## Contents

<table>
<thead>
<tr>
<th>Section</th>
<th>Description</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intro</td>
<td>Introduction to survey data manual</td>
<td>1</td>
</tr>
<tr>
<td>Survey</td>
<td>Introduction to survey commands</td>
<td>2</td>
</tr>
<tr>
<td>bootstrap_options</td>
<td>More options for bootstrap variance estimation</td>
<td>23</td>
</tr>
<tr>
<td>brr_options</td>
<td>More options for BRR variance estimation</td>
<td>25</td>
</tr>
<tr>
<td>Calibration</td>
<td>Calibration for survey data</td>
<td>27</td>
</tr>
<tr>
<td>Direct standardization</td>
<td>Direct standardization of means, proportions, and ratios</td>
<td>32</td>
</tr>
<tr>
<td>estat</td>
<td>Postestimation statistics for survey data</td>
<td>36</td>
</tr>
<tr>
<td>jackknife_options</td>
<td>More options for jackknife variance estimation</td>
<td>58</td>
</tr>
<tr>
<td>ml for svy</td>
<td>Maximum pseudolikelihood estimation for survey data</td>
<td>60</td>
</tr>
<tr>
<td>Poststratification</td>
<td>Poststratification for survey data</td>
<td>62</td>
</tr>
<tr>
<td>sdr_options</td>
<td>More options for SDR variance estimation</td>
<td>66</td>
</tr>
<tr>
<td>Subpopulation estimation</td>
<td>Subpopulation estimation for survey data</td>
<td>67</td>
</tr>
<tr>
<td>svy</td>
<td>The survey prefix command</td>
<td>73</td>
</tr>
<tr>
<td>svy bootstrap</td>
<td>Bootstrap for survey data</td>
<td>83</td>
</tr>
<tr>
<td>svy brr</td>
<td>Balanced repeated replication for survey data</td>
<td>91</td>
</tr>
<tr>
<td>svy estimation</td>
<td>Estimation commands for survey data</td>
<td>99</td>
</tr>
<tr>
<td>svy jackknife</td>
<td>Jackknife estimation for survey data</td>
<td>112</td>
</tr>
<tr>
<td>svy postestimation</td>
<td>Postestimation tools for svy</td>
<td>120</td>
</tr>
<tr>
<td>svy sdr</td>
<td>Successive difference replication for survey data</td>
<td>137</td>
</tr>
<tr>
<td>svy: tabulate oneway</td>
<td>One-way tables for survey data</td>
<td>143</td>
</tr>
<tr>
<td>svy: tabulate twoway</td>
<td>Two-way tables for survey data</td>
<td>150</td>
</tr>
<tr>
<td>svydescribe</td>
<td>Describe survey data</td>
<td>171</td>
</tr>
<tr>
<td>svymarkout</td>
<td>Mark observations for exclusion on the basis of survey characteristics</td>
<td>178</td>
</tr>
<tr>
<td>svyset</td>
<td>Declare survey design for dataset</td>
<td>179</td>
</tr>
<tr>
<td>Variance estimation</td>
<td>Variance estimation for survey data</td>
<td>198</td>
</tr>
<tr>
<td>Glossary</td>
<td></td>
<td>212</td>
</tr>
<tr>
<td>Subject and author index</td>
<td></td>
<td>216</td>
</tr>
</tbody>
</table>
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
[BAYES] Stata Bayesian Analysis Reference Manual
[FN] Stata Functions Reference Manual
[XT] Stata Longitudinal-Data/Panel-Data Reference Manual
[M] Stata Multiple-Imputation Reference Manual
[SVY] Stata Survey Data Reference Manual
[I] Stata Glossary and Index
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.
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
- **svyset**: Declare survey design for dataset
- **svydescribe**: Describe survey data

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

Survey data concepts
- **Variance estimation**: Variance estimation for survey data
- **Subpopulation estimation**: Subpopulation estimation for survey data
- **Calibration**: Calibration for survey data
- **Direct standardization**: Direct standardization of means, proportions, and ratios
- **Poststratification**: Poststratification for survey data

Tools for programmers of new survey commands
- **ml for svy**: Maximum pseudolikelihood estimation for survey data
- **svymarkout**: Mark observations for exclusion on the basis of survey characteristics
Remarks and examples

Remarks are presented under the following headings:

- Introduction
- Survey design tools
- Survey data analysis tools
- Survey data concepts
- Tools for programmers of new survey commands
- Video examples

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.
Survey commands

- **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`.

```stata
. use https://www.stata-press.com/data/r16/stage5a
. svyset su1 [pweight=pw], strata(strata) fpc(fpc1)

+----------------------------------+
|                              pweight: pw                        |
| VCE: linearized                  |
| Single unit: missing             |
| Strata 1: strata                 |
| SU 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).
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.

```stata
use https://www.stata-press.com/data/r16/multistage
svyset county [pw=sampwgt], strata(state) fpc(ncounties) || school, fpc(nschools)
save highschool
```

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

```stata
clear
describe
Contains data
obs: 0
vars: 0
Sorted by:
use highschool
svyset
pweight: sampwgt
VCE: linearized
Single unit: missing
Strata 1: state
SU 1: county
FPC 1: ncounties
Strata 2: <one>
SU 2: school
FPC 2: nschools
```

We saved the `svyset` dataset to `highschool.dta`. We can now use this new dataset without having to worry about respecifying the design characteristics.
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
    pweight: sampwgt
    VCE: linearized
    Single unit: missing
    Strata 1: state
    SU 1: county
    FPC 1: ncounties
    Strata 2: <one>
    SU 2: school
    FPC 2: nschools
```

```

<table>
<thead>
<tr>
<th>Stratum</th>
<th>#Units included</th>
<th>#Units omitted</th>
<th>#Obs with complete data</th>
<th>#Obs with missing data</th>
<th>#Obs per included Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>#</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>0</td>
<td>92</td>
<td>0</td>
<td>34</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>0</td>
<td>112</td>
<td>0</td>
<td>51</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>0</td>
<td>43</td>
<td>0</td>
<td>18</td>
</tr>
<tr>
<td>4</td>
<td>2</td>
<td>0</td>
<td>37</td>
<td>0</td>
<td>14</td>
</tr>
<tr>
<td>5</td>
<td>2</td>
<td>0</td>
<td>96</td>
<td>0</td>
<td>38</td>
</tr>
<tr>
<td></td>
<td>(output omitted)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>46</td>
<td>2</td>
<td>0</td>
<td>115</td>
<td>0</td>
<td>56</td>
</tr>
<tr>
<td>47</td>
<td>2</td>
<td>0</td>
<td>67</td>
<td>0</td>
<td>28</td>
</tr>
<tr>
<td>48</td>
<td>2</td>
<td>0</td>
<td>56</td>
<td>0</td>
<td>23</td>
</tr>
<tr>
<td>49</td>
<td>2</td>
<td>0</td>
<td>78</td>
<td>0</td>
<td>39</td>
</tr>
<tr>
<td>50</td>
<td>2</td>
<td>0</td>
<td>64</td>
<td>0</td>
<td>31</td>
</tr>
<tr>
<td></td>
<td>50</td>
<td>100</td>
<td>0</td>
<td>4,071</td>
<td>0</td>
</tr>
</tbody>
</table>

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.

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
```

<table>
<thead>
<tr>
<th>Linearized</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>weight</td>
<td>160.2863</td>
<td>.7412512</td>
<td>(158.7974, 161.7751)</td>
</tr>
</tbody>
</table>

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.

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
```

<table>
<thead>
<tr>
<th>Linearized</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>weight</td>
<td>.7163115</td>
<td>.0293908</td>
<td>(0.6572784, 0.7753447)</td>
</tr>
<tr>
<td>_cons</td>
<td>-149.6183</td>
<td>12.57265</td>
<td>(-174.9712, -124.3654)</td>
</tr>
</tbody>
</table>

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.

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/r16/nhefs
svyset psu2 [pw=swgt2], strata(strata2)
pweight: swgt2
VCE: linearized
Single unit: missing
Strata 1: strata2
SU 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)
   failure event: lung_cancer != 0 & lung_cancer < .
   obs. time interval: (0, age_lung_cancer]
   exit on or before: failure
   weight: [pweight=swgt2]
```

<table>
<thead>
<tr>
<th>total observations</th>
<th>event time missing (age_lung_cancer&gt;=.)</th>
</tr>
</thead>
<tbody>
<tr>
<td>14,407</td>
<td></td>
</tr>
<tr>
<td>5,126</td>
<td></td>
</tr>
</tbody>
</table>

9,281 observations remaining, representing
83 failures in single-record/single-failure data
599,691 total analysis time at risk and under observation

<table>
<thead>
<tr>
<th>at risk from t</th>
<th>earliest observed entry t</th>
<th>last observed exit t</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0</td>
<td>97</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Haz. Ratio</td>
<td>Std. Err.</td>
</tr>
<tr>
<td>former_smoker</td>
<td>2.788113</td>
<td>.6205102</td>
</tr>
<tr>
<td>smoker</td>
<td>7.849483</td>
<td>2.593249</td>
</tr>
<tr>
<td>male</td>
<td>1.187611</td>
<td>.3445315</td>
</tr>
<tr>
<td>urban1</td>
<td>.8035074</td>
<td>.3285144</td>
</tr>
<tr>
<td>rural</td>
<td>1.581674</td>
<td>.5281859</td>
</tr>
</tbody>
</table>

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.

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/r16/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

1=white, 2=black, 3=other

<table>
<thead>
<tr>
<th></th>
<th>diabetes, 1=yes, 0=no</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>White</td>
<td>0.9680</td>
<td>0.0320</td>
<td>1.0000</td>
</tr>
<tr>
<td></td>
<td>(0.0020)</td>
<td>(0.0020)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>[0.9638,0.9718]</td>
<td>[0.0282,0.0362]</td>
<td></td>
</tr>
<tr>
<td>Black</td>
<td>0.9410</td>
<td>0.0590</td>
<td>1.0000</td>
</tr>
<tr>
<td></td>
<td>(0.0061)</td>
<td>(0.0061)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>[0.9271,0.9523]</td>
<td>[0.0477,0.0729]</td>
<td></td>
</tr>
<tr>
<td>Other</td>
<td>0.9797</td>
<td>0.0203</td>
<td>1.0000</td>
</tr>
<tr>
<td></td>
<td>(0.0076)</td>
<td>(0.0076)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>[0.9566,0.9906]</td>
<td>[0.0094,0.0434]</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>0.9658</td>
<td>0.0342</td>
<td>1.0000</td>
</tr>
<tr>
<td></td>
<td>(0.0018)</td>
<td>(0.0018)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>[0.9619,0.9693]</td>
<td>[0.0307,0.0381]</td>
<td></td>
</tr>
</tbody>
</table>

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.

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/r16/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
Linearized
Mean 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: propor-
tion, 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

    Linearized
    Over     Mean    Std. Err.    DEFF    DEFT
    c.weight@sex
       male  175.4809    1.116802    2.61016    1.61519
       female  146.204    0.9004157    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     Coef.    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.

```stata
. use https://www.stata-press.com/data/r16/nhanes2
. svydescribe
Survey: Describing stage 1 sampling units
  pweight: finalwgt
  VCE: linearized
  Single unit: missing
  Strata 1: strata
  SU 1: psu
  FPC 1: <zero>

<table>
<thead>
<tr>
<th>Stratum</th>
<th>#Units</th>
<th>#Obs</th>
<th>min</th>
<th>mean</th>
<th>max</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>380</td>
<td>165</td>
<td>190.0</td>
<td>215</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>185</td>
<td>67</td>
<td>92.5</td>
<td>118</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>348</td>
<td>149</td>
<td>174.0</td>
<td>199</td>
</tr>
<tr>
<td>4</td>
<td>2</td>
<td>460</td>
<td>229</td>
<td>230.0</td>
<td>231</td>
</tr>
<tr>
<td>5</td>
<td>2</td>
<td>252</td>
<td>105</td>
<td>126.0</td>
<td>147</td>
</tr>
<tr>
<td>(output omitted)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>29</td>
<td>2</td>
<td>503</td>
<td>215</td>
<td>251.5</td>
<td>288</td>
</tr>
<tr>
<td>30</td>
<td>2</td>
<td>365</td>
<td>166</td>
<td>182.5</td>
<td>199</td>
</tr>
<tr>
<td>31</td>
<td>2</td>
<td>308</td>
<td>143</td>
<td>154.0</td>
<td>165</td>
</tr>
<tr>
<td>32</td>
<td>2</td>
<td>450</td>
<td>211</td>
<td>225.0</td>
<td>239</td>
</tr>
<tr>
<td>31</td>
<td>62</td>
<td>10,351</td>
<td>67</td>
<td>167.0</td>
<td>288</td>
</tr>
</tbody>
</table>
```

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)*.
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)

|   1   |   2   |   3   |   4   |   5   |

BRR results

command:  total weight height
WtoH:   _b[weight]/_b[height]

<table>
<thead>
<tr>
<th></th>
<th>BRR</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Coef.</td>
<td>Std. Err.</td>
<td>t</td>
<td>P&gt;</td>
</tr>
<tr>
<td>---------</td>
<td>---------------</td>
<td>----------</td>
<td>---------</td>
<td>---------</td>
</tr>
<tr>
<td>WtoH</td>
<td>.4268116</td>
<td>.0008904</td>
<td>479.36</td>
<td>0.000</td>
</tr>
</tbody>
</table>

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/r16/highschool
. describe sex
  
<table>
<thead>
<tr>
<th>variable</th>
<th>storage</th>
<th>display</th>
<th>value</th>
</tr>
</thead>
<tbody>
<tr>
<td>sex</td>
<td>byte</td>
<td>%9.0g</td>
<td>sex</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1=male, 2=female</td>
</tr>
</tbody>
</table>
  
. 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
  
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

| weight | Coef.  | 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/r16/stdize, clear
. list, noobs sep(0) sum
```

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

Sum 74088 1764 66453 1418

We can use svy: ratio to compute the death rates 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.
. gen fpc = 1
. svyset, fpc(fpc)
   pweight: <none>
   VCE: linearized
   Single unit: missing
   Strata 1: <one>
         SU 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

               | Linearized     | [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 death rates are 2.38% for Bethnal Green and 2.13% for St. George’s Hanover Square. These observed death rates
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
          Design df = 20

               | Linearized     | [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 death rate for St. George’s Hanover Square, 2.66%, is larger than the death rate 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).

```stata
. use https://www.stata-press.com/data/r16/poststrata, clear
. svyset, poststrata(type) postweight(postwgt) fpc(fpc)
   pweight: <none>
   VCE: linearized
   Poststrata: type
   Postweight: postwgt
   Single unit: missing
   Strata 1: <one>
      SU 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)
    pweight: <none>
    VCE: linearized
Single unit: missing
  Strata 1: <one>
    SU 1: <observations>
    FPC 1: fpc

. svy: mean totexp
(running mean on estimation sample)
Survey: Mean estimation

<table>
<thead>
<tr>
<th>Number of strata</th>
<th>Number of obs</th>
<th>Population size</th>
<th>Design df</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>50</td>
<td>50</td>
<td>49</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Linearized</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>totexp</td>
<td>39.7254</td>
<td>2.221747</td>
<td>35.26063 44.19017</td>
</tr>
</tbody>
</table>

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 Gould, Pitblado, and Poi (2010).

Example 14

The `ml` command requires a program that computes likelihood values to perform maximum likelihood. Here is a likelihood evaluator used in Gould, Pitblado, and Poi (2010) to fit linear regression models using the likelihood from the normal distribution.

```stata
program mynormal_lf
    version 16.1
    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.
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 U.S. 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.

References


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**

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

**Syntax**

```
bootstrap options

Description
```

<table>
<thead>
<tr>
<th>Options</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>SE</strong></td>
<td>use MSE formula for variance</td>
</tr>
<tr>
<td><strong>mse</strong></td>
<td>suppress replication dots</td>
</tr>
<tr>
<td><strong>nodots</strong></td>
<td>display dots every # replications</td>
</tr>
<tr>
<td><strong>dots(#)</strong></td>
<td>bootstrap mean-weight adjustment</td>
</tr>
<tr>
<td><strong>bsn(#)</strong></td>
<td>save results to filename</td>
</tr>
<tr>
<td><strong>saving()</strong></td>
<td>display the full table legend</td>
</tr>
<tr>
<td><strong>verbose</strong></td>
<td>display any output from command</td>
</tr>
<tr>
<td><strong>noisily</strong></td>
<td>trace command</td>
</tr>
<tr>
<td><strong>trace</strong></td>
<td>use text as the title for results</td>
</tr>
<tr>
<td><strong>title()</strong></td>
<td>do not drop observations</td>
</tr>
<tr>
<td><strong>reject()</strong></td>
<td>identify invalid results</td>
</tr>
</tbody>
</table>

**Options**

**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. A red ‘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
Description

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

Syntax

```
**brr_options**
```

<table>
<thead>
<tr>
<th><strong>Description</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>SE</strong></td>
</tr>
<tr>
<td><strong>mse</strong></td>
</tr>
<tr>
<td><strong>nodots</strong></td>
</tr>
<tr>
<td><strong>dots(#)</strong></td>
</tr>
<tr>
<td><strong>hadamard(matrix)</strong></td>
</tr>
<tr>
<td><strong>fay(#)</strong></td>
</tr>
<tr>
<td><strong>saving(filename, ...)</strong></td>
</tr>
<tr>
<td><strong>verbose</strong></td>
</tr>
<tr>
<td><strong>noisily</strong></td>
</tr>
<tr>
<td><strong>trace</strong></td>
</tr>
<tr>
<td><strong>title(text)</strong></td>
</tr>
<tr>
<td><strong>nodrop</strong></td>
</tr>
<tr>
<td><strong>reject(exp)</strong></td>
</tr>
</tbody>
</table>

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. A red ‘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:

<table>
<thead>
<tr>
<th>hosptype</th>
<th>beds</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>37,978</td>
</tr>
<tr>
<td>2</td>
<td>13,066</td>
</tr>
<tr>
<td>3</td>
<td>9,573</td>
</tr>
<tr>
<td>5</td>
<td>10,077</td>
</tr>
</tbody>
</table>

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.

```stata
. use https://www.stata-press.com/data/r16/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))
```

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

```stata
. svy: mean exptot
(running mean on estimation sample)
```

Survey: Mean estimation

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
</tr>
<tr>
<td>exptot</td>
<td>10.40552</td>
</tr>
</tbody>
</table>
```

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)
pweight: wt
VCE: linearized
Single unit: missing
Strata 1: hosptype
   SU 1: <observations>
   FPC 1: <zero>
.
svy: mean exptot
(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

```
<table>
<thead>
<tr>
<th>Linearized</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>------</td>
</tr>
<tr>
<td>exptotal</td>
</tr>
</tbody>
</table>
```

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

\[
w_j^* = w_j F(\mathbf{a}_j' \lambda)
\]

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

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

\[ z_j(\hat{R}_C) = \frac{\hat{X}_C z_j(\hat{Y}_C) - \hat{Y}_C z_j(\hat{X}_C)}{(\hat{X}_C)^2} \]

where \( \hat{X}_C \) 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 \( a_j \) using the adjusted weights \( w_j^* \).

References


**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 hsddeaths contains the number of people who died in Hanover Square that year.
We can use `svy: ratio` to compute the death rates 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.

```
. gen fpc = 1
. svyset, fpc(fpc)
    pweight: <none>
    VCE: linearized
    Single unit: missing
    Strata 1: <one>
    SU 1: <observations>
    FPC 1: fpc

. svy: ratio (Bethnal: bgdeaths/bgliving) (Hanover: hsdeaths/hsliving)
    (running ratio on estimation sample)
Survey: Ratio estimation

        Linearized
Number of strata =    1    Number of obs    =     21
Number of PSUs    =    21    Population size =     21
Design df    =     20

Bethnal: bgdeaths/bgliving
         Hanover: hsdeaths/hsliving

<table>
<thead>
<tr>
<th></th>
<th>Ratio</th>
<th>Std. Err.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bethnal</td>
<td>.0238095</td>
<td>0</td>
<td>.</td>
</tr>
<tr>
<td>Hanover</td>
<td>.0213384</td>
<td>0</td>
<td>.</td>
</tr>
</tbody>
</table>
```

Note: Zero standard errors because of 100% sampling rate detected for FPC in the first stage.
The death rates are 2.38% for Bethnal Green and 2.13% for St. George’s Hanover Square. These observed death rates 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

         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 death rate for St. George’s Hanover Square, 2.66%, is larger than the death rate for Bethnal Green.

