svy postestimation — Postestimation tools for svy

| Postestimation commands | predict | margins |
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Postestimation commands

The following postestimation commands are available after svy:

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

See [SVY] estat.

predict

The syntax of predict (and even if predict is allowed) after svy depends on the command used with svy. Specifically, predict is not allowed after svy: mean, svy: proportion, svy: ratio, svy: tabulate, or svy: total.

margins

The syntax of margins (and even if margins is allowed) after svy depends on the command used with svy. Specifically, margins is not allowed after svy: mean, svy: proportion, svy: ratio, svy: tabulate, or svy: total.

Remarks and examples

What follows are some examples of applications of postestimation commands using survey data. The examples are meant only to introduce the commands in a survey context and explore a few of the possibilities for postestimation analysis. See the individual entries for each command in the *Base Reference Manual* for complete syntax and many more examples.

Example 1: Linear and nonlinear combinations

lincom will display an estimate of a linear combination of parameters, along with its standard error, a confidence interval, and a test that the linear combination is zero. nlcom will do likewise for nonlinear combinations of parameters.

lincom is commonly used to compute the differences of two subpopulation means. For example, suppose that we wish to estimate the difference of zinc levels in white males versus black males in the population represented by the NHANES II data (McDowell et al. 1981). Because the survey design characteristics are already svyset in nhanes2.dta, we only need to generate a variable for identifying the male subpopulation before using svy: mean.

```
. use https://www.stata-press.com/data/r19/nhanes2
. generate male = (sex == 1)
. svy, subpop(male): mean zinc, over(race)
(running mean on estimation sample)
Survey: Mean estimation
Number of strata = 31
                                  Number of obs
                                                           9,811
                                                  =
Number of PSUs = 62
                                  Population size = 111,127,314
                                  Subpop. no. obs =
                                                           4,375
                                  Subpop. size
                                                  = 50,129,281
                                  Design df
                                                              31
                                                  =
                            Linearized
                     Mean
                            std. err.
                                           [95% conf. interval]
 c.zinc@race
      White
                 91.15725
                              .541625
                                            90.0526
                                                         92.2619
                             1.208336
                                                        90.73342
      Black
                   88.269
                                           85.80458
      Other
                 85.54716
                             2.608974
                                           80.22612
                                                         90.8682
```

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

```
. lincom zinc#1.race - zinc#2.race
```

| (1) | c.zinc0 | 01bn.race - c. | zinc@2.race | = 0 | | | |
|-----|---------|----------------|-------------|------|-------|------------|-----------|
| | Mean | Coefficient | Std. err. | t | P> t | [95% conf. | interval] |
| | (1) | 2.888249 | 1.103999 | 2.62 | 0.014 | .6366288 | 5.139868 |

The t statistic and its p-value give a survey analysis equivalent of a two-sample t test.

lincom and nlcom can be used after any of the estimation commands described in [SVY] svy estimation. lincom can, for example, display results as odds ratios after svy: logit and can be used to compute odds ratios for one covariate group relative to another. nlcom can display odds ratios, as well, and allows more general nonlinear combinations of the parameters. See [R] lincom and [R] nlcom for full details. Also see Eltinge and Sribney (1996) for an earlier implementation of lincom for survey data.

Finally, lincom and nlcom operate on the estimated parameters only. To obtain estimates and inference for functions of the parameters and of the data, such as for an exponentiated linear predictor or a predicted probability of success from a logit model, use predictnl; see [R] predictnl.

