------------------
                    |             Linearized
                    |       Mean   std. err.     [95% conf. interval]
--------------------+-----------------------------------------------
                  x |   5.448148   .7412683       3.63433    7.261966
--------------------------------------------------------------
```

Including an FPC always reduces the variance estimate. However, the reduction in the variance estimates will be small when the $N_h$ are large relative to the $n_h$.

Rather than having a variable that represents the total number of PSUs per stratum in the sampling frame, we sometimes have a variable that represents a sampling rate $f_h = n_h/N_h$. The syntax for `svyset` is the same whether the FPC variable contains $N_h$ or $f_h$. The survey variance-estimation routines in Stata are smart enough to identify what type of FPC information has been specified. If the FPC variable is less than or equal to 1, it is interpreted as a sampling rate; if it is greater than or equal to $n_h$, it is interpreted as containing $N_h$. It is an error for the FPC variable to have values between 1 and $n_h$ or to have a mixture of sampling rates and stratum sizes.

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## Multiple-stage designs and with-replacement sampling

Although survey data are seldom collected using with-replacement sampling, dropping the FPC information when the sampling fractions are small is common. In either case, `svyset` ignores the design variables specified in later sampling stages because this information is not necessary for variance estimation. In the following, we describe why this is true.

### ▷ Example 6

Consider the two-stage design where PSUs are sampled with replacement and individuals are sampled without replacement within the selected PSUs. Sampling the individuals with replacement would change some of the details in the following discussion, but the result would be the same.

Our population contains 100 PSUs, with five individuals in each, so our population size is 500. We will sample 10 PSUs with replacement and then sample two individuals without replacement from within each selected PSU. This results in a dataset with 10 PSUs, each with 2 observations, for a total of 20 observations. If our dataset contained the PSU information in variable `su1` and the second-stage FPC information in variable `fpc2`, our `svyset` command would be as follows.

```
. use https://www.stata-press.com/data/r19/svyset_wr
. svyset su1 || _n, fpc(fpc2)
note: stage 1 is sampled with replacement; further stages will be ignored for
      variance estimation.
Sampling weights: <none>
             VCE: linearized
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: su1
           FPC 1: <zero>
```

As expected, `svyset` tells us that it is ignoring the second-stage information because the first-stage units were sampled with replacement. Because we do not have an FPC variable for the first stage, we can regard the sampling of PSUs as a series of independently and identically distributed draws. The second-sampled PSU is drawn independently from the first and has the same sampling distribution because the first-sampled PSU is eligible to be sampled again.

Consider the following alternative scenario. Because there are 10 ways to pick two people of five, let's expand the 100 PSUs to form $100 \times 10 = 1{,}000$ "new PSUs" (NPSUs), each of size 2, representing all possible two-person groups that can be sampled from the original 100 groups of five people. We now have a population of $1{,}000 \times 2 = 2{,}000$ "new people"; each original person was replicated four times. We can select 10 NPSUs with replacement to end up with a dataset consisting of 10 groups of two to form samples of 20 people. If our "new" dataset contained the PSU information in variable `nsu1`, our `svyset` command would be as follows:

```
. svyset nsu1
Sampling weights: <none>
             VCE: linearized
     Single unit: missing
        Strata 1: <one>
 Sampling unit 1: nsu1
           FPC 1: <zero>
```

There is nothing from a sampling standpoint to distinguish between our two scenarios. The information contained in the variables `su1` and `nsu1` is equivalent; thus `svyset` can behave as if our dataset came from the second scenario.

The following questions may spring to mind after reading the above:

- The population in the first scenario has 500 people; the second has 2,000. Does that not invalidate the comparison between the two scenarios?

  Although the populations are different, the sampling schemes described for each scenario result in the same sampling space. By construction, each possible sample from the first scenario is also a possible sample from the second scenario. For the first scenario, the number of possible samples of 10 of 100 PSUs sampled with replacement, where two of five individuals are sampled without replacement, is

  $$100^{10} \times \binom{5}{2}^{10} = 10^{30}$$

  For the second scenario, the number of possible samples of 10 of 1,000 NPSUs sampled with replacement, where each NPSU is sampled as a whole, is

  $$1{,}000^{10} = 10^{30}$$

- Does the probability of being in the sample not depend on what happens in the first sampling stage?

  Not when the first stage is sampled with replacement. Sampling with replacement means that all PSUs have the same chance of being selected even after one of the PSUs has been selected. Thus each of the two-person groups that can possibly be sampled has the same chance of being sampled even after a specific two-person group has been selected.

- Is it valid to have replicated people in the population like the one in the second scenario?

  Yes, because each person in the population can be sampled more than once. Sampling with replacement allows us to construct the replicated people.

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## Replication-weight variables

Many groups that collect survey data for public use have taken steps to protect the privacy of the survey participants. This may result in datasets that have replicate-weight variables instead of variables that identify the strata and sampling units from the sampling stages. These datasets require replication methods for variance estimation.

The `brrweight()`, `jkrweight()`, `bsrweight()`, and `sdrweight()` options allow `svyset` to identify the set of replication weights for use with BRR, jackknife, bootstrap, and SDR variance estimation (`svy brr`, `svy jackknife`, `svy bootstrap`, and `svy sdr`), respectively. In addition to the weight variables, `svyset` also allows you to change the default variance estimation method from linearization to BRR, jackknife, bootstrap, or SDR.

## ▷ Example 7

Here are two simple examples using jackknife replication weights.

1. Data containing only sampling weights and jackknife replication weights, and we set the default variance estimator to the jackknife:

```
. use https://www.stata-press.com/data/r19/stage5a_jkw
. svyset [pweight=pw], jkrweight(jkw_*) vce(jackknife)
 Sampling weights: pw
              VCE: jackknife
              MSE: off
Jackknife weights: jkw_1 .. jkw_9
      Single unit: missing
         Strata 1: <one>
  Sampling unit 1: <observations>
           FPC 1: <zero>
```

2. Data containing only sampling weights and jackknife replication weights, and we set the default variance estimator to the jackknife by using the MSE formula:

```
. svyset [pweight=pw], jkrweight(jkw_*) vce(jackknife) mse
 Sampling weights: pw
              VCE: jackknife
              MSE: on
Jackknife weights: jkw_1 .. jkw_9
      Single unit: missing
         Strata 1: <one>
  Sampling unit 1: <observations>
           FPC 1: <zero>
```

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## ▷ Example 8: Characteristics for jackknife replicate-weight variables

The `jkrweight()` option has suboptions that allow you to identify certain characteristics of the jackknife replicate-weight variables. These characteristics include the following:

- An identifier for the stratum in which the sampling weights have been adjusted because one of its PSUs was dropped. We use the `stratum()` suboption to set these values. The default is one stratum for all the replicate-weight variables.
- The FPC value. We use the `fpc()` suboption to set these values. The default value is zero.

  This characteristic is ignored when the `mse` option is supplied to `svy jackknife`.
- A jackknife multiplier used in the formula for variance estimation. The multiplier for the standard leave-one-out jackknife method is

$$\frac{n_h - 1}{n_h}$$

  where $n_h$ is the number of PSUs sampled from stratum $h$. We use the `multiplier()` suboption to set these values. The default is derived from the above formula, assuming that $n_h$ is equal to the number of replicate-weight variables for stratum $h$.

Because of privacy concerns, public survey datasets may not contain stratum-specific information. However, the population size and an overall jackknife multiplier will probably be provided. You must then supply this information to `svyset` for the jackknife replicate-weight variables. We will use the 1999–2000 NHANES data to illustrate how to set these characteristics.

The NHANES datasets for years 1999–2000 are available for download from the Centers for Disease Control and Prevention (CDC) website, https://www.cdc.gov. This particular release of the NHANES data contains jackknife replication weights in addition to the usual PSU and stratum information. These variables are contained in the demographic dataset. In our web browser, we saved the demographic data from the CDC website https://wwwn.cdc.gov/Nchs/Nhanes/1999-2000/DEMO.XPT. We suggest that you rename the data to `demo.xpt`.

The 1999–2000 NHANES datasets are distributed in SAS Transport format, so we use Stata's `import sasxport8` command to read the data into memory. Because of the nature of the survey design, the demographic dataset `demo.xpt` has two sampling-weight variables. `wtint2yr` contains the sampling weights appropriate for the interview data, and `wtmec2yr` contains the sampling weights appropriate for the Mobile Examination Center (MEC) exam data. Consequently, there are two sets of jackknife replicate-weight variables. The jackknife replicate-weight variables for the interview data are named `wtirep01`, `wtirep02`, ..., `wtirep52`. The jackknife replicate-weight variables for the MEC exam data are named `wtmrep01`, `wtmrep02`, ..., `wtmrep52`. The documentation published with the NHANES data gives guidance on which weight variables to use.