For this example, we could have used stdize to compute the death rates; however, stdize will not compute the correct standard errors for survey data. Furthermore, stdize 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 \( LD \) be the number of standard strata, and let \( \pi_g \) be the proportion of the population that belongs to standard stratum \( g \).

\[
\sum_{g=1}^{LD} \pi_g = 1
\]  
(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

\[
\hat{R}^D = \sum_{g=1}^{LD} \pi_g \frac{\hat{Y}_g}{\hat{X}_g}
\]

where

\[
\hat{Y}_g = \sum_{j=1}^{m} I_{D_g}(j) w_j y_j
\]

with \( \hat{X}_g \) 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

\[
z_j(\hat{R}^D) = \sum_{g=1}^{LD} \pi_g I_{D_g}(j) \frac{\hat{X}_g y_j - \hat{Y}_g x_j}{\hat{X}_g^2}
\]

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


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

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

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
```

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

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]

<table>
<thead>
<tr>
<th>estat_effects_options</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>deff</td>
<td>report DEFF design effects</td>
</tr>
<tr>
<td>deft</td>
<td>report DEFT design effects</td>
</tr>
<tr>
<td>srs subpop</td>
<td>report design effects, assuming SRS within subpopulation</td>
</tr>
<tr>
<td>meff</td>
<td>report MEFF design effects</td>
</tr>
<tr>
<td>meft</td>
<td>report MEFT design effects</td>
</tr>
<tr>
<td>display_options</td>
<td>control spacing and display of omitted variables and base and empty cells</td>
</tr>
</tbody>
</table>
### estat lceffects_options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>deff</td>
<td>report DEFF design effects</td>
</tr>
<tr>
<td>deft</td>
<td>report DEFT design effects</td>
</tr>
<tr>
<td>srs*subpop</td>
<td>report design effects, assuming SRS within subpopulation</td>
</tr>
<tr>
<td>meff</td>
<td>report MEFF design effects</td>
</tr>
<tr>
<td>meft</td>
<td>report MEFT design effects</td>
</tr>
</tbody>
</table>

### estat size_options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>obs</td>
<td>report number of observations (within subpopulation)</td>
</tr>
<tr>
<td>size</td>
<td>report subpopulation sizes</td>
</tr>
</tbody>
</table>

### estat sd_options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>variance</td>
<td>report subpopulation variances instead of standard deviations</td>
</tr>
<tr>
<td>srs*subpop</td>
<td>report standard deviation, assuming SRS within subpopulation</td>
</tr>
</tbody>
</table>

### estat cv_options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>nolegend</td>
<td>suppress the table legend</td>
</tr>
<tr>
<td>display_options</td>
<td>control spacing and display of omitted variables and base and empty cells</td>
</tr>
</tbody>
</table>

### estat gof_options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>group(#)</td>
<td>compute test statistic using # quantiles</td>
</tr>
<tr>
<td>total</td>
<td>compute test statistic using the total estimator instead of the mean estimator</td>
</tr>
<tr>
<td>all</td>
<td>execute test for all observations in the data</td>
</tr>
</tbody>
</table>

### estat vce_options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>covariance</td>
<td>display as covariance matrix; the default</td>
</tr>
<tr>
<td>correlation</td>
<td>display as correlation matrix</td>
</tr>
<tr>
<td>equation(spec)</td>
<td>display only specified equations</td>
</tr>
<tr>
<td>block</td>
<td>display submatrices by equation</td>
</tr>
<tr>
<td>diag</td>
<td>display submatrices by equation; diagonal blocks only</td>
</tr>
<tr>
<td>format(%,fmt)</td>
<td>display format for covariances and correlations</td>
</tr>
<tr>
<td>nolines</td>
<td>suppress lines between equations</td>
</tr>
<tr>
<td>display_options</td>
<td>control display of omitted variables and base and empty cells</td>
</tr>
</tbody>
</table>
Options

Options are presented under the following headings:

- Options for estat effects
- Options for estat lceffects
- Options for estat size
- Options for estat sd
- Options for estat cv
- Options for estat gof
- Options for estat vce

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 MEF 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 MEF 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/r16/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

Linearized
Mean  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
    pweight: finalwgt
        VCE: linearized
    Single unit: missing
    Strata 1: strata
        SU 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

Linearized
Mean  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

Linearized
Mean  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
```

<table>
<thead>
<tr>
<th>Over</th>
<th>Linearized</th>
<th>Obs</th>
<th>Size</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
<td></td>
</tr>
<tr>
<td>c.tcresult@sex</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>210.7937</td>
<td>1.312967</td>
<td>4,915</td>
</tr>
<tr>
<td>Female</td>
<td>215.2188</td>
<td>1.193853</td>
<td>5,436</td>
</tr>
</tbody>
</table>

**estat sd** reports a table of subpopulation standard deviations.

```
estat sd
```

<table>
<thead>
<tr>
<th>Over</th>
<th>Mean</th>
<th>Std. Dev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>c.tcresult@sex</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>210.7937</td>
<td>45.79065</td>
</tr>
<tr>
<td>Female</td>
<td>215.2188</td>
<td>50.72563</td>
</tr>
</tbody>
</table>

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

```
estat cv
```

<table>
<thead>
<tr>
<th>Over</th>
<th>Linearized</th>
<th>CV (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
</tr>
<tr>
<td>c.tcresult@sex</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>210.7937</td>
<td>1.312967</td>
</tr>
<tr>
<td>Female</td>
<td>215.2188</td>
<td>1.193853</td>
</tr>
</tbody>
</table>

> **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/r16/nhanes2b
.svy: mean iron, over(sex)
(output omitted)
estat effects
```

<table>
<thead>
<tr>
<th>Over</th>
<th>Linearized Mean</th>
<th>Std. Err.</th>
<th>DEFF</th>
<th>DEFT</th>
</tr>
</thead>
<tbody>
<tr>
<td>c.iron@sex</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>104.7969</td>
<td>.557267</td>
<td>1.36097</td>
<td>1.16661</td>
</tr>
<tr>
<td>Female</td>
<td>97.16247</td>
<td>.6743344</td>
<td>2.01403</td>
<td>1.41916</td>
</tr>
</tbody>
</table>

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
```

<table>
<thead>
<tr>
<th>Over</th>
<th>Linearized Mean</th>
<th>Std. Err.</th>
<th>DEFF</th>
<th>DEFT</th>
</tr>
</thead>
<tbody>
<tr>
<td>c.iron@sex</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>104.7969</td>
<td>.557267</td>
<td>1.348</td>
<td>1.16104</td>
</tr>
<tr>
<td>Female</td>
<td>97.16247</td>
<td>.6743344</td>
<td>2.03132</td>
<td>1.42524</td>
</tr>
</tbody>
</table>

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/r16/nmihs
. svy: mean birthwgt, over(race)
(output omitted)
. estat effects
```

<table>
<thead>
<tr>
<th>Over</th>
<th>Linearized</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
<td>DEFF</td>
<td>DEFT</td>
</tr>
<tr>
<td>c.birthwgt@</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>race</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>nonblack</td>
<td>3402.32</td>
<td>7.609532</td>
<td>1.44376</td>
<td>1.20157</td>
</tr>
<tr>
<td>black</td>
<td>3127.834</td>
<td>6.529814</td>
<td>.172041</td>
<td>.414778</td>
</tr>
</tbody>
</table>

```
. estat effects, srssubpop
```

<table>
<thead>
<tr>
<th>Over</th>
<th>Linearized</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
<td>DEFF</td>
<td>DEFT</td>
</tr>
<tr>
<td>c.birthwgt@</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>race</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>nonblack</td>
<td>3402.32</td>
<td>7.609532</td>
<td>.826842</td>
<td>.909308</td>
</tr>
<tr>
<td>black</td>
<td>3127.834</td>
<td>6.529814</td>
<td>.528963</td>
<td>.727298</td>
</tr>
</tbody>
</table>

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

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

$$MEFT = \sqrt{MEFF}$$

where $\hat{V}$ is the appropriate design-based estimate of variance and $\hat{V}_{msp}$ 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.

```stata
. use https://www.stata-press.com/data/r16/nhanes2b
. svy: mean zinc, over(sex)
(output omitted)
. estat effects, meff meft
```

<table>
<thead>
<tr>
<th>Over</th>
<th>Linearized</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
</tr>
<tr>
<td>c.zinc@sex</td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>90.74543</td>
</tr>
<tr>
<td>Female</td>
<td>83.8635</td>
</tr>
</tbody>
</table>

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

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

<table>
<thead>
<tr>
<th>Variable</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>zinc</td>
<td>4,375</td>
<td>89.53143</td>
<td>.2334228</td>
<td>89.0738 89.98906</td>
</tr>
</tbody>
</table>

```stata
. display _se[zinc#1.sex]/r(se) 2.5064994
. display (_se[zinc#1.sex]/r(se))^2 6.2825393
```

```stata
. ci means zinc if sex == "Female":sex
```

<table>
<thead>
<tr>
<th>Variable</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>zinc</td>
<td>4,827</td>
<td>83.76652</td>
<td>.186444</td>
<td>83.40101 84.13204</td>
</tr>
</tbody>
</table>

```stata
. 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/r16/nhanes2
. svy: mean tcresult, over(sex)
```

```
Survey: Mean estimation
Number of strata = 31  Number of obs = 10,351
Number of PSUs = 62  Population size = 117,157,513
Design df = 31
```

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
</tr>
<tr>
<td>c.tcresult@sex</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>210.7937</td>
<td>1.312967</td>
</tr>
<tr>
<td>Female</td>
<td>215.2188</td>
<td>1.193853</td>
</tr>
</tbody>
</table>

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
```

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:

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

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/r16/nmihs
. svyset [pw=finwgt], strata(stratan)
  pweight: finwgt
  VCE: linearized
  Single unit: missing
  Strata 1: stratan
  SU 1: <observations>
  FPC 1: <zero>
. svy: mean birthwgt, over(stratan)
```

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

<table>
<thead>
<tr>
<th>Over</th>
<th>Linearized</th>
<th>Obs</th>
<th>Size</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>c.birthwgt@</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>stratan</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>1049.434</td>
<td>841</td>
<td>18,402.98161</td>
</tr>
<tr>
<td>2</td>
<td>2189.561</td>
<td>803</td>
<td>67,650.95932</td>
</tr>
<tr>
<td>3</td>
<td>3303.492</td>
<td>3,578</td>
<td>579,104.6188</td>
</tr>
<tr>
<td>4</td>
<td>1036.626</td>
<td>710</td>
<td>29,814.93215</td>
</tr>
<tr>
<td>5</td>
<td>2211.217</td>
<td>714</td>
<td>153,379.07445</td>
</tr>
<tr>
<td>6</td>
<td>3485.42</td>
<td>3,300</td>
<td>3,047,209.105</td>
</tr>
</tbody>
</table>

. 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

<table>
<thead>
<tr>
<th></th>
<th>Mean</th>
<th>Std. Dev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>c.birthwgt@stratan</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>1049.434</td>
<td>2305.931</td>
</tr>
<tr>
<td>2</td>
<td>2189.561</td>
<td>555.7971</td>
</tr>
<tr>
<td>3</td>
<td>3303.492</td>
<td>687.3575</td>
</tr>
<tr>
<td>4</td>
<td>1036.626</td>
<td>999.0867</td>
</tr>
<tr>
<td>5</td>
<td>2211.217</td>
<td>349.8068</td>
</tr>
<tr>
<td>6</td>
<td>3485.42</td>
<td>300.6945</td>
</tr>
</tbody>
</table>

. matrix p_neyman = 100 * hadamard(nsubp,r(sd))/el(nsubp*r(sd)',1,1)
. matrix list p_obs, format(%4.1f)

<p>| | | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>c.birthwgt@</td>
<td>c.birthwgt@</td>
<td>c.birthwgt@</td>
<td>c.birthwgt@</td>
<td>c.birthwgt@</td>
</tr>
<tr>
<td>1.stratan</td>
<td>2.stratan</td>
<td>3.stratan</td>
<td>4.stratan</td>
<td>5.stratan</td>
</tr>
<tr>
<td>r1</td>
<td>8.5</td>
<td>8.1</td>
<td>36.0</td>
<td>7.1</td>
</tr>
<tr>
<td>c.birthwgt@</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6.stratan</td>
<td>33.2</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

. matrix list p_neyman, format(%4.1f)

<p>| | | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>c.birthwgt@</td>
<td>c.birthwgt@</td>
<td>c.birthwgt@</td>
<td>c.birthwgt@</td>
<td>c.birthwgt@</td>
</tr>
<tr>
<td>1.stratan</td>
<td>2.stratan</td>
<td>3.stratan</td>
<td>4.stratan</td>
<td>5.stratan</td>
</tr>
<tr>
<td>r1</td>
<td>2.9</td>
<td>2.5</td>
<td>26.9</td>
<td>2.0</td>
</tr>
<tr>
<td>c.birthwgt@</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6.stratan</td>
<td>62.0</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

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/r16/strata5
. svy: total y
(output omitted)
. estat strata

<table>
<thead>
<tr>
<th>Stage</th>
<th>Singleton strata</th>
<th>Certainty strata</th>
<th>Total strata</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0</td>
<td>1</td>
<td>4</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>0</td>
<td>10</td>
</tr>
<tr>
<td>3</td>
<td>0</td>
<td>3</td>
<td>29</td>
</tr>
<tr>
<td>4</td>
<td>2</td>
<td>0</td>
<td>110</td>
</tr>
<tr>
<td>5</td>
<td>204</td>
<td>311</td>
<td>865</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Stage</th>
<th>Singleton strata</th>
<th>Certainty strata</th>
<th>Total strata</th>
<th>Scale factor</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0</td>
<td>1</td>
<td>4</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>0</td>
<td>10</td>
<td>1.11</td>
</tr>
<tr>
<td>3</td>
<td>0</td>
<td>3</td>
<td>29</td>
<td>1</td>
</tr>
<tr>
<td>4</td>
<td>2</td>
<td>0</td>
<td>110</td>
<td>1.02</td>
</tr>
<tr>
<td>5</td>
<td>204</td>
<td>311</td>
<td>865</td>
<td>1.58</td>
</tr>
</tbody>
</table>

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/r16/nhanes2d
. svyset pweight: finalwgt
    VCE: linearized
Single unit: missing
Strata 1: strata
    SU 1: psu
    FPC 1: <zero>
. svy: logistic highbp height weight age female
```

```
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
```

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.
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(vvar): 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 MEGT 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): MEGT estimate
**estat size** stores the following in \( r() \):

Matrices
- \( r(N) \): vector of numbers of nonmissing observations
- \( r(N_{\text{subp}}) \): vector of subpopulation size estimates

**estat sd** stores the following in \( r() \):

Macros
- \( r(srssubpop) \): srssubpop, if specified

Matrices
- \( r(\text{mean}) \): vector of subpopulation mean estimates
- \( r(\text{sd}) \): vector of subpopulation standard-deviation estimates
- \( r(\text{variance}) \): 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
- Linear combinations
- Misspecification effects
- Population and subpopulation standard deviations
- Coefficient of variation
- Goodness of fit for binary response models

**Design effects**

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

DEFF is estimated as described in [Kish (1965)](#) as

\[
\text{DEFF} = \frac{\hat{V}(\hat{\theta})}{\hat{V}_{\text{srswo}}(\tilde{\theta}_{\text{ars}})}
\]
where \( \hat{V}(\theta) \) is the design-based estimate of variance for a parameter, \( \theta \), and \( \hat{V}_{srswor}(\tilde{\theta}_{srs}) \) is an estimate of the variance for an estimator, \( \tilde{\theta}_{srs} \), 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

\[
\hat{V}_{srswor}(\tilde{\theta}_{srs}) = (1 - f) \frac{\hat{M}}{m - 1} \sum_{j=1}^{m} w_j (y_j - \hat{Y})^2
\]

(1)

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

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

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

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

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

\[
I_{S}(j) = \begin{cases} 
1, & \text{if } j \in S \\
0, & \text{otherwise}
\end{cases}
\]

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 \( S \). Here (1) is used with the sums restricted to those elements belonging to the subpopulation; \( m \) is replaced with \( m_S \), the number of sample elements from the subpopulation; \( \hat{M} \) is replaced with \( \hat{M}_S \), the sum of the weights from the subpopulation; and \( \hat{Y} \) is replaced with \( \hat{Y}_S = \bar{Y}_S/\hat{M}_S \), the weighted mean across the subpopulation.

**Linear combinations**

\texttt{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

\[
\hat{V}_{srswor}(\hat{\eta}_{srs}) = C\hat{V}_{srswor}(\hat{\theta}_{srs})C'
\]
and the SRS with replacement (srswr) variance estimator used in the computation of DEFT is

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

The variance estimator used in computing MEFF and MEFT is

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

_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.

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

$$MEFT = \sqrt{MEFF}$$

where $$\hat{V}(\hat{\theta})$$ is the design-based estimate of variance for a parameter, $$\theta$$, and $$\hat{V}_{msp}(\hat{\theta}_{msp})$$ is the variance estimate for $$\hat{\theta}_{msp}$$. These estimators, $$\hat{\theta}_{msp}$$ and $$\hat{V}_{msp}(\hat{\theta}_{msp})$$, 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:

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

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

When computing MEFF and MEFT for a subpopulation, sums are restricted to those elements belonging to the subpopulation, and $$m_S$$ and $$\overline{M}_S$$ are used in place of $$m$$ and $$\overline{M}$$.

**Population and subpopulation standard deviations**

For srswr designs, the variance of the mean estimator is

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

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

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

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

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

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 \texttt{group()} option; then the \( \hat{r}_j \) are placed in \( g \) quantile groups as described in \textit{Methods and formulas} for the \texttt{xtile} command in \texttt{[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

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

where \( \hat{V}(\overline{r}) \) is the design-based variance estimate for \( \overline{r} \). Here \( \hat{X}^2 \) 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). \texttt{estat gof} reports this statistic when the design degrees of freedom is missing, such as with \texttt{svy bootstrap} results.

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

\[
\hat{F} = \frac{\hat{X}^2(d - g + 2)}{(dg)}
\]

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 \texttt{total} option, \texttt{estat gof} uses the subpopulation total estimator instead of the subpopulation mean estimator.

References


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
Description

svy accepts more options when performing jackknife variance estimation.