Example 2: Quadratic terms

From example 2 in [SVY] svy estimation, we modeled the incidence of high blood pressure as a function of height, weight, age, and sex (using the female indicator variable). Here we also include c.age#c.age, a squared term for age.

| . use https:// | www.stata-pr | ess.com/data, | /r19/nhar | nes2d, cle | ear | | |
|---|--|---------------------------------|------------------------|--|--------------------------------------|--------------------|--|
| . svy: logisti (running logis | ic highbp heig s tic on estimation | ght weight ag ation sample) | ge c.age‡) | ¢c.age fem | nale | | |
| Survey: Logist | cic regression | n | | | | | |
| Number of stra Number of PSUs | ata = 31 s = 62 | | | Number Populat Design F(5, 27 Prob > | of obs tion size df 7) F | = = 1 = = | 10,351 17,157,513 31 284.33 0.0000 |
| highbp | Odds ratio | Linearized std. err. | t | P> t | [95% c | conf. | interval] |
| height weight age | .9656421 1.052911 1.055829 | .005163 .0026433 .0133575 | -6.54 20.54 4.29 | 0.000 0.000 0.000 | .95516 1.0475 1.0289 | 93 534 935 | .9762298 1.058316 1.083426 |
| c.age#c.age | .9999399 | .0001379 | -0.44 | 0.666 | .99965 | 88 | 1.000221 |
| female _cons | .6260988 .653647 | .0364945 .5744564 | -8.03 -0.48 | 0.000 0.632 | .55592 .1088 | 217 869 | .7051347 3.924483 |

Note: _cons estimates baseline odds.

Because our model includes a quadratic in the age variable, the peak incidence of high blood pressure with respect to age will occur at -b [age]/(2*b[c.age#c.age]), which we can estimate, along with its standard error, using nlcom.

| <pre>. nlcom peak:b[age]/(2*_b[c.age#c.age])</pre> | | | | | | | |
|--|------|-------------|-----------|------|-------|------------|-----------|
| hig | ghbp | Coefficient | Std. err. | Z | P> z | [95% conf. | interval] |
| P | eak | 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.

These data do not reject our theory. testnl allows multiple hypotheses to be tested jointly and applies the degrees-of-freedom adjustment for survey results; see [R] testnl.

Example 3: Predictive margins

Changing our logistic regression for high blood pressure slightly, we add a factor variable for the levels of race. Level 1 of race represents whites, level 2 represents blacks, and level 3 represents others. We also specify that female is a factor variable, which does not change its coefficient but does increase its functionality with some postestimation commands.

```
. svy: logistic highbp height weight age c.age#c.age i.female i.race, baselevels
(running logistic on estimation sample)
Survey: Logistic regression
Number of strata = 31
                                                    Number of obs
                                                                     =
                                                                             10,351
Number of PSUs
                = 62
                                                    Population size = 117,157,513
                                                    Design df
                                                                     =
                                                                                 31
                                                    F(7, 25)
                                                                     =
                                                                             230.16
                                                    Prob > F
                                                                     =
                                                                             0.0000
                            Linearized
                              std. err.
                                                   P>|t|
                                                              [95% conf. interval]
      highbp
                Odds ratio
                                              t
      height
                  .9675961
                              .0052361
                                          -6.09
                                                   0.000
                                                              .9569758
                                                                           .9783343
                  1.052683
                              .0026091
                                          20.72
                                                   0.000
                                                              1.047376
                                                                           1.058018
      weight
                                           4.33
                  1.056628
                              .0134451
                                                   0.000
                                                              1.029559
                                                                          1.084408
         age
 c.age#c.age
                  .9999402
                              .0001382
                                          -0.43
                                                   0.668
                                                              .9996585
                                                                           1.000222
      female
       Male
                         1
                             (base)
     Female
                  .6382331
                              .0377648
                                          -7.59
                                                   0.000
                                                              .5656774
                                                                            .720095
        race
                             (base)
      White
                         1
      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
                                          -0.96
                                                   0.345
                  .4312846
                               .378572
                                                              .0719901
                                                                          2.583777
```

Note: _cons estimates baseline odds.