```
. import sasxport5 demo.xpt
. describe wtint2yr wtmec2yr wtirep01 wtmrep01
Variable      Storage   Display    Value
    name         type    format    label      Variable label
------------------------------------------------------------------------------
wtint2yr        double  %10.0g                Full Sample 2 Year Interview
                                                Weight
wtmec2yr        double  %10.0g                Full Sample 2 Year MEC Exam Weight
wtirep01        double  %10.0g                Interview Weight Jack Knife
                                                Replicate 01
wtmrep01        double  %10.0g                MEC Exam Weight Jack Knife
                                                Replicate 01
```

The number of PSUs in the NHANES population is not apparent, so we will not set an FPC value, but we can set the standard jackknife multiplier for the 52 replicate-weight variables and save the results as a Stata dataset for future use. Also the NHANES datasets all contain a variable called `seqn`. This variable has a respondent sequence number that allows the dataset users to merge the demographic dataset with other 1999–2000 NHANES datasets, so we sort on `seqn` before saving `demo99_00.dta`.

```
. local mult = 51/52
. svyset, jkrweight(wtmrep*, multiplier('mult'))
  (output omitted)
. svyset, jkrweight(wtirep*, multiplier('mult'))
  (output omitted)
. svyset, clear
. sort seqn
. save demo99_00
file demo99_00.dta saved
```

To complete this example, we will perform a simple analysis using the blood pressure data; however, before we can perform any analysis, we have to merge the blood pressure dataset, `bpx.xpt`, with our demographic dataset, `demo99_00.dta`. In our web browser, we saved the blood pressure data from the CDC website https://wwwn.cdc.gov/Nchs/Nhanes/1999-2000/BPX.XPT. We suggest that you rename the data to `bpx.xpt`.

We can then use `import sasxport8` to read in the blood pressure data, sort on `seqn`, and save the resulting dataset to `bpx99_00.dta`. We read in our copy of the demographic data, drop the irrelevant weight variables, and merge in the blood pressure data from `bpx99_00.dta`. A quick call to `tabulate` on the `_merge` variable generated by `merge` indicates that 683 observations in the demographic data are not present in the blood pressure data. We do not `drop` these observations; otherwise, the estimate of the population size will be incorrect. Finally, we set the appropriate sampling and replicate-weight variables with `svyset` before replacing `bpx99_00.dta` with a more complete copy of the blood pressure data.

```
. import sasxport5 bpx.xpt, clear
. sort seqn
. save bpx99_00
file bpx99_00.dta saved
. use demo99_00
. drop wtint?yr wtirep*
. merge 1:1 seqn using bpx99_00
    Result                      Number of obs
    -----------------------------------------
    Not matched                           683
        from master                       683  (_merge==1)
        from using                          0  (_merge==2)
    Matched                             9,282  (_merge==3)
    -----------------------------------------
. drop _merge
. svyset [pw=wtmec2yr], jkrweight(wtmrep*) vce(jackknife)
  (output omitted)
. save bpx99_00, replace
file bpx99_00.dta saved
```

Having saved our merged dataset (with `svyset`tings), we estimate the mean systolic blood pressure for the population, using the MEC exam replication weights for jackknife variance estimation.

```
. svy: mean bpxsar
(running mean on estimation sample)
Jackknife replications (52): .........10.........20.........30.........40.......
> ..50.. done
Survey: Mean estimation
Number of strata = 1              Number of obs   =       7,898
                                  Population size = 231,756,417
                                  Replications    =          52
                                  Design df       =          51
------------------------------------------------------------------------------
             |             Jackknife
             |      Mean   std. err.     [95% conf. interval]
-------------+----------------------------------------------------------------
      bpxsar |   119.7056   .5109122      118.6799    120.7313
------------------------------------------------------------------------------
```

## Combining datasets from multiple surveys

The 2001–2002 NHANES datasets are also available from the CDC website, https://www.cdc.gov. The guidelines that are published with these datasets recommend that the 1999–2000 and 2001–2002 NHANES datasets be combined to increase the accuracy of results. Combining datasets from multiple surveys is a complicated process, and Stata has no specific tools for this task. However, the distributors of the

NHANES datasets provide sampling-weight variables for the 1999–2002 combined data in the respective demographic datasets. They also provide some simple instructions on how to combine the datasets from these two surveys.

In the previous example, we worked with the 1999–2000 NHANES data. The 2001–2002 NHANES demographics data are contained in demo_b.xpt, and the blood pressure data are contained in bpx_b.xpt. We follow the same steps as in the previous example to merge the blood pressure data with the demographic data for 2001–2002.

Visit the following CDC websites and save the data:

https://wwwn.cdc.gov/Nchs/Nhanes/2001-2002/BPX_B.XPT

https://wwwn.cdc.gov/Nchs/Nhanes/2001-2002/DEMO_B.XPT

We suggest that you rename the data to bpx_b.xpt and demo_b.xpt. We can then continue with our example:

```
. import sasxport5 bpx_b.xpt, clear
. sort seqn
. save bpx01_02
file bpx01_02.dta saved
. import sasxport5 demo_b.xpt, clear
. drop wtint?yr
. sort seqn
. merge 1:1 seqn using bpx01_02
    Result                      Number of obs
    -----------------------------------------
    Not matched                           562
        from master                       562  (_merge==1)
        from using                          0  (_merge==2)
    Matched                            10,477  (_merge==3)
    -----------------------------------------

. drop _merge
. svyset sdmvpsu [pw=wtmec2yr], strata(sdmvstra)
Sampling weights: wtmec2yr
             VCE: linearized
     Single unit: missing
        Strata 1: sdmvstra
 Sampling unit 1: sdmvpsu
           FPC 1: <zero>
. save bpx01_02, replace
file bpx01_02.dta saved
```

The demographic dataset for 2001–2002 does not contain replicate-weight variables, but there are variables that provide information on PSUs and strata for variance estimation. The PSU information is contained in sdmvpsu, and the stratum information is in sdmvstra. See the documentation that comes with the NHANES datasets for the details regarding these variables.

This new blood pressure dataset (bpx01_02.dta) is all we need if we are interested in analyzing blood pressure data only for 2001–2002. However, we want to use the 1999–2002 combined data, so we will follow the advice in the guidelines and just combine the datasets from the two surveys.

For those concerned about overlapping stratum identifiers between the two survey datasets, it is a simple exercise to check that sdmvstra ranges from 1 to 13 for 1999–2000 but ranges from 14 to 28 for 2001–2002. Thus the stratum identifiers do not overlap, so we can simply append the data.

The 2001–2002 NHANES demographic dataset has no jackknife replicate-weight variables, so we drop the replicate-weight variables from the 1999–2000 dataset. The sampling-weight variable `wtmec2yr` is no longer appropriate for use with the combined data because its values are based on the survey designs individually, so we drop it from the combined dataset. Finally, we use `svyset` to identify the design variables for the combined surveys. `wtmec4yr` is the sampling-weight variable for the MEC exam data developed by the data producers for the combined 1999–2002 NHANES data.

```
. use bpx99_00
. drop wt?rep*
. append using bpx01_02
. drop wtmec2yr
. svyset sdmvpsu [pw=wtmec4yr], strata(sdmvstra)
Sampling weights: wtmec4yr
             VCE: linearized
     Single unit: missing
        Strata 1: sdmvstra
 Sampling unit 1: sdmvpsu
           FPC 1: <zero>
. save bpx99_02
file bpx99_02.dta saved
```

Now we can estimate the mean systolic blood pressure for our population by using the combined surveys and jackknife variance estimation.

```
. svy jackknife: mean bpxsar
(running mean on estimation sample)
Jackknife replications (57): .........10.........20.........30.........40.......
