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

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

**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**

- **coef\_legend** display legend instead of statistics
  
**coef\_legend** is not shown in the dialog boxes for estimation commands.

**brr\_options**

- **hadamard(matrix)** Hadamard matrix
- **fay(#)** Fay’s adjustment

**Options**

- **saving(filename[, ...])** save results to filename; save statistics in double precision; save results to filename every # replications
- **mse** use MSE formula for variance

**Reporting**

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

**Advanced**

- **nodrop** do not drop observations
- **reject(exp)** identify invalid results
- **dof(#)** design degrees of freedom

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svy requires that the survey design variables be identified using \texttt{svyset}; see [SVY] 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

\begin{align*}
\text{name: } & \text{elist} \\
\text{elist} & \text{contains} \\
\text{newvarname} & = (\text{exp}) \\
(\text{exp}) & \\
\text{eexp} & \text{is} \\
\text{specname} & [\text{eqno}] \text{specname} \\
\text{specname} & \text{is} \\
\_b & \\
\_b[] & \\
\_se & \\
\_se[] & \\
\text{eqno} & \text{is} \\
\# \# & \\
\text{name} & \\
\end{align*}

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.

\begin{itemize}
\item hadamard(matrix) specifies the Hadamard matrix to be used to determine which PSUs are chosen for each replicate.
\item fay(#) specifies Fay's adjustment (Judkins 1990), where 0 ≤ # ≤ 2, but excluding 1. This option overrides the fay(#) option of svyset; see [SVY] svyset.
\item saving(filename[, suboptions]) creates a Stata data file (.dta file) consisting of (for each statistic in exp_list) a variable containing the replicates.
\item 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.
\item 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.
\item replace specifies that filename be overwritten if it exists. This option does not appear in the dialog box.
\item 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.
\end{itemize}
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, \( df = \frac{N_{psu} - N_{strata}}{} \).

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

<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>
</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>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>
</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>

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)  
1 2 3 4 5  

BRR results  
Number of obs = 10,351  
Population size = 117,157,513  
Replications = 32  
Design df = 31  

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

| BRR | Coef. | Std. Err. | t | P>|t| | [95% Conf. Interval] |
|-----|-------|-----------|---|------|-------------------|
| WtoH | .4268116 | .0008904 | 479.36 | 0.000 | .4249957 .4286276 |

The mse option causes svy brr to use the MSE form of the BRR variance estimator. This variance estimator will tend to be larger than the previous because of the addition of the familiar squared bias term in the MSE; see [SVY] Variance estimation for more details. The header for the column of standard errors in the table of results is BRR * for the BRR variance estimator using the MSE formula.

. svy brr WtoH = (_b[weight]/_b[height]), mse: total weight height  
(running total on estimation sample)  
BRR replications (32)  
1 2 3 4 5  

BRR results  
Number of obs = 10,351  
Population size = 117,157,513  
Replications = 32  
Design df = 31  

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

| BRR * | 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.
svy brr — Balanced repeated replication for survey data

. 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)
1 2 3 4 5

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></th>
<th>BRR</th>
<th></th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Ratio</td>
<td>Std. Err.</td>
<td></td>
</tr>
<tr>
<td>WtoH</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

\[
H_r' H_r = rI_r
\]

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.

```stata
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