manova postestimation — Postestimation tools for manova

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Postestimation commands

The following postestimation commands are of special interest after manova:

Command	Description
manovatest	multivariate tests after manova
screeplot	plot eigenvalues

The following standard postestimation commands are also available:

Command	Description
contrast	contrasts and ANOVA-style joint tests of parameters
estat summarize	summary statistics for the estimation sample
estat vce	variance-covariance matrix of the estimators (VCE)
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 parameters
predict	predictions and their SEs, residuals, etc.
predictnl	point estimates, standard errors, testing, and inference for generalized predictions
pwcompare	pairwise comparisons of parameters
test	Wald tests of simple and composite linear hypotheses
testnl	Wald tests of nonlinear hypotheses

predict

Description for predict

predict creates a new variable containing predictions such as fitted values, standard errors, residuals, and differences between the linear predictions.

Menu for predict

Statistics > Postestimation

Syntax for predict

predict [type] newval	[<i>if</i>][<i>in</i>]	, equation(eqno[, eqn	no]) statistic]
-----------------------	----------------------------	-----------------------	-----------------

statistic	Description
Main	
xb	$\mathbf{x}_i \mathbf{b}$, fitted values; the default
stdp	standard error of the fitted value
<u>r</u> esiduals	residuals
difference	difference between the linear predictions of two equations
<u>stdd</u> p	standard error of the fitted values for differences

These statistics are available both in and out of sample; type predict ... if e(sample) ... if wanted only for the estimation sample.

Options for predict

Main

equation(eqno[, eqno]) specifies the equation to which you are referring.

equation() is filled in with one *eqno* for the xb, stdp, and residuals options. equation(#1) would mean that the calculation is to be made for the first equation (that is, for the first dependent variable), equation(#2) would mean the second, and so on. You could also refer to the equations by their names. equation(income) would refer to the equation named income and equation(hours), to the equation named hours.

If you do not specify equation(), results are the same as if you had specified equation(#1).

difference and stddp refer to between-equations concepts. To use these options, you must specify two equations, for example, equation(#1,#2) or equation(income,hours). When two equations must be specified, equation() is required. With equation(#1,#2), difference computes the prediction of equation(#1) minus the prediction of equation(#2).

xb, the default, calculates the fitted values—the prediction of $\mathbf{x}_i \mathbf{b}$ for the specified equation.

stdp calculates the standard error of the prediction for the specified equation (the standard error of the estimated expected value or mean for the observation's covariate pattern). The standard error of the prediction is also referred to as the standard error of the fitted value.

residuals calculates the residuals.

difference calculates the difference between the linear predictions of two equations in the system.

stddp calculates the standard error of the difference in linear predictions $(\mathbf{x}_{1j}\mathbf{b}-\mathbf{x}_{2j}\mathbf{b})$ between equations 1 and 2.

For more information on using predict after multiple-equation estimation commands, see [R] predict.

margins

Description for margins

margins estimates margins of responses for linear predictions, fitted values, and differences between the linear predictions.

Menu for margins

Statistics > Postestimation

Syntax for margins

margins [marginlist] [, options]						
margins [margin	nlist], predict(statistic) [predict(statistic)] [options]					
statistic	Description					
default	linear predictions for each equation					
xb	$\mathbf{x}_i \mathbf{b}$, fitted values					
<u>d</u> ifference	difference between the linear predictions of two equations					
<u>r</u> esiduals	not allowed with margins					
stdp	not allowed with margins					
<u>stdd</u> p	not allowed with margins					

xb defaults to the first equation.

Statistics not allowed with margins are functions of stochastic quantities other than e(b).

For the full syntax, see [R] margins.

manovatest

Description of manovatest

manovatest provides multivariate tests involving *terms* or linear combinations of the underlying design matrix from the most recently fit manova. The four multivariate test statistics are Wilks's lambda, Pillai's trace, Lawley–Hotelling trace, and Roy's largest root. The format of the output is similar to that shown by manova; see [MV] manova.

Menu for manovatest

 $\label{eq:statistics} Statistics > Multivariate analysis > MANOVA, multivariate regression, and related > Multivariate tests after MANOVA$

Syntax for manovatest

manovatest term [term ...] [/ term [term ...]] [, ytransform(matname)]

manovatest, test(matname) [ytransform(matname)]

manovatest, showorder

where term is a term from the termlist in the previously run manova.