> ..50....... done
Survey: Mean estimation
Number of strata = 28            Number of obs   =      16,297
Number of PSUs   = 57            Population size = 237,466,080
                                 Replications    =          57
                                 Design df       =          29
------------------------------------------------------------------------------
             |                Jackknife
             |       Mean   std. err.      [95% conf. interval]
-------------+----------------------------------------------------------------
      bpxsar |   119.8914   .3828434      119.1084    120.6744
------------------------------------------------------------------------------
```

## Video example

Specifying the design of your survey data to Stata

## Stored results

svyset stores the following in r():

Scalars

| | |
|---|---|
| r(stages) | number of sampling stages |
| r(stages_wt) | last stage containing stage-level weights |
| r(bsn) | bootstrap mean-weight adjustment |
| r(fay) | Fay's adjustment |
| r(dof) | dof() value |

Macros

| | |
|---|---|
| r(wtype) | weight type |
| r(wexp) | weight expression |
| r(wvar) | weight variable name |
| r(weight#) | variable identifying weight for stage # |
| r(su#) | variable identifying sampling units for stage # |
| r(strata#) | variable identifying strata for stage # |
| r(fpc#) | FPC for stage # |
| r(bsrweight) | bsrweight() variable list |
| r(brrweight) | brrweight() variable list |
| r(jkrweight) | jkrweight() variable list |
| r(sdrweight) | sdrweight() variable list |
| r(sdrfpc) | fpc() value from within sdrweight() |
| r(vce) | *vcetype* specified in vce() |
| r(mse) | mse, if specified |
| r(poststrata) | poststrata() variable |
| r(postweight) | postweight() variable |
| r(rake) | rake() specification |
| r(regress) | regress() specification |
| r(settings) | svyset arguments to reproduce the current settings |
| r(singleunit) | singleunit() setting |

## References

Cochran, W. G. 1977. *Sampling Techniques.* 3rd ed. New York: Wiley.

Judkins, D. R. 1990. Fay's method for variance estimation. *Journal of Official Statistics* 6: 223–239.

O'Donnell, O., E. van Doorslaer, A. Wagstaff, and M. Lindelow. 2008. *Analyzing Health Equity Using Household Survey Data: A Guide to Techniques and Their Implementation.* Washington, DC: World Bank.

## Also see

[SVY] **Survey** — Introduction to survey commands

[SVY] **svy** — The survey prefix command

[SVY] **svydescribe** — Describe survey data

[SVY] **Calibration** — Calibration for survey data

[SVY] **Poststratification** — Poststratification for survey data

[SVY] **Subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **Variance estimation** — Variance estimation for survey data

Description Remarks and examples References Also see

# Description

Stata's suite of estimation commands for survey data use the most commonly used variance estimation techniques: bootstrap, balanced repeated replication, jackknife, successive difference replication, and linearization. The bootstrap, balanced repeated replication, jackknife, and successive difference replication techniques are known as replication methods in the survey literature. We stick with that nomenclature here, but note that these techniques are also known as resampling methods. This entry discusses the details of these variance estimation techniques.

Also see Cochran (1977), Wolter (2007), and Shao and Tu (1995) for some background on these variance estimators.

# Remarks and examples

Remarks are presented under the following headings:



## Variance of the total

This section describes the methods and formulas for `svy: total`. The variance estimators not using replication methods use the variance of a total as an important ingredient; this section therefore also introduces variance estimation for survey data.

We will discuss the variance estimators for two complex survey designs:

1. The stratified single-stage design is the simplest design that has the elements present in most complex survey designs.
2. Adding a second stage of clustering to the previous design results in a variance estimator for designs with multiple stages of clustered sampling.

### Stratified single-stage design

The population is partitioned into groups called *strata*. Clusters of observations are randomly sampled—with or without replacement—from within each stratum. These clusters are called *primary sampling units* (PSUs). In single-stage designs, data are collected from every member of the sampled PSUs. When the observed data are analyzed, sampling weights are used to account for the survey design. If the PSUs were sampled without replacement, a finite population correction (FPC) is applied to the variance estimator.

The `svyset` syntax to specify this design is

`svyset` *psu* `[pweight=`*weight*`], strata(`*strata*`) fpc(`*fpc*`)`

The stratum identifiers are contained in the variable named *strata*, PSU identifiers are contained in variable *psu*, the sampling weights are contained in variable *weight*, and the values for the FPC are contained in variable *fpc*.

Let $h = 1, \ldots, L$ count the strata and $(h, i)$ denote the $i$th PSU in stratum $h$, where $i = 1, \ldots, N_h$ and $N_h$ is the number of PSUs in stratum $h$. Let $(h, i, j)$ denote the $j$th individual from PSU $(h, i)$ and $M_{hi}$ be the number of individuals in PSU $(h, i)$; then

$$M = \sum_{h=1}^{L} \sum_{i=1}^{N_h} M_{hi}$$

is the number of individuals in the population. Let $Y_{hij}$ be a survey item for individual $(h, i, j)$; for example, $Y_{hij}$ might be income for adult $j$ living in block $i$ of county $h$. The associated population total is

$$Y = \sum_{h=1}^{L} \sum_{i=1}^{N_h} \sum_{j=1}^{M_{hi}} Y_{hij}$$

Let $y_{hij}$ denote the items for individuals who are members of the sampled PSUs; here $h = 1, \ldots, L$; $i = 1, \ldots, n_h$; and $j = 1, \ldots, m_{hi}$. The number of individuals in the sample (number of observations) is

$$m = \sum_{h=1}^{L} \sum_{i=1}^{n_h} m_{hi}$$

The estimator for $Y$ is

$$\hat{Y} = \sum_{h=1}^{L} \sum_{i=1}^{n_h} \sum_{j=1}^{m_{hi}} w_{hij} y_{hij}$$

where $w_{hij}$ is a sampling weight, and its unadjusted value for this design is $w_{hij} = N_h/n_h$. The estimator for the number of individuals in the population (population size) is

$$\widehat{M} = \sum_{h=1}^{L} \sum_{i=1}^{n_h} \sum_{j=1}^{m_{hi}} w_{hij}$$

The estimator for the variance of $\hat{Y}$ is

$$\hat{V}(\hat{Y}) = \sum_{h=1}^{L}(1-f_h)\frac{n_h}{n_h-1}\sum_{i=1}^{n_h}(y_{hi}-\overline{y}_h)^2 \tag{1}$$

where $y_{hi}$ is the weighted total for PSU $(h,i)$,

$$y_{hi} = \sum_{j=1}^{m_{hi}} w_{hij}y_{hij}$$

and $\overline{y}_h$ is the mean of the PSU totals for stratum $h$:

$$\overline{y}_h = \frac{1}{n_h}\sum_{i=1}^{n_h} y_{hi}$$

The factor $(1-f_h)$ is the FPC for stratum $h$, and $f_h$ is the sampling rate for stratum $h$. The sampling rate $f_h$ is derived from the variable specified in the `fpc()` option of `svyset`. If an FPC variable is not `svyset`, then $f_h = 0$. If an FPC variable is set and its values are greater than or equal to $n_h$, then the variable is assumed to contain the values of $N_h$, and $f_h$ is given by $f_h = n_h/N_h$. If its values are less than or equal to 1, then the variable is assumed to contain the sampling rates $f_h$.

If multiple variables are supplied to `svy: total`, covariances are also computed. The estimator for the covariance between $\hat{Y}$ and $\widehat{X}$ (notation for $X$ is defined similarly to that of $Y$) is

$$\widehat{\mathrm{Cov}}(\hat{Y},\widehat{X}) = \sum_{h=1}^{L}(1-f_h)\frac{n_h}{n_h-1}\sum_{i=1}^{n_h}(y_{hi}-\overline{y}_h)(x_{hi}-\overline{x}_h)$$

### Stratified two-stage design

The population is partitioned into strata. PSUs are randomly sampled without replacement from within each stratum. Clusters of observations are then randomly sampled—with or without replacement—from within the sampled PSUs. These clusters are called *secondary sampling units* (SSUs). Data are then collected from every member of the sampled SSUs. When the observed data are analyzed, sampling weights are used to account for the survey design. Each sampling stage provides a component to the variance estimator and has its own FPC.

The `svyset` syntax to specify this design is

`svyset` *psu* `[pweight=`*weight*`], strata(`*strata*`) fpc(`*fpc*$_1$`) || `*ssu*`, fpc(`*fpc*$_2$`)`

The stratum identifiers are contained in the variable named *strata*, PSU identifiers are contained in variable *psu*, the sampling weights are contained in variable *weight*, the values for the FPC for the first sampling stage are contained in variable *fpc*$_1$, SSU identifiers are contained in variable *ssu*, and the values for the FPC for the second sampling stage are contained in variable *fpc*$_2$.