Syntax

\begin{verbatim}
  jackknife_options
  Description
  SE
  mse        use MSE formula for variance
  nodots     suppress replication dots
  dots(#)    display dots every # replications
  saving(...) save results to filename
  keep       keep pseudovalues
  verbose    display the full table legend
  nosily     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
\end{verbatim}

Options

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. A red ‘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, nosily, 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

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 Gould, Pitblado, and Poi (2010) 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 Gould, Pitblado, and Poi (2010) to fit linear regression models using likelihood from the normal distribution.

```stata
program mynormal_lf
    version 16.1
    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/r16/multistage
. svyset county [pw=sampwgt], strata(state) fpc(ncounties) || school, > fpc(nschools)
    pweight: sampwgt
    VCE: linearized
    Single unit: missing
    Strata 1: state
    SU 1: county
    FPC 1: ncounties
    Strata 2: <one>
    SU 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 = -41226725 (not concave)
Iteration 2: log pseudolikelihood = -41221650 (not concave)
Iteration 3: log pseudolikelihood = -41176159 (not concave)
Iteration 4: log pseudolikelihood = -41154139 (not concave)
Iteration 5: log pseudolikelihood = -41052368
Iteration 6: log pseudolikelihood = -39379181 (backed up)
Iteration 7: log pseudolikelihood = -38333242
Iteration 8: log pseudolikelihood = -38328742
Iteration 9: 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 | Linearized | Log Coef. | Std. Err. | t | P>|t| | [95% Conf. Interval] |
|--------|------------|-----------|-----------|---|-----|----------------------|
| height | 0.716311   | .0293908  | 24.37     | 0.000 | .6572778 | .7753442 |
| _cons  | -149.6181  | 12.57266  | -11.90    | 0.000 | -174.871 | -124.3652 |
| /lnsigma | 3.372153 | .0180777  | 186.54    | 0.000 | 3.335843 | 3.408464 |

Reference

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
Description

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

See \texttt{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 \texttt{svyset} command has options to set variables for applying poststratification adjustments to the sampling weights. The \texttt{poststrata()} option takes a variable that contains poststratum identifiers, and the \texttt{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.

\textbf{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 \texttt{poststrata.dta} were collected using simple random sampling without replacement. The \texttt{totexp} variable contains the total expenses to the client, \texttt{type} identifies the cats and dogs, \texttt{postwgt} contains the poststratum sizes (450 for cats and 850 for dogs), and \texttt{fpc} contains the total number of clients (850 + 450 = 1300).
. use https://www.stata-press.com/data/r16/poststrata
. svyset, poststrata(type) postweight(postwgt) fpc(fpc)
  pweight: <none>
  VCE: linearized
  Poststrata: type
  Postweight: postwgt
  Single unit: missing
  Strata 1: <one>
    SU 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

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
</tr>
<tr>
<td>totexp</td>
<td>40.11513</td>
<td>1.163498</td>
</tr>
</tbody>
</table>

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 ≈ 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)
  pweight: <none>
  VCE: linearized
  Single unit: missing
  Strata 1: <one>
    SU 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

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
</tr>
<tr>
<td>totexp</td>
<td>39.7254</td>
<td>2.221747</td>
</tr>
</tbody>
</table>

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

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

where \( \hat{M}_k \) is

\[
\hat{M}_k = \sum_{j=1}^{m} I_{P_k}(j) w_j
\]

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

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

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

\[
z_j(\hat{R}^P) = \frac{\hat{X}^P z_j(\hat{Y}^P) - \hat{Y}^P z_j(\hat{X}^P)}{(\hat{X}^P)^2}
\]

where \( \hat{X}^P \) 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


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
```

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>SE</strong></td>
</tr>
<tr>
<td><strong>mse</strong></td>
</tr>
<tr>
<td><strong>nodots</strong></td>
</tr>
<tr>
<td><strong>dots(#)</strong></td>
</tr>
<tr>
<td><strong>saving(filename, ...)</strong></td>
</tr>
<tr>
<td><strong>verbose</strong></td>
</tr>
<tr>
<td><strong>noisily</strong></td>
</tr>
<tr>
<td><strong>trace</strong></td>
</tr>
<tr>
<td><strong>title(text)</strong></td>
</tr>
<tr>
<td><strong>nodrop</strong></td>
</tr>
<tr>
<td><strong>reject(exp)</strong></td>
</tr>
</tbody>
</table>

`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. A red ‘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 # replicates. **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/r16/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
                  
                  Linearized
          Mean  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 ≠ 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/r16/nmihs
.svymean birthwgt, over(race)
```

<table>
<thead>
<tr>
<th>Linearized</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>c.birthwgt@race</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>nonblack</td>
<td>3402.32</td>
<td>7.609532</td>
<td>3387.404 3417.236</td>
</tr>
<tr>
<td>black</td>
<td>3127.83</td>
<td>6.529814</td>
<td>3115.035 3140.634</td>
</tr>
</tbody>
</table>
```
More than one variable can be used in the `over()` option.

```
.svy: mean birthwgt, over(race marital)
```

(this running `mean` on estimation sample)

Survey: Mean estimation

<table>
<thead>
<tr>
<th>Number of strata = 6</th>
<th>Number of obs = 9,946</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of PSUs = 9,946</td>
<td>Population size = 3,895,562</td>
</tr>
<tr>
<td>Design df = 9,940</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Linearized</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>c.birthwgt@race#marital</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>nonblack#single</td>
<td>3291.045</td>
<td>20.18795</td>
<td>3251.472 3330.617</td>
</tr>
<tr>
<td>nonblack#married</td>
<td>3426.407</td>
<td>8.379497</td>
<td>3409.982 3442.833</td>
</tr>
<tr>
<td>black#single</td>
<td>3073.122</td>
<td>8.752553</td>
<td>3055.965 3090.279</td>
</tr>
<tr>
<td>black#married</td>
<td>3221.616</td>
<td>12.42687</td>
<td>3197.257 3245.975</td>
</tr>
</tbody>
</table>

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)
```

(this running `mean` on estimation sample)

Survey: Mean estimation

<table>
<thead>
<tr>
<th>Number of strata = 3</th>
<th>Number of obs = 4,724</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of PSUs = 4,724</td>
<td>Population size = 3,230,403</td>
</tr>
<tr>
<td>Subpop. no. obs = 4,724</td>
<td>Subpop. size = 3,230,403</td>
</tr>
<tr>
<td>Design df = 4,721</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Linearized</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>c.birthwgt@marital#age20</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>single#age20+</td>
<td>3312.012</td>
<td>24.2869</td>
<td>3264.398 3359.625</td>
</tr>
<tr>
<td>single#age&lt;20</td>
<td>3244.709</td>
<td>36.85934</td>
<td>3172.448 3316.971</td>
</tr>
<tr>
<td>married#age20+</td>
<td>3434.923</td>
<td>8.752553</td>
<td>3417.916 3451.929</td>
</tr>
<tr>
<td>married#age&lt;20</td>
<td>3287.301</td>
<td>34.15988</td>
<td>3220.332 3354.271</td>
</tr>
</tbody>
</table>

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

This time, we estimated means for the marital status and age (<20 or ≥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
- Subpopulation estimates other than the total
- Subpopulation with replication methods

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

$$\hat{Y}_S = \sum_{j=1}^{n} I_S(j)w_jy_j \quad (1)$$
where \( w_j = N/n \) is the unadjusted sampling weight for this design. The estimator for \( N_S \) is

\[
\hat{N}_S = \sum_{j=1}^{n} I_S(j)w_j
\]

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

\[
\hat{V}(\hat{Y}_S) = \left(1 - \frac{n}{N}\right) \frac{n}{n-1} \sum_{j=1}^{n} \left\{ I_S(j)w_jy_j - \frac{1}{n}\hat{Y}_S \right\}^2
\]

(2)

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

\[
\widehat{\text{Cov}}(\hat{Y}_S, \hat{X}_S) = \left(1 - \frac{n}{N}\right) \frac{n}{n-1} \sum_{j=1}^{n} \left\{ I_S(j)w_jy_j - \frac{1}{n}\hat{Y}_S \right\} \left\{ I_S(j)w_jx_j - \frac{1}{n}\hat{X}_S \right\}
\]

(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 \texttt{svyset} with the corresponding FPC) is

\[
\tilde{V}(\hat{Y}_S) = \left(1 - \frac{n_S}{N_S}\right) \frac{n_S}{n_S-1} \sum_{j=1}^{n_S} I_S(j) \left\{ w_jy_j - \frac{1}{n_S}\hat{Y}_S \right\}^2
\]

(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 \textit{if} and \textit{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 \textit{if} qualifier. For example, if you suspected laboratory error for a certain set of measurements, then using the \textit{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 [SVV] Variance estimation) is

\[
\hat{G}(\beta_S) = \sum_{j=1}^{n} I_S(j)w_jS(\beta_S; y_j, x_j) = 0
\]

(5)

You can write \( \hat{G}(\beta_S) \) as

\[
\hat{G}(\beta_S) = \sum_{j=1}^{n} I_S(j)w_jd_j
\]

which is an estimator for the subpopulation total \( G(\beta_S) \), 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


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 ...

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  Description

subpop([varname] [if])  identify a subpopulation

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 — The survey prefix command

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.

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

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

\[
[\text{varname}] \ [\text{if}]
\]

Thus the subpopulation is defined by the observations for which varname ≠ 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.

dof(#) specifies the design degrees of freedom, overriding the default calculation, df = N_{psu} − N_{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.

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, nolabel, fwrap(#), fwrapstyle, rformat(%fmt), 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/r16/nhanes2f
. svyset psuid [pweight=finalwgt], strata(stratid)
```

We then use the svy command to obtain our estimates:

```
. svy: mean zinc
```

We may also use the svy: regress command to estimate the relationship between zinc level and age:

```
. svy: regress zinc age
```

In both cases, the svy command takes into account the complex survey design characteristics of the data, including sampling weights, clustering, and stratification. This is crucial for obtaining accurate estimates of standard errors and for making valid inferences from the data.

In summary, the svy prefix command is essential for analyzing complex survey data, and it is important to carefully consider the effects of weights, clustering, and stratification when using the command. By carefully setting the appropriate options and using the svy command, we can obtain accurate estimates and standard errors for our analyses.
We now estimate the mean by using the proper design-based analysis:

```
.svys: 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
```

<table>
<thead>
<tr>
<th>Linearized</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>zinc</td>
<td>87.18207</td>
<td>.4944827</td>
<td>86.17356 88.19057</td>
</tr>
</tbody>
</table>

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

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

<table>
<thead>
<tr>
<th>Mean Std. Err. [95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>zinc 86.51518 .1510744 86.21904 86.81132</td>
</tr>
</tbody>
</table>

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]
  pweight: finalwgt
  VCE: linearized
  Single unit: missing
  Strata 1: <one>
  SU 1: <observations>
  FPC 1: <zero>
.svys: 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
```

<table>
<thead>
<tr>
<th>Linearized</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>zinc</td>
<td>87.18207</td>
<td>.1828747</td>
<td>86.82359 87.54054</td>
</tr>
</tbody>
</table>
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]
    pweight: finalwgt
    VCE: linearized
    Single unit: missing
    Strata 1: <one>
    SU 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

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
<td>[95% Conf. Interval]</td>
</tr>
<tr>
<td>zinc</td>
<td>87.18207</td>
<td>.7426221</td>
<td>77.74616</td>
</tr>
</tbody>
</table>
```

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)
pweight: finalwgt
VCE: linearized
Single unit: missing
Strata 1: stratid
SU 1: psuid
FPC 1: <zero>
```

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

Survey: Linear regression

| Number of strata | 31 |
| 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 |

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

<table>
<thead>
<tr>
<th>Source</th>
<th>SS</th>
<th>df</th>
<th>MS</th>
<th>Number of obs = 9,189</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>110417.827</td>
<td>7</td>
<td>15773.9753</td>
<td>Prob &gt; F = 0.0000</td>
</tr>
<tr>
<td>Residual</td>
<td>1816535.3</td>
<td>9,181</td>
<td>197.85811</td>
<td>R-squared = 0.0573</td>
</tr>
<tr>
<td>Total</td>
<td>1926953.13</td>
<td>9,188</td>
<td>209.724982</td>
<td>Root MSE = 14.066</td>
</tr>
</tbody>
</table>

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

svy — The survey prefix command

79
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(vtype)` weight type
- `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, $\hat{V}_{srs\text{worr}}$
svy — The survey prefix command

### Functions

- **e(V_srssub)**: subpopulation simple-random-sampling-without-replacement variance, $\hat{V}_{srswr}$ (created only when `subpop()` is specified)
- **e(V_srswr)**: simple-random-sampling-with-replacement variance, $\hat{V}_{srswr}$ (created only when `fpc()` option is `svyset`)
- **e(V_srssubwr)**: subpopulation simple-random-sampling-with-replacement variance, $\hat{V}_{srswr}$ (created only when `subpop()` is specified)
- **e(V_modelbased)**: model-based variance
- **e(V_msp)**: variance from misspecified model fit, $\hat{V}_{msp}$
- **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

### Matrices

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

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

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

- **r(sample)**: marks estimation sample

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


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
```

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
```

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

```bash
svy bootstrap exp_list [ , svy_options bootstrap_options eform_option ] : command
```

### svy_options

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>if/in</strong></td>
</tr>
</tbody>
</table>

**subpop([varname] [if])**
- identify a subpopulation

### Reporting

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>level(#)</strong></td>
</tr>
</tbody>
</table>
- set confidence level; default is `level(95)`

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>noheader</strong></td>
</tr>
</tbody>
</table>
- suppress table header

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>nolegend</strong></td>
</tr>
</tbody>
</table>
- suppress table legend

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>noadjust</strong></td>
</tr>
</tbody>
</table>
- do not adjust model Wald statistic

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>nocnsreport</strong></td>
</tr>
</tbody>
</table>
- do not display constraints

### display_options

```bash
display_options:
control columns and column formats, row spacing, line width,
display of omitted variables and base and empty cells, and
factor-variable labeling
```

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>coeflegend</strong></td>
</tr>
</tbody>
</table>
- display legend instead of statistics

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

### bootstrap_options

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Main</strong></td>
</tr>
</tbody>
</table>

**bsn(#)**
- bootstrap mean-weight adjustment

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Options</strong></td>
</tr>
</tbody>
</table>

**saving(filename[, ...])**
- save results to `filename`; save statistics in double precision;
  save results to `filename` every # replications

**mse**
- use MSE formula for variance

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Reporting</strong></td>
</tr>
</tbody>
</table>

**verbose**
- display the full table legend

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>nodots</strong></td>
</tr>
</tbody>
</table>
- suppress replication dots

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>dots(#)</strong></td>
</tr>
</tbody>
</table>
- display dots every # replications

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>noisily</strong></td>
</tr>
</tbody>
</table>
- display any output from `command`

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>trace</strong></td>
</tr>
</tbody>
</table>
- trace `command`

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>title(text)</strong></td>
</tr>
</tbody>
</table>
- use `text` as title for bootstrap results

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Advanced</strong></td>
</tr>
</tbody>
</table>

**nodrop**
- do not drop observations

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>reject(exp)</strong></td>
</tr>
</tbody>
</table>
- identify invalid results

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>dof(#)</strong></td>
</tr>
</tbody>
</table>
- design degrees of freedom

---

### svy Bootstrap for Survey Data

- `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`.
- 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`.

---

### Syntax Details

#### svy bootstrap

- `exp_list`: A list of expressions to be used in the bootstrap process.
- `svy_options`: Options for the `svy` command.
- `bootstrap_options`: Options for the bootstrap process.
- `eform_option`: An eform option.
- `command`: The statistical command to be executed.

---

### svy_options

- **if/in**: The `if` and `in` conditions can be used to specify subpopulations.

### Reporting

- **level(#)**: Sets the confidence level; default is `level(95)`.
- **noheader**: Suppresses the table header.
- **nolegend**: Suppresses the table legend.
- **noadjust**: Does not adjust the model Wald statistic.
- **nocnsreport**: Does 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

- Displays a legend instead of statistics.

#### coeflegend

- This option is not shown in the dialog boxes for estimation commands.

### bootstrap_options

- **Main**
  - **bsn(#)**: Bootstrap mean-weight adjustment.

- **Options**
  - **saving(filename[, ...])**: Saves results to `filename`; saves statistics in double precision; saves results to `filename` every # replications.
  - **mse**: Uses the MSE formula for variance.

- **Reporting**
  - **verbose**: Displays the full table legend.
  - **nodots**: Suppresses replication dots.
  - **dots(#)**: Displays dots every # replications.
  - **noisily**: Displays any output from `command`.
  - **trace**: Trace `command`.
  - **title(text)**: Uses `text` as title for bootstrap results.

- **Advanced**
  - **nodrop**: Does not drop observations.
  - **reject(exp)**: Identifies invalid results.
  - **dof(#)**: Designs degrees of freedom.
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.

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.

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.
verbose requests that the full table legend be displayed.

Note that the replication dots displayed by \texttt{dots(#)} are not the same as the replication dots displayed in the \texttt{svy:}
\texttt{regress} command. The replication dots displayed by \texttt{dots(#)} are
used to indicate which observations were included in the
replication. The replication dots displayed in the \texttt{svy:}
\texttt{regress} command are used to indicate which
replications were successful.

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

\texttt{nodots} suppresses display of the replication dots.
\texttt{dots(#)} displays dots every \# replications. \texttt{dots(0)} is a synonym for \texttt{nodots}.

\texttt{noisily} requests that any output from \texttt{command} be displayed. This option implies the \texttt{nodots} option.
\texttt{trace} causes a trace of the execution of \texttt{command} to be displayed. This option implies the \texttt{noisily} option.

\texttt{title(text)} specifies a title to be displayed above the table of bootstrap results; the default title is “Bootstrap results”.

\texttt{eform} option; see \texttt{[R eform option]}. This option is ignored if \texttt{exp_list} is not \texttt{b}.

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

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

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

\section*{Remarks and examples}


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.

\subsection*{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 \texttt{[SVY] svy estimation}, the dataset \texttt{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 \texttt{finalwgt} variable contains the sampling weights.
- The \texttt{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/r16/nmihs_bs
. svyset
     pweight: finwgt
     VCE: bootstrap
     MSE: off
     bsrweight: bsrw1 .. bsrw1000
     Single unit: missing
     Strata 1: <one>
      SU 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 Bootstrap Normal-based
  Mean Std. Err.    [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).
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

<table>
<thead>
<tr>
<th></th>
<th>Observed</th>
<th>Bootstrap</th>
<th>Normal-based</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
<td>[95% Conf. Interval]</td>
</tr>
<tr>
<td>birthwgt</td>
<td>3355.452</td>
<td>5.712574</td>
<td>3344.256</td>
</tr>
</tbody>
</table>
```

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.
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


