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Description

`contrast` tests linear hypotheses and forms contrasts involving factor variables and their interactions from the most recently fit model. The tests include ANOVA-style tests of main effects, simple effects, interactions, and nested effects. `contrast` can use named contrasts to decompose these effects into comparisons against reference categories, comparisons of adjacent levels, comparisons against the grand mean, orthogonal polynomials, and such. Custom contrasts may also be specified.

`contrast` can be used with `svy` estimation results; see [\[SVY\]](#) [svy postestimation](#).

Contrasts can also be computed for margins of linear and nonlinear responses; see [\[R\]](#) [margins, contrast](#).

Quick start

Contrasts for one-way models

Test the main effect of categorical variable `a` after `regress y i.a` or `anova y a`

```
contrast a
```

Reference category contrasts of cell means of `y` with the smallest value of `a` as the base category

```
contrast r.a
```

Same as above, but specify `a = 3` as the base category for comparisons

```
contrast rb3.a
```

Report tests instead of confidence intervals for each contrast

```
contrast r.a, pveffects
```

Report tests and confidence intervals for each contrast

```
contrast r.a, effects
```

Contrasts of the cell mean of `y` for each level of `a` with the grand mean of `y`

```
contrast g.a
```

Same as above, but compute grand mean as a weighted average of cell means with weights based on the number of observations for each level of `a`

```
contrast gw.a
```

User-defined contrast comparing the cell mean of `y` for `a = 1` with the average of the cell means for `a = 3` and `a = 4`

```
contrast {a -1 0 .5 .5}
```

Contrasts for two-way models

Test of the interaction effect after `regress y a##b` or `anova y a##b`

```
contrast a#b
```

Test of the main and interaction effects

```
contrast a b a#b
```

Same as above

```
contrast a##b
```

Individual reference category contrasts for the interaction of a and b

```
contrast r.a#r.b
```

Joint tests of the simple effects of a within each level of b

```
contrast a@b
```

Individual reference category contrasts for the simple effects of a within each level of b

```
contrast r.a@b
```

Orthogonal polynomial contrasts for a within each level of b

```
contrast p.a@b
```

Reference category contrasts of the marginal means of y for levels of a

```
contrast r.a
```

Same as above, but with marginal means for a computed as a weighted average of cell means, using the marginal frequencies of b rather than equal weights for each level

```
contrast r.a, asobserved
```

Contrasts of the marginal mean of y for each level of a with the previous level—reverse-adjacent contrasts

```
contrast ar.a
```

Contrasts for models with continuous covariates

Test of the interaction effect after `regress y a##c.x` or `anova y a##c.x`

```
contrast a#c.x
```

Reference category effects of a on the slope of x

```
contrast r.a#c.x
```

Reference category effects of a on the intercept

```
contrast r.a
```

Contrasts for nonlinear models

Orthogonal polynomial contrasts of log odds across levels of a after `logit y i.a`
`contrast p.a`

Test the main and interaction effects after `logit y a##b`
`contrast a##b`

Simple reference category effects for a within each level of b
`contrast r.a@b`

Contrasts for multiple-equation models

Test the main and interaction effects in the equation for y2 after `mvreg y1 y2 y3 = a##b`
`contrast a##b, equation(y2)`

Reference category contrasts of estimated marginal means of y3 for levels of a
`contrast r.a, equation(y3)`

Test for a difference in the overall estimated marginal means of y1, y2, and y3
`contrast _eqns`

Contrasts of estimated marginal means of y2 and y3 with y1
`contrast r._eqns`

Test whether interaction effects differ across equations
`contrast a#b#_eqns`

Menu

Statistics > Postestimation

Syntax

```
contrast termlist [ , options ]
```

where *termlist* is a list of factor variables or interactions that appear in the current estimation results. The variables may be typed with or without [contrast operators](#), and you may use any factor-variable syntax:

See the [operators \(op.\)](#) table below for the list of contrast operators.

<i>options</i>	Description
Main	
<code><u>overall</u></code>	add a joint hypothesis test for all specified contrasts
<code><u>asobserved</u></code>	treat all factor variables as observed
<code><u>lincom</u></code>	treat user-defined contrasts as linear combinations
Equations	
<code><u>equation</u>(<i>eqspec</i>)</code>	perform contrasts in <i>termlist</i> for equation <i>eqspec</i>
<code><u>atequations</u></code>	perform contrasts in <i>termlist</i> within each equation
Advanced	
<code><u>emptycells</u>(<i>empspec</i>)</code>	treatment of empty cells for balanced factors
<code><u>noestimcheck</u></code>	suppress estimability checks
Reporting	
<code><u>level</u>(#)</code>	confidence level; default is <code>level(95)</code>
<code><u>mcompare</u>(<i>method</i>)</code>	adjust for multiple comparisons; default is <code>mcompare(noadjust)</code>
<code><u>noeffects</u></code>	suppress table of individual contrasts
<code><u>cieffects</u></code>	show effects table with confidence intervals
<code><u>pveffects</u></code>	show effects table with <i>p</i> -values
<code><u>effects</u></code>	show effects table with confidence intervals and <i>p</i> -values
<code><u>nowald</u></code>	suppress table of Wald tests
<code><u>noatlevels</u></code>	report only the overall Wald test for terms that use the within @ or nested operator
<code><u>nosvyadjust</u></code>	compute unadjusted Wald tests for survey results
<code><u>sort</u></code>	sort the individual contrast values in each term
<code><u>post</u></code>	post contrasts and their VCEs as estimation results
<code><u>display_options</u></code>	control column formats, row spacing, line width, and factor-variable labeling
<code><u>eform_option</u></code>	report exponentiated contrasts
<code><u>df</u>(#)</code>	use <i>t</i> distribution with # degrees of freedom for computing <i>p</i> -values and confidence intervals

`collect` is allowed; see [\[U\] 11.1.10 Prefix commands](#).

`df(#)` does not appear in the dialog box.

Term	Description
Main effects	
A	joint test of the main effects of A
$r.A$	individual contrasts that decompose A using r .
Interaction effects	
A#B	joint test of the two-way interaction effects of A and B
A#B#C	joint test of the three-way interaction effects of A, B, and C
$r.A\#g.B$	individual contrasts for each interaction of A and B defined by r . and g .
Partial interaction effects	
$r.A\#B$	joint tests of interactions of A and B within each contrast defined by $r.A$
$A\#r.B$	joint tests of interactions of A and B within each contrast defined by $r.B$
Simple effects	
A@B	joint tests of the effects of A within each level of B
A@B#C	joint tests of the effects of A within each combination of the levels of B and C
$r.A@B$	individual contrasts of A that decompose A@B using r .
$r.A@B\#C$	individual contrasts of A that decompose A@B#C using r .
Other conditional effects	
A#B@C	joint tests of the interaction effects of A and B within each level of C
A#B@C#D	joint tests of the interaction effects of A and B within each combination of the levels of C and D
$r.A\#g.B@C$	individual contrasts for each interaction of A and B that decompose A#B@C using r . and g .
Nested effects	
A B	joint tests of the effects of A nested in each level of B
A B#C	joint tests of the effects of A nested in each combination of the levels of B and C
A#B C	joint tests of the interaction effects of A and B nested in each level of C
A#B C#D	joint tests of the interaction effects of A and B nested in each combination of the levels of C and D
$r.A B$	individual contrasts of A that decompose A B using r .
$r.A B\#C$	individual contrasts of A that decompose A B#C using r .
$r.A\#g.B C$	individual contrasts for each interaction of A and B defined by r . and g . nested in each level of C
Slope effects	
A#c.x	joint test of the effects of A on the slopes of x
A#c.x#c.y	joint test of the effects of A on the slopes of the product (interaction) of x and y
A#B#c.x	joint test of the interaction effects of A and B on the slopes of x
A#B#c.x#c.y	joint test of the interaction effects of A and B on the slopes of the product (interaction) of x and y
$r.A\#c.x$	individual contrasts of A's effects on the slopes of x using r .
Denominators	
$\dots / term2$	use <i>term2</i> as the denominator in the F tests of the preceding terms
$\dots /$	use the residual as the denominator in the F tests of the preceding terms (the default if no other /s are specified)

A, B, C, and D represent any factor variable in the current estimation results.

x and y represent any continuous variable in the current estimation results.

r. and g. represent any contrast operator. See the table [below](#).

c. specifies that a variable be treated as continuous; see [\[U\] 11.4.3 Factor variables](#).

Operators are allowed on any factor variable that does not appear to the right of @ or |. Operators decompose the effects of the associated factor variable into one-degree-of-freedom effects (contrasts).

Higher-level interactions are allowed anywhere an interaction operator (#) appears in the table.

Time-series operators are allowed if they were used in the estimation.

_eqns designates the equations in [manova](#), [mlogit](#), [mprobit](#), and [mvreg](#) and can be specified anywhere a factor variable appears.

/ is allowed only after [anova](#), [cnsreg](#), [manova](#), [mvreg](#), or [regress](#).