The notation for this design is based on the previous notation. There still are $L$ strata, and $(h, i)$ identifies the $i$th PSU in stratum $h$. Let $M_{hi}$ be the number of SSUs in PSU $(h, i)$, $M_{hij}$ be the number of individuals in SSU $(h, i, j)$, and

$$M = \sum_{h=1}^{L} \sum_{i=1}^{N_h} \sum_{j=1}^{M_h i} M_{hij}$$

be the population size. Let $Y_{hijk}$ be a survey item for individual $(h, i, j, k)$; for example, $Y_{hijk}$ might be income for adult $k$ living in block $j$ of county $i$ of state $h$. The associated population total is

$$Y = \sum_{h=1}^{L} \sum_{i=1}^{N_h} \sum_{j=1}^{M_{hi}} \sum_{k=1}^{M_{hij}} Y_{hijk}$$

Let $y_{hijk}$ denote the items for individuals who are members of the sampled SSUs; here $h = 1, \ldots, L$; $i = 1, \ldots, n_h$; $j = 1, \ldots, m_{hi}$; and $k = 1, \ldots, m_{hij}$. The number of observations is

$$m = \sum_{h=1}^{L} \sum_{i=1}^{n_h} \sum_{j=1}^{m_{hi}} m_{hij}$$

The estimator for $Y$ is

$$\hat{Y} = \sum_{h=1}^{L} \sum_{i=1}^{n_h} \sum_{j=1}^{m_{hi}} \sum_{k=1}^{m_{hij}} w_{hijk} y_{hijk}$$

where $w_{hijk}$ is a sampling weight, and its unadjusted value for this design is

$$w_{hijk} = \left(\frac{N_h}{n_h}\right)\left(\frac{M_{hi}}{m_{hi}}\right)$$

The estimator for the population size is

$$\widehat{M} = \sum_{h=1}^{L} \sum_{i=1}^{n_h} \sum_{j=1}^{m_{hi}} \sum_{k=1}^{m_{hij}} w_{hijk}$$

The estimator for the variance of $\hat{Y}$ is

$$\begin{aligned} \hat{V}(\hat{Y}) = &\sum_{h=1}^{L} (1 - f_h) \frac{n_h}{n_h - 1} \sum_{i=1}^{n_h} (y_{hi} - \overline{y}_h)^2 \\ &+ \sum_{h=1}^{L} f_h \sum_{i=1}^{n_h} (1 - f_{hi}) \frac{m_{hi}}{m_{hi} - 1} \sum_{j=1}^{m_{hi}} (y_{hij} - \overline{y}_{hi})^2 \end{aligned} \tag{2}$$

where $y_{hi}$ is the weighted total for PSU $(h, i)$; $\overline{y}_h$ is the mean of the PSU totals for stratum $h$; $y_{hij}$ is the weighted total for SSU $(h, i, j)$,

$$y_{hij} = \sum_{k=1}^{m_{hij}} w_{hijk} y_{hijk}$$

and $\overline{y}_{hi}$ is the mean of the SSU totals for PSU $(h, i)$,

$$\overline{y}_{hi} = \frac{1}{m_{hi}} \sum_{j=1}^{m_{hi}} y_{hij}$$

Equation (2) is equivalent to (1) with an added term representing the increase in variability because of the second stage of sampling. The factor $(1-f_h)$ is the FPC, and $f_h$ is the sampling rate for the first stage of sampling. The factor $(1-f_{hi})$ is the FPC, and $f_{hi}$ is the sampling rate for PSU $(h,i)$. The sampling rate $f_{hi}$ is derived in the same manner as $f_h$.

If multiple variables are supplied to `svy: total`, covariances are also computed. For estimated totals $\widehat{Y}$ and $\widehat{X}$ (notation for $X$ is defined similarly to that of $Y$), the covariance estimator is

$$\widehat{\mathrm{Cov}}(\widehat{Y},\widehat{X}) = \sum_{h=1}^{L}(1-f_h)\frac{n_h}{n_h-1}\sum_{i=1}^{n_h}(y_{hi}-\overline{y}_h)(x_{hi}-\overline{x}_h) + \sum_{h=1}^{L}f_h\sum_{i=1}^{n_h}(1-f_{hi})\frac{m_{hi}}{m_{hi}-1}\sum_{j=1}^{m_{hi}}(y_{hij}-\overline{y}_{hi})(x_{hij}-\overline{x}_{hi})$$

On the basis of the formulas (1) and (2), writing down the variance estimator for a survey design with three or more stages is a matter of deriving the variance component for each sampling stage. The sampling units from a given stage pose as strata for the next sampling stage.

All but the last stage must be sampled without replacement to get nonzero variance components from each stage of clustered sampling. For example, if $f_h = 0$ in (2), the second stage contributes nothing to the variance estimator.

## Variance for census data

The point estimates that result from the analysis of census data, in which the entire population was sampled without replacement, are the population's parameters instead of random variables. As such, there is no sample-to-sample variation if we consider the population fixed. Here the sampling fraction is one; thus, if the FPC variable you `svyset` for the first sampling stage is one, Stata will report a standard error of zero.

## Certainty sampling units

Stata's `svy` commands identify strata with an FPC equal to one as units sampling with certainty. To properly determine the design degrees of freedom, certainty sampling units should be contained within their own strata, one for each certainty unit, in each sampling stage. Although the observations contained in certainty units from a given sampling stage play a role in parameter estimation, they contribute nothing to the variance for that stage.

## Strata with one sampling unit

By default, Stata's `svy` commands report missing standard errors when they encounter a stratum with one sampling unit. Although the best way to solve this problem is to reassign the sampling unit to another appropriately chosen stratum, there are three automatic alternatives that you can choose from, in the `singleunit()` option, when you `svyset` your data.

`singleunit(certainty)` treats the strata with single sampling units as certainty units.

`singleunit(scaled)` treats the strata with single sampling units as certainty units but multiplies the variance components from each stage by a scaling factor. For a given sampling stage, suppose that $L$ is the total number of strata, $L_c$ is the number of certainty strata, and $L_s$ is the number of strata with

one sampling unit, and then the scaling factor is $(L - L_c)/(L - L_c - L_s)$. Using this scaling factor is the same as using the average of the variances from the strata with multiple sampling units for each stratum with one sampling unit.

`singleunit(centered)` specifies that strata with one sampling unit are centered at the population mean instead of the stratum mean. The quotient $n_h/(n_h - 1)$ in the variance formula is also taken to be 1 if $n_h = 1$.

## Ratios and other functions of survey data

Shah (2004) points out a simple procedure for deriving the linearized variance for functions of survey data that are continuous functions of the sampling weights. Let $\theta$ be a (possibly vector-valued) function of the population data and $\hat{\theta}$ be its associated estimator based on survey data.

1. Define the $j$th observation of the score variable by

$$z_j = \frac{\partial \hat{\theta}}{\partial w_j}$$

   If $\hat{\theta}$ is implicitly defined through estimating equations, $z_j$ can be computed by taking the partial derivative of the estimating equations with respect to $w_j$.

2. Define the weighted total of the score variable by

$$\widehat{Z} = \sum_{j=1}^{m} w_j z_j$$

3. Estimate the variance $V(\widehat{Z})$ by using the design-based variance estimator for the total $\widehat{Z}$. This variance estimator is an approximation of $V(\hat{\theta})$.

### Revisiting the total estimator

As a first example, we derive the variance of the total from a stratified single-stage design. Here you have $\hat{\theta} = \hat{Y}$, and deriving the score variable for $\hat{Y}$ results in the original values of the variable of interest.

$$z_j(\hat{\theta}) = z_j(\hat{Y}) = \frac{\partial \hat{Y}}{\partial w_j} = y_j$$

Thus you trivially recover the variance of the total given in (1) and (2).

### The ratio estimator

The estimator for the population ratio is

$$\widehat{R} = \frac{\hat{Y}}{\widehat{X}}$$

and its score variable is

$$z_j(\widehat{R}) = \frac{\partial \widehat{R}}{\partial w_j} = \frac{y_j - \widehat{R}\, x_j}{\widehat{X}}$$

Plugging this into (1) or (2) results in a variance estimator that is algebraically equivalent to the variance estimator derived from directly applying the delta method (a first-order Taylor expansion with respect to $y$ and $x$)

$$\hat{V}(\widehat{R}) = \frac{1}{\widehat{X}^2}\{\hat{V}(\hat{Y}) - 2\widehat{R}\,\widehat{\mathrm{Cov}}(\hat{Y}, \widehat{X}) + \widehat{R}^2\,\hat{V}(\widehat{X})\}$$

### A note about score variables

The functional form of the score variable for each estimation command is detailed in the *Methods and formulas* section of its manual entry; see [R] **total**, [R] **ratio**, and [R] **mean**.