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
```

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

\[
\texttt{[svy] brr \ exp\_list \ [\ , \ svy\_options \ brr\_options \ eform\_option] : command}
\]

svy_options Description

\texttt{if/in}
\texttt{subpop([varname] \ [if])} identify a subpopulation

Reporting
\texttt{level(#)} set confidence level; default is \texttt{level(95)}
\texttt{noheader} suppress table header
\texttt{nolegend} suppress table legend
\texttt{noadjust} do not adjust model Wald statistic
\texttt{nocnsreport} do not display constraints
\texttt{display_options} control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling

\texttt{coeflegend} display legend instead of statistics
\texttt{coeflegend} is not shown in the dialog boxes for estimation commands.

brr_options Description

Main
\texttt{hadamard(matrix)} Hadamard matrix
\texttt{fay(#)} Fay’s adjustment

Options
\texttt{saving(filename[, ...])} save results to \texttt{filename}; save statistics in double precision; save results to \texttt{filename} every \# replications
\texttt{mse} use MSE formula for variance

Reporting
\texttt{verbose} display the full table legend
\texttt{nodots} suppress replication dots
\texttt{dots(#)} display dots every \# replications
\texttt{noisily} display any output from \texttt{command}
\texttt{trace} trace \texttt{command}
\texttt{title(text)} use \texttt{text} as title for BRR results

Advanced
\texttt{nodrop} do not drop observations
\texttt{reject(exp)} identify invalid results
\texttt{dof(#)} design degrees of freedom

svy requires that the survey design variables be identified using \texttt{svyset}; see [SVY] \texttt{svyset}.
\texttt{command} defines the statistical command to be executed. The \texttt{by} prefix cannot be part of \texttt{command}.
See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.
Warning: Using \texttt{if} or \texttt{in} restrictions will often not produce correct variance estimates for subpopulations. To compute estimates for subpopulations, use the \texttt{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 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 ≤ # ≤ 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. A red ‘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, \( df = N_{psu} - N_{strata} \).

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.
Survey: Describing stage 1 sampling units

#Obs per Unit

<table>
<thead>
<tr>
<th>Stratum</th>
<th>#Units</th>
<th>#Obs</th>
<th>min</th>
<th>mean</th>
<th>max</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>380</td>
<td>165</td>
<td>190.0</td>
<td>215</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>185</td>
<td>67</td>
<td>92.5</td>
<td>118</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>348</td>
<td>149</td>
<td>174.0</td>
<td>199</td>
</tr>
<tr>
<td>4</td>
<td>2</td>
<td>460</td>
<td>229</td>
<td>230.0</td>
<td>231</td>
</tr>
<tr>
<td>5</td>
<td>2</td>
<td>252</td>
<td>105</td>
<td>126.0</td>
<td>147</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(output omitted)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>29</td>
<td>2</td>
<td>503</td>
<td>215</td>
<td>251.5</td>
<td>288</td>
</tr>
<tr>
<td>30</td>
<td>2</td>
<td>365</td>
<td>166</td>
<td>182.5</td>
<td>199</td>
</tr>
<tr>
<td>31</td>
<td>2</td>
<td>308</td>
<td>143</td>
<td>154.0</td>
<td>165</td>
</tr>
<tr>
<td>32</td>
<td>2</td>
<td>450</td>
<td>211</td>
<td>225.0</td>
<td>239</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>31</td>
<td>62</td>
<td>10,351</td>
<td>67</td>
<td>167.0</td>
<td>288</td>
</tr>
</tbody>
</table>

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).

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)

<table>
<thead>
<tr>
<th></th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
</tr>
</thead>
</table>

BRR results

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of obs</td>
<td>10,351</td>
</tr>
<tr>
<td>Population size</td>
<td>117,157,513</td>
</tr>
<tr>
<td>Replications</td>
<td>32</td>
</tr>
<tr>
<td>Design df</td>
<td>31</td>
</tr>
</tbody>
</table>

command: total weight height
WtoH: _b[weight]/_b[height]

| BRR *          | Coef. | 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/r16/nhanes2
. svy brr, hadamard(h32): ratio (WtoH: weight/height)
(running ratio on estimation sample)
BRR replications (32)
................................
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

<table>
<thead>
<tr>
<th>BRR</th>
<th>Ratio</th>
<th>Std. Err.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>.4268116</td>
<td>.0008904</td>
<td>.4249957 .4286276</td>
</tr>
</tbody>
</table>

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).
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


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

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/r16/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
- `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` ([TE] `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
- **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** [TE] 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

- **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

Multilevel mixed-effects models

- mecloglog  
  [ME] mecloglog — Multilevel mixed-effects complementary log-log regression
- meglm  
  [ME] meglm — Multilevel mixed-effects generalized linear model
- 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
- mepoisson  
  [ME] mepoisson — Multilevel mixed-effects Poisson regression
- meoprobit  
  [ME] meoprobit — Multilevel mixed-effects ordered probit 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
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
  - Descriptive statistics
  - Regression models
  - Health surveys

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 \texttt{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 \texttt{svyset iweights} instead of \texttt{pweights}; no standard command will allow negative sampling weights.

The \texttt{svy} commands compute finite population corrections (FPCs). After a \texttt{svy} command, \texttt{estat effects} will compute the design effects DEFF and DEFT and the misspecification effects MEFF and MEFT.

\texttt{svy} commands can perform variance estimation that accounts for multiple stages of clustered sampling.

\texttt{svy} commands can perform variance estimation that accounts for poststratification adjustments to the sampling weights.

Some standard options are not allowed with the \texttt{svy} prefix. For example, \texttt{vce()} and weights cannot be specified when using the \texttt{svy} prefix because \texttt{svy} is already using the variance estimation and sampling weights identified by \texttt{svyset}. Some options are not allowed with survey data because they would be statistically invalid, such as \texttt{no skip} for producing optional likelihood-ratio tests. Other options are not allowed because they change how estimation results are reported (for example, \texttt{nodisplay}, \texttt{first}, \texttt{plus}) or are not compatible with \texttt{svy}'s variance estimation methods (for example, \texttt{irls}, \texttt{mse1}, \texttt{hc2}, \texttt{hc3}).

Estimation results are presented in the standard way, except that \texttt{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), \texttt{svy} will also report the following information in the header:

\begin{itemize}
  \item number of strata and PSUs
  \item number of poststrata, if specified to \texttt{svyset}
  \item population size estimate
  \item subpopulation sizes, if the \texttt{subpop()} option was specified
  \item design degrees of freedom
\end{itemize}

\textbf{Descriptive statistics}

Use \texttt{svy: mean}, \texttt{svy: ratio}, \texttt{svy: proportion}, and \texttt{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 \texttt{[SVY] Direct standardization}. Estimates for multiple subpopulations can be obtained using the \texttt{over()} option; see \texttt{[SVY] Subpopulation estimation}.

\textbf{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:

\begin{itemize}
  \item Primary sampling units are mothers; that is, PSUs are individual observations—there is no separate PSU variable.
  \item The \texttt{finalwgt} variable contains the sampling weights.
  \item The \texttt{stratan} variable identifies strata.
  \item There is no variable for the finite population correction.
\end{itemize}
Then we use `svyset` to identify the variables for sampling weights and stratification.

```
. use https://www.stata-press.com/data/r16/nmihs
. svyset [pweight=finwgt], strata(stratan)
    pweight: finwgt
    VCE: linearized
    Single unit: missing
    Strata 1: stratan
     SU 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

                      Linearized
               Mean  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/r16/nhanes2d
. svyset
    pweight: finalwgt
    VCE: linearized
    Single unit: missing
    Strata 1: strata
     SU 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

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
</tr>
</thead>
<tbody>
<tr>
<td>highbp</td>
<td>Odds Ratio Std. Err. t P&gt;</td>
</tr>
<tr>
<td>height</td>
<td>.9657022 .0051511 -6.54 0.000 .9552534 .9762654</td>
</tr>
<tr>
<td>weight</td>
<td>1.053023 .0026902 20.22 0.000 1.047551 1.058524</td>
</tr>
<tr>
<td>age</td>
<td>1.050059 .0019761 25.96 0.000 1.046037 1.054097</td>
</tr>
<tr>
<td>female</td>
<td>.6272129 .0368195 -7.95 0.000 .5564402 .706987</td>
</tr>
<tr>
<td>_cons</td>
<td>.716868 .6106878 -0.39 0.699 .1261491 4.073749</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
</tr>
</thead>
<tbody>
<tr>
<td>highbp</td>
<td>Odds Ratio Std. Err. t P&gt;</td>
</tr>
<tr>
<td>height</td>
<td>.9630557 .0074892 -4.84 0.000 .9479018 .9784518</td>
</tr>
<tr>
<td>weight</td>
<td>1.053197 .003579 15.25 0.000 1.045923 1.060522</td>
</tr>
<tr>
<td>age</td>
<td>1.066112 .0034457 19.81 0.000 1.059107 1.073163</td>
</tr>
<tr>
<td>_cons</td>
<td>.3372393 .4045108 -0.91 0.372 .029208 3.893807</td>
</tr>
</tbody>
</table>

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 Midhune 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?


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/r16/nhefs
. svyset psu2 [pw=swgt2], strata(strata2)
```

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)
failure event:  lung_cancer != 0 & lung_cancer < .
obs. 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)

|           | Linearized |            |           |            |            |
|-----------|------------|------------|------------|------------|
|           | Haz. Ratio | 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      | 0.565   | 0.6658757 | 2.118142 |
| urban1     | .8035074  | .3285144   | -0.54     | 0.594   | 0.3555123 | 1.816039 |
| rural      | 1.581674  | .5281859   | 1.37      | 0.174   | 0.8125799 | 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] `stcox PH-assumption tests`, 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(col(1))
  
  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`.

As an example, consider the `revised_race` variable and its categories.
. svy: stcox former_smoker smoker male urban1 rural, strata(revised_race)
(running stcox on estimation sample)

Survey: Cox regression

<table>
<thead>
<tr>
<th>Number of strata = 35</th>
<th>Number of obs = 9,149</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of PSUs = 105</td>
<td>Population size = 151,327,827</td>
</tr>
<tr>
<td>Design df = 70</td>
<td>F( 5, 66) = 13.95</td>
</tr>
<tr>
<td>Prob &gt; F = 0.0000</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
<th></th>
<th></th>
<th></th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>_t</td>
<td>Haz. Ratio</td>
<td>Std. Err.</td>
<td>t</td>
<td>P&gt;</td>
</tr>
<tr>
<td>former_smoker</td>
<td></td>
<td>2.801797</td>
<td>.6280352</td>
<td>4.60</td>
<td>0.000</td>
</tr>
<tr>
<td>smoker</td>
<td></td>
<td>7.954921</td>
<td>2.640022</td>
<td>6.25</td>
<td>0.000</td>
</tr>
<tr>
<td>male</td>
<td></td>
<td>1.165724</td>
<td>.3390339</td>
<td>0.53</td>
<td>0.600</td>
</tr>
<tr>
<td>urban1</td>
<td></td>
<td>.784031</td>
<td>.3120525</td>
<td>-0.61</td>
<td>0.543</td>
</tr>
<tr>
<td>rural</td>
<td></td>
<td>1.490269</td>
<td>.5048569</td>
<td>1.18</td>
<td>0.243</td>
</tr>
</tbody>
</table>

Stratified by revised_race

References


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
[1] 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

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

**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

**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.

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 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.

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 \( x_3 \) equal to missing. The 42nd observation plays no role in obtaining the estimates, but \texttt{svy jackknife} has no way of knowing that and will use the wrong \( N \). If, on the other hand, you specify

\[
\texttt{. svy jackknife coef=_b[x2], n(e(n))}: \texttt{myreg y x1 x2 x3}
\]

Then \texttt{svy jackknife} will notice that observation 42 plays no role. The \( n(e(n)) \) option is specified because \texttt{myreg} is an estimation command, but it stores the number of observations used in \( e(n) \) (instead of the standard \( e(N) \)). When \texttt{svy jackknife} runs the regression omitting the 42nd observation, \texttt{svy jackknife} will observe that \( e(n) \) has the same value as when \texttt{svy jackknife} previously ran the regression by using all the observations. Thus \texttt{svy jackknife} will know that \texttt{myreg} did not use the observation.

### Options

\texttt{saving(} \textit{filename} [\texttt{, suboptions}] \texttt{)} creates a Stata data file (.dta file) consisting of (for each statistic in \textit{exp_list}) a variable containing the replicates.

- \texttt{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 \texttt{saving()} option to compute the variance estimates by using double precision.
- \texttt{every(#)} specifies that results be written to disk every \#th replication. \texttt{every()} should be specified in conjunction with \texttt{saving()} only when \texttt{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.
- \texttt{replace} specifies that \textit{filename} be overwritten if it exists. This option does not appear in the dialog box.
- \texttt{keep} specifies that new variables be added to the dataset containing the pseudovalues of the requested statistics. For instance, if you typed

\[
\texttt{. svy jackknife coef=_b[x2], eclass keep: regress y x1 x2 x3}
\]

Then the new variable \texttt{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

\[
pseudovalue_j = N \times \{b - b(j)\} + b(j)
\]

where \( N \) is the number of observations used to produce \( b \). \texttt{keep} implies the \texttt{nodrop} option.

- \texttt{mse} specifies that \texttt{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, \texttt{svy jackknife} computes the variance by using deviations of the pseudovalues from their mean.

### Reporting

- \texttt{verbose} requests that the full table legend be displayed.
- \texttt{nodots} and \texttt{dots(#)} specify whether to display replication dots. By default, one dot character is printed for each successful replication. A red ‘x’ is displayed if \texttt{command} returns an error, ‘e’ is displayed if at least one value in \textit{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, df = N_{psu} - N_{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 \( \bar{y} \) is the sample mean of \( y \) using the entire dataset and \( \bar{y}_{(j)} \) is the mean when the \( j \)th observation is omitted, then

\[
\bar{y} = \frac{(N - 1) \bar{y}_{(j)} + y_j}{N}
\]

Solving for \( y_j \), we obtain

\[
y_j = N \bar{y} - (N - 1) \bar{y}_{(j)}
\]

These are the pseudovalues that \texttt{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/r16/nhanes2
. svyset
   pweight: finalwgt
   VCE: linearized
   Single unit: missing
   Strata 1: strata
   SU 1: psu
   FPC 1: <zero>
. svy jackknife slope = _b[height]: regress weight height
   (running regress on estimation sample)
Jackknife replications (62)
.................................................. 50
............
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)

<table>
<thead>
<tr>
<th></th>
<th>Jackknife</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Coef.</td>
</tr>
<tr>
<td>slope</td>
<td>.8014753</td>
</tr>
</tbody>
</table>
```

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)`.`
Here we perform the same analysis as in the previous example, using jackknife replication weights.

```
. svy jackknife slope = _b[height], nodots: regress weight height
```

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
```
Stored results

In addition to the results documented in \texttt{[SVY] svy}, \texttt{svy jackknife} stores the following in \texttt{e()}: 

Scalars

- \texttt{e(N_reps)}: number of replications
- \texttt{e(N_misreps)}: number of replications with missing values
- \texttt{e(k_exp)}: number of standard expressions
- \texttt{e(k_eexp)}: number of \texttt{\_b/\_se} expressions
- \texttt{e(k_extra)}: number of extra estimates added to \texttt{\_b}

Macros

- \texttt{e(cmdname)}: command name from \texttt{command}
- \texttt{e(cmd)}: same as \texttt{e(cmdname)} or \texttt{jackknife}
- \texttt{e(vce)}: \texttt{jackknife}
- \texttt{e(exp#)}: \#th expression
- \texttt{e(jkrweight)}: \texttt{jkrweight()} variable list

Matrices

- \texttt{e(b_jk)}: jackknife means
- \texttt{e(V)}: jackknife variance estimates

When \texttt{exp_list} is \texttt{\_b}, \texttt{svy jackknife} will also carry forward most of the results already in \texttt{e()} from \texttt{command}.

Methods and formulas

See \texttt{[SVY] Variance estimation} for details regarding jackknife variance estimation.

References


Also see

- \texttt{[SVY] svy postestimation} — Postestimation tools for \texttt{svy}
- \texttt{[SVY] svy bootstrap} — Bootstrap for survey data
- \texttt{[SVY] svy brr} — Balanced repeated replication for survey data
- \texttt{[SVY] svy sdr} — Successive difference replication for survey data
- \texttt{[SVY] Calibration} — Calibration for survey data
- \texttt{[SVY] Poststratification} — Poststratification for survey data
- \texttt{[SVY] Subpopulation estimation} — Subpopulation estimation for survey data
- \texttt{[SVY] Variance estimation} — Variance estimation for survey data
- \texttt{[R] jackknife} — Jackknife estimation
- \texttt{[U] 20 Estimation and postestimation commands}
svy postestimation — Postestimation tools for svy

Postestimation commands predict margins
Remarks and examples References Also see

Postestimation commands

The following postestimation commands are available after svy:

<table>
<thead>
<tr>
<th>command</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>contrast</td>
<td>contrasts and ANOVA-style joint tests of estimates</td>
</tr>
<tr>
<td>estat (svy)</td>
<td>postestimation statistics for survey data</td>
</tr>
<tr>
<td>estimates</td>
<td>cataloging estimation results</td>
</tr>
<tr>
<td>lincom</td>
<td>point estimates, standard errors, testing, and inference for linear</td>
</tr>
<tr>
<td></td>
<td>combinations of coefficients</td>
</tr>
<tr>
<td>margins</td>
<td>marginal means, predictive margins, marginal effects, and average marginal</td>
</tr>
<tr>
<td></td>
<td>effects</td>
</tr>
<tr>
<td>marginsplot</td>
<td>graph the results from margins (profile plots, interaction plots, etc.)</td>
</tr>
<tr>
<td>nlcom</td>
<td>point estimates, standard errors, testing, and inference for nonlinear</td>
</tr>
<tr>
<td></td>
<td>combinations of coefficients</td>
</tr>
<tr>
<td>predict</td>
<td>predictions, residuals, influence statistics, and other diagnostic measures</td>
</tr>
<tr>
<td>predictnl</td>
<td>point estimates, standard errors, testing, and inference for generalized</td>
</tr>
<tr>
<td></td>
<td>predictions</td>
</tr>
<tr>
<td>pwcompare</td>
<td>pairwise comparisons of estimates</td>
</tr>
<tr>
<td>suest</td>
<td>seemingly unrelated estimation</td>
</tr>
<tr>
<td>test</td>
<td>Wald tests of simple and composite linear hypotheses</td>
</tr>
<tr>
<td>testnl</td>
<td>Wald tests of nonlinear hypotheses</td>
</tr>
</tbody>
</table>

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`.

```stata
. use https://www.stata-press.com/data/r16/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

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
<td>[95% Conf. Interval]</td>
</tr>
<tr>
<td>c.zinc@race</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>White</td>
<td>91.15725</td>
<td>.541625</td>
<td>90.0526</td>
</tr>
<tr>
<td>Black</td>
<td>88.269</td>
<td>1.208336</td>
<td>85.80458</td>
</tr>
<tr>
<td>Other</td>
<td>85.54716</td>
<td>2.608974</td>
<td>80.22612</td>
</tr>
</tbody>
</table>
```

Then we run `lincom` to estimate the difference of zinc levels between the two subpopulations.

```stata
. lincom zinc#1.race - zinc#2.race
( 1) c.zinc@1bn.race - c.zinc@2.race = 0

| Mean | Coef.  | 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.

```stata
use https://www.stata-press.com/data/r16/nhanes2d, clear
.svy: logistic highbp height weight age c.age#c.age female
(running logistic on estimation sample)
```

Survey: Logistic regression

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Odds Ratio</td>
</tr>
<tr>
<td>height</td>
<td>.9656421</td>
</tr>
<tr>
<td>weight</td>
<td>1.052911</td>
</tr>
<tr>
<td>age</td>
<td>1.055829</td>
</tr>
<tr>
<td>c.age#c.age</td>
<td>.9999399</td>
</tr>
</tbody>
</table>

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`.

```stata
.nlcom peak: -_b[age]/(2*_b[c.age#c.age])
```

|                    | Coef. | 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.

```stata
.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

<table>
<thead>
<tr>
<th>Number of strata</th>
<th>31</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of PSUs</td>
<td>62</td>
</tr>
<tr>
<td>Population size</td>
<td>117,157,513</td>
</tr>
<tr>
<td>Design df</td>
<td>31</td>
</tr>
<tr>
<td>F(7, 25)</td>
<td>230.16</td>
</tr>
<tr>
<td>Prob &gt; F</td>
<td>0.0000</td>
</tr>
</tbody>
</table>

| Odds Ratio | 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     |           |       |       |       |                     |
| 0          |           |       |       |       |                     |
| 1          | .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

<table>
<thead>
<tr>
<th>Expression</th>
<th>Linearized</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Margin</td>
<td>Std. Err.</td>
<td>t</td>
<td>P&gt;</td>
</tr>
<tr>
<td>race</td>
<td>White</td>
<td>.3600722</td>
<td>.0150121</td>
<td>23.99</td>
</tr>
<tr>
<td></td>
<td>Black</td>
<td>.4256413</td>
<td>.0211311</td>
<td>20.14</td>
</tr>
<tr>
<td></td>
<td>Other</td>
<td>.4523404</td>
<td>.0311137</td>
<td>14.54</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Dy/dx w.r.t.</th>
<th>Linearized</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>dy/dx</td>
<td>Std. Err.</td>
<td>t</td>
<td>P&gt;</td>
</tr>
<tr>
<td>race</td>
<td>Black</td>
<td>.0655691</td>
<td>.0204063</td>
<td>3.21</td>
</tr>
<tr>
<td></td>
<td>Other</td>
<td>.0922682</td>
<td>.0343809</td>
<td>2.68</td>
</tr>
</tbody>
</table>

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)
```

<table>
<thead>
<tr>
<th>Expression</th>
<th>Number of strata =  31</th>
<th>Number of obs =     10,351</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of PSUs = 62</td>
<td>Population size = 117,157,513</td>
<td></td>
</tr>
<tr>
<td>Design df = 31</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Expression : Pr(highbp), predict()</td>
<td>dy/dx w.r.t. : 2.race 3.race</td>
<td></td>
</tr>
<tr>
<td>over : region</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

| dy/dx | 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 16.1
    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)
.................................................. 50
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

                Jackknife             
                  Coef.       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/r16/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