Our point estimates indicate that the odds of females having high blood pressure is about 64% of the odds for men and that the odds of blacks having high blood pressure is about 1.4 times that of whites. The odds ratios give us the relative effects of their covariates, but they do not give us any sense of the absolute size of the effects. The odds ratio comparing blacks with whites is clearly large and statistically significant, but does it represent a sizable change? One way to answer that question is to explore the probabilities of high blood pressure from our fitted model. Let's first look at the predictive margins of the probability of high blood pressure for the three levels of race.

```
. margins race, vce(unconditional)
Predictive margins
Number of strata = 31
                                                  Number of obs =
                                                                          10,351
Number of PSUs = 62
                                                  Population size = 117, 157, 513
                                                  Design df
                                                                   _
                                                                              31
Expression: Pr(highbp), predict()
                            Linearized
                   Margin
                            std. err.
                                            t
                                                 P>|t|
                                                            [95% conf. interval]
        race
                 .3600722
                             .0150121
                                         23.99
                                                 0.000
                                                            .3294548
                                                                        .3906895
      White
                                                            .3825441
      Black
                 .4256413
                            .0211311
                                         20.14
                                                 0.000
                                                                        .4687385
      Other
                 .4523404
                            .0311137
                                         14.54
                                                 0.000
                                                            .3888836
                                                                        .5157972
```

Because our response is a probability, these margins are sometimes called predicted marginal proportions or model-adjusted risks. They let us compare the effect of our three racial groups while controlling for the distribution of other covariates in the groups. Computationally, these predictive margins are the weighted average of the predicted probabilities for each observation in the estimation sample. The marginal probability for whites is the average probability, assuming that everyone in the sample is white; the margin for blacks assumes that everyone is black; and the margin for others assumes that everyone is something other than black or white.

There is a sizable difference in blood pressure between whites and blacks, with the marginal probability of high blood pressure for whites being about 36% and that for blacks being almost 43%. These are the adjusted probability levels. A more direct answer to our question about whether the odds ratios represent a substantial effect requires looking at the differences of these marginal probabilities. Researchers in the health-related sciences call such differences risk differences, whereas researchers in the social sciences usually call them average marginal effects or average partial effects.

Regardless of terminology, we are interested in the difference in the probability of blacks having high blood pressure as compared with whites, while adjusting for all other covariates in the model. We request risk differences by specifying the variables of interest in a dydx() option.

| . margins, vce | e(uncondition | al) dydx(race | e) | | | |
|----------------------------------|------------------------------|----------------------|------|----------------------------|-----------------------------------|----------------------------|
| Average margin | nal effects | | | | | |
| Number of stra Number of PSUs | ata = 31 s = 62 | | | Number Popula Design | of obs = tion size = 1 df = | 10,351 17,157,513 31 |
| Expression: Pi dy/dx wrt: 2 | (highbp), pr .race 3.race | edict() | | | | |
| | dy/dx | Linearized std. err. | t | P> t | [95% conf. | interval] |
| race | | | | | | |
| Black | .0655691 | .0204063 | 3.21 | 0.003 | .0239501 | .1071881 |
| Other | .0922682 | .0343809 | 2.68 | 0.012 | .0221478 | .1623886 |

Note: dy/dx for factor levels is the discrete change from the base level.

Looking in the column labeled dy/dx, we see that the risk difference between blacks and whites is about 6.6% (0.6557). That is a sizable as well as significant difference.

Because they are population-weighted averages over the whole sample, these margins are estimates of the population average risk differences. And because we specified the vce(unconditional) option, their standard errors and confidence intervals can be used to make inferences about the population average risk differences. See *Methods and formulas* in [R] margins for details.