Although Deville (1999) and Demnati and Rao (2004) refer to $z_j$ as the *linearized variable*, here it is referred to as the *score variable* to tie it more closely to the model-based estimators discussed in the following section.

## Linearized/robust variance estimation

The regression models for survey data that allow the `vce(linearized)` option use *linearization*-based variance estimators that are natural extensions of the variance estimator for totals. For general background on regression and generalized linear model analysis of complex survey data, see Binder (1983); Cochran (1977); Fuller (1975); Godambe (1991); Kish and Frankel (1974); Särndal, Swensson, and Wretman (1992); and Skinner (1989).

Suppose that you observed $(Y_j, \mathbf{x}_j)$ for the entire population and are interested in modeling the relationship between $Y_j$ and $\mathbf{x}_j$ by the vector of parameters $\boldsymbol{\beta}$ that solve the following estimating equations:

$$G(\boldsymbol{\beta}) = \sum_{j=1}^{M} S(\boldsymbol{\beta}; Y_j, \mathbf{x}_j) = 0$$

For ordinary least squares, $G(\boldsymbol{\beta})$ is the normal equations

$$G(\boldsymbol{\beta}) = X'Y - X'X\boldsymbol{\beta} = 0$$

where $Y$ is the vector of outcomes for the full population and $X$ is the matrix of explanatory variables for the full population. For a pseudolikelihood model—such as logistic regression—$G(\boldsymbol{\beta})$ is the first derivative of the log-pseudolikelihood function with respect to $\boldsymbol{\beta}$. Estimate $\boldsymbol{\beta}$ by solving for $\widehat{\boldsymbol{\beta}}$ from the weighted sample estimating equations

$$\widehat{G}(\boldsymbol{\beta}) = \sum_{j=1}^{m} w_j S(\boldsymbol{\beta}; y_j, \mathbf{x}_j) = 0 \tag{3}$$

The associated estimation command with `iweights` will produce point estimates $\widehat{\boldsymbol{\beta}}$ equal to the solution of (3).

A first-order matrix Taylor-series expansion yields

$$\widehat{\boldsymbol{\beta}} - \boldsymbol{\beta} \approx -\left\{ \frac{\partial \widehat{G}(\boldsymbol{\beta})}{\partial \boldsymbol{\beta}} \right\}^{-1} \widehat{G}(\boldsymbol{\beta})$$

with the following variance estimator for $\widehat{\boldsymbol{\beta}}$:

$$\hat{V}(\widehat{\boldsymbol{\beta}}) = \left[ \left\{ \frac{\partial \widehat{G}(\boldsymbol{\beta})}{\partial \boldsymbol{\beta}} \right\}^{-1} \hat{V}\{\widehat{G}(\boldsymbol{\beta})\} \left\{ \frac{\partial \widehat{G}(\boldsymbol{\beta})}{\partial \boldsymbol{\beta}} \right\}^{-\mathrm{T}} \right] \Bigg|_{\boldsymbol{\beta}=\widehat{\boldsymbol{\beta}}} = D\hat{V}\{\widehat{G}(\boldsymbol{\beta})\}\Big|_{\boldsymbol{\beta}=\widehat{\boldsymbol{\beta}}} D'$$

where $D$ is $(X_s' W X_s)^{-1}$ for linear regression (where $W$ is a diagonal matrix of the sampling weights and $X_s$ is the matrix of sampled explanatory variables) or the inverse of the negative Hessian matrix from the pseudolikelihood model. Write $\widehat{G}(\boldsymbol{\beta})$ as

$$\widehat{G}(\boldsymbol{\beta}) = \sum_{j=1}^{m} w_j \mathbf{d}_j$$

where $\mathbf{d}_j = s_j \mathbf{x}_j$ and $s_j$ is a residual for linear regression or an equation-level score from the pseudolikelihood model. The term *equation-level score* means the derivative of the log pseudolikelihood with respect to $\mathbf{x}_j\boldsymbol{\beta}$. In either case, $\widehat{G}(\widehat{\boldsymbol{\beta}})$ is an estimator for the total $G(\boldsymbol{\beta})$, and the variance estimator $\hat{V}\{\widehat{G}(\boldsymbol{\beta})\}|_{\boldsymbol{\beta}=\widehat{\boldsymbol{\beta}}}$ is computed using the design-based variance estimator for a total.

The above result is easily extended to models with ancillary parameters, multiple regression equations, or both.

## The bootstrap

The bootstrap methods for survey data used in recent years are largely due to McCarthy and Snowden (1985), Rao and Wu (1988), and Rao, Wu, and Yue (1992). For example, Yeo, Mantel, and Liu (1999) cite Rao, Wu, and Yue (1992) with the method for variance estimation used in the National Population Health Survey conducted by Statistics Canada.

In the survey bootstrap, the model is fit multiple times, once for each of a set of adjusted sampling weights that mimic bootstrap resampling. The variance is estimated using the resulting replicated point estimates.

Let $\hat{\boldsymbol{\theta}}$ be the vector of point estimates computed using the sampling weights for a given survey dataset (for example, $\hat{\boldsymbol{\theta}}$ could be a vector of means, ratios, or regression coefficients). Each bootstrap replicate is produced by fitting the model with adjusted sampling weights. The adjusted sampling weights are derived from the method used to resample the original survey data.

According to Yeo, Mantel, and Liu (1999), if $n_h$ is the number of observed PSUs in stratum $h$, then $n_h - 1$ PSUs are sampled with replacement from within stratum $h$. This sampling is performed independently across the strata to produce one bootstrap sample of the survey data. Let $r$ be the number of bootstrap samples. Suppose that we are about to generate the adjusted-weight variable for the $i$th bootstrap replication and $w_{hij}$ is the sampling weight attached to the $j$th observation in the $i$th PSU of stratum $h$. The adjusted weight is

$$w^*_{hij} = \frac{n_h}{n_h - 1} m^*_{hi} w_{hij}$$

where $m^*_{hi}$ is the number of times the $i$th cluster in stratum $h$ was resampled.

To accommodate privacy concerns, many public-use datasets contain replicate-weight variables derived from the "mean bootstrap" described by Yung (1997). In the mean bootstrap, each adjusted weight is derived from $b$ bootstrap samples instead of one. The adjusted weight is

$$w^*_{hij} = \frac{n_h}{n_h - 1}\overline{m}^*_{hi} w_{hij}$$

where

$$\overline{m}^*_{hi} = \frac{1}{b}\sum_{k=1}^{b} m^*_{hik}$$

is the average of the number of times the $i$th cluster in stratum $h$ was resampled among the $b$ bootstrap samples.

Each replicate is produced using an adjusted-weight variable with the estimation command that computed $\hat{\boldsymbol{\theta}}$. The adjusted-weight variables must be supplied to `svyset` with the `bsrweight()` option. For the mean bootstrap, $b$ must also be supplied to `svyset` with the `bsn()` option; otherwise, `bsn(1)` is assumed. We call the variables supplied to the `bsrweight()` option *bootstrap replicate-weight variables* when $b = 1$ and *mean bootstrap replicate-weight variables* when $b > 1$.

Let $\hat{\boldsymbol{\theta}}_{(i)}$ be the vector of point estimates from the $i$th replication. When the `mse` option is specified, the variance estimator is

$$\hat{V}(\hat{\boldsymbol{\theta}}) = \frac{b}{r}\sum_{i=1}^{r}\{\hat{\boldsymbol{\theta}}_{(i)} - \hat{\boldsymbol{\theta}}\}\{\hat{\boldsymbol{\theta}}_{(i)} - \hat{\boldsymbol{\theta}}\}'$$

Otherwise, the variance estimator is

$$\hat{V}(\hat{\boldsymbol{\theta}}) = \frac{b}{r}\sum_{i=1}^{r}\{\hat{\boldsymbol{\theta}}_{(i)} - \overline{\boldsymbol{\theta}}_{(.)}\}\{\hat{\boldsymbol{\theta}}_{(i)} - \overline{\boldsymbol{\theta}}_{(.)}\}'$$

where $\overline{\boldsymbol{\theta}}_{(.)}$ is the bootstrap mean,

$$\overline{\boldsymbol{\theta}}_{(.)} = \frac{1}{r}\sum_{i=1}^{r}\hat{\boldsymbol{\theta}}_{(i)}$$

## BRR

BRR was first introduced by McCarthy (1966, 1969a, and 1969b) as a method of variance estimation for designs with two PSUs in every stratum. The BRR variance estimator tends to give more reasonable variance estimates for this design than the linearized variance estimator, which can result in large values and undesirably wide confidence intervals.