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

Options for manovatest

ytransform (matname) specifies a matrix for transforming the y variables (the depvarlist from manova) as part of the test. The multivariate tests are based on $(AEA')^{-1}(AHA')$. By default, A is the identity matrix. ytransform() is how you specify an A matrix to be used in the multivariate tests. Specifying ytransform() provides the same results as first transforming the y variables with YA', where Y is the matrix formed by binding the y variables by column and A is the matrix stored in matname; then performing manova on the transformed y's; and finally running manovatest without ytransform().

The number of columns of *matname* must equal the number of variables in the *depvarlist* from manova. The number of rows must be less than or equal to the number of variables in the *depvarlist* from manova. *matname* should have columns in the same order as the *depvarlist* from manova. The column and row names of *matname* are ignored.

When ytransform() is specified, a listing of the transformations is presented before the table containing the multivariate tests. You should examine this table to verify that you have applied the transformation you desired.

test (*matname*) is required with the second syntax of manovatest. The rows of *matname* specify linear combinations of the underlying design matrix of the MANOVA that are to be jointly tested. The columns correspond to the underlying design matrix (including the constant if it has not been suppressed). The column and row names of *matname* are ignored.

A listing of the constraints imposed by the test() option is presented before the table containing the multivariate tests. You should examine this table to verify that you have applied the linear combinations you desired. Typing manovatest, showorder allows you to examine the ordering of the columns for the design matrix from the MANOVA.

showorder causes manovatest to list the definition of each column in the design matrix. showorder is not allowed with any other option or when *terms* are specified.

test

Description for test

In addition to the standard syntax of test (see [R] test), test after manova has two additionally allowed syntaxes; see below. test performs Wald tests of expressions involving the coefficients of the underlying regression model. Simple and composite linear hypotheses are possible.

Menu for test

Statistics > Multivariate analysis > MANOVA, multivariate regression, and related > Wald test after MANOVA

Syntax for test

In addition to the standard syntax of test (see [R] test), test after manova also allows the following.

<u>te</u> st, test(<i>matname</i>)	$[\underline{m}test[(opt)]]$] matvlc(<i>matname</i>)	syntax A
<u>te</u> st, <u>showord</u> er			syntax B

- syntax A test expression involving the coefficients of the underlying multivariate regression model; you provide information as a matrix
- syntax B show underlying order of design matrix, which is useful when constructing the *matname* argument of the test() option

Options for test

Main

test (*matname*) is required with syntax A of test. The rows of *matname* specify linear combinations of the underlying design matrix of the MANOVA that are to be jointly tested. The columns correspond to the underlying design matrix (including the constant if it has not been suppressed). The column and row names of *matname* are ignored.

A listing of the constraints imposed by the test() option is presented before the table containing the tests. You should examine this table to verify that you have applied the linear combinations you desired. Typing test, showorder allows you to examine the ordering of the columns for the design matrix from the MANOVA.

matname should have as many columns as the number of dependent variables times the number of columns in the basic design matrix. The design matrix is repeated for each dependent variable.

showorder causes test to list the definition of each column in the design matrix. showorder is not allowed with any other option.

Options

mtest[(opt)] specifies that tests be performed for each condition separately. opt specifies the method
for adjusting p-values for multiple testing. Valid values for opt are

<u>b</u> onferroni	Bonferroni's method
holm	Holm's method
<u>s</u> idak	Šidák's method
noadjust	no adjustment is to be made

Specifying mtest without an argument is equivalent to specifying mtest(noadjust).

The following option is available with test after manova but is not shown in the dialog box:

matvlc(*matname*), a programmer's option, saves the variance-covariance matrix of the linear combinations involved in the suite of tests. For the test of H_0 : $\mathbf{Lb} = \mathbf{c}$, what is returned in *matname* is \mathbf{LVL}' , where V is the estimated variance-covariance matrix of b.

Remarks and examples

Several postestimation tools are available after manova. We demonstrate these tools by extending examples 1, 2, 4, and 8 of [MV] manova.

Example 1: test and lincom

(1)

Example 1 of [MV] manova presented a balanced one-way MANOVA on the rootstock data.

```
. use https://www.stata-press.com/data/r19/rootstock
(Table 6.2. Rootstock data, Rencher and Christensen (2012))
. manova y1 y2 y3 y4 = rootstock
(output omitted)
```

test provides Wald tests on expressions involving the underlying coefficients of the model, and lincom provides linear combinations along with standard errors and confidence intervals.