Linearized

|            | Coef. | Std. Err. | t     | P>|t|  | [95% Conf. Interval] |
|------------|-------|-----------|-------|-----|----------------------|
| loglead    |       |           |       |     |                      |
| age        | .0158388 | .0027352 | 5.79  | 0.000 | .0102603 -.0214173 |
| c.age#c.age| -.0001464 | .0000295 | -4.96 | 0.000 | -.0002066 -.0000862 |
| 1.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 leadhat
. generate showobs = inrange(_n,1,5) + inrange(_n,2501,2505) +
> inrange(_n,4945,4948)
```
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

\[ F(3, 29) = 2.96 \]

\[ \text{Prob} > F = 0.0486 \]

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

\[ F(3, 31) = 3.17 \]

\[ \text{Prob} > F = 0.0382 \]

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:

\[
\text{. test 2.region 3.region 4.region, mtest(bonferroni)}
\]

Adjusted Wald test

\[
\begin{align*}
( 1) & \quad 2.\text{region} = 0 \\
( 2) & \quad 3.\text{region} = 0 \\
( 3) & \quad 4.\text{region} = 0
\end{align*}
\]

<table>
<thead>
<tr>
<th></th>
<th>( F(\text{df}, 29) )</th>
<th>( \text{df} )</th>
<th>( p )</th>
</tr>
</thead>
<tbody>
<tr>
<td>(1)</td>
<td>0.34</td>
<td>1</td>
<td>1.0000 #</td>
</tr>
<tr>
<td>(2)</td>
<td>9.06</td>
<td>1</td>
<td>0.0155 #</td>
</tr>
<tr>
<td>(3)</td>
<td>0.87</td>
<td>1</td>
<td>1.0000 #</td>
</tr>
</tbody>
</table>

\[ \text{all} 2.96 3 0.0486 \]  
\[ \text{# Bonferroni-adjusted } p \text{-values} \]

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 \texttt{svy} commands, we can estimate contrasts and make pairwise comparisons with the \texttt{contrast} and \texttt{pwcompare} commands. First, we will fit a regression of serum zinc levels on health status:

\[
\text{. use https://www.stata-press.com/data/r16/nhanes2f, clear}
\]
\[
\text{. label list hlthgrp}
\]

hlthgrp:

1 poor
2 fair
3 average
4 good
5 excellent

\[
\text{. svy: regress zinc i.health}
\]

(running \texttt{regress} on estimation sample)

Survey: Linear regression

| Number of strata | = 31 |
| 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 |

| \( \text{zinc} \) | Coef. | Std. Err. | t | P>|t| | [95% Conf. Interval] |
|-----------------|-------|-----------|---|-------|------------------|
| health          |       |           |   |       |                  |
| fair            | .9272308 | .7690396 | 1.21 | 0.237 | -0.6412357 | 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

Margins : asbalanced

<table>
<thead>
<tr>
<th></th>
<th>df</th>
<th>F</th>
<th>P&gt;F</th>
</tr>
</thead>
<tbody>
<tr>
<td>health</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(fair vs poor)</td>
<td>1</td>
<td>1.45</td>
<td>0.2371</td>
</tr>
<tr>
<td>(average vs fair)</td>
<td>1</td>
<td>5.49</td>
<td>0.0257</td>
</tr>
<tr>
<td>(good vs average)</td>
<td>1</td>
<td>10.92</td>
<td>0.0024</td>
</tr>
<tr>
<td>(excellent vs good)</td>
<td>1</td>
<td>1.93</td>
<td>0.1744</td>
</tr>
<tr>
<td>Joint</td>
<td>4</td>
<td>15.61</td>
<td>0.0000</td>
</tr>
<tr>
<td>Design</td>
<td>31</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
```

Note: F statistics are adjusted for the survey design.

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

Margins : asbalanced

<table>
<thead>
<tr>
<th>Number of Comparisons</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>health</td>
<td>10</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Contrast</th>
<th>Std. Err.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>fair vs poor</td>
<td>0.9</td>
<td>-1.4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3.2</td>
</tr>
<tr>
<td>average vs poor</td>
<td>2.4</td>
<td>0.5</td>
</tr>
<tr>
<td></td>
<td></td>
<td>4.4</td>
</tr>
<tr>
<td>good vs poor</td>
<td>4.0</td>
<td>2.0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>6.1</td>
</tr>
<tr>
<td>excellent vs poor</td>
<td>4.8</td>
<td>2.6</td>
</tr>
<tr>
<td></td>
<td></td>
<td>6.9</td>
</tr>
<tr>
<td>average vs fair</td>
<td>1.5</td>
<td>-0.4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3.5</td>
</tr>
<tr>
<td>good vs fair</td>
<td>3.1</td>
<td>1.5</td>
</tr>
<tr>
<td></td>
<td></td>
<td>4.8</td>
</tr>
<tr>
<td>excellent vs fair</td>
<td>3.8</td>
<td>1.7</td>
</tr>
<tr>
<td></td>
<td></td>
<td>6.0</td>
</tr>
<tr>
<td>good vs average</td>
<td>1.6</td>
<td>0.1</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3.0</td>
</tr>
<tr>
<td>excellent vs average</td>
<td>2.3</td>
<td>0.3</td>
</tr>
<tr>
<td></td>
<td></td>
<td>4.4</td>
</tr>
<tr>
<td>excellent vs good</td>
<td>0.7</td>
<td>-0.9</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.3</td>
</tr>
</tbody>
</table>

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/r16/nhanes2f, clear
.svyset psuid [pw=finalwgt], strata(stratid)
pweight: finalwgt
VCE: linearized
Single unit: missing
Strata 1: stratid
SU 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

Coef.  Std. Err.  t  P>|t|  [95% Conf. Interval]
female -0.1615219  0.0523678  -3.08  0.004  -0.2683267  -0.054717
black -0.986568  0.0790277  -12.48  0.000  -1.147746  -0.8253899
age -0.0119491  0.0082974  -1.44  0.160  -0.0288717  0.0049736
c.age#c.age -0.0003234  0.000091  -3.55  0.001  -0.000509  -0.0001377
/cut1 -4.566229  0.1632651  -4.899192  -4.233266
/cut2 -3.057415  0.1699944  -4.147746  -2.710709
/cut3 -1.520596  0.1714342  -1.870954  -1.170954
/cut4 -0.242785  0.1703965  -5.90311  0.104741
```

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`.

```plaintext
. 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

<table>
<thead>
<tr>
<th>Number of strata</th>
<th>= 31</th>
<th>Number of obs</th>
<th>= 10,335</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of PSUs</td>
<td>= 62</td>
<td>Population size</td>
<td>= 116,997,257</td>
</tr>
<tr>
<td>Design df</td>
<td>= 31</td>
<td>F(   4,    28)</td>
<td>= 197.08</td>
</tr>
<tr>
<td>Prob &gt; F</td>
<td>= 0.0000</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

| health3          | Coef.  | Std. Err. | t     | P>|t| | [95% Conf. Interval] |
|------------------|--------|-----------|-------|-------|---------------------|
| female           | -.1551238 | .0563809 | -2.75 | 0.010 | -.2701133 to -.0401342 |
| black            | -1.046316 | .0728274 | -14.37| 0.000 | -1.194849 to -.8977836 |
| age              | -.0365408 | .0073653 | -4.96 | 0.000 | -.0515624 to -.0215192 |
| c.age#c.age      | -.00009 | .0000791 | -1.14 | 0.264 | -.0002512 to .0000713 |
| /cut1            | -3.655498 | .1610211 | -3.983903 | -3.327093 |
| /cut2            | -2.109584 | .1597057 | -2.435306 | -1.783862 |
```

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

<table>
<thead>
<tr>
<th>Number of strata</th>
<th>Number of obs</th>
<th>Population size</th>
<th>Design df</th>
</tr>
</thead>
<tbody>
<tr>
<td>31</td>
<td>10,335</td>
<td>116,997,257</td>
<td>31</td>
</tr>
</tbody>
</table>

| Linearized       | Coef.  | Std. Err. | t     | P>|t| [95% Conf. Interval] |
|------------------|--------|-----------|-------|-----------------------|
| H5_health        |        |           |       |                       |
| female           | -0.1615219 | 0.0523678 | -3.08 | 0.004 | -0.2683267 | -0.054717 |
| black            | -0.986568  | 0.0790277  | -12.48| 0.000 | -1.147746  | -0.8253899|
| age              | -0.0119491 | 0.0082974  | -1.44 | 0.160 | -0.0288717 | 0.0049736 |
| c.age#c.age      | -0.0003234 | 0.000091   | -3.55 | 0.001 | -.000509   | -.0001377 |
| /H5              |         |           |       |                       |
| cut1             | -4.566229  | 1.632561   | -4.89 | 0.000 | -4.899192  | -4.233266 |
| cut2             | -3.057415  | 1.699944   | -3.40 | 0.001 | -3.404121  | -2.710709 |
| cut3             | -1.520596  | 1.714342   | -1.87 | 0.067 | -1.870239  | -1.170954 |
| cut4             | -0.242785  | 0.170396   | -1.59 | 0.118 | -.0003512  | .104741   |
| H3_health3       |         |           |       |                       |
| female           | -0.1551238 | 0.0563809  | -2.75 | 0.006 | -.2701133  | -.0401342 |
| black            | -1.046316  | 0.0728274  | -14.37| 0.000 | -1.194849  | -.8977836 |
| age              | -0.0365408 | 0.0073653  | -4.96 | 0.000 | -0.051562  | -.0215192 |
| c.age#c.age      | -0.00009   | 0.0000791  | -0.14 | 0.891 | -.0002512  | .0000713  |
| /H3              |         |           |       |                       |
| cut1             | -3.655498  | 1.610211   | -3.98 | 0.002 | -3.983903  | -3.327093 |
| cut2             | -2.109584  | 1.597057   | -1.36 | 0.176 | -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.

```
```

<table>
<thead>
<tr>
<th>H5</th>
<th>latent</th>
<th>cut1</th>
<th>cut2</th>
<th>cut3</th>
<th>cut4</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>observed</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>4</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>H3</th>
<th>latent</th>
<th>cut1</th>
<th>cut2</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>observed</td>
<td>2</td>
<td>3</td>
</tr>
</tbody>
</table>

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/r16/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]
```

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


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

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

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>if/in</td>
<td></td>
</tr>
<tr>
<td>subpop([varname] [if])</td>
<td>identify a subpopulation</td>
</tr>
</tbody>
</table>

Reporting

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>level(#)</td>
<td>set confidence level; default is level(95)</td>
</tr>
<tr>
<td>noheader</td>
<td>suppress table header</td>
</tr>
<tr>
<td>nolegend</td>
<td>suppress table legend</td>
</tr>
<tr>
<td>noadjust</td>
<td>do not adjust model Wald statistic</td>
</tr>
<tr>
<td>nocnsreport</td>
<td>do not display constraints</td>
</tr>
<tr>
<td>display_options</td>
<td>control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>coeflegend</td>
<td>display legend instead of statistics</td>
</tr>
</tbody>
</table>

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

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

sdr_options  Description

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Options</td>
<td></td>
</tr>
<tr>
<td>saving([filename] , ...)</td>
<td>save results to filename; save statistics in double precision; save results to filename every # replications</td>
</tr>
<tr>
<td>mse</td>
<td>use MSE formula for variance</td>
</tr>
</tbody>
</table>

Reporting

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>verbose</td>
<td>display the full table legend</td>
</tr>
<tr>
<td>nodots</td>
<td>suppress replication dots</td>
</tr>
<tr>
<td>dots(#)</td>
<td>display dots every # replications</td>
</tr>
<tr>
<td>noisyly</td>
<td>display any output from command</td>
</tr>
<tr>
<td>trace</td>
<td>trace command</td>
</tr>
<tr>
<td>title(text)</td>
<td>use text as title for SDR results</td>
</tr>
</tbody>
</table>

Advanced

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>nodrop</td>
<td>do not drop observations</td>
</tr>
<tr>
<td>reject(exp)</td>
<td>identify invalid results</td>
</tr>
<tr>
<td>dof(#)</td>
<td>design degrees of freedom</td>
</tr>
</tbody>
</table>

`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`.
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:

\[
\text{exp_list contains } (\text{name: elist}) \\
\text{elist contains } newvarname = (exp) \\
\text{(exp)} \\
\text{eexp is } specname \\
\text{[eqno]specname} \\
\text{specname is } _b \\
\text{_b[]} \\
\text{_se} \\
\text{_se[]} \\
\text{eqno is } ## \\
\text{name}
\]

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.

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.

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. A red ‘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.

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 U.S. 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/r16/ss07ptx
    . svyset pweight: pwgtp
        VCE: sdr
        MSE: off
        sdrweight: pwgtp1 .. pwgtp80
        Single unit: missing
        Strata 1: <one>
        SU 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 sdr — Successive difference replication for survey data

```
. svy: mean agep, over(sex)
(running mean on estimation sample)
SDR replications (80)

<table>
<thead>
<tr>
<th></th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>50</th>
</tr>
</thead>
</table>

Survey: Mean estimation
Number of obs = 230,817
Population size = 23,904,380
Replications = 80

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>SDR Mean</td>
<td>Std. Err.</td>
<td>[95% Conf. Interval]</td>
</tr>
<tr>
<td>c.agep@sex</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>33.24486</td>
<td>.0470986</td>
<td>33.15255</td>
</tr>
<tr>
<td>Female</td>
<td>35.23908</td>
<td>.0386393</td>
<td>35.16335</td>
</tr>
</tbody>
</table>

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

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


Quick start

One-way table showing weighted proportions for categories of \texttt{v1} using \texttt{svyset} data

\texttt{svy: tabulate v1}

Add 95\% confidence intervals and weighted counts

\texttt{svy: tabulate v1, ci count}

As above, and display large counts in a more readable format

\texttt{svy: tabulate v1 ci count format(\%11.3g)}

Unweighted numbers of observations and weighted proportions for categories of \texttt{v2}

\texttt{svy: tabulate v2, obs}

Weighted proportions and CIs for categories of \texttt{v3} in the subpopulation defined by \texttt{v4} $>$ 40

\texttt{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 ]
```

<table>
<thead>
<tr>
<th>vcetype</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>SE</td>
<td></td>
</tr>
<tr>
<td>linearized</td>
<td>Taylor-linearized variance estimation</td>
</tr>
<tr>
<td>bootstrap</td>
<td>bootstrap variance estimation; see [SVY] svy bootstrap</td>
</tr>
<tr>
<td>brr</td>
<td>BRR variance estimation; see [SVY] svy brr</td>
</tr>
<tr>
<td>jackknife</td>
<td>jackknife variance estimation; see [SVY] svy jackknife</td>
</tr>
<tr>
<td>sdr</td>
<td>SDR variance estimation; see [SVY] svy sdr</td>
</tr>
</tbody>
</table>

Specifying a vcetype overrides the default from svyset.

<table>
<thead>
<tr>
<th>svy_options</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>if/in</td>
<td></td>
</tr>
<tr>
<td>subpop( varname</td>
<td>if )</td>
</tr>
</tbody>
</table>

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.
## svy: tabulate oneway — One-way tables for survey data

### Model

<table>
<thead>
<tr>
<th>Model</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>stdize(varname)</td>
<td>variable identifying strata for standardization</td>
</tr>
<tr>
<td>stddfweight(varname)</td>
<td>weight variable for standardization</td>
</tr>
<tr>
<td>tab(varname)</td>
<td>variable for which to compute cell totals/proportions</td>
</tr>
<tr>
<td>missing</td>
<td>treat missing values like other values</td>
</tr>
</tbody>
</table>

### display_items

<table>
<thead>
<tr>
<th>Table items</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cell</td>
<td>cell proportions</td>
</tr>
<tr>
<td>count</td>
<td>weighted cell counts</td>
</tr>
<tr>
<td>se</td>
<td>standard errors</td>
</tr>
<tr>
<td>ci</td>
<td>confidence intervals</td>
</tr>
<tr>
<td>deff</td>
<td>display the DEFF design effects</td>
</tr>
<tr>
<td>deft</td>
<td>display the DEFT design effects</td>
</tr>
<tr>
<td>cv</td>
<td>display the coefficient of variation</td>
</tr>
<tr>
<td>srssubpop</td>
<td>report design effects assuming SRS within subpopulation</td>
</tr>
<tr>
<td>obs</td>
<td>cell observations</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Reporting</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>_level(#)</td>
<td>set confidence level; default is level(95)</td>
</tr>
<tr>
<td>proportion</td>
<td>display proportions; the default</td>
</tr>
<tr>
<td>percent</td>
<td>display percentages instead of proportions</td>
</tr>
<tr>
<td>nomarginal</td>
<td>suppress column marginal</td>
</tr>
<tr>
<td>nolabel</td>
<td>suppress displaying value labels</td>
</tr>
<tr>
<td>cellwidth(#)</td>
<td>cell width</td>
</tr>
<tr>
<td>csepwidth(#)</td>
<td>column-separation width</td>
</tr>
<tr>
<td>stubwidth(#)</td>
<td>stub width</td>
</tr>
<tr>
<td>format(%fmt)</td>
<td>cell format; default is format(%6.0g)</td>
</tr>
</tbody>
</table>

Proportion is not shown in the dialog box.

### Options

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

**stdize(varname)** specifies that the point estimates be adjusted by direct standardization across the strata identified by varname. This option requires the stddfweight() 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.
\texttt{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.

\texttt{missing} specifies that missing values of \texttt{varname} be treated as another row category rather than be omitted from the analysis (the default).

<table>
<thead>
<tr>
<th>Table items</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>cell</td>
<td>requests that cell proportions (or percentages) be displayed. This is the default if \texttt{count} is not specified.</td>
</tr>
<tr>
<td>count</td>
<td>requests that weighted cell counts be displayed.</td>
</tr>
<tr>
<td>se</td>
<td>requests that the standard errors of cell proportions (the default) or weighted counts be displayed.</td>
</tr>
<tr>
<td>\texttt{ci}</td>
<td>requests confidence intervals for cell proportions or weighted counts.</td>
</tr>
<tr>
<td>deff</td>
<td>and \texttt{deft} request that the design-effect measures DEFF and DEFT be displayed for each cell proportion or weighted count. See [\texttt{SVY}] estat for details.</td>
</tr>
<tr>
<td>cv</td>
<td>requests that the coefficient of variation be displayed for each cell proportion, count, or row or column proportion. See [\texttt{SVY}] estat for details.</td>
</tr>
<tr>
<td>\texttt{srssubpop}</td>
<td>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, \texttt{srssubpop} would be given when computing subpopulation estimates by strata or by groups of strata.</td>
</tr>
<tr>
<td>obs</td>
<td>requests that the number of observations for each cell be displayed.</td>
</tr>
</tbody>
</table>

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

\texttt{proportion}, the default, requests that proportions be displayed.

\texttt{percent} requests that percentages be displayed instead of proportions.

\texttt{nomarginal} requests that the column marginal not be displayed.

\texttt{nolabel} requests that variable labels and value labels be ignored.

\texttt{cellwidth(#)}, \texttt{csepwidth(#)}, and \texttt{stubwidth(#)} specify widths of table elements in the output; see [\texttt{P}] tabdisp. Acceptable values for the \texttt{stubwidth()} option range from 4 to 32.

\texttt{format(\%fmt)} specifies a format for the items in the table. The default is \texttt{format(\%6.0g)}. See [\texttt{U}] 12.5 Formats: Controlling how data are displayed.

\texttt{svy: tabulate} uses the \texttt{tabdisp} command (see [\texttt{P}] tabdisp) to produce the table. Only five items can be displayed in the table at one time. The \texttt{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

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.

```stata
use https://www.stata-press.com/data/r16/nhanes2b
svyset psuid [pweight=finalwgt], strata(stratid)
pweight: finalwgt
VCE: linearized
Single unit: missing
Strata 1: stratid
SU 1: psuid
FPC 1: <zero>
svy: tabulate race
```

<table>
<thead>
<tr>
<th>race</th>
<th>proportion</th>
</tr>
</thead>
<tbody>
<tr>
<td>White</td>
<td>.8792</td>
</tr>
<tr>
<td>Black</td>
<td>.0955</td>
</tr>
<tr>
<td>Other</td>
<td>.0253</td>
</tr>
<tr>
<td>Total</td>
<td>1</td>
</tr>
</tbody>
</table>

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

1=white,  2=black,  3=other

<table>
<thead>
<tr>
<th></th>
<th>count</th>
<th>lb</th>
<th>ub</th>
<th>deff</th>
<th>deft</th>
</tr>
</thead>
<tbody>
<tr>
<td>White</td>
<td>102999549</td>
<td>97060400</td>
<td>108938698</td>
<td>60.2</td>
<td>7.76</td>
</tr>
<tr>
<td>Black</td>
<td>11189236</td>
<td>8213964</td>
<td>14164508</td>
<td>18.6</td>
<td>4.31</td>
</tr>
<tr>
<td>Other</td>
<td>2968728</td>
<td>414930</td>
<td>5522526</td>
<td>47.9</td>
<td>6.92</td>
</tr>
<tr>
<td>Total</td>
<td>117157513</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

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.