The model is fit multiple times, once for each of a balanced set of combinations where one PSU is dropped (or downweighted) from each stratum. The variance is estimated using the resulting replicated point estimates (replicates). Although the BRR method has since been generalized to include other designs, Stata's implementation of BRR requires two PSUs per stratum.

Let $\hat{\boldsymbol{\theta}}$ be the vector of point estimates computed using the sampling weights for a given stratified survey design (for example, $\hat{\boldsymbol{\theta}}$ could be a vector of means, ratios, or regression coefficients). Each BRR replicate is produced by dropping (or downweighting) a PSU from every stratum. This could result in as many as $2^L$ replicates for a dataset with $L$ strata; however, the BRR method uses Hadamard matrices to identify a balanced subset of the combinations from which to produce the replicates.

A Hadamard matrix is a square matrix, $H_r$ (with $r$ rows and columns), such that $H_r' H_r = rI$, where $I$ is the identity matrix. The elements of $H_r$ are $+1$ and $-1$; $-1$ causes the first PSU to be downweighted and $+1$ causes the second PSU to be downweighted. Thus $r$ must be greater than or equal to the number of strata.

Suppose that we are about to generate the adjusted-weight variable for the $i$th replication and $w_j$ is the sampling weight attached to the $j$th observation, which happens to be in the first PSU of stratum $h$. The adjusted weight is

$$w_j^* = \begin{cases} f w_j, & \text{if } H_r[i,h] = -1 \\ (2-f) w_j, & \text{if } H_r[i,h] = +1 \end{cases}$$

where $f$ is Fay's adjustment (Judkins 1990). By default, $f = 0$.

Each replicate is produced using an adjusted-weight variable with the estimation command that computed $\hat{\boldsymbol{\theta}}$. The adjusted-weight variables can be generated by Stata or supplied to `svyset` with the `brrweight()` option. We call the variables supplied to the `brrweight()` option *BRR replicate-weight variables*.

Let $\hat{\boldsymbol{\theta}}_{(i)}$ be the vector of point estimates from the $i$th replication. When the `mse` option is specified, the variance estimator is

$$\hat{V}(\hat{\boldsymbol{\theta}}) = \frac{1}{r(1-f)^2} \sum_{i=1}^{r} \{\hat{\boldsymbol{\theta}}_{(i)} - \hat{\boldsymbol{\theta}}\}\{\hat{\boldsymbol{\theta}}_{(i)} - \hat{\boldsymbol{\theta}}\}'$$

Otherwise, the variance estimator is

$$\hat{V}(\hat{\boldsymbol{\theta}}) = \frac{1}{r(1-f)^2} \sum_{i=1}^{r} \{\hat{\boldsymbol{\theta}}_{(i)} - \overline{\boldsymbol{\theta}}_{(.)}\}\{\hat{\boldsymbol{\theta}}_{(i)} - \overline{\boldsymbol{\theta}}_{(.)}\}'$$

where $\overline{\boldsymbol{\theta}}_{(.)}$ is the BRR mean,

$$\overline{\boldsymbol{\theta}}_{(.)} = \frac{1}{r} \sum_{i=1}^{r} \hat{\boldsymbol{\theta}}_{(i)}$$

## The jackknife

The jackknife method for variance estimation is appropriate for many models and survey designs. The model is fit multiple times, and each time one or more PSUs are dropped from the estimation sample. The variance is estimated using the resulting replicates (replicated point estimates).

Let $\hat{\boldsymbol{\theta}}$ be the vector of point estimates computed using the sampling weights for a given survey design (for example, $\hat{\boldsymbol{\theta}}$ could be a vector of means, ratios, or regression coefficients). The dataset is resampled by dropping one or more PSUs from one stratum and adjusting the sampling weights before recomputing a replicate for $\hat{\boldsymbol{\theta}}$.

Let $w_{hij}$ be the sampling weight for the $j$th individual from PSU $i$ in stratum $h$. Suppose that you are about to generate the adjusted weights for the replicate resulting from dropping $k$ PSUs from stratum $h$. The adjusted weight is

$$w_{abj}^* = \begin{cases} 0, & \text{if } a = h \text{ and } b \text{ is dropped} \\ \frac{n_h}{n_h - k} w_{abj}, & \text{if } a = h \text{ and } b \text{ is not dropped} \\ w_{abj}, & \text{otherwise} \end{cases}$$

Each replicate is produced by using the adjusted-weight variable with the estimation command that produced $\hat{\boldsymbol{\theta}}$. For the delete-one jackknife (where one PSU is dropped for each replicate), adjusted weights can be generated by Stata or supplied to `svyset` with the `jkrweight()` option. For the delete-$k$ jackknife (where $k > 1$ PSUs are dropped for each replicate), the adjusted-weight variables must be supplied to `svyset` using the `jkrweight()` option. The variables supplied to the `jkrweight()` option are called *jackknife replicate-weight variables*.

### The delete-one jackknife

Let $\hat{\boldsymbol{\theta}}_{(h,i)}$ be the point estimates (replicate) from leaving out the $i$th PSU from stratum $h$. The pseudovalue for replicate $(h, i)$ is

$$\hat{\boldsymbol{\theta}}^*_{h,i} = \hat{\boldsymbol{\theta}}_{(h,i)} + n_h\{\hat{\boldsymbol{\theta}} - \hat{\boldsymbol{\theta}}_{(h,i)}\}$$

When the `mse` option is specified, the variance estimator is

$$\hat{V}(\hat{\boldsymbol{\theta}}) = \sum_{h=1}^{L}(1 - f_h)\, m_h \sum_{i=1}^{n_h}\{\hat{\boldsymbol{\theta}}_{(h,i)} - \hat{\boldsymbol{\theta}}\}\{\hat{\boldsymbol{\theta}}_{(h,i)} - \hat{\boldsymbol{\theta}}\}'$$

and the jackknife mean is

$$\overline{\boldsymbol{\theta}}_{(.)} = \frac{1}{n}\sum_{h=1}^{L}\sum_{i=1}^{n_h}\hat{\boldsymbol{\theta}}_{(h,i)}$$

where $f_h$ is the sampling rate and $m_h$ is the jackknife multiplier associated with stratum $h$. Otherwise, the variance estimator is

$$\hat{V}(\hat{\boldsymbol{\theta}}) = \sum_{h=1}^{L}(1 - f_h)\, m_h \sum_{i=1}^{n_h}\{\hat{\boldsymbol{\theta}}_{(h,i)} - \overline{\boldsymbol{\theta}}_h\}\{\hat{\boldsymbol{\theta}}_{(h,i)} - \overline{\boldsymbol{\theta}}_h\}', \qquad \overline{\boldsymbol{\theta}}_h = \frac{1}{n_h}\sum_{i=1}^{n_h}\hat{\boldsymbol{\theta}}_{(h,i)}$$

and the jackknife mean is

$$\overline{\boldsymbol{\theta}}^* = \frac{1}{n}\sum_{h=1}^{L}\sum_{i=1}^{n_h}\hat{\boldsymbol{\theta}}^*_{h,i}$$

The multiplier for the delete-one jackknife is

$$m_h = \frac{n_h - 1}{n_h}$$

### The delete-k jackknife

Let $\tilde{\boldsymbol{\theta}}_{(h,d)}$ be one of the point estimates that resulted from leaving out $k$ PSUs from stratum $h$. Let $c_h$ be the number of such combinations that were used to generate a replicate for stratum $h$; then $d = 1, \ldots, c_h$. If all combinations were used, then

$$c_h = \frac{n_h!}{(n_h - k)!k!}$$

The pseudovalue for replicate $(h, d)$ is

$$\tilde{\boldsymbol{\theta}}^*_{h,d} = \tilde{\boldsymbol{\theta}}_{(h,d)} + c_h\{\hat{\boldsymbol{\theta}} - \tilde{\boldsymbol{\theta}}_{(h,d)}\}$$

When the mse option is specified, the variance estimator is

$$\hat{V}(\hat{\boldsymbol{\theta}}) = \sum_{h=1}^{L}(1-f_h)\,m_h \sum_{d=1}^{c_h}\{\tilde{\boldsymbol{\theta}}_{(h,d)} - \hat{\boldsymbol{\theta}}\}\{\tilde{\boldsymbol{\theta}}_{(h,d)} - \hat{\boldsymbol{\theta}}\}'$$

and the jackknife mean is

$$\overline{\boldsymbol{\theta}}_{(.)} = \frac{1}{C}\sum_{h=1}^{L}\sum_{d=1}^{c_h}\tilde{\boldsymbol{\theta}}_{(h,d)}, \quad C = \sum_{h=1}^{L} c_h$$

Otherwise, the variance estimator is

$$\hat{V}(\hat{\boldsymbol{\theta}}) = \sum_{h=1}^{L}(1-f_h)\,m_h \sum_{d=1}^{c_h}\{\tilde{\boldsymbol{\theta}}_{(h,d)} - \overline{\boldsymbol{\theta}}_h\}\{\tilde{\boldsymbol{\theta}}_{(h,d)} - \overline{\boldsymbol{\theta}}_h\}', \qquad \overline{\boldsymbol{\theta}}_h = \frac{1}{c_h}\sum_{d=1}^{c_h}\tilde{\boldsymbol{\theta}}_{(h,d)}$$

and the jackknife mean is

$$\overline{\boldsymbol{\theta}}^* = \frac{1}{C}\sum_{h=1}^{L}\sum_{d=1}^{c_h}\tilde{\boldsymbol{\theta}}^*_{h,d}$$

The multiplier for the delete-$k$ jackknife is

$$m_h = \frac{n_h - k}{c_h k}$$

Variables containing the values for the stratum identifier $h$, the sampling rate $f_h$, and the jackknife multiplier $m_h$ can be svyset using the respective suboptions of the jkrweight() option: stratum(), fpc(), and multiplier().