We can also compute margins or risk differences for subpopulations. To compute risk differences for the four subpopulations that are the regions of the United States—Northeast, Midwest, South, and West—we add the over(region) option.

```
. margins, vce(unconditional) dydx(race) over(region)
Average marginal effects
Number of strata = 31
                                                     Number of obs
                                                                              10,351
                                                                      =
Number of PSUs
                 = 62
                                                     Population size = 117, 157, 513
                                                     Design df
                                                                      =
                                                                                  31
Expression: Pr(highbp), predict()
dy/dx wrt:
            2.race 3.race
Over:
            region
                             Linearized
                                                   P>|t|
                                                               [95% conf. interval]
                     dy/dx
                              std. err.
                                              t
                 (base outcome)
1.race
2.race
      region
         NE
                  .0662951
                              .0207354
                                            3.20
                                                   0.003
                                                               .0240051
                                                                            .1085852
         MW
                   .065088
                              .0204357
                                            3.19
                                                   0.003
                                                               .0234091
                                                                             .106767
          S
                                            3.28
                                                   0.003
                                                               .0251112
                  .0663448
                              .0202173
                                                                            .1075783
          W
                  .0647221
                              .0203523
                                            3.18
                                                   0.003
                                                               .0232134
                                                                            .1062308
3.race
      region
         NF.
                   .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.

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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.

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)
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
             Coefficient
                        std. err.
                                     t
                                         P>|t|
                                                  [95% conf. interval]
      race
     White
               .3600722
                        .0150128
                                  23.98
                                         0.000
                                                  .3294534
                                                              .390691
                        .0211504
     Black
               .4256413
                                  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.

R-squared

4,948

156.24

0.0000

0.2379

=

31

Example 5: Nonlinear predictions and their standard errors

Continuing with the NHANES II data, we fit a linear regression of log of blood lead level on age, age-squared, gender, race, and region.

```
. use https://www.stata-press.com/data/r19/nhanes2d
. svy: regress loglead age c.age#c.age i.female i.race i.region
(running regress on estimation sample)
Survey: Linear regression
Number of strata = 31
                                                Number of obs =
Number of PSUs = 62
                                                Population size = 56,405,414
                                                Design df =
                                                F(8, 24)
                                                              =
                                               Prob > F
                                                              =
```

| loglead | Coefficient | Linearized std. err. | t | P> t | [95% conf. | interval] |
|------------------------|-----------------------------|---------------------------------|-------------------------|-------------------------|-------------------------------|---------------------------------|
| age | .0158388 | .0027352 | 5.79 | 0.000 | .0102603 | .0214173 |
| c.age#c.age | 0001464 | .0000295 | -4.96 | 0.000 | 0002066 | 0000862 |
| female Female | 3655338 | .0116157 | -31.47 | 0.000 | 3892242 | 3418434 |
| race Black Other | .178402 0516952 | .0314173 .0402381 | 5.68 -1.28 | 0.000 0.208 | .114326 1337614 | .242478 .030371 |
| region MW S W | 02283 1685453 0362295 | .0389823 .056004 .0387508 | -0.59 -3.01 -0.93 | 0.562 0.005 0.357 | 1023349 2827662 1152623 | .0566749 0543244 .0428032 |
| _cons | 2.440671 | .0627987 | 38.86 | 0.000 | 2.312592 | 2.568749 |

Given that we modeled the natural log of the lead measurement, we can use predictnl to compute the exponentiated linear prediction (in the original units of the lead variable), along with its standard error.

```
. predictnl leadhat = exp(xb()) if e(sample), se(leadhat_se)
(5,403 missing values generated)
. sort lead leadhat
. generate showobs = inrange(_n,1,5) + inrange(_n,2501,2505) +
> inrange(_n,4945,4948)
```

| | lead | leadhat | leadhat_se | age | c.age# c.age |
|-------|------|----------|------------|-----|-----------------|
| 1. | 2 | 9.419804 | .5433255 | 29 | 841 529 |
| 3. | 3 | 9.046788 | .5298448 | 24 | 576 |
| 4. | 3 | 9.046788 | .5298448 | 24 | 576 |
| 5. | 3 | 9.27693 | .5347956 | 27 | 729 |
| 2501. | 13 | 16.88317 | .7728783 | 37 | 1369 |
| 2502. | 13 | 16.90057 | 2.296082 | 71 | 5041 |
| 2503. | 13 | 16.90057 | 2.296082 | 71 | 5041 |
| 2504. | 13 | 16.90237 | 1.501056 | 48 | 2304 |
| 2505. | 13 | 16.90852 | 2.018708 | 60 | 3600 |
| 4945. | 61 | 17.18581 | 2.052034 | 58 | 3364 |
| 4946. | 64 | 15.08437 | .647629 | 24 | 576 |
| 4947. | 66 | 17.78698 | 1.641349 | 56 | 3136 |
| 4948. | 80 | 16.85864 | 1.333927 | 42 | 1764 |

. list lead leadhat leadhat_se age c.age#c.age if showobs, abbrev(10)

Example 6: Multiple-hypothesis testing

Joint-hypothesis tests can be performed after svy commands with the test command. Using the results from the regression model fit in the previous example, we can use test to test the joint significance of 2.region, 3.region, and 4.region. (1.region is the Northeast, 2.region is the Midwest, 3.region is the South, and 4.region is the West.) We test the hypothesis that 2.region = 0, 3.region = 0, and 4.region = 0.