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 U.S. 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 U.S. 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 U.S. 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 U.S. 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


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 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

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

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
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**

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>SE</strong></td>
</tr>
<tr>
<td><strong>linearized</strong> Taylor-linearized variance estimation</td>
</tr>
<tr>
<td><strong>bootstrap</strong> bootstrap variance estimation; see [SVY] svy bootstrap</td>
</tr>
<tr>
<td><strong>brr</strong>  BRR variance estimation; see [SVY] svy brr</td>
</tr>
<tr>
<td><strong>jackknife</strong> jackknife variance estimation; see [SVY] svy jackknife</td>
</tr>
<tr>
<td><strong>sdr</strong>  SDR variance estimation; see [SVY] svy sdr</td>
</tr>
</tbody>
</table>

Specifying a vcetype overrides the default from svyset.

**svy_options**

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>if/in</strong></td>
</tr>
<tr>
<td><strong>subpop([ varname ] [ if ])</strong> identify a subpopulation</td>
</tr>
</tbody>
</table>

**SE**

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>bootstrap_options</strong> more options allowed with bootstrap variance estimation; see [SVY] bootstrap_options</td>
</tr>
<tr>
<td><strong>brr_options</strong> more options allowed with BRR variance estimation; see [SVY] brr_options</td>
</tr>
<tr>
<td><strong>jackknife_options</strong> more options allowed with jackknife variance estimation; see [SVY] jackknife_options</td>
</tr>
<tr>
<td><strong>sdr_options</strong> more options allowed with SDR variance estimation; see [SVY] sdr_options</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Model</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>stdize(varname)</td>
<td>variable identifying strata for standardization</td>
</tr>
<tr>
<td>stdweight(varname)</td>
<td>weight variable for standardization</td>
</tr>
<tr>
<td>tab(varname)</td>
<td>variable for which to compute cell totals/proportions</td>
</tr>
<tr>
<td>missing</td>
<td>treat missing values like other values</td>
</tr>
</tbody>
</table>

### display_items

<table>
<thead>
<tr>
<th>Table items</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cell</td>
<td>cell proportions</td>
</tr>
<tr>
<td>count</td>
<td>weighted cell counts</td>
</tr>
<tr>
<td>column</td>
<td>within-column proportions</td>
</tr>
<tr>
<td>row</td>
<td>within-row proportions</td>
</tr>
<tr>
<td>se</td>
<td>standard errors</td>
</tr>
<tr>
<td>ci</td>
<td>confidence intervals</td>
</tr>
<tr>
<td>deff</td>
<td>display the DEFF design effects</td>
</tr>
<tr>
<td>deft</td>
<td>display the DEFT design effects</td>
</tr>
<tr>
<td>cv</td>
<td>display the coefficient of variation</td>
</tr>
<tr>
<td>srssubpop</td>
<td>report design effects assuming SRS within subpopulation</td>
</tr>
<tr>
<td>obs</td>
<td>cell observations</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Reporting</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>level(#)</td>
<td>set confidence level; default is <code>level(95)</code></td>
</tr>
<tr>
<td>proportion</td>
<td>display proportions; the default</td>
</tr>
<tr>
<td>percent</td>
<td>display percentages instead of proportions</td>
</tr>
<tr>
<td>vertical</td>
<td>stack confidence interval endpoints vertically</td>
</tr>
<tr>
<td>nomarginals</td>
<td>suppress row and column marginals</td>
</tr>
<tr>
<td>nofactor</td>
<td>suppress displaying value labels</td>
</tr>
<tr>
<td>notable</td>
<td>suppress displaying the table</td>
</tr>
<tr>
<td>cellwidth(#)</td>
<td>cell width</td>
</tr>
<tr>
<td>csepwidth(#)</td>
<td>column-separation width</td>
</tr>
<tr>
<td>stubwidth(#)</td>
<td>stub width</td>
</tr>
<tr>
<td>format(%)fmt</td>
<td>cell format; default is <code>format(6.0g)</code></td>
</tr>
</tbody>
</table>

`proportion` and `notable` are not shown in the dialog box.
svy: tabulate twoway — Two-way tables for survey data

<table>
<thead>
<tr>
<th>statistic_options</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>pearson</strong></td>
<td>Pearson’s chi-squared</td>
</tr>
<tr>
<td><strong>lr</strong></td>
<td>likelihood ratio</td>
</tr>
<tr>
<td><strong>null</strong></td>
<td>display null-based statistics</td>
</tr>
<tr>
<td><strong>wald</strong></td>
<td>adjusted Wald</td>
</tr>
<tr>
<td><strong>llwald</strong></td>
<td>adjusted log-linear Wald</td>
</tr>
<tr>
<td><strong>noadjust</strong></td>
<td>report unadjusted Wald statistics</td>
</tr>
</tbody>
</table>

**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).

**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.

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.

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 counts 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 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 in order 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
- The Rao and Scott correction
- Wald statistics
- Properties of the statistics

**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 twoway — Two-way tables for survey data

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 def, 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/r16/nhanes2b
. svyset psuid [pweight=finalwgt], strata(stratid)
    pweight: finalwgt
    VCE: linearized
    Single unit: missing
    Strata 1: stratid
    SU 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
                 1=white, 2=black, 3=other
diabetes, 1=yes, 0=no          0     1     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
                 1=white, 2=black, 3=other
diabetes, 1=yes, 0=no          0     1     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)
```

```
<table>
<thead>
<tr>
<th></th>
<th>diabetes, 1=yes, 0=no</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0</td>
<td>1</td>
<td>Total</td>
</tr>
<tr>
<td>1=white</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>White</td>
<td>0.9680</td>
<td>0.0320</td>
<td>1.0000</td>
</tr>
<tr>
<td></td>
<td>(0.0020)</td>
<td>(0.0020)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>[0.9638,0.9718]</td>
<td>[0.0282,0.0362]</td>
<td></td>
</tr>
<tr>
<td>2=black</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Black</td>
<td>0.9410</td>
<td>0.0590</td>
<td>1.0000</td>
</tr>
<tr>
<td></td>
<td>(0.0061)</td>
<td>(0.0061)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>[0.9271,0.9523]</td>
<td>[0.0477,0.0729]</td>
<td></td>
</tr>
<tr>
<td>3=other</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Other</td>
<td>0.9797</td>
<td>0.0203</td>
<td>1.0000</td>
</tr>
<tr>
<td></td>
<td>(0.0076)</td>
<td>(0.0076)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>[0.9566,0.9906]</td>
<td>[0.0094,0.0434]</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>0.9658</td>
<td>0.0342</td>
<td>1.0000</td>
</tr>
<tr>
<td></td>
<td>(0.0018)</td>
<td>(0.0018)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>[0.9619,0.9693]</td>
<td>[0.0307,0.0381]</td>
<td></td>
</tr>
</tbody>
</table>
```

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
```

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Ratio</td>
<td>Std. Err.</td>
<td>[95% Conf. Interval]</td>
</tr>
<tr>
<td>_ratio_1</td>
<td>.0590349</td>
<td>.0061443</td>
<td>.0465035</td>
</tr>
</tbody>
</table>

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:
svy: tabulate twoway — Two-way tables for survey data

```stata
use https://www.stata-press.com/data/r16/svy_tabopt, clear
svy: tabulate gender race, tab(income) row
```

<table>
<thead>
<tr>
<th>Number of strata = 31</th>
<th>Number of obs  = 10,351</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of PSUs = 62</td>
<td>Population size = 117,157,513</td>
</tr>
<tr>
<td>Design df = 31</td>
<td>Design df = 31</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Race</th>
<th>Gender</th>
<th>White</th>
<th>Black</th>
<th>Other</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Male</td>
<td>.8857</td>
<td>.0875</td>
<td>.0268</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>Female</td>
<td>.884</td>
<td>.094</td>
<td>.022</td>
<td>1</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>.8848</td>
<td>.0909</td>
<td>.0243</td>
<td>1</td>
</tr>
</tbody>
</table>

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

$$X_P^2 = m \sum_{r=1}^{R} \sum_{c=1}^{C} (\hat{p}_{rc} - \hat{p}_{0rc})^2 / \hat{p}_{0rc}$$

and the likelihood-ratio $\chi^2$ statistic

$$X_{LR}^2 = 2m \sum_{r=1}^{R} \sum_{c=1}^{C} \hat{p}_{rc} \ln (\hat{p}_{rc} / \hat{p}_{0rc})$$

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, $\hat{p}_{0rc} = \hat{p}_r \hat{p}_c$, the product of the row and column marginals: $\hat{p}_r = \sum_{c=1}^{C} \hat{p}_{rc}$ and $\hat{p}_c = \sum_{r=1}^{R} \hat{p}_{rc}$.

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, $X^2_F$ and $X^2_{LR}$ 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*.

Rao and Scott (1981, 1984) derived the asymptotic distribution of $X^2_F$ and $X^2_{LR}$ 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

$$\hat{\chi}_{rc} = \hat{N}_{rc} - \hat{N}_r \cdot \hat{N}_c / \hat{N},$$

where $\hat{N}_{rc}$ is the estimated weighted count for the $r$th, $c$th cell. The delta method can be used to approximate the variance of $\hat{\chi}_{rc}$, 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 *nooladjust* option is specified with *wald* or *lwald*.

Another technique is to adjust the $F$ statistic by using

$$F_{adj} = (\nu - d_0 + 1)W / (\nu d_0) \quad \text{with} \quad F_{adj} \sim F(d_0, \nu - d_0 + 1)$$

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/r16/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  ```

<table>
<thead>
<tr>
<th>bpsystol &gt;= 140</th>
<th>bpdia &gt;= 90, 0 otherwise</th>
<th>1=urban,..., 8=rural</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total</td>
<td>526</td>
<td>607</td>
</tr>
<tr>
<td>0</td>
<td>.4949</td>
<td>.5884</td>
</tr>
<tr>
<td>241 326 381 228 121 135 186 993 2611</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>.5051</td>
<td>.4116</td>
</tr>
<tr>
<td>285 281 241 217 101 95 185 899 2304</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

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
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 $\chi^2$ 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 $\chi^2$ statistics yield smaller $p$-values than the adjusted $\chi^2$ 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 $\chi^2$ 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 $\chi^2$ statistic than that for the default-corrected Pearson and likelihood-ratio statistics.

The $p$-value for the adjusted log-linear Wald $\chi^2$ 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 “uncorrected” Wald $\chi^2$ statistics, on the other hand, are completely different. They are valid asymptotically as the variance degrees of freedom becomes large.

Properties of the statistics


`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 $\text{LR}$ statistic in most situations. It often appears to be more powerful than the adjusted “Pearson” Wald $\chi^2$ 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.

**Stored results**

In addition to the results documented in `svy` `svy: tabulate` stores the following in `e()`:

<table>
<thead>
<tr>
<th>Scalars</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>e(r)</td>
<td>number of rows</td>
</tr>
<tr>
<td>e(c)</td>
<td>number of columns</td>
</tr>
<tr>
<td>e(cvgdeff)</td>
<td>coefficient of variation of generalized DEFF eigenvalues</td>
</tr>
<tr>
<td>e(mgdeff)</td>
<td>mean generalized DEFF</td>
</tr>
<tr>
<td>e(total)</td>
<td>weighted sum of <code>tab()</code> variable</td>
</tr>
<tr>
<td>e(F_Pear)</td>
<td>default-corrected Pearson $F$</td>
</tr>
<tr>
<td>e(F_Penl)</td>
<td>null-corrected Pearson $F$</td>
</tr>
<tr>
<td>e(df1_Pear)</td>
<td>numerator d.f. for <code>e(F_Pear)</code></td>
</tr>
<tr>
<td>e(df2_Pear)</td>
<td>denominator d.f. for <code>e(F_Pear)</code></td>
</tr>
<tr>
<td>e(df1_Penl)</td>
<td>numerator d.f. for <code>e(F_Penl)</code></td>
</tr>
<tr>
<td>e(df2_Penl)</td>
<td>denominator d.f. for <code>e(F_Penl)</code></td>
</tr>
<tr>
<td>e(p_Pear)</td>
<td>$p$-value for <code>e(F_Pear)</code></td>
</tr>
<tr>
<td>e(p_Penl)</td>
<td>$p$-value for <code>e(F_Penl)</code></td>
</tr>
<tr>
<td>e(cun_Pear)</td>
<td>uncorrected Pearson $\chi^2$</td>
</tr>
<tr>
<td>e(cun_Penl)</td>
<td>null variant uncorrected Pearson $\chi^2$</td>
</tr>
<tr>
<td>e(F_LR)</td>
<td>default-corrected likelihood-ratio $F$</td>
</tr>
<tr>
<td>e(F_LRnl)</td>
<td>null-corrected likelihood-ratio $F$</td>
</tr>
<tr>
<td>e(df1_LR)</td>
<td>numerator d.f. for <code>e(F_LR)</code></td>
</tr>
<tr>
<td>e(df2_LR)</td>
<td>denominator d.f. for <code>e(F_LR)</code></td>
</tr>
<tr>
<td>e(df1_LRnl)</td>
<td>numerator d.f. for <code>e(F_LRnl)</code></td>
</tr>
</tbody>
</table>
Methods and formulas

Methods and formulas are presented under the following headings:

The table items
Confidence intervals
The test statistics

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

$$y_{(rc)} = \begin{cases} 
1 & \text{if the } j\text{th observation of the data is in the } r, c\text{th cell} \\
0 & \text{otherwise}
\end{cases}$$
where \( j = 1, \ldots, m \) indexes individuals in the sample. Weighted cell counts (count option) are

\[
\hat{N}_{rc} = \sum_{j=1}^{m} w_j y_{(rc)j}
\]

where \( w_j \) is a sampling weight. If a variable, \( x_j \), is specified with the \( \text{tab()} \) option, \( \hat{N}_{rc} \) becomes

\[
\hat{N}_{rc} = \sum_{j=1}^{m} w_j x_j y_{(rc)j}
\]

Let

\[
\hat{N}_r = \sum_{c=1}^{C} \hat{N}_{rc}, \quad \hat{N}_c = \sum_{r=1}^{R} \hat{N}_{rc}, \quad \text{and} \quad \hat{N}_. = \sum_{r=1}^{R} \sum_{c=1}^{C} \hat{N}_{rc}
\]

Estimated cell proportions are \( \hat{p}_{rc} = \hat{N}_{rc} / \hat{N}_. \); estimated row proportions (row option) are \( \hat{p}_{row rc} = \hat{N}_{rc} / \hat{N}_r \); estimated column proportions (column option) are \( \hat{p}_{col rc} = \hat{N}_{rc} / \hat{N}_c \); estimated row marginals are \( \hat{p}_r = \hat{N}_r / \hat{N}_. \); and estimated column marginals are \( \hat{p}_c = \hat{N}_c / \hat{N}_. \).

\( \hat{N}_{rc} \) is a total, the proportion estimators are ratios, and their variances can be estimated using linearization methods as outlined in [SVY] Variance estimation. \texttt{svy: tabulate} computes the variance estimates by using \texttt{svy: mean}, \texttt{svy: ratio}, and \texttt{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

\[
\hat{SE}\{f(\hat{p})\} = f'(\hat{p})\hat{s} = \frac{\hat{s}}{\hat{p}(1-\hat{p})}
\]

Thus a \(100(1 - \alpha)\)% confidence interval in this metric is

\[
\ln\left(\frac{\hat{p}}{1-\hat{p}}\right) \pm t_{1-\alpha/2, \nu} \frac{\hat{s}}{\hat{p}(1-\hat{p})}
\]

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

\[
f^{-1}\left\{ \ln\left(\frac{\hat{p}}{1-\hat{p}}\right) \pm t_{1-\alpha/2, \nu} \frac{\hat{s}}{\hat{p}(1-\hat{p})} \right\}
\]

Confidence intervals for weighted counts are untransformed and are identical to the intervals produced by \texttt{svy: total}.
The test statistics

The uncorrected Pearson $\chi^2$ statistic is

$$X^2_p = m \sum_{r=1}^{R} \sum_{c=1}^{C} (\hat{p}_{rc} - \hat{p}_{0rc})^2 / \hat{p}_{0rc}$$

and the uncorrected likelihood-ratio $\chi^2$ statistic is

$$X^2_{LR} = 2m \sum_{r=1}^{R} \sum_{c=1}^{C} \hat{p}_{rc} \ln (\hat{p}_{rc} / \hat{p}_{0rc})$$

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 as defined earlier, and $\hat{p}_{0rc}$ is the estimated proportion under the null hypothesis of independence; that is, $\hat{p}_{0rc} = \hat{p}_r \cdot \hat{p}_c$, the product of the row and column marginals.

Rao and Scott (1981, 1984) show that, asymptotically, $X^2_p$ and $X^2_{LR}$ are distributed as

$$X^2 \sim \sum_{k=1}^{(R-1)(C-1)} \delta_k W_k$$

where the $W_k$ are independent $\chi^2_1$ variables and the $\delta_k$ are the eigenvalues of

$$\Delta = (\tilde{X}'_2 V_{srs} \tilde{X}_2)^{-1} (\tilde{X}'_2 V \tilde{X}_2)$$

where $V$ is the variance of the $\hat{p}_{rc}$ under the survey design and $V_{srs}$ is the variance of the $\hat{p}_{rc}$ that you would have if the design were simple random sampling; namely, $V_{srs}$ has diagonal elements $p_{rc}(1 - p_{rc})/m$ and off-diagonal elements $-p_{rcp_{st}}/m$.

$\tilde{X}_2$ is calculated as follows. Rao and Scott do their development in a log-linear modeling context, so consider $[1 \mid X_1 \mid X_2]$ as predictors for the cell counts of the $R \times C$ table in a log-linear model. The $X_1$ 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 $X_2$ matrix of dimension $RC \times (R - 1)(C - 1)$ contains the row and column “interactions”. Hence, fitting $[1 \mid X_1 \mid X_2]$ gives the fully saturated model (that is, fits the observed values perfectly) and $[1 \mid X_1]$ gives the independence model. The $\tilde{X}_2$ matrix is the projection of $X_2$ onto the orthogonal complement of the space spanned by the columns of $X_1$, where the orthogonality is defined with respect to $V_{srs}$; that is, $\tilde{X}'_2 V_{srs} X_1 = 0$.

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

$$DEFF = \frac{\hat{V}(\hat{p}_{rc})}{V_{srsor}(\hat{p}_{rc})}$$

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 $V$ and $V_{srs}$ is easy. Rao and Scott (1984) derive a simpler formula for $\hat{\Delta}$:

$$
\hat{\Delta} = (C'\hat{D}_p^{-1}\hat{V}_{srs}D_{\hat{\pi}}^{-1}C)^{-1}(C'\hat{D}_p^{-1}\hat{V}\hat{D}_p^{-1}C)
$$

Here $C$ is a contrast matrix that is any $RC \times (R - 1)(C - 1)$ full-rank matrix orthogonal to $[1 \mid X_1]$; that is, $C'1 = 0$ and $C'X_1 = 0$. $D_{\hat{\pi}}$ 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 $D_{\hat{\pi}}^{-1}$ is immaterial for computing $\hat{\Delta}$.