.1443917

.2075001

If the equation portion of the expression is omitted, the first equation (first dependent variable) is assumed.

1.44

0.158

-.0838941

.4988943

The manovatest postestimation command provides multivariate tests of *terms* or linear combinations of the underlying design matrix from the most recent MANOVA model.

Example 2: manovatest

. manovatest group

In example 2 of [MV] manova, a one-way MANOVA on the metabolic dataset was shown.

```
. use https://www.stata-press.com/data/r19/metabolic
(Table 4.5. Metabolic comparisons of rabbits, Rencher (1998))
. manova y1 y2 = group
(output omitted)
```

manovatest can test *terms* from the preceding manova. Here we test the group term from our one-way MANOVA:

	W P	= Wilks' la = Pillai's	ambda trace	L = Lawley-Hotelling trace R = Roy's largest root					
Source	S	tatistic	df	F(df1,	df2) =	F	Prob>F	_	
group	W P L R	0.1596 1.2004 3.0096 1.5986	3	6.0 6.0 6.0 3.0	32.0 34.0 30.0 17.0	8.02 8.51 7.52 9.06	0.0000 0.0000 0.0001 0.0008	e a a u	
Residual			17					-	

e = exact, a = approximate, u = upper bound on F

Using manovatest to test model *terms* is not interesting here. It merely repeats information already presented by manova. Later we will see useful applications of *term* testing via manovatest.

manovatest can also be used to test linear combinations of the underlying design matrix of the MANOVA model. Whereas the MANOVA indicates that there are differences in the groups, it does not indicate the nature of those differences. Rencher discusses three linear contrasts of interest for this example: group one (the control) versus the rest, group four versus groups two and three, and group two versus group three. The test() option of manovatest allows us to test these hypotheses.

Because we did not use the noconstant option with our manova, the underlying parameterization of the design matrix has the last column corresponding to the constant in the model, whereas the first four columns correspond to the four groups of rabbits. The showorder option of manovatest illustrates this point. The tests on the three contrasts of interest follow.

```
. manovatest, showorder
Order of columns in the design matrix
1: (group==1)
2: (group==2)
3: (group==3)
4: (group==4)
5: _cons
. matrix c1 = (3,-1,-1,-1,0)
```

```
. manovatest, test(c1)
Test constraint
(1)
        3*1.group - 2.group - 3.group - 4.group = 0
                        W = Wilks' lambda
                                                 L = Lawley-Hotelling trace
                        P = Pillai's trace
                                                 R = Roy's largest root
              Source
                        Statistic
                                           df
                                                 F(df1,
                                                             df2) =
                                                                       F
                                                                           Prob>F
                       W
                           0.4063
                                            1
                                                   2.0
                                                            16.0
                                                                     11.69 0.0007 e
          manovatest
                       Ρ
                           0.5937
                                                   2.0
                                                            16.0
                                                                     11.69 0.0007 e
                       L
                           1.4615
                                                   2.0
                                                            16.0
                                                                     11.69 0.0007 e
                       R
                           1.4615
                                                   2.0
                                                            16.0
                                                                     11.69 0.0007 e
            Residual
                                           17
                        e = exact, a = approximate, u = upper bound on F
. matrix c2 = (0, -1, -1, 2, 0)
. manovatest, test(c2)
Test constraint
        -2.group - 3.group + 2*4.group = 0
(1)
                        W = Wilks' lambda
                                                 L = Lawley-Hotelling trace
                        P = Pillai's trace
                                                 R = Roy's largest root
                                                             df2) =
              Source
                        Statistic
                                           df
                                                 F(df1.
                                                                       F
                                                                           Prob>F
                           0.9567
                                                   2.0
                                                                      0.36 0.7018 e
          manovatest
                       W
                                            1
                                                            16.0
                       Ρ
                           0.0433
                                                   2.0
                                                            16.0
                                                                      0.36 0.7018 e
                       T.
                           0.0453
                                                   2.0
                                                            16.0
                                                                      0.36 0.7018 e
                       R.
                           0.0453
                                                   2.0
                                                            16.0
                                                                      0.36 0.7018 e
                                           17
            Residual
                        e = exact, a = approximate, u = upper bound on F
matrix c3 = (0, 1, -1, 0, 0)
. manovatest, test(c3)
Test constraint
(1)
        2.\text{group} - 3.\text{group} = 0
                        W = Wilks' lambda
                                                 L = Lawley-Hotelling trace
                        P = Pillai's trace
                                                 R = Roy's largest root
                        Statistic
                                           df
                                                 F(df1,
                                                             df2) =
                                                                       F
                                                                           Prob>F
              Source
          manovatest
                           0.4161
                                            1
                                                   2.0
                                                            16.0
                                                                     11.23 0.0009 e
                       W
                       Ρ
                           0.5839
                                                            16.0
                                                                     11.23 0.0009 e
                                                   2.0
                           1.4033
                                                   2.0
                                                            16.0
                                                                     11.23 0.0009 e
                       L
                       R
                           1.4033
                                                   2.0
                                                            16.0
                                                                     11.23 0.0009 e
            Residual
                                           17
```