```
. test 2.region 3.region 4.region
Adjusted Wald test
( 1) 2.region = 0
( 2) 3.region = 0
( 3) 4.region = 0
F( 3, 29) = 2.96
Prob > F = 0.0486
```

The nosvyadjust option on test produces an unadjusted Wald test.

```
. test 2.region 3.region 4.region, nosvyadjust
Unadjusted Wald test
(1) 2.region = 0
(2) 3.region = 0
(3) 4.region = 0
F(3, 31) = 3.17
Prob > F = 0.0382
```

For one-dimensional tests, the adjusted and unadjusted F statistics are identical, but they differ for higher-dimensional tests. Using the nosvyadjust option is not recommended because the unadjusted Fstatistic 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.

4

Bonferroni-adjusted *p*-values can also be computed:

. test 2.region 3.region 4.region, mtest(bonferroni) Adjusted Wald test (1) 2.region = 03.region = 0(2) (3) 4.region = 0p > F F(df,29) df 0.34 1.0000* (1)1 (2)9.06 0.0155* 1 (3) 0.87 1.0000* 1 A11 2.96 3 0.0486

* Bonferroni-adjusted p-values

See Korn and Graubard (1990) for a discussion of these three different procedures for conducting joint-hypothesis tests. See Eltinge and Sribney (1996) for an earlier implementation of test for survey data.

Example 7: Contrasts

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