<i>operators (op.)</i>	Description
r.	differences from the reference (base) level; the default
a.	differences from the next level (adjacent contrasts)
ar.	differences from the previous level (reverse adjacent contrasts)
As-balanced operators	
g.	differences from the balanced grand mean
h.	differences from the balanced mean of subsequent levels (Helmert contrasts)
j.	differences from the balanced mean of previous levels (reverse Helmert contrasts)
p.	orthogonal polynomial in the level values
q.	orthogonal polynomial in the level sequence
As-observed operators	
gw.	differences from the observation-weighted grand mean
hw.	differences from the observation-weighted mean of subsequent levels
jw.	differences from the observation-weighted mean of previous levels
pw.	observation-weighted orthogonal polynomial in the level values
qw.	observation-weighted orthogonal polynomial in the level sequence

One or more individual contrasts may be selected by using the *op#.* or *op(numlist)* . syntax. For example, *a3.A* selects the adjacent contrast for level 3 of A, and *p(1/2).B* selects the linear and quadratic effects of B. Also see [Orthogonal polynomial contrasts](#) and [Beyond linear models](#).

Custom contrasts	Description
{A <i>numlist</i> }	user-defined contrast on the levels of factor A
{A#B <i>numlist</i> }	user-defined contrast on the levels of interaction between A and B

Custom contrasts may be part of a term, such as {A *numlist*}#B, {A *numlist*}@B, {A *numlist*}|B, {A#B *numlist*}, and {A *numlist*}#{B *numlist*}. The same is true of higher-order custom contrasts, such as {A#B *numlist*}@C, {A#B *numlist*}#r.C, and {A#B *numlist*}#c.x.

Higher-order interactions with at most eight factor variables are allowed with custom contrasts.

method	Description
noadjust	do not adjust for multiple comparisons; the default
<u>bonferroni</u> [adjustall]	Bonferroni's method; adjust across all terms
<u>sidak</u> [adjustall]	Šidák's method; adjust across all terms
<u>scheffe</u>	Scheffé's method

Options

Main

- `overall` specifies that a joint hypothesis test over all terms be performed.
- `asobserved` specifies that factor covariates be evaluated using the cell frequencies observed in the estimation sample. The default is to treat all factor covariates as though there were an equal number of observations in each level.
- `lincom` specifies that user-defined contrasts be treated as linear combinations. The default is to require that all user-defined contrasts sum to zero. (Summing to zero is part of the definition of a contrast.)

Equations

- `equation(eqspec)` specifies the equation from which contrasts are to be computed. The default is to compute contrasts from the first equation.
- `atequations` specifies that the contrasts be computed within each equation.

Advanced

- `emptycells(empspec)` specifies how empty cells are handled in interactions involving factor variables that are being treated as balanced.
 - `emptycells(strict)` is the default; it specifies that contrasts involving empty cells be treated as not estimable.
 - `emptycells(reweight)` specifies that the effects of the observed cells be increased to accommodate any missing cells. This makes the contrast estimable but changes its interpretation.
- `noestimcheck` specifies that contrast not check for estimability. By default, the requested contrasts are checked and those found not estimable are reported as such. Nonestimability is usually caused by empty cells. If `noestimcheck` is specified, estimates are computed in the usual way and reported even though the resulting estimates are manipulable, which is to say they can differ across equivalent models having different parameterizations.

Reporting

- `level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [\[U\] 20.8 Specifying the width of confidence intervals](#).
- `mcompare(method)` specifies the method for computing *p*-values and confidence intervals that account for multiple comparisons within a factor-variable term.
 - Most methods adjust the comparisonwise error rate, α_c , to achieve a prespecified experimentwise error rate, α_e .

`mcompare(noadjust)` is the default; it specifies no adjustment.

$$\alpha_c = \alpha_e$$

`mcompare(bonferroni)` adjusts the comparisonwise error rate based on the upper limit of the Bonferroni inequality

$$\alpha_e \leq m\alpha_c$$

where m is the number of comparisons within the term.

The adjusted comparisonwise error rate is

$$\alpha_c = \alpha_e / m$$

`mcompare(sidak)` adjusts the comparisonwise error rate based on the upper limit of the probability inequality

$$\alpha_e \leq 1 - (1 - \alpha_c)^m$$

where m is the number of comparisons within the term.

The adjusted comparisonwise error rate is

$$\alpha_c = 1 - (1 - \alpha_e)^{1/m}$$

This adjustment is exact when the m comparisons are independent.

`mcompare(scheffe)` controls the experimentwise error rate using the F or χ^2 distribution with degrees of freedom equal to the rank of the term.

`mcompare(method adjustall)` specifies that the multiple-comparison adjustments count all comparisons across all terms rather than performing multiple comparisons term by term. This leads to more conservative adjustments when multiple variables or terms are specified in *marginslist*. This option is compatible only with the `bonferroni` and `sidak` methods.

`noeffects` suppresses the table of individual contrasts with confidence intervals. This table is produced by default when the `mcompare()` option is specified or when a term in *termlist* implies all individual contrasts.

`cieffects` specifies that a table containing a confidence interval for each individual contrast be reported.

`pveffects` specifies that a table containing a p -value for each individual contrast be reported.

`effects` specifies that a single table containing a confidence interval and p -value for each individual contrast be reported.

`nowald` suppresses the table of Wald tests.

`noatlevels` indicates that only the overall Wald test be reported for each term containing within or nested (@ or |) operators.

`nosvyadjust` is for use with `svy` estimation commands. It specifies that the Wald test be carried out without the default adjustment for the design degrees of freedom. That is to say the test is carried out as $W/k \sim F(k, d)$ rather than as $(d - k + 1)W/(kd) \sim F(k, d - k + 1)$, where k is the dimension of the test and d is the total number of sampled PSUs minus the total number of strata.

`sort` specifies that the table of individual contrasts be sorted by the contrast values within each term.

post causes contrast to behave like a Stata estimation (`e-class`) command. `contrast` posts the vector of estimated contrasts along with the estimated variance–covariance matrix to `e()`, so you can treat the estimated contrasts just as you would results from any other estimation command. For example, you could use `test` to perform simultaneous tests of hypotheses on the contrasts, or you could use `lincom` to create linear combinations.

display_options: `vsquish`, `nofvlabel`, `fvwrap(#)`, `fvwrapon(style)`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`.

`vsquish` specifies that the blank space separating factor-variable terms or time-series–operated variables from other variables in the model be suppressed.

`nofvlabel` displays factor-variable level values rather than attached value labels. This option overrides the `fvlabel` setting; see [R] [set showbaselevels](#).

`fvwrap(#)` specifies how many lines to allow when long value labels must be wrapped. Labels requiring more than `#` lines are truncated. This option overrides the `fvwrap` setting; see [R] [set showbaselevels](#).

`fvwrapon(style)` specifies whether value labels that wrap will break at word boundaries or break based on available space.

`fvwrapon(word)`, the default, specifies that value labels break at word boundaries.

`fvwrapon(width)` specifies that value labels break based on available space.

This option overrides the `fvwrapon` setting; see [R] [set showbaselevels](#).

`cformat(%fmt)` specifies how to format contrasts, standard errors, and confidence limits in the table of estimated contrasts.

`pformat(%fmt)` specifies how to format *p*-values in the table of estimated contrasts.

`sformat(%fmt)` specifies how to format test statistics in the table of estimated contrasts.

`nolstretch` specifies that the width of the table of estimated contrasts not be automatically widened to accommodate longer variable names. The default, `lstretch`, is to automatically widen the table of estimated contrasts up to the width of the Results window. Specifying `lstretch` or `nolstretch` overrides the setting given by [set lstretch](#). If `set lstretch` has not been set, the default is `lstretch`. `nolstretch` is not shown in the dialog box.

eform_option specifies that the contrasts table be displayed in exponentiated form. e^{contrast} is displayed rather than contrast. Standard errors and confidence intervals are also transformed. See [R] [eform_option](#) for the list of available options.

The following option is available with `contrast` but is not shown in the dialog box:

`df(#)` specifies that the *t* distribution with `#` degrees of freedom be used for computing *p*-values and confidence intervals. The default is to use `e(df_r)` degrees of freedom or the standard normal distribution if `e(df_r)` is missing.

Remarks and examples

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Introduction

`contrast` performs ANOVA-style tests of main effects, interactions, simple effects, and nested effects. It can easily decompose these tests into constituent contrasts using either named contrasts (codings) or user-specified contrasts. Comparing levels of factor variables—whether as main effects, interactions, or simple effects—is as easy as adding a contrast operator to the variable. The operators can compare each level with the previous level, each level with a reference level, each level with the mean of previous levels, and more.

`contrast` tests and estimates contrasts. A contrast of the parameters $\mu_1, \mu_2, \dots, \mu_p$ is a linear combination $\sum_i c_i \mu_i$ whose c_i sum to zero. A difference of population means such as $\mu_1 - \mu_2$ is a contrast, as are most other comparisons of population or model quantities (Coster 2005). Some contrasts may be estimated with `lincom`, but `contrast` is much more powerful. `contrast` can handle multiple contrasts simultaneously, and the command's contrast operators make it easy to specify complicated linear combinations.

Both the contrast operation and the creation of the margins for comparison can be performed as though the data were balanced (typical for experimental designs) or using the observed frequencies in the estimation sample (typical for observational studies). `contrast` can perform these analyses on the results of almost all of Stata's estimators, not just the linear-models estimators.