e = exact, a = approximate, u = upper bound on F

Because there is only 1 degree of freedom for each of the hypotheses, the F tests are exact (and identical for the four multivariate methods). The first test indicates that the mean vector for the control group is significantly different from the mean vectors for the other three groups. The second test, with a p-value of 0.7018, fails to reject the null hypothesis that group four equals groups two and three. The third test, with a p-value of 0.0009, indicates differences between the mean vectors of groups two and three.

Rencher also tests using weighted orthogonal contrasts. manovatest can do these tests as well.

```
matrix c1w = (14, -7, -5, -2, 0)
. manovatest, test(c1w)
Test constraint
(1)
        14*1.group - 7*2.group - 5*3.group - 2*4.group = 0
                        W = Wilks' lambda
                                                L = Lawley-Hotelling trace
                        P = Pillai's trace
                                                R = Roy's largest root
                       Statistic
                                          df
                                                F(df1,
                                                            df2) =
                                                                     F
                                                                          Prob>F
              Source
          manovatest
                      W
                           0.3866
                                           1
                                                  2.0
                                                           16.0
                                                                   12.70 0.0005 e
                      Ρ
                                                  2.0
                                                           16.0
                                                                   12.70 0.0005 e
                           0.6134
                      L
                           1.5869
                                                  2.0
                                                           16.0
                                                                   12.70 0.0005 e
                      R
                           1.5869
                                                  2.0
                                                           16.0
                                                                   12.70 0.0005 e
            Residual
                                          17
                        e = exact, a = approximate, u = upper bound on F
matrix c2w = (0, -7, -5, 12, 0)
. manovatest, test(c2w)
Test constraint
        -7*2.group - 5*3.group + 12*4.group = 0
(1)
                        W = Wilks' lambda
                                                L = Lawley-Hotelling trace
                        P = Pillai's trace
                                                R = Roy's largest root
                       Statistic
                                          df
                                                F(df1.
                                                            df2) =
                                                                     F
                                                                          Prob>F
              Source
                           0.9810
                                                  2.0
                                                           16.0
                                                                    0.15 0.8580 e
          manovatest
                      W
                                           1
                      Ρ
                           0.0190
                                                           16.0
                                                  2.0
                                                                    0.15 0.8580 e
                      L
                           0.0193
                                                  2.0
                                                           16.0
                                                                    0.15 0.8580 e
                      R
                           0.0193
                                                  2.0
                                                           16.0
                                                                    0.15 0.8580 e
            Residual
                                          17
```

e = exact, a = approximate, u = upper bound on F

These two weighted contrasts do not lead to different conclusions compared with their unweighted counterparts.

Technical note

manovatest, test(*matname*) displays the linear combination (labeled "Test constraint") indicated by *matname*. You should examine this listing to make sure that the matrix you specify in test() provides the test you want.

The margins postestimation command provides, among other things, tables of predicted means and confidence intervals that are based on the most recently fit model.

Example 3: Margins, contrasts, and predictions

Example 4 of [MV] manova presented a two-way MANOVA model on the jaw data.

```
. use https://www.stata-press.com/data/r19/jaw
(Table 4.6. Two-way unbalanced data for fractures of the jaw, Rencher (1998))
. manova y1 y2 y3 = gender fracture gender#fracture
 (output omitted)
```

4

The interaction term, gender#fracture, was significant. margins may be used to examine the interaction; see [R] margins.