```
. use https://www.stata-press.com/data/r19/nhanes2f, clear
. label list hlthgrp
hlthgrp:
           1 Poor
           2 Fair
           3 Average
           4 Good
           5 Excellent
. svy: regress zinc i.health
(running regress on estimation sample)
Survey: Linear regression
Number of strata = 31
                                                   Number of obs
                                                                    =
Number of PSUs
                = 62
                                                   Population size = 104, 162, 204
                                                   Design df
                                                                    =
                                                   F(4, 28)
                                                                    =
                                                   Prob > F
                                                                    =
                                                                            0.0000
                                                   R-squared
                                                                    =
                                                                            0.0098
                            Linearized
        zinc
               Coefficient
                            std. err.
                                             t
                                                  P>|t|
                                                             [95% conf. interval]
      health
       Fair
                  .9272308
                             .7690396
                                           1.21
                                                  0.237
                                                            -.6412357
                                                                         2.495697
                  2.444004
                             .6407097
                                           3.81
                                                  0.001
                                                             1.137268
                                                                          3.75074
    Average
       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
                                                  0.000
                 83.94729
                             .8523379
                                          98.49
                                                             82.20893
                                                                         85.68564
```

4

9,188

15.61

31

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

| | عد | F | DNE |
|---------------------|----|-------|--------|
| | di | F | P>F |
| health | | | |
| (Fair vs Poor) | 1 | 1.45 | 0.2371 |
| (Average vs Fair) | 1 | 5.49 | 0.0257 |
| (Good vs Average) | 1 | 10.92 | 0.0024 |
| (Excellent vs Good) | 1 | 1.93 | 0.1744 |
| Joint | 4 | 15.61 | 0.0000 |
| Design | 31 | | |

Note: F statistics are adjusted for the survey design.

| | Contrast | Std. err. | [95% conf. | interval] |
|---|--|--|--|--|
| health (Fair vs Poor) (Average vs Fair) (Good vs Average) (Excellent vs Good) | .9272308 1.516773 1.594281 .7326264 | .7690396 .6474771 .4824634 .5270869 | 6412357 .1962347 .6102904 3423744 | 2.495697 2.837311 2.578271 1.807627 |

The first table reports significance tests for each contrast, along with a joint test of all the contrasts. The row labeled (Fair vs Poor), for example, tests the null hypothesis that the first two health statuses have the same mean zinc level. The test statistics are automatically adjusted for the survey design.

The second table reports estimates, standard errors, and confidence limits for each contrast. The row labeled (Good vs Average), for example, shows that those in good health have a mean zinc level about 1.6 units higher than those of average health. The standard errors and confidence intervals also account for the survey design.

Design df = 31

If we would like to go further and make all possible pairwise comparisons of the health groups, we can use the pwcompare command. We will specify the mcompare(sidak) option to account for multiple comparisons and the cformat(%3.1f) option to reduce the number of decimal places in the output:

. pwcompare health, mcompare(sidak) cformat(%3.1f) Pairwise comparisons of marginal linear predictions

Design df = 31

Margins: asbalanced

| | Number of comparisons |
|--------|--------------------------|
| health | 10 |

| | | | Sidak | | | |
|--------------|---------|----------|-----------|------------|-----------|--|
| | | Contrast | Std. err. | [95% conf. | interval] | |
| | health | | | | | |
| Fair | vs Poor | 0.9 | 0.8 | -1.4 | 3.2 | |
| Average | vs Poor | 2.4 | 0.6 | 0.5 | 4.4 | |
| Good | vs Poor | 4.0 | 0.7 | 2.0 | 6.1 | |
| Excellent | vs Poor | 4.8 | 0.7 | 2.6 | 6.9 | |
| Average | vs Fair | 1.5 | 0.6 | -0.4 | 3.5 | |
| Good | vs Fair | 3.1 | 0.5 | 1.5 | 4.8 | |
| Excellent | vs Fair | 3.8 | 0.7 | 1.7 | 6.0 | |
| Good vs | Average | 1.6 | 0.5 | 0.1 | 3.0 | |
| Excellent vs | Average | 2.3 | 0.7 | 0.3 | 4.4 | |
| Excellent | vs Good | 0.7 | 0.5 | -0.9 | 2.3 | |

Seven of the ten Šidák intervals exclude the null value of zero. See [R] **pwcompare** for more information on pairwise comparisons and multiple-comparison adjustments.

4

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-pre | ess.com/data | /r19/nhar | nes2f, cl | ear | | |
|--|---|--|-----------------------------------|--|---------------------------------------|----------------------|--|
| . svyset psuid | d [pw=finalwgt |], strata(s | tratid) | | | | |