Most of `contrast`'s computations can be considered comparisons of estimated cell means from a model fit. Tests of interactions are tests of whether the cell means for the interaction are all equal. Tests of main effects are tests of whether the marginal cell means for the factor are all equal. More focused comparisons of cell means (for example, is level 2 equal to level 1) are specified using contrast operators. More formally, all of `contrast`'s computations are comparisons of conditional expectations; cell means are one type of conditional expectation.

All contrasts can also easily be graphed; see [\[R\] marginsplot](#).

For a discussion of contrasts and testing for linear models, see [Searle and Gruber \(2017\)](#) and [Searle \(1997\)](#). For discussions specifically related to experimental design, see [Winer, Brown, and Michels \(1991\)](#) and [Milliken and Johnson \(2009\)](#). [Rosenthal, Rosnow, and Rubin \(2000\)](#) focus on contrasts with applications in behavioral sciences. [Mitchell \(2021, 2015\)](#) and [Baldwin \(2019\)](#) focus on contrasts in Stata.

`contrast` is a flexible tool for understanding the effects of categorical covariates. If your model contains categorical covariates, and especially if it contains interactions, you will want to use `contrast`.

One-way models

Suppose we have collected data on cholesterol levels for individuals from five age groups. To study the effect of age group on cholesterol, we can begin by fitting a one-way model using `regress`:

```
. use https://www.stata-press.com/data/r19/cholesterol
(Artificial cholesterol data)
```

```
. label list ages
ages:
```

```
1 10-19
2 20-29
3 30-39
4 40-59
5 60-79
```

```
. regress chol i.agegrp
```

Source	SS	df	MS	Number of obs	=	75
Model	14943.3997	4	3735.84993	F(4, 70)	=	35.02
Residual	7468.21971	70	106.68853	Prob > F	=	0.0000
				R-squared	=	0.6668
				Adj R-squared	=	0.6477
Total	22411.6194	74	302.859722	Root MSE	=	10.329

chol	Coefficient	Std. err.	t	P> t	[95% conf. interval]	
agegrp						
20-29	8.203575	3.771628	2.18	0.033	.6812991	15.72585
30-39	21.54105	3.771628	5.71	0.000	14.01878	29.06333
40-59	30.15067	3.771628	7.99	0.000	22.6284	37.67295
60-79	38.76221	3.771628	10.28	0.000	31.23993	46.28448
_cons	180.5198	2.666944	67.69	0.000	175.2007	185.8388

Estimated cell means

margins will show us the estimated cell means for each age group based on our fitted model:

```
. margins agegrp
```

Adjusted predictions

Number of obs = 75

Model VCE: OLS

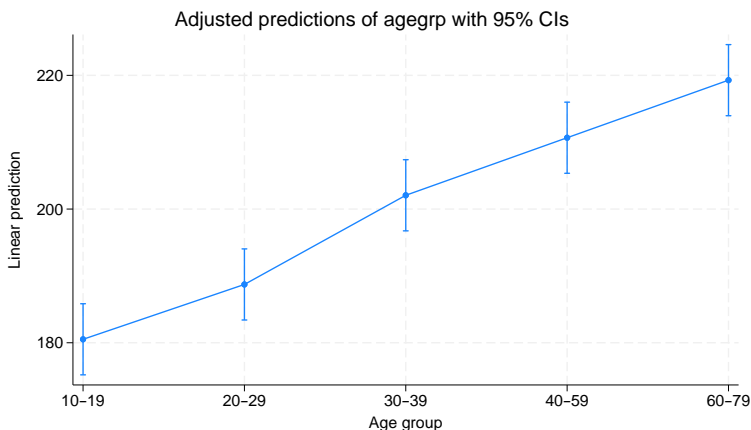
Expression: Linear prediction, predict()

	Delta-method				[95% conf. interval]	
	Margin	std. err.	t	P> t		
agegrp						
10-19	180.5198	2.666944	67.69	0.000	175.2007	185.8388
20-29	188.7233	2.666944	70.76	0.000	183.4043	194.0424
30-39	202.0608	2.666944	75.76	0.000	196.7418	207.3799
40-59	210.6704	2.666944	78.99	0.000	205.3514	215.9895
60-79	219.282	2.666944	82.22	0.000	213.9629	224.601

We can graph those means with marginsplot:

```
. marginsplot
```

Variables that uniquely identify margins: **agegrp**



Testing equality of cell means

Are all the means equal? That is to say is there an effect of age group on cholesterol level? We can answer that by asking contrast to test whether the means of the age groups are identical.

```
. contrast agegrp
```

Contrasts of marginal linear predictions

Margins: asbalanced

	df	F	P>F
agegrp	4	35.02	0.0000
Denominator	70		

The means are clearly different. We could have obtained this same test directly had we fit our model using `anova` rather than `regress`.

```
. anova chol agegrp
```

Number of obs = 75					
R-squared = 0.6668					
Root MSE = 10.329					
Adj R-squared = 0.6477					
Source	Partial SS	df	MS	F	Prob>F
Model	14943.4	4	3735.8499	35.02	0.0000
agegrp	14943.4	4	3735.8499	35.02	0.0000
Residual	7468.2197	70	106.68885		
Total	22411.619	74	302.85972		

Achieving a more direct test result is why we recommend using `anova` instead of `regress` for models where our focus is on the categorical covariates. The models fit by `anova` and `regress` are identical; they merely parameterize the effects differently. The results of `contrast` will be identical regardless of which command is used to fit the model. If, however, we were fitting models whose responses are nonlinear functions of the covariates, such as logistic regression, then there would be no analogue to `anova`, and we would appreciate `contrast`'s ability to quickly test main effects and interactions.

Reference category contrasts

Now that we know that the overall effect of age group is statistically significant, we can explore the effects of each age group. One way to do that is to use the reference category operator, `r.:`

```
. contrast r.agegrp
```

Contrasts of marginal linear predictions

Margins: asbalanced

	df	F	P>F
agegrp			
(20-29 vs 10-19)	1	4.73	0.0330
(30-39 vs 10-19)	1	32.62	0.0000
(40-59 vs 10-19)	1	63.91	0.0000
(60-79 vs 10-19)	1	105.62	0.0000
Joint	4	35.02	0.0000
Denominator	70		

	Contrast	Std. err.	[95% conf. interval]	
agegrp				
(20-29 vs 10-19)	8.203575	3.771628	.6812991	15.72585
(30-39 vs 10-19)	21.54105	3.771628	14.01878	29.06333
(40-59 vs 10-19)	30.15067	3.771628	22.6284	37.67295
(60-79 vs 10-19)	38.76221	3.771628	31.23993	46.28448

The cell mean of each age group is compared against the base age group (ages 10–19). The first table shows that each difference is significant. The second table gives an estimate and confidence interval for each contrast. These are the comparisons that linear regression gives with a factor covariate and no interactions. The contrasts are identical to the coefficients from our linear regression.

Reverse adjacent contrasts

We have far more flexibility with `contrast`. Age group is ordinal, so it is interesting to compare each age group with the preceding age group (rather than against one reference group). We specify that analysis by using the reverse adjacent operator, `ar`:

```
. contrast ar.agegrp
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
agegrp			
(20–29 vs 10–19)	1	4.73	0.0330
(30–39 vs 20–29)	1	12.51	0.0007
(40–59 vs 30–39)	1	5.21	0.0255
(60–79 vs 40–59)	1	5.21	0.0255
Joint	4	35.02	0.0000
Denominator	70		

	Contrast	Std. err.	[95% conf. interval]	
agegrp				
(20–29 vs 10–19)	8.203575	3.771628	.6812991	15.72585
(30–39 vs 20–29)	13.33748	3.771628	5.815204	20.85976
(40–59 vs 30–39)	8.60962	3.771628	1.087345	16.1319
(60–79 vs 40–59)	8.611533	3.771628	1.089257	16.13381

The 20–29 age group’s cholesterol level is 8.2 points higher than the 10–19 age group’s cholesterol level; the 30–39 age group’s level is 13.3 points higher than the 20–29 age group’s level; and so on. Each age group is statistically different from the preceding age group at the 5% level.

Orthogonal polynomial contrasts

The relationship between age group and cholesterol level looked almost linear in our graph. We can examine that relationship further by using the orthogonal polynomial operator, `p`:

```
. contrast p.agegrp, noeffects
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
agegrp			
(linear)	1	139.11	0.0000
(quadratic)	1	0.15	0.6962
(cubic)	1	0.37	0.5448
(quartic)	1	0.43	0.5153
Joint	4	35.02	0.0000
Denominator	70		

Only the linear effect is statistically significant.

We can even perform the joint test that all effects beyond linear are zero. We do that by selecting all polynomial contrasts above linear—that is, polynomial contrasts 2, 3, and 4.

```
. contrast p(2 3 4).agegrp, noeffects
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
agegrp			
(quadratic)	1	0.15	0.6962
(cubic)	1	0.37	0.5448
(quartic)	1	0.43	0.5153
Joint	3	0.32	0.8129
Denominator	70		

The joint test has three degrees of freedom and is clearly insignificant. A linear effect of age group seems adequate for this model.

Two-way models

Suppose we are investigating the effects of different dosages of a blood pressure medication and believe that the effects may be different for men and women. We can fit the following ANOVA model for `bpchange`, the change in diastolic blood pressure. Change is defined as the after measurement minus the before measurement, so that negative values of `bpchange` correspond to decreases in blood pressure.