<pre>. margins gender#fracture, predict(equation(y1))</pre>					
Adjusted predictions	Number	of	obs	=	27
<pre>Expression: Linear prediction, predict(equation(y1))</pre>					

			Delta-method	l			
		Margin	std. err.	t	P> t	[95% conf	. interval]
	gender#						
	fracture						
	Male #						
One	compou	39.5	4.171386	9.47	0.000	30.82513	48.17487
	Male #						
Two	compou	26.875	3.612526	7.44	0.000	19.36234	34.38766
	Male #						
One	simple	45.16667	4.171386	10.83	0.000	36.49179	53.84154
	Female #						
One	compou	22	10.21777	2.15	0.043	.7509887	43.24901
	Female #						
Two	compou	30.75	5.108884	6.02	0.000	20.12549	41.37451
	Female #						
One	simple	36.5	7.225053	5.05	0.000	21.47468	51.52532

. margins gender#fracture, predict(equation(y2))

Adjusted predictions

Number of obs = 27

Expression: Linear prediction, predict(equation(y2))

		Margin	Delta-method std. err.	d t	P> t	[95% conf	. interval]
	gender# fracture Male #						
One	compou Male #	35.5	2.150966	16.50	0.000	31.02682	39.97318
Тwo	compou Male #	32.375	1.862791	17.38	0.000	28.50111	36.24889
One	simple Female #	36.16667	2.150966	16.81	0.000	31.69349	40.63984
One	compou Female #	56	5.268768	10.63	0.000	45.043	66.957
Two	compou Female #	33.25	2.634384	12.62	0.000	27.7715	38.7285
One	simple	33	3.725582	8.86	0.000	25.25223	40.74777

. margins gender#fracture, predict(equation(y3))
Adjusted predictions

Number of obs = 27

Expression: Linear prediction, predict(equation(y3))

		Margin	Delta-method std. err.	t	P> t	[95% conf	. interval]
	gender# fracture Male #						
One	compou Male #	61.16667	2.038648	30.00	0.000	56.92707	65.40627
Тwо	compou Male #	62.25	1.765521	35.26	0.000	58.5784	65.9216
One	simple Female #	58.16667	2.038648	28.53	0.000	53.92707	62.40627
One	compou Female #	43	4.993647	8.61	0.000	32.61514	53.38486
Two	compou Female #	64	2.496823	25.63	0.000	58.80757	69.19243
One	simple	63.5	3.531041	17.98	0.000	56.1568	70.8432

The first margins table shows the predicted mean (marginal mean), standard error, z statistic, p-value, and confidence interval of y1 (age of patient) for each combination of fracture and gender. The second and third margins tables provide this information for y2 (blood lymphocytes) and y3 (blood polymorphonuclears). These three tables of predictions are the same as those you would obtain from margins after running anova for each of the three dependent variables separately.

The predicted y2 value is larger than the predicted y3 value for females with one compound fracture. For the other five combinations of gender and fracture, the relationship is reversed. There is only 1 observation for the combination of female and one compound fracture.

There are nine possible contrasts if we contrast women with men for every fracture type and every dependent variable. We will use contrast to estimate all nine contrasts and apply Scheffé's adjustment for multiple comparisons.

. contrast gender@fracture#_eqns, mcompare(scheffe)
Contrasts of marginal linear predictions
Margins: asbalanced

	df	F	P>F	Scheffe P>F
gender@fracture# eqns				
One compound fracture 1	1	2.51	0.1278	0.9733
One compound fracture 2	1	12.98	0.0017	0.2333
One compound fracture 3	1	11.34	0.0029	0.3137
Two compound fractures 1	1	0.38	0.5424	1.0000
Two compound fractures 2	1	0.07	0.7889	1.0000
Two compound fractures 3	1	0.33	0.5732	1.0000
One simple fracture 1	1	1.08	0.3107	0.9987
One simple fracture 2	1	0.54	0.4698	0.9999
One simple fracture 3	1	1.71	0.2050	0.9929
Joint	9	2.57	0.0361	
Denominator	21			

Note: Scheffe-adjusted p-values are reported for tests on individual contrasts only.