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 $\hat{\Delta}$; namely, you compute

$$
X_P^2(\hat{\delta}) = X_P^2/\hat{\delta} \quad \text{and} \quad X_{LR}^2(\hat{\delta}) = X_{LR}^2/\hat{\delta}.
$$

where $\hat{\delta}$ is the mean-generalized DEFF

$$
\hat{\delta} = \frac{1}{(R - 1)(C - 1)} \sum_{k=1}^{(R-1)(C-1)} \delta_k
$$

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 $X_P^2$ and $X_{LR}^2$ as being “too big” by a factor of $\hat{\delta}$ 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

$$
X_P^2(\hat{\delta}, \hat{\alpha}) = \frac{X_P^2}{\hat{\delta}(\hat{\alpha}^2 + 1)}
$$

(3)

where $\hat{\alpha}$ is the coefficient of variation of the eigenvalues:

$$
\hat{\alpha}^2 = \frac{\sum \hat{\delta}_k^2}{(R - 1)(C - 1)\hat{\delta}^2} - 1
$$

Because $\sum \hat{\delta}_k = \text{tr} \hat{\Delta}$ and $\sum \hat{\delta}_k^2 = \text{tr} \hat{\Delta}^2$, (3) can be written in an easily computable form as

$$
X_P^2(\hat{\delta}, \hat{\alpha}) = \frac{\text{tr} \hat{\Delta}}{\text{tr} \hat{\Delta}^2} X_P^2
$$

These corrected statistics are asymptotically distributed as $\chi^2_d$, with

$$
d = \frac{(R - 1)(C - 1)}{\hat{\alpha}^2 + 1} = \frac{(\text{tr} \hat{\Delta})^2}{\text{tr} \hat{\Delta}^2}
$$

that is, a $\chi^2$ with, in general, noninteger degrees of freedom. The likelihood-ratio statistic $X_{LR}^2$ 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 $\hat{V}_{\text{hrs}}$, which is used to compute $\hat{\Delta}$. $V_{\text{hrs}}$ 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, $\hat{p}_{0rc} = \hat{p}_r\cdot\hat{p}_c$? 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 $\hat{V}_{\text{hrs}}$, `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, $\hat{V}$, 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

$$F_P = \frac{X^2_p}{\text{tr} \hat{\Delta}} \quad \text{with} \quad F_P \sim F(d, \nu d) \quad \text{where} \quad d = \frac{(\text{tr} \hat{\Delta})^2}{\text{tr} \hat{\Delta}^2} \quad \text{and} \quad \nu = n - L \quad (4)$$

This is the corrected statistic that `svy: tabulate` displays by default or when the `pearson` option is specified. When the `1r` option is specified, an identical correction is produced for the likelihood-ratio statistic $X^2_{LR}$. When `null` is specified, (4) is also used. For the statistic labeled “D-B (null)”, $\hat{\Delta}$ is computed using $\hat{p}_{0rc}$. For the statistic labeled “Design-based”, $\hat{\Delta}$ 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

$$\hat{Y}_{rc} = \hat{N}_{rc} - \hat{N}_r\cdot\hat{N}_c/\hat{N}.$$  

where $r = 1, \ldots, R - 1$ and $c = 1, \ldots, C - 1$. The delta method can be used to estimate the variance of $\hat{Y}$ (which is $\hat{Y}_{rc}$ stacked into a vector), and a Wald statistic can be constructed in the usual manner:

$$W = \hat{Y}'\{J_N\hat{V}(\hat{N})J_N'\}^{-1}\hat{Y} \quad \text{where} \quad J_N = \partial \hat{Y}/\partial \hat{N}'$$

The statistic given by the `llwald` option is based on the log-linear model with predictors $[1|X_1|X_2]$ that was mentioned earlier. This Wald statistic is

$$W_{LL} = (X_2' \ln \hat{p})'\{X_2' J_P \hat{V}(\hat{p}) J_P' X_2\}^{-1}(X_2' \ln \hat{p})$$

where $J_P$ is the matrix of first derivatives of $\ln \hat{p}$ with respect to $\hat{p}$, which is, of course, just a matrix with $\hat{p}^{-1}$ 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

$$F_{\text{unadj}} = W/d_0 \quad \text{with} \quad F_{\text{unadj}} \sim F(d_0, \nu)$$
Adjusted $F$ statistics are produced using

$$F_{\text{adj}} = \frac{(\nu - d_0 + 1)W}{(\nu d_0)_{\nu - d_0 + 1}} \quad \text{with} \quad F_{\text{adj}} \sim F(d_0, \nu - d_0 + 1)$$

The other \texttt{svy} estimators also use this adjustment procedure for $F$ statistics. See Korn and Graubard (1990) for a justification of the procedure.

References


Also see

\[SVY\] \texttt{svy postestimation} — Postestimation tools for \texttt{svy}

\[SVY\] \texttt{svy} — The survey prefix command

\[SVY\] \texttt{svy: tabulate oneway} — One-way tables for survey data

\[SVY\] \texttt{svydescribe} — Describe survey data

\[SVY\] \texttt{Calibration} — Calibration for survey data

\[SVY\] \texttt{Direct standardization} — Direct standardization of means, proportions, and ratios

\[SVY\] \texttt{Poststratification} — Poststratification for survey data

\[SVY\] \texttt{Subpopulation estimation} — Subpopulation estimation for survey data

\[SVY\] \texttt{Variance estimation} — Variance estimation for survey data

\[R\] \texttt{tabulate twoway} — Two-way table of frequencies

\[R\] \texttt{test} — Test linear hypotheses after estimation

\[U\] 20 Estimation and postestimation commands
Title

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]
```

<table>
<thead>
<tr>
<th>options</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>stage(#)</code></td>
<td>sampling stage to describe; default is <code>stage(1)</code></td>
</tr>
<tr>
<td><code>finalstage</code></td>
<td>display information per sampling unit in the final stage</td>
</tr>
<tr>
<td><code>single</code></td>
<td>display only the strata with one sampling unit</td>
</tr>
<tr>
<td><code>generate(newvar)</code></td>
<td>generate a variable identifying strata with one sampling unit</td>
</tr>
</tbody>
</table>

`svydescribe` requires that the survey design variables be identified using `svyset`; see [SVY] `svyset`. 171
Options

- **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.

svy describe 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, svy describe 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.

```stata
. use https://www.stata-press.com/data/r16/nhanes2b
. svyset psuid [pweight=finalwgt], strata(stratid)
```

```stata
  pweight: finalwgt
  VCE: linearized
  Single unit: missing
  Strata 1: stratid
  SU 1: psuid
  FPC 1: <zero>
```
svydescribe will display the strata and PSU arrangement of the dataset.

```
. svydescribe
Survey: Describing stage 1 sampling units
    pweight: finalwgt
    VCE: linearized
Single unit: missing
Strata 1: stratid
SU 1: psuid
FPC 1: <zero>

<table>
<thead>
<tr>
<th>Stratum</th>
<th>#Units</th>
<th>#Obs</th>
<th>min</th>
<th>mean</th>
<th>max</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>380</td>
<td>165</td>
<td>190.0</td>
<td>215</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>185</td>
<td>67</td>
<td>92.5</td>
<td>118</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>348</td>
<td>149</td>
<td>174.0</td>
<td>199</td>
</tr>
</tbody>
</table>

(output omitted)

<table>
<thead>
<tr>
<th>Stratum</th>
<th>#Units</th>
<th>#Obs</th>
<th>min</th>
<th>mean</th>
<th>max</th>
</tr>
</thead>
<tbody>
<tr>
<td>17</td>
<td>2</td>
<td>393</td>
<td>180</td>
<td>196.5</td>
<td>213</td>
</tr>
<tr>
<td>18</td>
<td>2</td>
<td>359</td>
<td>144</td>
<td>179.5</td>
<td>215</td>
</tr>
<tr>
<td>20</td>
<td>2</td>
<td>285</td>
<td>125</td>
<td>142.5</td>
<td>160</td>
</tr>
<tr>
<td>21</td>
<td>2</td>
<td>214</td>
<td>102</td>
<td>107.0</td>
<td>112</td>
</tr>
</tbody>
</table>

(output omitted)

<table>
<thead>
<tr>
<th>Stratum</th>
<th>#Units</th>
<th>#Obs</th>
<th>min</th>
<th>mean</th>
<th>max</th>
</tr>
</thead>
<tbody>
<tr>
<td>31</td>
<td>2</td>
<td>308</td>
<td>143</td>
<td>154.0</td>
<td>165</td>
</tr>
<tr>
<td>32</td>
<td>2</td>
<td>450</td>
<td>211</td>
<td>225.0</td>
<td>239</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Stratum</th>
<th>#Units</th>
<th>#Obs</th>
<th>min</th>
<th>mean</th>
<th>max</th>
</tr>
</thead>
<tbody>
<tr>
<td>31</td>
<td>62</td>
<td>10,351</td>
<td>67</td>
<td>167.0</td>
<td>288</td>
</tr>
</tbody>
</table>
```

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

<table>
<thead>
<tr>
<th>Linearized</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
</tr>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>Std. Err.</td>
</tr>
<tr>
<td>[95% Conf. Interval]</td>
</tr>
</tbody>
</table>

| 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
  pweight: finalwgt
  VCE: linearized
  Single unit: missing
  Strata 1: stratid
  SU 1: psuid
  FPC 1: <zero>

<table>
<thead>
<tr>
<th>Stratum</th>
<th>#Units included</th>
<th>#Units omitted</th>
<th>#Obs with complete data</th>
<th>#Obs with missing data</th>
<th>#Obs per included Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1*</td>
<td>1</td>
<td>114</td>
<td>266</td>
<td>114.0</td>
</tr>
<tr>
<td>2</td>
<td>1*</td>
<td>1</td>
<td>98</td>
<td>87</td>
<td>98.0</td>
</tr>
</tbody>
</table>

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
  pweight: finalwgt
  VCE: linearized
  Single unit: missing
  Strata 1: stratid
  SU 1: psuid
  FPC 1: <zero>

<table>
<thead>
<tr>
<th>Stratum</th>
<th>Unit</th>
<th>#Obs with complete data</th>
<th>#Obs with missing data</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>0</td>
<td>215</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>114</td>
<td>51</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>98</td>
<td>20</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>0</td>
<td>67</td>
</tr>
</tbody>
</table>

(output omitted)

<table>
<thead>
<tr>
<th>Stratum</th>
<th>Unit</th>
<th>#Obs with complete data</th>
<th>#Obs with missing data</th>
</tr>
</thead>
<tbody>
<tr>
<td>32</td>
<td>2</td>
<td>203</td>
<td>8</td>
</tr>
<tr>
<td>31</td>
<td>62</td>
<td>8,720</td>
<td>1,631</td>
</tr>
</tbody>
</table>

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)
   pweight: finalwgt
   VCE: linearized
   Single unit: missing
   Strata 1: newstr
   SU 1: newpsu
   FPC 1: <zero>

Then use svydescribe to check what we have done.

. svydescribe hdresult, finalstage

Survey: Describing final stage sampling units
   pweight: finalwgt
   VCE: linearized
   Single unit: missing
   Strata 1: newstr
   SU 1: newpsu
   FPC 1: <zero>

<table>
<thead>
<tr>
<th>Stratum</th>
<th>Unit</th>
<th>#Obs with complete data</th>
<th>#Obs with missing data</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>1</td>
<td>98</td>
<td>20</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>0</td>
<td>67</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>0</td>
<td>215</td>
</tr>
<tr>
<td>2</td>
<td>4</td>
<td>114</td>
<td>51</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>161</td>
<td>38</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>116</td>
<td>33</td>
</tr>
<tr>
<td>(output omitted)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>32</td>
<td>1</td>
<td>180</td>
<td>59</td>
</tr>
<tr>
<td>32</td>
<td>2</td>
<td>203</td>
<td>8</td>
</tr>
<tr>
<td>30</td>
<td>62</td>
<td>8,720</td>
<td>1,631</td>
</tr>
</tbody>
</table>

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.
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.

```stata
use https://www.stata-press.com/data/r16/nhanes2b, clear
svy: mean hdresult
```

```
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.

```stata
svydescribe if e(sample), single
```

```
Survey: Describing strata with a single sampling unit in stage 1
```

```
#Obs per Unit

<table>
<thead>
<tr>
<th>Stratum</th>
<th>#Units</th>
<th>#Obs</th>
<th>min</th>
<th>mean</th>
<th>max</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1*</td>
<td>114</td>
<td>114</td>
<td>114.0</td>
<td>114</td>
</tr>
<tr>
<td>2</td>
<td>1*</td>
<td>98</td>
<td>98</td>
<td>98.0</td>
<td>98</td>
</tr>
</tbody>
</table>
```

2
Methods and formulas

See Eltinge and Sribney (1996) for an earlier implementation of `svydescribe`.

References


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

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*)
```

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.

<table>
<thead>
<tr>
<th><code>design_options</code></th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>strata(varname)</code></td>
<td>variable identifying strata</td>
</tr>
<tr>
<td><code>fpc(varname)</code></td>
<td>finite population correction</td>
</tr>
<tr>
<td><code>weight(varname)</code></td>
<td>stage-level sampling weight</td>
</tr>
</tbody>
</table>
svyset – Declare survey design for dataset

Options

Weights

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>brrweight(varlist)</td>
<td>balanced repeated replicate (BRR) weights</td>
</tr>
<tr>
<td>fay(#)</td>
<td>Fay’s adjustment</td>
</tr>
<tr>
<td>bsrweight(varlist)</td>
<td>bootstrap replicate weights</td>
</tr>
<tr>
<td>bsn(#)</td>
<td>bootstrap mean-weight adjustment</td>
</tr>
<tr>
<td>jkrweight(varlist, jkropts)</td>
<td>jackknife replicate weights</td>
</tr>
<tr>
<td>sdrweight(varlist, sdropts)</td>
<td>successive difference replicate (SDR) weights</td>
</tr>
</tbody>
</table>

SE

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>vce(linearized)</td>
<td>Taylor linearized variance estimation</td>
</tr>
<tr>
<td>vce(bootstrap)</td>
<td>bootstrap variance estimation</td>
</tr>
<tr>
<td>vce(brr)</td>
<td>BRR variance estimation</td>
</tr>
<tr>
<td>vce(jackknife)</td>
<td>jackknife variance estimation</td>
</tr>
<tr>
<td>vce(sdr)</td>
<td>SDR variance estimation</td>
</tr>
<tr>
<td>dof(#)</td>
<td>design degrees of freedom</td>
</tr>
<tr>
<td>mse</td>
<td>use the MSE formula with vce(bootstrap), vce(brr), vce(jackknife), or vce(sdr)</td>
</tr>
<tr>
<td>singleunit(method)</td>
<td>strata with a single sampling unit; method may be missing, certainty, scaled, or centered</td>
</tr>
</tbody>
</table>

Poststratification

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>poststrata(varname)</td>
<td>variable identifying poststrata</td>
</tr>
<tr>
<td>postweight(varname)</td>
<td>poststratum population sizes</td>
</tr>
</tbody>
</table>

Calibration

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rake(varlist, calopts)</td>
<td>adjust weights using the raking-ratio method</td>
</tr>
<tr>
<td>regress(varlist, calopts)</td>
<td>adjust weights using linear regression calibration</td>
</tr>
<tr>
<td>clear</td>
<td>clear all settings from the data</td>
</tr>
<tr>
<td>noclear</td>
<td>change some of the settings without clearing the others; opnames may be one or more of weight, vce, dof, mse, bsrweight, brrweight, jkrweight, sdrweight, poststrata, rake, or regress</td>
</tr>
<tr>
<td>clear(opnames)</td>
<td>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</td>
</tr>
</tbody>
</table>

pweights and iweights are allowed; see [U] 11.1.6 weight.
clear, noclear, and clear() are not shown in the dialog box.

jkropts

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>stratum(# [# ...])</td>
<td>stratum identifier for each jackknife replicate weight</td>
</tr>
<tr>
<td>fpc(# [# ...])</td>
<td>finite population correction for each jackknife replicate weight</td>
</tr>
<tr>
<td>multiplier(# [# ...])</td>
<td>variance multiplier for each jackknife replicate weight</td>
</tr>
<tr>
<td>reset</td>
<td>reset characteristics for each jackknife replicate weight</td>
</tr>
</tbody>
</table>

sdropts

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>fpc(# [# ...])</td>
<td>finite population correction for each SDR weight</td>
</tr>
</tbody>
</table>
**calopts**

**Description**

* **totals()**
  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.

**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, \( df = N_{psu} - N_{strata} \).

**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.

**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.

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
- Finite population correction (FPC)
- Multiple-stage designs and with-replacement sampling
- Replication-weight variables
- Combining datasets from multiple surveys
- Video example

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/r16/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
   pweight: <none>
   VCE: linearized
   Single unit: missing
   Strata 1: <one>
   SU 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.
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)
pweight: pw
VCE: linearized
Single unit: missing
Strata 1: strata
  SU 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)
pweight: pw
VCE: linearized
Single unit: missing
Strata 1: <one>
  SU 1: su1
  FPC 1: fpc1
Strata 2: <one>
  SU 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)
pweight: pw
VCE: linearized
Single unit: missing
Strata 1: <one>
  SU 1: su1
  FPC 1: fpc1
Strata 2: <one>
  SU 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)

    pweight: pw
      VCE: linearized
    Single unit: missing
     Strata 1: <one>
         SU 1: su1
         FPC 1: fpc1
     Strata 2: strata
         SU 2: su2
         FPC 2: fpc2
```

**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)

    pweight: pw
      VCE: linearized
    Single unit: missing
     Strata 1: strata
         SU 1: su1
         FPC 1: fpc1
     Strata 2: <one>
         SU 2: su2
         FPC 2: fpc2
     Strata 3: <one>
         SU 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
   pweight: pw
   VCE: linearized
   Single unit: missing
   Strata 1: strata
      SU 1: su1
      FPC 1: fpc1
   Strata 2: <one>
      SU 2: su2
      FPC 2: fpc2
   Strata 3: <one>
      SU 3: su3
      FPC 3: fpc3
   Strata 4: <one>
      SU 4: <observations>
      FPC 4: <zero>
```

### 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/r16/fpc
. list
```

<table>
<thead>
<tr>
<th></th>
<th>stratid</th>
<th>psuid</th>
<th>weight</th>
<th>nh</th>
<th>Nh</th>
<th>x</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>1</td>
<td>1</td>
<td>3</td>
<td>5</td>
<td>15</td>
<td>2.8</td>
</tr>
<tr>
<td>2.</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>5</td>
<td>15</td>
<td>4.1</td>
</tr>
<tr>
<td>3.</td>
<td>1</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>15</td>
<td>6.8</td>
</tr>
<tr>
<td>4.</td>
<td>1</td>
<td>4</td>
<td>3</td>
<td>5</td>
<td>15</td>
<td>6.8</td>
</tr>
<tr>
<td>5.</td>
<td>1</td>
<td>5</td>
<td>3</td>
<td>5</td>
<td>15</td>
<td>9.2</td>
</tr>
<tr>
<td>6.</td>
<td>2</td>
<td>1</td>
<td>4</td>
<td>3</td>
<td>12</td>
<td>3.7</td>
</tr>
<tr>
<td>7.</td>
<td>2</td>
<td>2</td>
<td>4</td>
<td>3</td>
<td>12</td>
<td>6.6</td>
</tr>
<tr>
<td>8.</td>
<td>2</td>
<td>3</td>
<td>4</td>
<td>3</td>
<td>12</td>
<td>4.2</td>
</tr>
</tbody>
</table>

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)
    pweight: weight
    VCE: linearized
    Single unit: missing
    Strata 1: stratid
    SU 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

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
</tr>
<tr>
<td>x</td>
<td>5.448148</td>
<td>.6160407</td>
</tr>
<tr>
<td></td>
<td>[95% Conf. Interval]</td>
<td></td>
</tr>
<tr>
<td>x</td>
<td>3.940751</td>
<td>6.955545</td>
</tr>
</tbody>
</table>

We must respecify the survey design before estimating the population mean of x assuming sampling with replacement.

. svyset psuid [pweight=weight], strata(stratid)
    pweight: weight
    VCE: linearized
    Single unit: missing
    Strata 1: stratid
    SU 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

<table>
<thead>
<tr>
<th></th>
<th>Linearized</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
</tr>
<tr>
<td>x</td>
<td>5.448148</td>
<td>.7412683</td>
</tr>
<tr>
<td></td>
<td>[95% Conf. Interval]</td>
<td></td>
</tr>
<tr>
<td>x</td>
<td>3.63433</td>
<td>7.261966</td>
</tr>
</tbody>
</table>

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.
**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/r16/svyset_wr
. svyset su1 || _n, fpc(fpc2)
```

Note: Stage 1 is sampled with replacement; further stages will be ignored for variance estimation.