```
. use https://www.stata-press.com/data/r19/bpchange
(Artificial blood pressure data)
. label list gender
gender:
      1 Male
      2 Female
. anova bpchange dose##gender
```

	Number of obs =	30	R-squared =	0.9647	
	Root MSE =	1.4677	Adj R-squared =	0.9573	
Source	Partial SS	df	MS	F	Prob>F
Model	1411.9087	5	282.38174	131.09	0.0000
dose	963.48179	2	481.7409	223.64	0.0000
gender	355.11882	1	355.11882	164.85	0.0000
dose#gender	93.308093	2	46.654046	21.66	0.0000
Residual	51.699253	24	2.1541355		
Total	1463.608	29	50.46924		

Estimated interaction cell means

Everything is significant, including the interaction. So increasing dosage is effective and differs by gender. Let's explore the effects. First, let's look at the estimated cell mean of blood pressure change for each combination of gender and dosage.

```
. margins dose#gender
Adjusted predictions                                Number of obs = 30
Expression: Linear prediction, predict()
```

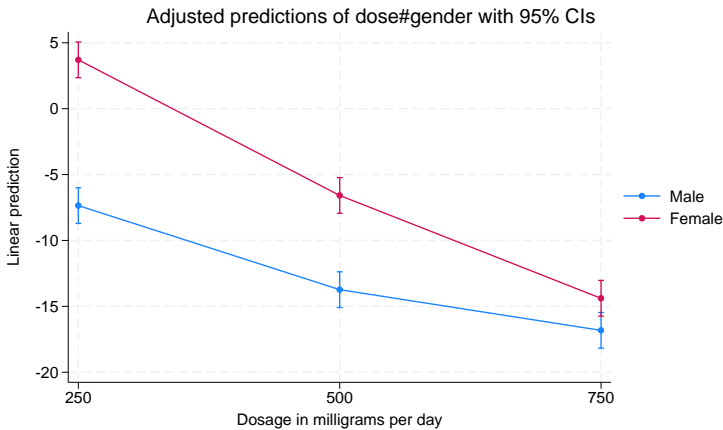
	Delta-method					
	Margin	std. err.	t	P> t	[95% conf. interval]	
dose#gender						
250#Male	-7.35384	.6563742	-11.20	0.000	-8.708529	-5.99915
250#Female	3.706567	.6563742	5.65	0.000	2.351877	5.061257
500#Male	-13.73386	.6563742	-20.92	0.000	-15.08855	-12.37917
500#Female	-6.584167	.6563742	-10.03	0.000	-7.938857	-5.229477
750#Male	-16.82108	.6563742	-25.63	0.000	-18.17576	-15.46639
750#Female	-14.38795	.6563742	-21.92	0.000	-15.74264	-13.03326

Our data are balanced, so these results will not be affected by the many different ways that margins can compute cell means. Moreover, because our model consists of only dose and gender, these are also the point estimates for each combination.

We can graph the results:

```
. marginsplot
```

Variables that uniquely identify margins: **dose gender**



The lines are not parallel, which we expected because the interaction term is significant. Males experience a greater decline in blood pressure at every dosage level, but the effect of increasing dosage is greater for females. In fact, it is not clear if we can tell the difference between male and female response at the maximum dosage.

Simple effects

We can contrast the male and female responses within dosage to see the simple effects of gender. Because there are only two levels in gender, the choice of contrast operator is largely irrelevant. Aside from orthogonal polynomials, all operators produce the same estimates, although the effects can change signs.

```
. contrast r.gender@dose
```

Contrasts of marginal linear predictions

Margins: asbalanced

	df	F	P>F
gender@dose			
(Female vs Male) 250	1	141.97	0.0000
(Female vs Male) 500	1	59.33	0.0000
(Female vs Male) 750	1	6.87	0.0150
Joint	3	69.39	0.0000
Denominator	24		

	Contrast	Std. err.	[95% conf. interval]	
gender@dose				
(Female vs Male) 250	11.06041	.9282533	9.144586	12.97623
(Female vs Male) 500	7.149691	.9282533	5.23387	9.065512
(Female vs Male) 750	2.433124	.9282533	.5173031	4.348944

The effect for females is about 11 points higher than for males at a dosage of 250, and that shrinks to 2.4 points higher at the maximum dosage of 750.

We can form the simple effects the other way by contrasting the effect of dose at each level of gender:

```
. contrast ar.dose@gender
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
dose@gender			
(500 vs 250) Male	1	47.24	0.0000
(500 vs 250) Female	1	122.90	0.0000
(750 vs 500) Male	1	11.06	0.0028
(750 vs 500) Female	1	70.68	0.0000
Joint	4	122.65	0.0000
Denominator	24		

	Contrast	Std. err.	[95% conf. interval]	
dose@gender				
(500 vs 250) Male	-6.380018	.9282533	-8.295839	-4.464198
(500 vs 250) Female	-10.29073	.9282533	-12.20655	-8.374914
(750 vs 500) Male	-3.087217	.9282533	-5.003038	-1.171396
(750 vs 500) Female	-7.803784	.9282533	-9.719605	-5.887963

Here we use the `ar.` reverse adjacent contrast operator so that first we are comparing a dosage of 500 with a dosage of 250, and then we are comparing 750 with 500. We see that increasing the dosage has a larger effect on females—10.3 points when going from 250 to 500 compared with 6.4 points for males, and 7.8 points when going from 500 to 750 versus 3.1 points for males.

Interaction effects

By specifying contrast operators on both factors, we can decompose the interaction effect into separate interaction contrasts.

```
. contrast ar.dose#r.gender
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
dose#gender			
(500 vs 250) (Female vs Male)	1	8.87	0.0065
(750 vs 500) (Female vs Male)	1	12.91	0.0015
Joint	2	21.66	0.0000
Denominator	24		

	Contrast	Std. err.	[95% conf. interval]	
dose#gender				
(500 vs 250)				
(Female vs Male)	-3.910716	1.312748	-6.620095	-1.201336
(750 vs 500)				
(Female vs Male)	-4.716567	1.312748	-7.425947	-2.007187

Look for departures from zero to indicate an interaction effect between dose and gender. Both contrasts are significantly different from zero. Of course, we already knew the overall interaction was significant from our [ANOVA results](#). The effect of increasing dose from 250 to 500 is 3.9 points greater in females than in males, and the effect of increasing dose from 500 to 750 is 4.7 points greater in females than in males. The confidence intervals for both estimates easily exclude zero, meaning that there is an interaction effect.

The joint test of these two interaction effects reproduces the test of interaction effects in the anova output. We can see that the F statistic of 21.66 matches the statistic from our original ANOVA results.

Main effects

We can perform tests of the main effects by listing each variable individually in contrast.

```
. contrast dose gender
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
dose	2	223.64	0.0000
gender	1	164.85	0.0000
Denominator	24		

The F tests are equivalent to the tests of main effects in the anova output. This is true only for linear models. `contrast` provides an easy way to obtain main effects and other ANOVA-style tests for models whose responses are not linear in the parameters—logistic, probit, `glm`, etc.

If we include contrast operators on the variables, we can also decompose the main effects into individual contrasts:

```
. contrast ar.dose r.gender
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
dose			
(500 vs 250)	1	161.27	0.0000
(750 vs 500)	1	68.83	0.0000
Joint	2	223.64	0.0000
gender	1	164.85	0.0000
Denominator	24		

	Contrast	Std. err.	[95% conf. interval]	
dose				
(500 vs 250)	-8.335376	.6563742	-9.690066	-6.980687
(750 vs 500)	-5.4455	.6563742	-6.80019	-4.090811
gender				
(Female vs Male)	6.881074	.5359273	5.774974	7.987173

By specifying the `ar.` operator on `dose`, we decompose the main effect for `dose` into two one-degree-of-freedom contrasts, comparing the marginal mean of blood pressure change for each dosage level with that of the previous level. Because `gender` has only two levels, we cannot decompose this main effect any further. However, specifying a contrast operator on `gender` allowed us to calculate the difference in the marginal means for women and men.

Partial interaction effects

At this point, we have looked at the total interaction effects and at the main effects of each variable. The partial interaction effects are a midpoint between these two types of effects where we collect the individual interaction effects along the levels of one of the variables and perform a joint test of those interactions. If we think of the interaction effects as forming a table, with the levels of one factor variable forming the rows and the levels of the other forming the columns, partial interaction effects are joint tests of the interactions in a row or a column. To perform these tests, we specify a contrast operator on only one of the variables in our interaction. For this particular model, these are not very interesting because our variables have only two and three levels. Therefore, the tests of the partial interaction effects reproduce the tests that we obtained for the total interaction effects. We specify a contrast operator only on `dose` to decompose the overall test for interaction effects into joint tests for each `ar.dose` contrast:

```
. contrast ar.dose#gender
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
dose#gender			
(500 vs 250) (joint)	1	8.87	0.0065
(750 vs 500) (joint)	1	12.91	0.0015
Joint	2	21.66	0.0000
Denominator	24		

The first row is a joint test of all the interaction effects involving the (500 vs 250) comparison of dosages. The second row is a joint test of all the interaction effects involving the (750 vs 500) comparison. If we look back at our output in [Interaction effects](#), we can see that there was only one of each of these interaction effects. Therefore, each test labeled (joint) has only one degree-of-freedom.