## Successive difference replication

Successive difference replication (SDR) was first introduced by Fay and Train (1995) as a method of variance estimation for annual demographic supplements to the Current Population Survey. This method is typically applied to systematic samples, where the observed sampling units are somehow ordered.

In SDR, the model is fit multiple times, once for each of a set of adjusted sampling weights. The variance is estimated using the resulting replicated point estimates.

Let $\hat{\boldsymbol{\theta}}$ be the vector of point estimates computed using the sampling weights for a given survey dataset (for example, $\hat{\boldsymbol{\theta}}$ could be a vector of means, ratios, or regression coefficients). Each SDR replicate is produced by fitting the model with adjusted sampling weights. The SDR method uses Hadamard matrices to generate these adjustments.

A Hadamard matrix is a square matrix, $H_r$ (with $r$ rows and columns), such that $H_r'H_r = rI$, where $I$ is the identity matrix. Let $h_{ij}$ be an element of $H_r$; then $h_{ij} = 1$ or $h_{ij} = -1$. In SDR, if $n$ is the number of PSUs, then we must find $H_r$ with $r \geq n + 2$.

Without loss of generality, we will assume the ordered PSUs are individuals instead of clusters. Suppose that we are about to generate the adjusted-weight variable for the $i$th replication and that $w_j$ is the sampling weight attached to the $j$th observation. The adjusted weight is $w_j^* = f_{ji}w_j$, where $f_{ji}$ is

$$f_{ji} = 1 + \frac{1}{2\sqrt{2}}(h_{j+1,i} - h_{j+2,i})$$

Here we assume that the elements of the first row of $H_r$ are all 1.

Each replicate is produced using an adjusted-weight variable with the estimation command that computed $\hat{\boldsymbol{\theta}}$. The adjusted-weight variables must be supplied to `svyset` with the `sdrweight()` option. We call the variables supplied to the `sdrweight()` option *SDR replicate-weight variables*.

Let $\hat{\boldsymbol{\theta}}_{(i)}$ be the vector of point estimates from the $i$th replication, and let $f$ be the sampling fraction computed using the FPC information `svyset` in the `fpc()` suboption of the `sdrweight()` option, where $f = 0$ when `fpc()` is not specified. When the `mse` option is specified, the variance estimator is

$$\hat{V}(\hat{\boldsymbol{\theta}}) = (1-f)\frac{4}{r}\sum_{i=1}^{r}\{\hat{\boldsymbol{\theta}}_{(i)} - \hat{\boldsymbol{\theta}}\}\{\hat{\boldsymbol{\theta}}_{(i)} - \hat{\boldsymbol{\theta}}\}'$$

Otherwise, the variance estimator is

$$\hat{V}(\hat{\boldsymbol{\theta}}) = (1-f)\frac{4}{r}\sum_{i=1}^{r}\{\hat{\boldsymbol{\theta}}_{(i)} - \overline{\boldsymbol{\theta}}_{(.)}\}\{\hat{\boldsymbol{\theta}}_{(i)} - \overline{\boldsymbol{\theta}}_{(.)}\}'$$

where $\overline{\boldsymbol{\theta}}_{(.)}$ is the SDR mean,

$$\overline{\boldsymbol{\theta}}_{(.)} = \frac{1}{r}\sum_{i=1}^{r}\hat{\boldsymbol{\theta}}_{(i)}$$

## Confidence intervals

In survey data analysis, the customary number of degrees of freedom attributed to a test statistic is $d = n - L$, where $n$ is the number of PSUs and $L$ is the number of strata. Under regularity conditions, an approximate $100(1-\alpha)\%$ confidence interval for a parameter $\theta$ (for example, $\theta$ could be a total, ratio, or regression coefficient) is

$$\hat{\theta} \pm t_{1-\alpha/2,d}\,\{\hat{V}(\hat{\theta})\}^{1/2}$$

Cochran (1977, sec. 2.8) and Korn and Graubard (1990) give some theoretical justification for using $d = n - L$ to compute univariate confidence intervals and $p$-values. However, for some cases, inferences based on the customary $n - L$ degrees-of-freedom calculation may be excessively liberal; the resulting confidence intervals may have coverage rates substantially less than the nominal $1 - \alpha$. This problem generally is of the greatest practical concern when the population of interest has a skewed or heavy-tailed distribution or is concentrated in a few PSUs. In some of these cases, the user may want to consider constructing confidence intervals based on alternative degrees-of-freedom terms, based on the Satterthwaite (1941, 1946) approximation and modifications thereof; see, for example, Cochran (1977, sec. 5.4) and Eltinge and Jang (1996).

Sometimes there is no information on $n$ or $L$ for datasets that contain replicate-weight variables but no PSU or strata variables. Each of `svy`'s replication commands has its own default behavior when the design degrees of freedom are not `svyset` or specified using the `dof()` option. `svy brr:` and `svy jackknife:` use $d = r - 1$, where $r$ is the number of replications. `svy bootstrap:` and `svy sdr:` use $z_{1-\alpha/2}$ for the critical value instead of $t_{1-\alpha/2,d}$.

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## Also see

[SVY] **svy** — The survey prefix command

[SVY] **svyset** — Declare survey design for dataset

[SVY] **Survey** — Introduction to survey commands

[P] **_robust** — Robust variance estimates

# Glossary

**100% sample**. See *census*.

**balanced repeated replication**. Balanced repeated replication (BRR) is a method of variance estimation for designs with two PSUs in every stratum. The BRR variance estimator tends to give more reasonable variance estimates for this design than does the linearized variance estimator, which can result in large values and undesirably wide confidence intervals. The BRR variance estimator is described in [SVY] **Variance estimation**.

**bootstrap**. The bootstrap is a method of variance estimation. The bootstrap variance estimator for survey data is described in [SVY] **Variance estimation**.

**BRR**. See *balanced repeated replication*.

**calibration**. Calibration is a method for adjusting sampling weights, most often to account for underrepresented groups in the population. This usually results in decreased bias because it adjusts for nonresponse and underrepresented groups in the population. Calibration also tends to result in smaller variance estimates.

The standard application of calibration uses population totals to adjust the sampling weights. Population totals are typically taken from a census or other source separate from the survey.

**census**. When a census of the population is conducted, every individual in the population participates in the survey. Because of the time, cost, and other constraints, the data collected in a census are typically limited to items that can be quickly and easily determined, usually through a questionnaire.

**cluster sampling**. A cluster is a collection of individuals that are sampled as a group. Although the cost in time and money can be greatly decreased, cluster sampling usually results in larger variance estimates when compared with designs in which individuals are sampled independently.