	Number of comparisons
gender@fracture#_eqns	9

			Sche	effe
	Contrast	Std. err.	[95% conf.	interval]
One compound fracture 1 (Female vs base)	-17.5	11.03645	-68.42869	33.42869
One compound fracture 2 (Female vs base)	20.5	5.69092	-5.76126	46.76126
One compound fracture 3 (Female vs base)	-18.16667	5.393755	-43.05663	6.723297
Two compound fractures 1 (Female vs base)	3.875	6.257079	-24.99885	32.74885
Two compound fractures 2 (Female vs base)	.875	3.226449	-14.01373	15.76373
Two compound fractures 3 (Female vs base)	1.75	3.057972	-12.36128	15.86128
One simple fracture 1 (Female vs base)	-8.666667	8.342772	-47.16513	29.8318
One simple fracture 2 (Female vs base)	-3.166667	4.301931	-23.01831	16.68498
One simple fracture 3	5.333333	4.077296	-13.48171	24.14838

Women do not differ significantly from men in any of the nine comparisons.

Let's examine the residuals with the predict command:

- . predict y1res, residual equation(y1)
- . predict y2res, residual equation(y2)
- . predict y3res, residual equation(y3)
- . list gender fracture y1res y2res y3res

gender	fracture	y1res	y2res	y3res
Male	One compound fracture	2.5	5	1666667
Male	One compound fracture	2.5	7.5	-6.166667
Male	One compound fracture	8.5	5	2.833333
Male	One compound fracture	-4.5	-2.5	3.833333
Male	One compound fracture	-14.5	-4.5	2.833333
Male	One compound fracture	5.5	.5	-3.166667
Male	Two compound fractures	-3.875	-5.375	1.75
Male	Two compound fractures	-4.875	375	1.75
Male	Two compound fractures	-1.875	-2.375	1.75
Male	Two compound fractures	1.125	6.625	-6.25
Male	Two compound fractures	-2.875	-1.375	6.75
Male	Two compound fractures	25.125	-4.375	-2.25
Male	Two compound fractures	-9.875	-2.375	1.75
Male	Two compound fractures	-2.875	9.625	-5.25
Male	One simple fracture	-13.16667	.8333333	-4.166667
Male	One simple fracture	6.833333	-2.166667	3.833333
Male	One simple fracture	7.833333	8.833333	-7.166667
Male	One simple fracture	3.833333	-1.166667	1.833333
Male	One simple fracture	9.833333	-4.166667	1.833333
Male	One simple fracture	-15.16667	-2.166667	3.833333
Female	One compound fracture	0	0	-2.84e-14
Female	Two compound fractures	-8.75	-4.25	4
Female	Two compound fractures	7.25	-8.25	9
Female	Two compound fractures	-9.75	3.75	-5
Female	Two compound fractures	11.25	8.75	-8
Female	One simple fracture	6.5	-3	3.5
Female	One simple fracture	-6.5	3	-3.5
	gender Male Male Male Male Male Male Male Male	genderfractureMaleOne compound fractureMaleOne compound fractureMaleOne compound fractureMaleOne compound fractureMaleOne compound fractureMaleOne compound fracturesMaleTwo compound fracturesMaleOne simple fractureMaleOne simple fractureMaleOne simple fractureMaleOne simple fractureMaleOne simple fractureMaleOne compound fracturesFemaleTwo compound fracturesFemaleTwo compound fracturesFemaleOne compound fracturesFemaleTwo compound fracturesFemaleOne compound fracturesFemaleOne simple fractureFemaleOne simple fracturesFemaleOne simple fractures <td>genderfractureylresMaleOne compound fracture2.5MaleOne compound fracture2.5MaleOne compound fracture8.5MaleOne compound fracture-4.5MaleOne compound fracture-14.5MaleOne compound fractures-3.875MaleTwo compound fractures-3.875MaleTwo compound fractures-1.875MaleTwo compound fractures1.125MaleTwo compound fractures-2.875MaleTwo compound fractures-9.875MaleTwo compound fractures-2.875MaleTwo