We could have instead included a contrast operator on gender to compute the partial interaction effects along the other dimension:

```
. contrast dose#r.gender
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
dose#gender	2	21.66	0.0000
Denominator	24		

Here we obtain a joint test of all the interaction effects involving the (Female vs Male) comparison for gender. Because gender has only two levels, the (Female vs Male) contrast is the only reference category contrast possible. Therefore, we obtain a single joint test of all the interaction effects.

Clearly, the partial interaction effects are not interesting for this particular model. However, if our factors had more levels, the partial interaction effects would produce tests that are not available in the total interaction effects. For example, if our model included factors for four dosage levels and three races, then typing

```
. contrast ar.dose#race
```

would produce three joint tests, one for each of the reverse adjacent contrasts for dosage. Each of these tests would be a two-degree-of-freedom test because race has three levels.

Three-way and higher-order models

All the contrasts and tests that we reviewed above for two-way models can be used with models that have more terms. For instance, we could fit a three-way full factorial model by using the `anova` command:

```
. use https://www.stata-press.com/data/r19/cont3way
. anova y race##sex##group
```

We could then test the simple effects of `race` within each level of the interaction between `sex` and `group`:

```
. contrast race@sex#group
```

To see the reference category contrasts that decompose these simple effects, type

```
. contrast r.race@sex#group
```

We could test the three-way interaction effects by typing

```
. contrast race#sex#group
```

or the interaction effects for the interaction of `race` and `sex` by typing

```
. contrast race#sex
```

To see the individual reference category contrasts that decompose this interaction effect, type

```
. contrast r.race#r.sex
```

We could even obtain joint tests for the interaction of `race` and `sex` within each level of `group` by typing

```
. contrast race#sex@group
```

For tests of the main effects of each factor, we can type

```
. contrast race sex group
```

We can calculate the individual reference category contrasts that decompose these main effects:

```
. contrast r.race r.sex r.group
```

For the partial interaction effects, we could type

```
. contrast r.race#group
```

to obtain a joint test of the two-way interaction effects of `race` and `group` for each of the individual `r.race` contrasts.

We could type

```
. contrast r.race#sex#group
```

to obtain a joint test of all the three-way interaction terms for each of the individual `r.race` contrasts.

Contrast operators

`contrast` recognizes a set of contrast operators that are used to specify commonly used contrasts. When these operators are used, `contrast` will report a test for each individual contrast in addition to the joint test for the term. We have already seen a few of these, like `r.` and `ar.`, in the previous examples. Here we will take a closer look at each of the unweighted operators.

Here we use the cholesterol dataset and the one-way ANOVA model from the example in [One-way models](#):

```
. use https://www.stata-press.com/data/r19/cholesterol
(Artificial cholesterol data)

. anova chol agegrp
(output omitted)
```

The `margins` command reports the estimated cell means, $\hat{\mu}_1, \dots, \hat{\mu}_5$, for each of the five age groups.

```
. margins agegrp
Adjusted predictions                                Number of obs = 75
Expression: Linear prediction, predict()
```

	Delta-method		t	P> t	[95% conf. interval]	
	Margin	std. err.				
agegrp						
10-19	180.5198	2.666944	67.69	0.000	175.2007	185.8388
20-29	188.7233	2.666944	70.76	0.000	183.4043	194.0424
30-39	202.0608	2.666944	75.76	0.000	196.7418	207.3799
40-59	210.6704	2.666944	78.99	0.000	205.3514	215.9895
60-79	219.282	2.666944	82.22	0.000	213.9629	224.601

Contrast operators provide an easy way to make certain types of comparisons of these cell means. We use the ordinal factor `agegrp` to demonstrate these operators because some types of contrasts are meaningful only when the levels of the factor have a natural ordering. We demonstrate these contrast operators using a one-way model; however, they are equally applicable to main effects, simple effects, and interactions for more complicated models.

Differences from a reference level (r.)

The `r.` operator specifies that each level of the attached factor variable be compared with a reference level. These are referred to as reference-level or reference-category contrasts (or effects), and `r.` is the reference-level operator.

In the following, we use the `r.` operator to test the effect of each category of age group when that category is compared with a reference category.

```
. contrast r.agegrp
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
agegrp			
(20–29 vs 10–19)	1	4.73	0.0330
(30–39 vs 10–19)	1	32.62	0.0000
(40–59 vs 10–19)	1	63.91	0.0000
(60–79 vs 10–19)	1	105.62	0.0000
Joint	4	35.02	0.0000
Denominator	70		

	Contrast	Std. err.	[95% conf. interval]	
agegrp				
(20–29 vs 10–19)	8.203575	3.771628	.6812991	15.72585
(30–39 vs 10–19)	21.54105	3.771628	14.01878	29.06333
(40–59 vs 10–19)	30.15067	3.771628	22.6284	37.67295
(60–79 vs 10–19)	38.76221	3.771628	31.23993	46.28448

In the first table, the row labeled (20–29 vs 10–19) is a test of $\mu_2 = \mu_1$, a test that the mean cholesterol levels for the 10–19 age group and the 20–29 age group are equal. The tests in the next three rows are defined similarly. The row labeled Joint provides the joint test for these four hypotheses, which is just the test of the main effects of age group.

The second table provides the contrasts of each category with the reference category along with confidence intervals. The contrast in the row labeled (20–29 vs 10–19) is the difference in the cell means of the second age group and the first age group, $\hat{\mu}_2 - \hat{\mu}_1$.

The first level of a factor is the default reference level, but we can specify a different reference level by using the `b.` operator; see [U] 11.4.3.2 Base levels. Here we use the last age group, (60–79), instead of the first as the reference category. We also include the `nowald` option so that only the table of contrasts and their confidence intervals is produced.

```
. contrast rb5.agegrp, nowald
Contrasts of marginal linear predictions
Margins: asbalanced
```

	Contrast	Std. err.	[95% conf. interval]	
agegrp				
(10–19 vs 60–79)	-38.76221	3.771628	-46.28448	-31.23993
(20–29 vs 60–79)	-30.55863	3.771628	-38.08091	-23.03636
(30–39 vs 60–79)	-17.22115	3.771628	-24.74343	-9.698877
(40–59 vs 60–79)	-8.611533	3.771628	-16.13381	-1.089257

Now, the first row is labeled (10–19 vs 60–79) and is the difference in the cell means of the first and fifth age groups.

Differences from the next level (a.)

The `a.` operator specifies that each level of the attached factor variable be compared with the next level. These are referred to as adjacent contrasts (or effects), and `a.` is the adjacent operator. This operator is meaningful only with factor variables that have a natural ordering in the levels.

We can use the `a.` operator to perform tests that each level of age group differs from the next adjacent level.

```
. contrast a.agegrp
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
agegrp			
(10-19 vs 20-29)	1	4.73	0.0330
(20-29 vs 30-39)	1	12.51	0.0007
(30-39 vs 40-59)	1	5.21	0.0255
(40-59 vs 60-79)	1	5.21	0.0255
Joint	4	35.02	0.0000
Denominator	70		

	Contrast	Std. err.	[95% conf. interval]	
agegrp				
(10-19 vs 20-29)	-8.203575	3.771628	-15.72585	-.6812991
(20-29 vs 30-39)	-13.33748	3.771628	-20.85976	-5.815204
(30-39 vs 40-59)	-8.60962	3.771628	-16.1319	-1.087345
(40-59 vs 60-79)	-8.611533	3.771628	-16.13381	-1.089257

In the first table, the row labeled (10-19 vs 20-29) tests the effect of belonging to the 10-19 age group instead of the 20-29 age group. Likewise, the rows labeled (20-29 vs 30-39), (30-39 vs 40-59), and (40-59 vs 60-79) are tests for the effects of being in the younger of the two age groups instead of the older one.

In the second table, the contrast in the row labeled (10-19 vs 20-29) is the difference in the cell means of the first and second age groups, $\hat{\mu}_1 - \hat{\mu}_2$. The contrasts in the other rows are defined similarly.

Differences from the previous level (ar.)

The `ar.` operator specifies that each level of the attached factor variable be compared with the previous level. These are referred to as reverse adjacent contrasts (or effects), and `ar.` is the reverse adjacent operator. As with the `a.` operator, this operator is meaningful only with factor variables that have a natural ordering in the levels.

In the following, we use the `ar.` operator to report tests for the individual reverse adjacent effects of `agegrp`.