| Sampling weigh N Single ur Strata Sampling unit FPC | nts: finalwgt /CE: linearize nit: missing a 1: stratid t 1: psuid C 1: <zero></zero> | d | | | | | |
| . svy: ologit (running ologi | health female it on estimati | e black age .on sample) | c.age#c.a | ıge | | | |
| Survey: Ordere | ed logistic re | gression | | | | | |
| Number of stra Number of PSUs | ata = 31 s = 62 | | | Number Popula Design F(4, 2 Prob > | of obs ation size df 8) F | = = 1 = = | 10,335 16,997,257 31 223.27 0.0000 |
| health | Coefficient | Linearized std. err. | t | P> t | [95% c | onf. | interval] |
| female black age c.age#c.age | 1615219 986568 0119491 0003234 | .0523678 .0790277 .0082974 .000091 | -3.08 -12.48 -1.44 -3.55 | 0.004 0.000 0.160 0.001 | 26832 -1.1477 02887 0005 | 67 46 17 09 | 054717 8253899 .0049736 0001377 |
| /cut1 /cut2 /cut3 /cut4 | -4.566229 -3.057415 -1.520596 242785 | .1632561 .1699944 .1714342 .1703965 | | | -4.8991 -3.4041 -1.8702 5903 | 92 21 39 11 | -4.233266 -2.710709 -1.170954 .104741 |

The self-reported health variable takes five categories. Categories 1 and 2 denote negative categories, whereas categories 4 and 5 denote positive categories. We wonder whether the distinctions between the two positive categories and between the two negative categories are produced in accordance with one latent dimension, which is an assumption of the ordered logistic model. To test one-dimensionality, we will collapse the five-point health measure into a three-point measure, refit the ordered logistic model, and compare the regression coefficients and cutpoints between the two analyses. If the single latent variable assumption is valid, the coefficients and cutpoints should match. This can be seen as a Hausman-style specification test. Estimation of the ordered logistic model parameters for survey data is by maximum pseudolikelihood. Neither estimator is fully efficient, and thus the assumptions for the classic Hausman test and for the hausman command are not satisfied. With suest, we can obtain an appropriate Hausman test for survey data.

To perform the Hausman test, we are already almost halfway there by following steps 1 and 2 for one of the models. We just need to store the current estimation results before moving on to the next model. Here we store the results with estimates store under the name H5, indicating that in this analysis, the dependent variable health has five categories.

. estimates store H5

We proceed by generating a new dependent variable health3, which maps values 1 and 2 into 2, 3 into 3, and 4 and 5 into 4. This transformation is conveniently accomplished with the clip() function. We then fit an ologit model with this new dependent variable and store the estimation results under the name H3.

| . generate hea (2 missing val | alth3 = clip(h lues generated | lealth, 2, 4 l) | .) | | | |
|---|----------------------------------|----------------------------------|--------------------------|--|---|---|
| . svy: ologit (running olog i | health3 femal it on estimati | .e black age .on sample) | c.age#c | .age | | |
| Survey: Ordere | ed logistic re | gression | | | | |
| Number of stra Number of PSUs | ata = 31 s = 62 | | | Number Popula Design F(4, 2 Prob > | r of obs = tion size = d df = 28) = F = | 10,335 116,997,257 31 197.08 0.0000 |
| health3 | Coefficient | Linearized std. err. | t | P> t | [95% conf | . interval] |
| female black age | 1551238 -1.046316 0365408 | .0563809 .0728274 .0073653 | -2.75 -14.37 -4.96 | 0.010 0.000 0.000 | 2701133 -1.194849 0515624 | 0401342 8977836 0215192 |
| c.age#c.age | 00009 | .0000791 | -1.14 | 0.264 | 0002512 | .0000713 |
| /cut1 /cut2 | -3.655498 -2.109584 | .1610211 .1597057 | | | -3.983903 -2.435306 | -3.327093 -1.783862 |

. estimates store H3

We can now obtain the combined estimation results of the two models stored under H5 and H3 with design-based standard errors.

| . suest H5 H3 | | | | | | | |
|--|----------------|------------|--------|---|------------|-----------|--|
| Simultaneous a | survey results | for H5, H3 | 3 | | | | |
| Number of strata = 31 Number of PSUs = 62 | | | | Number of obs = 10,335 Population size = 116,997,257 Design df = 31 | | | |
| | | Linearized | | | | | |
| | Coefficient | std. err. | t | P> t | [95% conf. | interval] | |
| H5_health | | | | | | | |
| female | 1615219 | .0523678 | -3.08 | 0.004 | 2683267 | 054717 | |
| black | 986568 | .0790277 | -12.48 | 0.000 | -1.147746 | 8253899 | |
| age | 0119491 | .0082974 | -1.44 | 0.160 | 0288717 | .0049736 | |
| c.age#c.age | 0003234 | .000091 | -3.55 | 0.001 | 000509 | 0001377 | |
| /Н5 | | | | | | | |
| cut1 | -4.566229 | .1632561 | | | -4.899192 | -4.233266 | |
| cut2 | -3.057415 | .1699944 | | | -3.404121 | -2.710709 | |
| cut3 | -1.520596 | .1714342 | | | -1.870239 | -1.170954 | |
| cut4 | 242785 | .1703965 | | | 590311 | .104741 | |
| H3_health3 | | | | | | | |
| female | 1551238 | .0563809 | -2.75 | 0.010 | 2701133 | 0401342 | |
| black | -1.046316 | .0728274 | -14.37 | 0.000 | -1.194849 | 8977836 | |
| age | 0365408 | .0073653 | -4.96 | 0.000 | 0515624 | 0215192 | |
| c.age#c.age | 00009 | .0000791 | -1.14 | 0.264 | 0002512 | .0000713 | |
| /НЗ | | | | | | | |
| cut1 | -3.655498 | .1610211 | | | -3.983903 | -3.327093 | |
| cut2 | -2.109584 | .1597057 | | | -2.435306 | -1.783862 | |

The coefficients of H3 and H5 look rather similar. We now use test to perform a formal Hausmantype test for the hypothesis that the regression coefficients are indeed the same, as we would expect if there is indeed a one-dimensional latent dimension for health. Thus we test that the coefficients in the equation H5_health are equal to those in H3_health3.