**DEFF** and **DEFT**. DEFF and DEFT are design effects. Design effects compare the sample-to-sample variability from a given survey dataset with a hypothetical SRS design with the same number of individuals sampled from the population.

DEFF is the ratio of two variance estimates. The design-based variance is in the numerator; the hypothetical SRS variance is in the denominator.

DEFT is the ratio of two standard-error estimates. The design-based standard error is in the numerator; the hypothetical SRS with-replacement standard error is in the denominator. If the given survey design is sampled with replacement, DEFT is the square root of DEFF.

**delta method**. See *linearization*.

**design effects**. See *DEFF* and *DEFT*.

**direct standardization**. Direct standardization is an estimation method that allows comparing rates that come from different frequency distributions.

Estimated rates (means, proportions, and ratios) are adjusted according to the frequency distribution from a standard population. The standard population is partitioned into categories called standard strata. The stratum frequencies for the standard population are called standard weights. The standardizing frequency distribution typically comes from census data, and the standard strata are most commonly identified by demographic information such as age, sex, and ethnicity.

**finite population correction**. Finite population correction (FPC) is an adjustment applied to the variance of a point estimator because of sampling without replacement, resulting in variance estimates that are smaller than the variance estimates from comparable with-replacement sampling designs.

**FPC**. See *finite population correction*.

**Hadamard matrix**. A Hadamard matrix is a square matrix with $r$ rows and columns that has the property

$$H_r' H_r = r I_r$$

where $I_r$ is the identity matrix of order $r$. Generating a Hadamard matrix with order $r = 2^p$ is easily accomplished. Start with a Hadamard matrix of order 2 ($H_2$), and build your $H_r$ by repeatedly applying Kronecker products with $H_2$.

**jackknife**. The jackknife is a data-dependent way to estimate the variance of a statistic, such as a mean, ratio, or regression coefficient. Unlike BRR, the jackknife can be applied to practically any survey design. The jackknife variance estimator is described in [SVY] **Variance estimation**.

**linearization**. Linearization is short for Taylor linearization. Also known as the delta method or the Huber/White/robust sandwich variance estimator, linearization is a method for deriving an approximation to the variance of a point estimator, such as a ratio or regression coefficient. The linearized variance estimator is described in [SVY] **Variance estimation**.

**MEFF** and **MEFT**. MEFF and MEFT are misspecification effects. Misspecification effects compare the variance estimate from a given survey dataset with the variance from a misspecified model. In Stata, the misspecified model is fit without weighting, clustering, or stratification.

MEFF is the ratio of two variance estimates. The design-based variance is in the numerator; the misspecified variance is in the denominator.

MEFT is the ratio of two standard-error estimates. The design-based standard error is in the numerator; the misspecified standard error is in the denominator. MEFT is the square root of MEFF.

**misspecification effects**. See *MEFF* and *MEFT*.

**point estimate**. A point estimate is another name for a statistic, such as a mean or regression coefficient.

**poststratification**. Poststratification is a method for adjusting sampling weights, usually to account for underrepresented groups in the population. This usually results in decreased bias because of nonresponse and underrepresented groups in the population. Poststratification also tends to result in smaller variance estimates.

The population is partitioned into categories, called poststrata. The sampling weights are adjusted so that the sum of the weights within each poststratum is equal to the respective poststratum size. The poststratum size is the number of individuals in the population that are in the poststratum. The frequency distribution of the poststrata typically comes from census data, and the poststrata are most commonly identified by demographic information such as age, sex, and ethnicity.

**predictive margins**. Predictive margins provide a way of exploring the response surface of a fitted model in any response metric of interest—means, linear predictions, probabilities, marginal effects, risk differences, and so on. Predictive margins are estimates of responses (or outcomes) for the groups represented by the levels of a factor variable, controlling for the differing covariate distributions across the groups. They are the survey-data and nonlinear response analogue to what are often called estimated marginal means or least-squares means for linear models.

Because these margins are population-weighted averages over the estimation sample or subsamples, and because they take account of the sampling distribution of the covariates, they can be used to make inferences about treatment effects for the population.

**primary sampling unit**. Primary sampling unit (PSU) is a cluster that was sampled in the first sampling stage; see *cluster sampling*.

**probability weight**. Probability weight is another term for sampling weight.

**pseudolikelihood**. A pseudolikelihood is a weighted likelihood that is used for point estimation. Pseudolikelihoods are not true likelihoods because they do not represent the distribution function for the sample data from a survey. The sampling distribution is instead determined by the survey design.

**PSU**. See *primary sampling unit*.

**replicate-weight variable**. A replicate-weight variable contains sampling weight values that were adjusted for resampling the data; see [SVY] **Variance estimation** for more details.

**resampling**. Resampling refers to the process of sampling from the dataset. In the delete-one jackknife, the dataset is resampled by dropping one PSU and producing a replicate of the point estimates. In the BRR method, the dataset is resampled by dropping combinations of one PSU from each stratum. The resulting replicates of the point estimates are used to estimate their variances and covariances.

**sample**. A sample is the collection of individuals in the population that were chosen as part of the survey. Sample is also used to refer to the data, typically in the form of answered questions, collected from the sampled individuals.

**sampling stage**. Complex survey data are typically collected using multiple stages of clustered sampling. In the first stage, the PSUs are independently selected within each stratum. In the second stage, smaller sampling units are selected within the PSUs. In later stages, smaller and smaller sampling units are selected within the clusters from the previous stage.

**sampling unit**. A sampling unit is an individual or collection of individuals from the population that can be selected in a specific stage of a given survey design. Examples of sampling units include city blocks, high schools, hospitals, and houses.

**sampling weight**. Given a survey design, the sampling weight for an individual is the reciprocal of the probability of being sampled. The probability for being sampled is derived from stratification and clustering in the survey design. A sampling weight is typically considered to be the number of individuals in the population represented by the sampled individual.

**sampling with and without replacement**. Sampling units may be chosen more than once in designs that use sampling with replacement. Sampling units may be chosen at most once in designs that use sampling without replacement. Variance estimates from with-replacement designs tend to be larger than those from corresponding without-replacement designs.

**SDR**. See *successive difference replication*.

**secondary sampling unit**. Secondary sampling unit (SSU) is a cluster that was sampled from within a PSU in the second sampling stage. SSU is also used as a generic term unit to indicate any sampling unit that is not from the first sampling stage.

**simple random sample**. In a simple random sample (SRS), individuals are independently sampled—each with the same probability of being chosen.

**SRS**. See *simple random sample*.

**SSU**. See *secondary sampling unit*.

**standard strata**. See *direct standardization*.

**standard weights**. See *direct standardization*.

**stratification**. The population is partitioned into well-defined groups of individuals, called strata. In the first sampling stage, PSUs are independently sampled from within each stratum. In later sampling stages, SSUs are independently sampled from within each stratum for that stage.

Survey designs that use stratification typically result in smaller variance estimates than do similar designs that do not use stratification. Stratification is most effective in decreasing variability when sampling units are more similar within the strata than between them.

**subpopulation estimation**. Subpopulation estimation focuses on computing point and variance estimates for part of the population. The variance estimates measure the sample-to-sample variability, assuming that the same survey design is used to select individuals for observation from the population. This approach results in a different variance than measuring the sample-to-sample variability by restricting the samples to individuals within the subpopulation; see [SVY] **Subpopulation estimation**.

**successive difference replication**. Successive difference replication (SDR) is a method of variance typically applied to systematic samples, where the observed sampling units are somehow ordered. The SDR variance estimator is described in [SVY] **Variance estimation**.

**survey data**. Survey data consist of information about individuals that were sampled from a population according to a survey design. Survey data distinguishes itself from other forms of data by the complex nature under which individuals are selected from the population.

In survey data analysis, the sample is used to draw inferences about the population. Furthermore, the variance estimates measure the sample-to-sample variability that results from the survey design applied to the fixed population. This approach differs from standard statistical analysis, in which the sample is used to draw inferences about a physical process and the variance measures the sample-to-sample variability that results from independently collecting the same number of observations from the same process.

**survey design**. A survey design describes how to sample individuals from the population. Survey designs typically include stratification and cluster sampling at one or more stages.

**Taylor linearization**. See *linearization*.

**variance estimation**. Variance estimation refers to the collection of methods used to measure the amount of sample-to-sample variation of point estimates; see [SVY] **Variance estimation**.

# Subject and author index

See the combined subject index and the combined author index in the *Stata Index*.