```
. contrast ar.agegrp
```

```
Contrasts of marginal linear predictions
```

```
Margins: asbalanced
```

	df	F	P>F
agegrp			
(20–29 vs 10–19)	1	4.73	0.0330
(30–39 vs 20–29)	1	12.51	0.0007
(40–59 vs 30–39)	1	5.21	0.0255
(60–79 vs 40–59)	1	5.21	0.0255
Joint	4	35.02	0.0000
Denominator	70		

	Contrast	Std. err.	[95% conf. interval]	
agegrp				
(20–29 vs 10–19)	8.203575	3.771628	.6812991	15.72585
(30–39 vs 20–29)	13.33748	3.771628	5.815204	20.85976
(40–59 vs 30–39)	8.60962	3.771628	1.087345	16.1319
(60–79 vs 40–59)	8.611533	3.771628	1.089257	16.13381

Here the Wald tests in the first table for the individual reverse adjacent effects are equivalent to the tests for the adjacent effects in the [previous example](#). However, if we compare values of the contrasts in the bottom tables, we see the difference between the `r.` and the `ar.` operators. This time, the contrast in the first row is labeled (20–29 vs 10–19) and is the difference in the cell means of the second and first age groups, $\hat{\mu}_2 - \hat{\mu}_1$. This is the estimated effect of belonging to the 20–29 age group instead of the 10–19 age group. The remaining rows make similar comparisons with the previous level.

Differences from the grand mean (g.)

The `g.` operator specifies that each level of a factor variable be compared with the grand mean of all levels. For this operator, the grand mean is computed using a simple average of the cell means.

Here are the grand mean effects of `agegrp`:

```
. contrast g.agegrp
```

Contrasts of marginal linear predictions

Margins: asbalanced

	df	F	P>F
agegrp			
(10-19 vs mean)	1	68.42	0.0000
(20-29 vs mean)	1	23.36	0.0000
(30-39 vs mean)	1	0.58	0.4506
(40-59 vs mean)	1	19.08	0.0000
(60-79 vs mean)	1	63.65	0.0000
Joint	4	35.02	0.0000
Denominator	70		

	Contrast	Std. err.	[95% conf. interval]	
agegrp				
(10-19 vs mean)	-19.7315	2.385387	-24.48901	-14.974
(20-29 vs mean)	-11.52793	2.385387	-16.28543	-6.770423
(30-39 vs mean)	1.809552	2.385387	-2.947953	6.567057
(40-59 vs mean)	10.41917	2.385387	5.661668	15.17668
(60-79 vs mean)	19.0307	2.385387	14.2732	23.78821

There are five age groups in our estimation sample. Thus, the row labeled (10-19 vs mean) tests $\mu_1 = (\mu_1 + \mu_2 + \mu_3 + \mu_4 + \mu_5)/5$. The row labeled (20-29 vs mean) tests $\mu_2 = (\mu_1 + \mu_2 + \mu_3 + \mu_4 + \mu_5)/5$. The remaining rows perform similar tests for the third, fourth, and fifth age groups. In our example, the means for all age groups except the 30-39 age group are statistically different from the grand mean.

Differences from the mean of subsequent levels (h.)

The `h.` operator specifies that each level of the attached factor variable be compared with the mean of subsequent levels. These are referred to as Helmert contrasts (or effects), and `h.` is the Helmert operator. For this operator, the mean is computed using a simple average of the cell means. This operator is meaningful only with factor variables that have a natural ordering in the levels.

Here are the Helmert contrasts for `agegrp`:

```
. contrast h.agegrp
```

```
Contrasts of marginal linear predictions
```

```
Margins: asbalanced
```

	df	F	P>F
agegrp			
(10-19 vs >10-19)	1	68.42	0.0000
(20-29 vs >20-29)	1	50.79	0.0000
(30-39 vs >30-39)	1	15.63	0.0002
(40-59 vs 60-79)	1	5.21	0.0255
Joint	4	35.02	0.0000
Denominator	70		

	Contrast	Std. err.	[95% conf. interval]	
agegrp				
(10-19 vs >10-19)	-24.66438	2.981734	-30.61126	-18.7175
(20-29 vs >20-29)	-21.94774	3.079522	-28.08965	-15.80583
(30-39 vs >30-39)	-12.91539	3.266326	-19.42987	-6.400905
(40-59 vs 60-79)	-8.611533	3.771628	-16.13381	-1.089257

The row labeled (10-19 vs >10-19) tests $\mu_1 = (\mu_2 + \mu_3 + \mu_4 + \mu_5)/4$, that is, that the cell mean for the youngest age group is equal to the average of the cell means for the older age groups. The row labeled (20-29 vs >20-29) tests $\mu_2 = (\mu_3 + \mu_4 + \mu_5)/3$. The tests in the other rows are defined similarly.

Differences from the mean of previous levels (j.)

The `j.` operator specifies that each level of the attached factor variable be compared with the mean of the previous levels. These are referred to as reverse Helmert contrasts (or effects), and `j.` is the reverse Helmert operator. For this operator, the mean is computed using a simple average of the cell means. This operator is meaningful only with factor variables that have a natural ordering in the levels.

Here are the reverse Helmert contrasts of agegrp:

```
. contrast j.agegrp
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
agegrp			
(20-29 vs 10-19)	1	4.73	0.0330
(30-39 vs <30-39)	1	28.51	0.0000
(40-59 vs <40-59)	1	43.18	0.0000
(60-79 vs <60-79)	1	63.65	0.0000
Joint	4	35.02	0.0000
Denominator	70		

	Contrast	Std. err.	[95% conf. interval]	
agegrp				
(20-29 vs 10-19)	8.203575	3.771628	.6812991	15.72585
(30-39 vs <30-39)	17.43927	3.266326	10.92479	23.95375
(40-59 vs <40-59)	20.2358	3.079522	14.09389	26.37771
(60-79 vs <60-79)	23.78838	2.981734	17.8415	29.73526

The row labeled (20-29 vs 10-19) tests $\mu_2 = \mu_1$, that is, that the cell means for the 20-29 and the 10-19 age groups are equal. The row labeled (30-39 vs <30-39) tests $\mu_3 = (\mu_1 + \mu_2)/2$, that is, that the cell mean for the 30-39 age group is equal to the average of the cell means for the 10-19 and 20-29 age groups. The tests in the remaining rows are defined similarly.

Orthogonal polynomials (p. and q.)

The p. and q. operators specify that orthogonal polynomials be applied to the attached factor variable. Orthogonal polynomial contrasts allow us to partition the effects of a factor variable into linear, quadratic, cubic, and higher-order polynomial components. The p. operator applies orthogonal polynomials using the values of the factor variable. The q. operator applies orthogonal polynomials using the level indices. If the level values of the factor variable are equally spaced, as with our agegrp variable, then the p. and q. operators yield the same result. These operators are meaningful only with factor variables that have a natural ordering in the levels.

Because `agegrp` has five levels, `contrast` can test the linear, quadratic, cubic, and quartic effects of `agegrp`.

```
. contrast p.agegrp, noeffects
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
agegrp			
(linear)	1	139.11	0.0000
(quadratic)	1	0.15	0.6962
(cubic)	1	0.37	0.5448
(quartic)	1	0.43	0.5153
Joint	4	35.02	0.0000
Denominator	70		

The row labeled (linear) tests the linear effect of `agegrp`, the only effect that appears to be significant in this case.

The labels for our `agegrp` variable show the age ranges that correspond to each level.

```
. label list ages
ages:
      1 10-19
      2 20-29
      3 30-39
      4 40-59
      5 60-79
```

Notice that these groups do not have equal widths. Now, let's refit our model using the `agemidpt` variable. The values of `agemidpt` indicate the midpoint of each age group that was defined by the `agegrp` variable and are, therefore, not equally spaced.

```
. anova chol agemidpt
```

		Number of obs =	75	R-squared =	0.6668
		Root MSE =	10.329	Adj R-squared =	0.6477
Source	Partial SS	df	MS	F	Prob>F
Model	14943.4	4	3735.8499	35.02	0.0000
agemidpt	14943.4	4	3735.8499	35.02	0.0000
Residual	7468.2197	70	106.68885		
Total	22411.619	74	302.85972		

Now if we use the `q.` operator, we will obtain the same results as above because the level indices of `agemidpt` are equivalent to the values of `agegrp`.

