

**svy** — The survey prefix command

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## 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
```

<i>vcetype</i>	Description
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SE

<u>linearized</u>	Taylor-linearized variance estimation
<u>bootstrap</u>	bootstrap variance estimation; see [SVY] <a href="#">svy bootstrap</a>
<u>brr</u>	BRR variance estimation; see [SVY] <a href="#">svy brr</a>
<u>jackknife</u>	jackknife variance estimation; see [SVY] <a href="#">svy jackknife</a>
<u>sdr</u>	SDR variance estimation; see [SVY] <a href="#">svy sdr</a>

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

<i>svy_options</i>	Description
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if/in

<u>subpop</u> ( [ <i>varname</i> ] [ <i>if</i> ] )	identify a subpopulation
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SE

<u>dof</u> (#)	design degrees of freedom
<u>bootstrap_options</u>	more options allowed with bootstrap variance estimation; see [SVY] <a href="#">bootstrap_options</a>
<u>brr_options</u>	more options allowed with BRR variance estimation; see [SVY] <a href="#">brr_options</a>
<u>jackknife_options</u>	more options allowed with jackknife variance estimation; see [SVY] <a href="#">jackknife_options</a>
<u>sdr_options</u>	more options allowed with SDR variance estimation; see [SVY] <a href="#">sdr_options</a>

Reporting

<u>level</u> (#)	set confidence level; default is <code>level(95)</code>
<u>nocnsreport</u>	do not display constraints
<u>display_options</u>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
<u>noheader</u>	suppress table header
<u>nolegend</u>	suppress table legend
<u>noadjust</u>	do not adjust model Wald statistic
<u>noisily</u>	display any output from <i>command</i>
<u>trace</u>	trace <i>command</i>
<u>coeflegend</u>	display legend instead of statistics

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

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

`mi estimate` may be used with `svy linearized` if the estimation command allows `mi estimate`; it may not be used with `svy bootstrap`, `svy brr`, `svy jackknife`, or `svy sdr`.

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

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

See [U] [20 Estimation and postestimation commands](#) for more capabilities of estimation commands.

## Options

if/in

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

[*varname*] [*if*]

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

See [SVY] [subpopulation estimation](#) and [SVY] [estat](#).

SE

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

*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](#).

Reporting

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

`nocnsreport`; see [R] [estimation options](#).

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

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

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

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

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

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

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

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

`coeflegend`; see [\[R\] estimation options](#).

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

*eform\_option*; see [\[R\] eform\\_option](#).

## Remarks and examples

[stata.com](http://www.stata.com)

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 http://www.stata-press.com/data/r15/nhanes2f
. svyset psuid [pweight=finalwgt], strata(stratid)
      pweight: finalwgt
      VCE: linearized
Single unit: missing
Strata 1: stratid
SU 1: psuid
FPC 1: <zero>
```

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

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

Survey: Mean estimation
Number of strata =      31      Number of obs   =      9,189
Number of PSUs   =      62      Population size = 104,176,071
                                   Design df       =       31
```

	Linearized		
	Mean	Std. Err.	[95% Conf. Interval]
zinc	87.18207	.4944827	86.17356 88.19057

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

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

	Linearized		
	Mean	Std. Err.	[95% Conf. Interval]
zinc	86.51518	.1510744	86.21904 86.81132

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

◀

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

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

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

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

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

Survey: Mean estimation
Number of strata =      1      Number of obs   =      9,189
Number of PSUs   =  9,189      Population size = 104,176,071
                                   Design df       =       9,188
```

	Linearized		
	Mean	Std. Err.	[95% Conf. Interval]
zinc	87.18207	.1828747	86.82359 87.54054

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

```
. svyset psuid [pweight=finalwgt]
      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
```

	Linearized		
	Mean	Std. Err.	[95% Conf. Interval]
zinc	87.18207	.7426221	77.74616 96.61798

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



### ▷ Example 3

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

Here is our design-based analysis:

```
. svyset psuid [pweight=finalwgt], strata(stratid)
      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
(running regress on estimation sample)

Survey: Linear regression
Number of strata   =      31      Number of obs   =      9,189
Number of PSUs    =      62      Population size = 104,176,071
Design df         =           31
F( 7, 25)        =      62.500
Prob > F         =      0.0000
R-squared        =      0.0698
```

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

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

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

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

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

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

## Stored results

svy stores the following in `e()`:

### Scalars

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

### Macros

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

### Matrices

<code>e(b)</code>	estimates
<code>e(V)</code>	design-based variance
<code>e(V_srs)</code>	simple-random-sampling-without-replacement variance, $\widehat{V}_{\text{srsor}}$



<code>e(V_srssub)</code>	subpopulation simple-random-sampling-without-replacement variance, $\widehat{V}_{srswor}$ (created only when <code>subpop()</code> is specified)
<code>e(V_srswr)</code>	simple-random-sampling-with-replacement variance, $\widehat{V}_{srswr}$ (created only when <code>fpc()</code> option is <code>svyset</code> )
<code>e(V_srssubwr)</code>	subpopulation simple-random-sampling-with-replacement variance, $\widehat{V}_{srswr}$ (created only when <code>subpop()</code> is specified)
<code>e(V_modelbased)</code>	model-based variance
<code>e(V_msp)</code>	variance from misspecified model fit, $\widehat{V}_{msp}$
<code>e(_N_strata_single)</code>	number of strata with one sampling unit
<code>e(_N_strata_certain)</code>	number of certainty strata
<code>e(_N_strata)</code>	number of strata
Functions	
<code>e(sample)</code>	marks estimation sample

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

## Methods and formulas

See [\[SVY\] variance estimation](#) for all the details behind the point estimate and variance calculations made by `svy`.

## References

- Korn, E. L., and B. I. Graubard. 1990. Simultaneous testing of regression coefficients with complex survey data: Use of Bonferroni *t* statistics. *American Statistician* 44: 270–276.
- McDowell, A., A. Engel, J. T. Massey, and K. Maurer. 1981. Plan and operation of the Second National Health and Nutrition Examination Survey, 1976–1980. *Vital and Health Statistics* 1(15): 1–144.

## 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
- [\[P\] \\_robust](#) — Robust variance estimates
- [\[U\] 20 Estimation and postestimation commands](#)
- [\[SVY\] 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