```
pweight: <none>
VCE: linearized
Single unit: missing
Strata 1: <one>
SU 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
```

```
pweight: <none>
VCE: linearized
Single unit: missing
Strata 1: <one>
SU 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.

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 \texttt{brrweight()}, \texttt{jkrweight()}, \texttt{bsrweight()}, and \texttt{sdrweight()} options allow \texttt{svyset} to identify the set of replication weights for use with BRR, jackknife, bootstrap, and SDR variance estimation (\texttt{svy brr}, \texttt{svy jackknife}, \texttt{svy bootstrap}, and \texttt{svy sdr}), respectively. In addition to the weight variables, \texttt{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/r16/stage5a_jkw
. svyset [pweight=pw], jkrweight(jkw_*) vce(jackknife)
  pweight: pw
  VCE: jackknife
  MSE: off
  jkrweight: jkw_1 .. jkw_9
  Single unit: missing
  Strata 1: <one>
  SU 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
  pweight: pw
  VCE: jackknife
  MSE: on
  jkrweight: jkw_1 .. jkw_9
  Single unit: missing
  Strata 1: <one>
  SU 1: <observations>
  FPC 1: <zero>
```

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.

```stata
. import sasxport5 demo.xpt
. describe wtint2yr wtmec2yr wtirep01 wtmrep01

variable name  storage  display         value
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.

```stata
. 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.

```stata
.import sasxport5 bpx.xpt, clear
.sort seqn
.save bpx99_00ile bpx99_00.dta saved
.use demo99_00
.drop wtint?yr wtirep*
.merge 1:1 seqn using bpx99_00
```

<table>
<thead>
<tr>
<th>Result</th>
<th># of obs.</th>
</tr>
</thead>
<tbody>
<tr>
<td>not matched</td>
<td>683</td>
</tr>
<tr>
<td>from master</td>
<td>683</td>
</tr>
<tr>
<td>from using</td>
<td>0</td>
</tr>
<tr>
<td>matched</td>
<td>9,282</td>
</tr>
</tbody>
</table>

```stata
.drop _merge
.svys et [pw=wtmec2yr], jkrweight(wtmrep*) vce(jackknife)
(output omitted)
.save bpx99_00, replace
file bpx99_00.dta saved
```

Having saved our merged dataset (with `svysettings`), we estimate the mean systolic blood pressure for the population, using the MEC exam replication weights for jackknife variance estimation.

```stata
.svy: mean bpxsar
```

```
Jackknife replications (52)
.................................................. 50
```

Survey: Mean estimation

<table>
<thead>
<tr>
<th>Number of strata</th>
<th>Number of obs</th>
<th>Population size</th>
<th>Replications</th>
<th>Design df</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>7,898</td>
<td>231,756,417</td>
<td>52</td>
<td>51</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>Jackknife</th>
<th>95% Conf. Interval</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
</tr>
<tr>
<td>bpxsar</td>
<td>119.7056</td>
<td>.5109122</td>
</tr>
</tbody>
</table>
```

**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:


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

<table>
<thead>
<tr>
<th>Result</th>
<th># of obs.</th>
</tr>
</thead>
<tbody>
<tr>
<td>not matched</td>
<td>562</td>
</tr>
<tr>
<td>from master</td>
<td>562</td>
</tr>
<tr>
<td>from using</td>
<td>0</td>
</tr>
<tr>
<td>matched</td>
<td>10,477</td>
</tr>
</tbody>
</table>

. drop _merge
. svyset sdmvpsu [pw=wtmec2yr], strata(sdmvstra)

pweight: wtmec2yr
VCE: linearized
Single unit: missing
Strata 1: sdmvstra
SU 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)
    pweight: wtmec4yr
    VCE: linearized
    Single unit: missing
    Strata 1: sdmvstra
        SU 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)

                           .................................................. 50
                           .......
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

<table>
<thead>
<tr>
<th></th>
<th>Jackknife</th>
<th></th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Std. Err.</td>
<td></td>
</tr>
<tr>
<td>bpxsar</td>
<td>119.8914</td>
<td>.3828434</td>
<td>119.1084 120.6744</td>
</tr>
</tbody>
</table>

Video example

Specifying the design of your survey data to Stata
Store results

svyset stores the following in \( r() \):

 Scalars

- \( r(\text{stages}) \): number of sampling stages
- \( r(\text{stages}\_\text{wt}) \): last stage containing stage-level weights
- \( r(\text{bsn}) \): bootstrap mean-weight adjustment
- \( r(\text{fay}) \): Fay's adjustment
- \( r(\text{dof}) \): \( \text{dof}() \) value

 Macros

- \( r(\text{wtype}) \): weight type
- \( r(\text{wexp}) \): weight expression
- \( r(\text{wvar}) \): weight variable name
- \( r(\text{weight}\#) \): variable identifying weight for stage \# 
- \( r(\text{su}\#) \): variable identifying sampling units for stage \# 
- \( r(\text{strata}\#) \): variable identifying strata for stage \# 
- \( r(\text{fpc}\#) \): \( \text{FPC} \) for stage \# 
- \( r(\text{bsrweight}) \): \( \text{bsrweight}() \) variable list
- \( r(\text{brrweight}) \): \( \text{brrweight}() \) variable list
- \( r(\text{jkrweight}) \): \( \text{jkrweight}() \) variable list
- \( r(\text{sdrweight}) \): \( \text{sdrweight}() \) variable list
- \( r(\text{sdrfpc}) \): \( \text{fpc}() \) value from within \( \text{sdrweight}() \)
- \( r(\text{vce}) \): \( \text{vce}() \) specified in \( \text{vce}() \)
- \( r(\text{mse}) \): \( \text{mse} \), if specified
- \( r(\text{poststrata}) \): \( \text{poststrata}() \) variable
- \( r(\text{postweight}) \): \( \text{postweight}() \) variable
- \( r(\text{rake}) \): \( \text{rake}() \) specification
- \( r(\text{regress}) \): \( \text{regress}() \) specification
- \( r(\text{settings}) \): \( \text{svyset} \) arguments to reproduce the current settings
- \( r(\text{singleunit}) \): \( \text{singleunit}() \) setting

References


Also see

[SVY] Survey — Introduction to survey commands

[SVY] svy — The survey prefix command

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

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
  - Stratified single-stage design
  - Stratified two-stage design
- Variance for census data
- Certainty sampling units
- Strata with one sampling unit
- Ratios and other functions of survey data
  - Revisiting the total estimator
  - The ratio estimator
  - A note about score variables
- Linearized/robust variance estimation
  - The bootstrap
  - BRR
  - The jackknife
    - The delete-one jackknife
    - The delete-k jackknife
- Successive difference replication
  - Confidence intervals

Variance of the total

This section describes the methods and formulas for \texttt{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

\[
m = \sum_{h=1}^{L} n_h \sum_{i=1}^{m_{hi}}
\]

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

\[
\hat{M} = \sum_{h=1}^{L} \sum_{i=1}^{n_h} \sum_{j=1}^{m_{hi}} w_{hij}
\]
The estimator for the variance of $\hat{Y}$ is

$$\hat{V}(\hat{Y}) = \sum_{h=1}^{L} (1 - f_h) \frac{n_h}{n_h - 1} \sum_{i=1}^{n_h} (y_{hi} - \overline{y}_h)^2$$

(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 $\hat{X}$ (notation for $X$ is defined similarly to that of $Y$) is

$$\hat{\text{Cov}}(\hat{Y}, \hat{X}) = \sum_{h=1}^{L} (1 - f_h) \frac{n_h}{n_h - 1} \sum_{i=1}^{n_h} (y_{hi} - \overline{y}_h)(x_{hi} - \overline{x}_h)$$

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

```bash
svyset psu [pweight=weight], strata(strata) fpc(fpc1) || ssu, fpc(fpc2)
```

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 `fpc1`, SSU identifiers are contained in variable `ssu`, and the values for the FPC for the second sampling stage are contained in variable `fpc2`.

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

$$M = \sum_{h=1}^{L} \sum_{i=1}^{N_h} \sum_{j=1}^{M_{hij}}$$
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

$$m = \sum_{h=1}^{L} \sum_{i=1}^{n_h} \sum_{j=1}^{m_{hi}} \sum_{k=1}^{m_{hij}}$$

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

$$\hat{M} = \sum_{h=1}^{L} \sum_{i=1}^{n_h} \sum_{j=1}^{m_{hi}} \sum_{k=1}^{m_{hij}} w_{hijk}$$

The estimator for the variance of $\hat{Y}$ is

$$\hat{V}(\hat{Y}) = \sum_{h=1}^{L} (1 - f_h) \frac{n_h}{n_h - 1} \sum_{i=1}^{n_h} \frac{y_{hi} - \overline{y}_h}{2} + \sum_{h=1}^{L} f_h \sum_{i=1}^{n_h} (1 - f_{hi}) \frac{m_{hi}}{m_{hi} - 1} \sum_{j=1}^{m_{hi}} \frac{y_{hij} - \overline{y}_{hi}}{2}$$

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 \(\hat{Y}\) and \(\hat{X}\) (notation for \(X\) is defined similarly to that of \(Y\)), the covariance estimator is

\[
\hat{\text{Cov}}(\hat{Y}, \hat{X}) = \sum_{h=1}^{L} (1 - f_h) \frac{n_h}{n_h - 1} \sum_{i=1}^{n_h} (y_{hi} - \overline{y}_h)(x_{hi} - \overline{x}_h)
+ \sum_{h=1}^{L} f_h \sum_{i=1}^{m_{hi}} (1 - f_{hi}) \frac{m_{hi}}{m_{hi} - 1} \sum_{j=1}^{m_{hi}} (y_{hij} - \overline{y}_{hi})(x_{hij} - \overline{x}_{hi})
\]

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
   \[
   \hat{Z} = \sum_{j=1}^{m} w_j z_j
   \]

3. Estimate the variance \( V(\hat{Z}) \) by using the design-based variance estimator for the total \( \hat{Z} \). 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

\[
\hat{R} = \frac{\hat{Y}}{\hat{X}}
\]

and its score variable is

\[
z_j(\hat{R}) = \frac{\partial \hat{R}}{\partial w_j} = \frac{y_j - \hat{R} x_j}{\hat{X}}
\]

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 \( x \))

\[
\hat{V}(\hat{R}) = \frac{1}{\hat{X}^2} \left\{ \hat{V}(\hat{Y}) - 2\hat{R} \hat{Cov}(\hat{Y}, \hat{X}) + \hat{R}^2 \hat{V}(\hat{X}) \right\}
\]
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 $(Y_j, x_j)$ for the entire population and are interested in modeling the relationship between $Y_j$ and $x_j$ by the vector of parameters $\beta$ that solve the following estimating equations:

$$ G(\beta) = \sum_{j=1}^{M} S(\beta; Y_j, x_j) = 0 $$

For ordinary least squares, $G(\beta)$ is the normal equations

$$ G(\beta) = X'Y - X'X\beta = 0 $$

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—$G'(\beta)$ is the first derivative of the log-pseudolikelihood function with respect to $\beta$. Estimate $\beta$ by solving for $\hat{\beta}$ from the weighted sample estimating equations

$$ \hat{G}(\beta) = \sum_{j=1}^{m} w_j S(\beta; y_j, x_j) = 0 $$

(3)

The associated estimation command with iweights will produce point estimates $\hat{\beta}$ equal to the solution of (3).

A first-order matrix Taylor-series expansion yields

$$ \hat{\beta} - \beta \approx - \left( \frac{\partial \hat{G}(\beta)}{\partial \beta} \right)^{-1} \hat{G}(\beta) $$

with the following variance estimator for $\hat{\beta}$:

$$ \hat{V}(\hat{\beta}) = \left[ \left( \frac{\partial \hat{G}(\beta)}{\partial \beta} \right)^{-1} \hat{V}(\hat{G}(\beta)) \left( \frac{\partial \hat{G}(\beta)}{\partial \beta} \right)^{-T} \right]_{\beta=\hat{\beta}} = D\hat{V}(\hat{G}(\beta))D' $$
where $D$ is $(X_s' WX_s)^{-1}$ 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 $\hat{G}(\beta)$ as

$$\hat{G}(\beta) = \sum_{j=1}^{m} w_j d_j$$

where $d_j = s_j x_j$ 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 $x_j \beta$. In either case, $\hat{G}(\beta)$ is an estimator for the total $G(\beta)$, and the variance estimator $\hat{V}\{\hat{G}(\beta)\}|_{\beta=\hat{\beta}}$ 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


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 $\hat{\theta}$ be the vector of point estimates computed using the sampling weights for a given survey dataset (for example, $\hat{\theta}$ 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 $\theta$. 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 $\hat{\theta}_{(i)}$ be the vector of point estimates from the $i$th replication. When the `mse` option is specified, the variance estimator is

$$\hat{V}(\theta) = \frac{b}{r} \sum_{i=1}^{r} \{\hat{\theta}_{(i)} - \hat{\theta}\} \{\hat{\theta}_{(i)} - \hat{\theta}\}'$$

Otherwise, the variance estimator is

$$\hat{V}(\theta) = \frac{b}{r} \sum_{i=1}^{r} \{\hat{\theta}_{(i)} - \bar{\theta}_{(.)}\} \{\hat{\theta}_{(i)} - \bar{\theta}_{(.)}\}'$$

where $\bar{\theta}_{(.)}$ is the bootstrap mean,

$$\bar{\theta}_{(.)} = \frac{1}{r} \sum_{i=1}^{r} \hat{\theta}_{(i)}$$

**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 $\hat{\theta}$ be the vector of point estimates computed using the sampling weights for a given stratified survey design (for example, $\hat{\theta}$ 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

$$w_j^* = \begin{cases} 
fw_j, & \text{if } H_r[i, h] = -1 \\
(2 - f)w_j, & \text{if } H_r[i, h] = +1 
\end{cases}$$

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 \( \hat{\theta} \). 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 \( \hat{\theta}_{(i)} \) be the vector of point estimates from the \( i \)th replication. When the `mse` option is specified, the variance estimator is

\[
\hat{V}(\theta) = \frac{1}{r(1-f)^2} \sum_{i=1}^{r} \{\hat{\theta}_{(i)} - \bar{\theta}\} \{\hat{\theta}_{(i)} - \bar{\theta}\}'
\]

Otherwise, the variance estimator is

\[
\hat{V}(\theta) = \frac{1}{r(1-f)^2} \sum_{i=1}^{r} \{\hat{\theta}_{(i)} - \bar{\theta}_{(.)}\} \{\hat{\theta}_{(i)} - \bar{\theta}_{(.)}\}'
\]

where \( \bar{\theta}_{(.)} \) is the BRR mean,

\[
\bar{\theta}_{(.)} = \frac{1}{r} \sum_{i=1}^{r} \hat{\theta}_{(i)}
\]

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 \( \hat{\theta} \) be the vector of point estimates computed using the sampling weights for a given survey design (for example, \( \hat{\theta} \) 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 \( \hat{\theta} \).

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

\[
w_{ab}^{*} = \begin{cases} 
0, & \text{if } a = h \text{ and } b \text{ is dropped} \\
\frac{n_{h}}{n_{h} - k} w_{ab}, & \text{if } a = h \text{ and } b \text{ is not dropped} \\
w_{ab}, & \text{otherwise}
\end{cases}
\]

Each replicate is produced by using the adjusted-weight variable with the estimation command that produced \( \hat{\theta} \). 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 \( \hat{\theta}_{(h,i)} \) be the point estimates (replicate) from leaving out the \( i \)th PSU from stratum \( h \). The pseudovalue for replicate \( (h, i) \) is

\[
\hat{\theta}^*_{h,i} = \hat{\theta}_{(h,i)} + n_h \{ \hat{\theta} - \hat{\theta}_{(h,i)} \}
\]

When the \texttt{mse} option is specified, the variance estimator is

\[
\hat{V}(\hat{\theta}) = \sum_{h=1}^{L} (1 - f_h) m_h \sum_{i=1}^{n_h} \{ \hat{\theta}_{(h,i)} - \bar{\theta} \} \{ \hat{\theta}_{(h,i)} - \bar{\theta} \}'
\]

and the jackknife mean is

\[
\bar{\theta}(\cdot) = \frac{1}{n} \sum_{h=1}^{L} \sum_{i=1}^{n_h} \hat{\theta}_{(h,i)}
\]

where \( f_h \) is the sampling rate and \( m_h \) is the jackknife multiplier associated with stratum \( h \). Otherwise, the variance estimator is

\[
\hat{V}(\hat{\theta}) = \sum_{h=1}^{L} (1 - f_h) m_h \sum_{i=1}^{n_h} \{ \hat{\theta}_{(h,i)} - \bar{\theta} \} \{ \hat{\theta}_{(h,i)} - \bar{\theta} \}', \quad \bar{\theta} = \frac{1}{n_h} \sum_{i=1}^{n_h} \hat{\theta}_{(h,i)}
\]

and the jackknife mean is

\[
\bar{\theta}^*(\cdot) = \frac{1}{n} \sum_{h=1}^{L} \sum_{i=1}^{n_h} \hat{\theta}^*_{h,i}
\]

The multiplier for the delete-one jackknife is

\[
m_h = \frac{n_h - 1}{n_h}
\]

The delete-\( k \) jackknife

Let \( \tilde{\theta}_{(h,d)} \) 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

\[
\tilde{\theta}^*_{h,d} = \tilde{\theta}_{(h,d)} + c_h \{ \hat{\theta} - \tilde{\theta}_{(h,d)} \}
\]

When the \texttt{mse} option is specified, the variance estimator is

\[
\tilde{V}(\tilde{\theta}) = \sum_{h=1}^{L} (1 - f_h) m_h \sum_{d=1}^{c_h} \{ \tilde{\theta}_{(h,d)} - \bar{\theta} \} \{ \tilde{\theta}_{(h,d)} - \bar{\theta} \}'
\]

and the jackknife mean is

\[
\bar{\theta}(\cdot) = \frac{1}{C} \sum_{h=1}^{L} \sum_{d=1}^{c_h} \tilde{\theta}_{(h,d)}, \quad C = \sum_{h=1}^{L} c_h
\]
Otherwise, the variance estimator is

\[
\hat{V}(\hat{\theta}) = \sum_{h=1}^{L} (1 - f_h) m_h \sum_{d=1}^{c_h} \{\hat{\theta}(h,d) - \bar{\theta}_h\} \{\hat{\theta}(h,d) - \bar{\theta}_h\}',
\]

and the jackknife mean is

\[
\bar{\theta}^* = \frac{1}{C} \sum_{h=1}^{L} \sum_{d=1}^{c_h} \hat{\theta}^*_{h,d}
\]

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 \(\hat{\theta}\) be the vector of point estimates computed using the sampling weights for a given survey dataset (for example, \(\hat{\theta}\) 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 \(H_r' H_r = r I\), 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 \(\hat{\theta}\). 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 \(\hat{\theta}(i)\) 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
\[ \hat{V}(\hat{\theta}) = (1 - f) \frac{4}{r} \sum_{i=1}^{r} \{\hat{\theta}(i) - \hat{\theta}\} \{\hat{\theta}(i) - \hat{\theta}\}' \]

Otherwise, the variance estimator is
\[ \hat{V}(\hat{\theta}) = (1 - f) \frac{4}{r} \sum_{i=1}^{r} \{\hat{\theta}(i) - \bar{\theta} \} \{\hat{\theta}(i) - \bar{\theta} \}' \]

where \( \bar{\theta} \) is the SDR mean,
\[ \bar{\theta} = \frac{1}{r} \sum_{i=1}^{r} \hat{\theta}(i) \]

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
\[ \hat{\theta} \pm \frac{t_{1-\alpha/2,d}}{\sqrt{\hat{V}(\hat{\theta})}} \]

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 \texttt{svy}'s replication commands has its own default behavior when the design degrees of freedom are not \texttt{svyset} or specified using the \texttt{dof()} option. \texttt{svy brr}: use \( d = r - 1 \), where \( r \) is the number of replications. \texttt{svy bootstrap}: and \texttt{svy sdr}: use \( z_{1-\alpha/2} \) for the critical value instead of \( t_{1-\alpha/2,d} \).

References


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
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.
**Glossary**

**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 Glossary and Index.