```
. contrast q.agemidpt, noeffects
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
agemidpt			
(linear)	1	139.11	0.0000
(quadratic)	1	0.15	0.6962
(cubic)	1	0.37	0.5448
(quartic)	1	0.43	0.5153
Joint	4	35.02	0.0000
Denominator	70		

However, if we use the `p.` operator, we will instead fit an orthogonal polynomial to the midpoint values.

```
. contrast p.agemidpt, noeffects
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
agemidpt			
(linear)	1	133.45	0.0000
(quadratic)	1	5.40	0.0230
(cubic)	1	0.05	0.8198
(quartic)	1	1.16	0.2850
Joint	4	35.02	0.0000
Denominator	70		

Using the values of the midpoints, the quadratic effect is also significant at the 5% level.

□ Technical note

We used the `noeffects` option when working with orthogonal polynomial contrasts. Apart from perhaps the sign of the contrast, the values of the individual contrasts are not meaningful for orthogonal polynomial contrasts. In addition, many textbooks provide tables with contrast coefficients that can be used to compute orthogonal polynomial contrasts where the levels of a factor are equally spaced. If we use these coefficients and calculate the contrasts manually with user-defined contrasts, as described below, the Wald tests for the polynomial terms will be equivalent, but the values of the individual contrasts will not necessarily match those that we obtain when using the polynomial contrast operator. When we use one of these contrast operators, an algorithm is used to calculate the coefficients of the polynomial contrast that will allow for unequal spacing in the levels of the factor as well as in the weights for the cell frequencies (when using `pw.` or `qw.`), as described in [Methods and formulas](#).



User-defined contrasts

In the previous examples, we performed tests using contrast operators. When there is not a contrast operator available to calculate the contrast in which we are interested, we can specify custom contrasts.

Here we fit a one-way model for cholesterol on the factor race, which has three levels:

```
. label list race
race:
      1 Black
      2 White
      3 Other
. anova chol race
```

	Number of obs =	75	R-squared =	0.0299	
	Root MSE =	17.3775	Adj R-squared =	0.0029	
Source	Partial SS	df	MS	F	Prob>F
Model	669.27823	2	334.63912	1.11	0.3357
race	669.27823	2	334.63912	1.11	0.3357
Residual	21742.341	72	301.97696		
Total	22411.619	74	302.85972		

margins calculates the estimated cell mean cholesterol level for each race:

```
. margins race
```

Adjusted predictions

Number of obs = 75

Expression: Linear prediction, predict()

	Delta-method				
	Margin	std. err.	t	P> t	[95% conf. interval]
race					
Black	204.4279	3.475497	58.82	0.000	197.4996 211.3562
White	197.6132	3.475497	56.86	0.000	190.6849 204.5415
Other	198.7127	3.475497	57.18	0.000	191.7844 205.6409

Suppose we want to test the following linear combination:

$$\sum_{i=1}^3 c_i \mu_i$$

where μ_i is the cell mean of chol when race is equal to its i th level (the means estimated using margins above). Assuming the c_i elements sum to zero, this linear combination is a contrast. We can specify this type of custom contrast by using the following syntax:

```
{race c1 c2 c3}
```


The null hypothesis for the test of the main effects of race is

$$H_{0_{\text{race}}} : \mu_1 = \mu_2 = \mu_3$$

Although $H_{0_{\text{race}}}$ can be tested using any of several different contrasts on the cell means, we will test it by comparing the second and third cell means with the first. To test that the cell means for blacks and whites are equal, $\mu_1 = \mu_2$, we can specify the contrast

$$\{\text{race } -1 \ 1 \ 0\}$$

To test that the cell means for blacks and other races are equal, $\mu_1 = \mu_3$, we can specify the contrast

$$\{\text{race } -1 \ 0 \ 1\}$$

We can use both in a single call to `contrast`.

```
. contrast {race -1 1 0} {race -1 0 1}
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
race			
(1)	1	1.92	0.1699
(2)	1	1.35	0.2488
Joint	2	1.11	0.3357
Denominator	72		

	Contrast	Std. err.	[95% conf. interval]	
race				
(1)	-6.814717	4.915095	-16.61278	2.983345
(2)	-5.715261	4.915095	-15.51332	4.082801

The row labeled (1) is the test for $\mu_1 = \mu_2$, the first specified contrast. The row labeled (2) is the test for $\mu_1 = \mu_3$, the second specified contrast. The row labeled Joint is the overall test for the main effects of race.

Now, let's fit a model with two factors, race and age group:

```
. anova chol race##agegrp
```

Number of obs =		75	R-squared =	0.7524	
Root MSE =		9.61785	Adj R-squared =	0.6946	
Source	Partial SS	df	MS	F	Prob>F
Model	16861.438	14	1204.3884	13.02	0.0000
race	669.27823	2	334.63912	3.62	0.0329
agegrp	14943.4	4	3735.8499	40.39	0.0000
race#agegrp	1248.7601	8	156.09501	1.69	0.1201
Residual	5550.1814	60	92.503024		
Total	22411.619	74	302.85972		

The null hypothesis for the test of the main effects of race is now

$$H_{0_{\text{race}}} : \mu_{1.} = \mu_{2.} = \mu_{3.}$$

where $\mu_{i.}$ is the marginal mean of chol when race is equal to its i th level.

We can use the same syntax as above to perform this test by specifying contrasts on the marginal means of race:

```
. contrast {race -1 1 0} {race -1 0 1}
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
race			
(1)	1	6.28	0.0150
(2)	1	4.41	0.0399
Joint	2	3.62	0.0329
Denominator	60		

	Contrast	Std. err.	[95% conf. interval]	
race				
(1)	-6.814717	2.720339	-12.2562	-1.37323
(2)	-5.715261	2.720339	-11.15675	-.2737739

Custom contrasts may be specified on the cell means of interactions, too. Here we use margins to calculate the mean of chol for each cell in the interaction of race and agegrp:

```
. margins race#agegrp
Adjusted predictions                                Number of obs = 75
Expression: Linear prediction, predict()
```

	Delta-method		t	P> t	[95% conf. interval]	
	Margin	std. err.				
race#agegrp						
Black#10-19	179.2309	4.301233	41.67	0.000	170.6271	187.8346
Black#20-29	196.4777	4.301233	45.68	0.000	187.874	205.0814
Black#30-39	210.6694	4.301233	48.98	0.000	202.0656	219.2731
Black#40-59	214.097	4.301233	49.78	0.000	205.4933	222.7008
Black#60-79	221.6646	4.301233	51.54	0.000	213.0609	230.2684
White#10-19	186.0727	4.301233	43.26	0.000	177.469	194.6765
White#20-29	184.6714	4.301233	42.93	0.000	176.0676	193.2751
White#30-39	196.2633	4.301233	45.63	0.000	187.6595	204.867
White#40-59	209.9953	4.301233	48.82	0.000	201.3916	218.5991
White#60-79	211.0633	4.301233	49.07	0.000	202.4595	219.667
Other#10-19	176.2556	4.301233	40.98	0.000	167.6519	184.8594
Other#20-29	185.0209	4.301233	43.02	0.000	176.4172	193.6247
Other#30-39	199.2498	4.301233	46.32	0.000	190.646	207.8535
Other#40-59	207.9189	4.301233	48.34	0.000	199.3152	216.5227
Other#60-79	225.118	4.301233	52.34	0.000	216.5143	233.7218

Now, we are interested in testing the following linear combination of these cell means:

$$\sum_{i=1}^3 \sum_{j=1}^5 c_{ij} \mu_{ij}$$

We can specify this type of custom contrast using the following syntax:

```
{race#agegrp c11 c12 ... c15 c21 c22 ... c25 c31 c32 ... c35}
```

Because the marginal means of `chol` for each level of `race` are linear combinations of the cell means, we can compose the test for the main effects of `race` in terms of the cell means directly. The constraint that the marginal means for blacks and whites are equal, $\mu_{1\cdot} = \mu_{2\cdot}$, translates to the following constraint on the cell means:

$$\frac{1}{5}(\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15}) = \frac{1}{5}(\mu_{21} + \mu_{22} + \mu_{23} + \mu_{24} + \mu_{25})$$

Ignoring the common factor, we can specify this contrast as

```
{race#agegrp -1 -1 -1 -1 -1 1 1 1 1 1 0 0 0 0 0}
```

`contrast` will fill in the trailing zeros for us if we neglect to specify them, so

```
{race#agegrp -1 -1 -1 -1 -1 1 1 1 1 1}
```

is also allowed. The other constraint, $\mu_{1\cdot} = \mu_{3\cdot}$, translates to

$$\frac{1}{5}(\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15}) = \frac{1}{5}(\mu_{31} + \mu_{32} + \mu_{33} + \mu_{34} + \mu_{35})$$

This can be specified to `contrast` as

```
{race#agegrp -1 -1 -1 -1 -1 0 0 0 0 0 1 1 1 1 1}
```

The following call to `contrast` yields the same test results as above.

```
. contrast {race#agegrp -1 -1 -1 -1 -1 1 1 1 1 1}
> {race#agegrp -1 -1 -1 -1 -1 0 0 0 0 0 1 1 1 1 1}, noeffects
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
race#agegrp			
(1) (1)	1	6.28	0.0150
(2) (2)	1	4.41	0.0399
Joint	2	3.62	0.0329
Denominator	60		

The row labeled (1) (1) is the test for

$$\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15} = \mu_{21} + \mu_{22} + \mu_{23} + \mu_{24} + \mu_{25}$$

It was the first specified contrast. The row labeled (2) (2) is the test for

$$\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15} = \mu_{31} + \mu_{32} + \mu_{33} + \mu_{34} + \mu_{35}$$

It was the second specified contrast. The row labeled Joint tests (1) (1) and (2) (2) simultaneously.