compound fractures-2.875MaleTwo compound fractures-2.875MaleTwo compound fractures-2.875MaleOne simple fracture-9.875MaleOne simple fractures-13.16667MaleOne simple fracture-13.16667MaleOne simple fracture0.833333MaleOne simple fracture-15.16667FemaleOne compound fractures7.25FemaleTwo compound fractures-9.75FemaleTwo compound fractures-9.75FemaleOne simple fracture-9.75FemaleOne simple fractures-9.75FemaleOne simple fractures-9.75FemaleOne simple fractures-9.75FemaleOne simple fractures-9.75FemaleOne simple fractures-9.75FemaleOne simple fra</td> <td>genderfracturey1resy2resMaleOne compound fracture2.55MaleOne compound fracture2.57.5MaleOne compound fracture8.55MaleOne compound fracture-4.5-2.5MaleOne compound fracture-4.5-4.5MaleOne compound fractures-3.875-5.375MaleTwo compound fractures-4.875375MaleTwo compound fractures-4.875-2.375MaleTwo compound fractures1.1256.625MaleTwo compound fractures1.125-4.375MaleTwo compound fractures-2.875-1.375MaleTwo compound fractures-9.875-2.375MaleTwo compound fractures-9.875-2.375MaleTwo compound fractures-2.8759.625MaleOne simple fracture-13.16667.833333MaleOne simple fracture7.833333-2.166667MaleOne simple fracture-15.16667-2.166667MaleOne simple fracture-8.75-4.25FemaleOne compound fractures-2.5-2.166667MaleOne simple fracture00FemaleOne compound fractures-2.5-3.75FemaleOne compound fractures-2.5-4.25FemaleOne compound fractures-2.5-4.25FemaleOne compound fractures-2.5-2.166667Female<td< td=""></td<></td>	genderfractureylresMaleOne compound fracture2.5MaleOne compound fracture2.5MaleOne compound fracture8.5MaleOne compound fracture-4.5MaleOne compound fracture-14.5MaleOne compound fractures-3.875MaleTwo compound fractures-3.875MaleTwo compound fractures-1.875MaleTwo compound fractures1.125MaleTwo compound fractures-2.875MaleTwo compound fractures-9.875MaleTwo compound fractures-2.875MaleTwo compound fractures-2.875MaleTwo compound fractures-2.875MaleTwo compound fractures-2.875MaleOne simple fracture-9.875MaleOne simple fractures-13.16667MaleOne simple fracture-13.16667MaleOne simple fracture0.833333MaleOne simple fracture-15.16667FemaleOne compound fractures7.25FemaleTwo compound fractures-9.75FemaleTwo compound fractures-9.75FemaleOne simple fracture-9.75FemaleOne simple fractures-9.75FemaleOne simple fractures-9.75FemaleOne simple fractures-9.75FemaleOne simple fractures-9.75FemaleOne simple fractures-9.75FemaleOne simple fra	genderfracturey1resy2resMaleOne compound fracture2.55MaleOne compound fracture2.57.5MaleOne compound fracture8.55MaleOne compound fracture-4.5-2.5MaleOne compound fracture-4.5-4.5MaleOne compound fractures-3.875-5.375MaleTwo compound fractures-4.875375MaleTwo compound fractures-4.875-2.375MaleTwo compound fractures1.1256.625MaleTwo compound fractures1.125-4.375MaleTwo compound fractures-2.875-1.375MaleTwo compound fractures-9.875-2.375MaleTwo compound fractures-9.875-2.375MaleTwo compound fractures-2.8759.625MaleOne simple fracture-13.16667.833333MaleOne simple fracture7.833333-2.166667MaleOne simple fracture-15.16667-2.166667MaleOne simple fracture-8.75-4.25FemaleOne compound fractures-2.5-2.166667MaleOne simple fracture00FemaleOne compound fractures-2.5-3.75FemaleOne compound fractures-2.5-4.25FemaleOne compound fractures-2.5-4.25FemaleOne compound fractures-2.5-2.166667Female <td< td=""></td<>