```
. test [H5_health=H3_health3]
Adjusted Wald test
( 1) [H5_health]female - [H3_health3]female = 0
( 2) [H5_health]black - [H3_health3]black = 0
( 3) [H5_health]age - [H3_health3]age = 0
( 4) [H5_health]c.age#c.age - [H3_health3]c.age#c.age = 0
F( 4, 28) = 17.13
Prob > F = 0.0000
```

We can reject the null hypothesis, which indicates that the ordered logistic regression model is indeed misspecified. Another specification test can be conducted with respect to the cutpoints. Variable health3 was constructed from health by collapsing the two worst categories into value 2 and the two best categories into value 4. This action effectively has removed two cutpoints, but if the model fits the data, it should not affect the other two cutpoints. The comparison is hampered by a difference in the names of the cutpoints between the models, as illustrated in the figure below:



Cutpoint /cut2 of model H5 should be compared with cutpoint /cut1 of H3, and similarly, /cut3 of H5 with /cut2 of H3.

```
. test (/H5:cut2=/H3:cut1) (/H5:cut3=/H3:cut2)
Adjusted Wald test
( 1) [/H5]cut2 - [/H3]cut1 = 0
( 2) [/H5]cut3 - [/H3]cut2 = 0
F( 2, 30) = 33.49
Prob > F = 0.0000
```

We conclude that the invariance of the cutpoints under the collapse of categories is not supported by the data, again providing evidence against the reduced specification of the ordered logistic model in this case.

4

Example 9: Using suest with survey data, the svy option

Not all estimation commands support the svy prefix, but you can use the svy option with suest to get survey estimation results. If you can use suest after a command, you can use suest, svy. Here are the corresponding Stata commands to perform the analysis in the previous example, using the svy option instead of the svy prefix.

```
. use https://www.stata-press.com/data/r19/nhanes2f, clear
. svyset psuid [pw=finalwgt], strata(stratid)
. ologit health female black age c.age#c.age [iw=finalwgt]
. estimates store H5
. generate health3 = clip(health,2,4)
. ologit health3 female black age c.age#c.age [iw=finalwgt]
. estimates store H3
. suest H5 H3, svy
. test [H5_health=H3_health3]
. test (/H5:cut2=/H3:cut1) (/H5:cut3=/H3:cut2)
```

The calls to ologit now use iweights instead of the svy prefix, and the svy option was added to suest. No other changes are required.

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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

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