The single observation for a female with one compound fracture has residuals that are within roundoff of zero. With only 1 observation for that cell of the design, this MANOVA model is forced to fit to that point. The largest residual (in absolute value) appears for observation 12, which has an age 25.125 higher than the model prediction for a male with two compound fractures.

4

Example 4: manovatest

Example 8 of [MV] manova presents a nested MANOVA on the videotrainer data.

```
. use https://www.stata-press.com/data/r19/videotrainer, clear (Video training)
```

```
. manova primary extra = video / store|video / associate|store|video /,
```

```
> dropemptycells
```

```
(output omitted)
```

The MANOVA indicated that store was not significant.

.

You decide to follow the rule of thumb that says to pool terms whose *p*-values are larger than 0.25. Wilks's lambda reports a *p*-value of 0.5775 for the test of store | video (see example 8 of [MV] manova). You decide to pool the store and associate terms in the MANOVA to gain power for the test of video. The forward-slash notation of manova is also allowed with manovatest to indicate nonresidual error terms. Here is the multivariate test of video using the pooled store and associate terms and then the multivariate test of the pooled term:

mar	novatest video / :	stor	e video a	ssociate s	tore video				
		W P	= Wilks' = Pillai'	lambda s trace	L = Lawl R = Roy'	ey-Hotelli s largest	ng tra root	ace	
_	Source	St	atistic	df	F(df1,	df2) =	F	Prob>F	
_	video	W	0.4079	1	2.0	9.0	6.53	0.0177	е
		P	0.5921		2.0	9.0	6.53	0.0177	е
		L	1.4516		2.0	9.0	6.53	0.0177	е
		R	1.4516		2.0	9.0	6.53	0.0177	е
a	store video associate store video			10					_
mar	novatest store vi	e deo	= exact, associate	a = approx store vid	imate, u = eo	upper bou	nd on	F	
		W P	= Wilks' = Pillai'	lambda s trace	L = Lawl B = Boy'	ey-Hotelli s largest	ng tra	ace	
	Source	St	atistic	df	F(df1,	df2) =	F	Prob>F	
-	store video	W	0.3925	10	20.0	58.0	1.73	0.0546	_ e
a	associate store	P	0.7160		20.0	60.0	1.67	0.0647	a
	video	L	1.2711		20.0	56.0	1.78	0.0469	a
		R	0.9924		10.0	30.0	2.98	0.0100	u
_	Residual			30					_

e = exact, a = approximate, u = upper bound on F

Pooling store with associate helps increase the power for the test of video.

You can show the univariate analysis for one of your dependent variables by using the ytransform() option of manovatest:

<pre>mat primonly = (1,0)</pre>)						
manovatest video / s	store video as	ssociate st	ore video	, ytransfo	rm(pr:	imonly)	
Transformation of the (1) primary	e dependent va	ariables					
	W = Wilks' 1 P = Pillai's	Lambda s trace	L = Lawl R = Roy'	ey-Hotelli s largest	ng tra root	ace	
Source	Statistic	df	F(df1,	df2) =	F	Prob>F	
video	W 0.8449 P 0.1551 L 0.1835 R 0.1835	1	1.0 1.0 1.0 1.0	10.0 10.0 10.0 10.0	1.84 1.84 1.84 1.84	0.2053 0.2053 0.2053 0.2053	e e e
store video associate store video		10					
manovatest store vid Transformation of the (1) primary	e = exact, a deo associate e dependent va	a = approxi store vide ariables	mate, u = 20, ytrans	upper bou form(primo	nd on nly)	F	
(-) <u>F</u> j	W = Wilks' I P = Pillai's	lambda s trace	L = Lawl R = Roy'	ey-Hotelli s largest	ng tra root	ace	
Source	Statistic	df	F(df1,	df2) =	F	Prob>F	
store video associate store video	W 0.6119 P 0.3881 L 0.6344 R 0.6344	10	10.0 10.0 10.0 10.0	30.0 30.0 30.0 30.0	1.90 1.90 1.90 1.90	0.0846 0.0846 0.0846 0.0846	e e e e
Residual		30					_

e = exact, a = approximate, u = upper bound on F

See the second manova run from example 8 of [MV] manova for an alternate way of pooling the terms by refitting the MANOVA model.

See examples 6, 10, 11, 12, and 13 of [MV] **manova** for more examples of manovatest, including examples involving both the test() and the ytransform() options.

4

Stored results

Scalars r(df) hypothesis degrees of freedom r(df_r) residual degrees of freedom Matrices hypothesis SSCP matrix r(H) residual-error SSCP matrix r(E)multivariate statistics r(stat) eigenvalues of E⁻¹H r(eigvals) s, m, and n values r(aux)

manovatest stores the following in r():

test after manova stores the following in r():

Scalars	
r(p)	two-sided p-value
r(F)	F statistic
r(df)	hypothesis degrees of freedom
r(df_r)	residual degrees of freedom
r(drop)	0 if no constraints dropped, 1 otherwise
r(dropped_#)	index of #th constraint dropped
Macros	
r(mtmethod)	method of adjustment for multiple testing
Matrices	
r(mtest)	multiple test results

Methods and formulas

See [MV] manova for methods and formulas for the multivariate tests performed by manovatest.

Also see

- [MV] manova Multivariate analysis of variance and covariance
- [MV] screeplot Scree plot of eigenvalues
- [U] 20 Estimation and postestimation commands

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