We used the `noeffects` option above to suppress the table of contrasts. We can omit the $1/5$ from the equations for $\mu_{1.} = \mu_{2.}$ and $\mu_{1.} = \mu_{3.}$ and still obtain the appropriate tests. However, if we want to calculate the differences in the marginal means, we must include the $1/5 = 0.2$ on each of the contrast coefficients as follows:

```
. contrast {race#agegrp -0.2 -0.2 -0.2 -0.2 -0.2 ///
              0.2  0.2  0.2  0.2  0.2} ///
      {race#agegrp -0.2 -0.2 -0.2 -0.2 -0.2 ///
              0      0      0      0      0 ///
              0.2  0.2  0.2  0.2  0.2}
```

So far, we have reproduced the reference category contrasts by specifying user-defined contrasts on the marginal means and then on the cell means. For this test, it would have been easier to use the `r. contrast` operator:

```
. contrast r.race, noeffects
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
race			
(White vs Black)	1	6.28	0.0150
(Other vs Black)	1	4.41	0.0399
Joint	2	3.62	0.0329
Denominator	60		

In most cases, we can use contrast operators to perform tests. However, if we want to compare, for instance, the second and third age groups with the fourth and fifth age groups with the test

$$\frac{1}{2}(\mu_{.2} + \mu_{.3}) = \frac{1}{2}(\mu_{.4} + \mu_{.5})$$

there is not a contrast operator that corresponds to this particular contrast. A custom contrast is necessary.

```
. contrast {agegrp 0 -0.5 -0.5 0.5 0.5}
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
agegrp	1	62.19	0.0000
Denominator	60		

	Contrast	Std. err.	[95% conf. interval]	
agegrp (1)	19.58413	2.483318	14.61675	24.5515

Empty cells

An empty cell is a combination of the levels of factor variables that is not observed in the estimation sample. In the previous examples, we have seen data with three levels of `race`, five levels of `agegrp`, and all level combinations of `race` and `agegrp` present. Suppose there are no observations for white individuals in the second age group (ages 20–29).

```
. use https://www.stata-press.com/data/r19/cholesterol2
(Artificial cholesterol data, empty cells)
. label list
race:
      1 Black
      2 White
      3 Other
ages:
      1 10–19
      2 20–29
      3 30–39
      4 40–59
      5 60–79
```

```
. regress chol race##agegrp
```

note: **2.race#2.agegrp** identifies no observations in the sample.

Source	SS	df	MS	Number of obs	=	70
Model	15751.6113	13	1211.66241	F(13, 56)	=	13.51
Residual	5022.71559	56	89.6913498	Prob > F	=	0.0000
				R-squared	=	0.7582
				Adj R-squared	=	0.7021
Total	20774.3269	69	301.077201	Root MSE	=	9.4706

chol	Coefficient	Std. err.	t	P> t	[95% conf. interval]	
race						
White	12.84185	5.989703	2.14	0.036	.8430383	24.84067
Other	-.167627	5.989703	-0.03	0.978	-12.16644	11.83119
agegrp						
20-29	17.24681	5.989703	2.88	0.006	5.247991	29.24562
30-39	31.43847	5.989703	5.25	0.000	19.43966	43.43729
40-59	34.86613	5.989703	5.82	0.000	22.86732	46.86495
60-79	44.43374	5.989703	7.42	0.000	32.43492	56.43256
race#agegrp						
White#20-29	0 (empty)					
White#30-39	-22.83983	8.470719	-2.70	0.009	-39.80872	-5.870939
White#40-59	-14.67558	8.470719	-1.73	0.089	-31.64447	2.293306
White#60-79	-10.51115	8.470719	-1.24	0.220	-27.48004	6.457735
Other#20-29	-6.054425	8.470719	-0.71	0.478	-23.02331	10.91446
Other#30-39	-11.48083	8.470719	-1.36	0.181	-28.44971	5.488063
Other#40-59	-.6796112	8.470719	-0.08	0.936	-17.6485	16.28928
Other#60-79	-1.578052	8.470719	-0.19	0.853	-18.54694	15.39084
_cons	175.2309	4.235359	41.37	0.000	166.7464	183.7153

Now, let's use contrast to test the main effects of race:

```
. contrast race
```

Contrasts of marginal linear predictions

Margins: asbalanced

	df	F	P>F
race	(not testable)		
Denominator	56		

By “not testable”, contrast means that it cannot form a test for the main effects of race based on estimable functions of the model coefficients. `agegrp` has five levels, so contrast constructs an estimate of the i th margin for race as

$$\hat{\mu}_i = \frac{1}{5} \sum_{j=1}^5 \hat{\mu}_{ij} = \hat{\mu}_0 + \hat{\alpha}_i + \frac{1}{5} \sum_{j=1}^5 \left\{ \hat{\beta}_j + (\widehat{\alpha\beta})_{ij} \right\}$$

but $(\widehat{\alpha\beta})_{22}$ was constrained to zero because of the empty cell, so $\hat{\mu}_2$ is not an estimable function of the model coefficients.

See *Estimable functions* in *Methods and formulas of [R] margins* for a technical description of estimable functions. The `emptycells(reweight)` option causes `contrast` to estimate $\mu_{2.}$ by

$$\hat{\mu}_{2.} = \frac{\hat{\mu}_{21} + \hat{\mu}_{23} + \hat{\mu}_{24} + \hat{\mu}_{25}}{4}$$

which is an estimable function of the model coefficients.

```
. contrast race, emptycells(reweight)
Contrasts of marginal linear predictions
Margins:      asbalanced
Empty cells: reweight
```

	df	F	P>F
race	2	3.17	0.0498
Denominator	56		

We can reconstruct the effect of the `emptycells(reweight)` option by using custom contrasts.

```
. contrast {race#agegrp -4 -4 -4 -4 -4 5 0 5 5 5}
>          {race#agegrp -1 -1 -1 -1 -1 0 0 0 0 1 1 1 1}, noeffects
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
race#agegrp			
(1) (1)	1	1.06	0.3080
(2) (2)	1	2.37	0.1291
Joint	2	3.17	0.0498
Denominator	56		

The row labeled (1) (1) is the test for

$$\frac{1}{5}(\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15}) = \frac{1}{4}(\mu_{21} + \mu_{23} + \mu_{24} + \mu_{25})$$

It was the first specified contrast. The row labeled (2) (2) is the test for

$$\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15} = \mu_{31} + \mu_{32} + \mu_{33} + \mu_{34} + \mu_{35}$$

It was the second specified contrast. The row labeled Joint is the overall test of the main effects of race.

Empty cells, ANOVA style

Let's refit the linear model from the [previous example](#) with `anova` to compare with `contrast`'s test for the main effects of `race`.

```
. anova chol race##agegrp
```

	Number of obs =	70	R-squared =	0.7582	
	Root MSE =	9.47055	Adj R-squared =	0.7021	
Source	Partial SS	df	MS	F	Prob>F
Model	15751.611	13	1211.6624	13.51	0.0000
race	305.49046	2	152.74523	1.70	0.1914
agegrp	14387.856	4	3596.964	40.10	0.0000
race#agegrp	795.80757	7	113.6868	1.27	0.2831
Residual	5022.7156	56	89.69135		
Total	20774.327	69	301.0772		

`contrast` and `anova` handled the empty cell differently; the F statistic reported by `contrast` was 3.17, but `anova` reported 1.70. To see how they differ, consider the following table of the cell means and margins for our situation.

		agegrp				
		1	2	3	4	5
race	1	μ_{11}	μ_{12}	μ_{13}	μ_{14}	μ_{15}
	2	μ_{21}		μ_{23}	μ_{24}	μ_{25}
	3	μ_{31}	μ_{32}	μ_{33}	μ_{34}	μ_{35}
		$\mu_{\cdot 1}$		$\mu_{\cdot 3}$	$\mu_{\cdot 4}$	$\mu_{\cdot 5}$

For testing the main effects of `race`, we know that we will be testing the equality of the marginal means for rows 1 and 3, that is, $\mu_{1\cdot} = \mu_{3\cdot}$. This translates into the following constraint:

$$\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15} = \mu_{31} + \mu_{32} + \mu_{33} + \mu_{34} + \mu_{35}$$

Because row 2 contains an empty cell in column 2, `anova` dropped column 2 and tested the equality of the marginal mean for row 2 with the average of the marginal means from rows 1 and 3, using only the remaining cell means. This translates into the following constraint:

$$2(\mu_{21} + \mu_{23} + \mu_{24} + \mu_{25}) = \mu_{11} + \mu_{13} + \mu_{14} + \mu_{15} + \mu_{31} + \mu_{33} + \mu_{34} + \mu_{35} \quad (1)$$

Now that we know the constraints that anova used to test for the main effects of race, we can use custom contrasts to reproduce the anova test result.

```
. contrast {race#agegrp -1 -1 -1 -1 -1 0 0 0 0 0 1 1 1 1}
> {race#agegrp 1 0 1 1 1 -2 0 -2 -2 -2 1 0 1 1}, noeffects
```

Contrasts of marginal linear predictions

Margins: asbalanced

	df	F	P>F
race#agegrp			
(1) (1)	1	2.37	0.1291
(2) (2)	1	1.03	0.3138
Joint	2	1.70	0.1914
Denominator	56		

The row labeled (1) (1) is the test for $\mu_1 = \mu_3$; it was the first specified contrast. The row labeled (2) (2) is the test for the constraint in (1); it was the second specified contrast. The row labeled Joint is an overall test for the main effects of race.

Nested effects

contrast has the | operator for computing simple effects when the levels of one factor are nested within the levels of another. Here is a fictional example where we are interested in the effect of five methods of teaching algebra on students' scores for the math portion of the SAT. Suppose three algebra classes are randomly sampled from classes using each of the five methods so that class is nested in method as demonstrated in the following tabulation.

```
. use https://www.stata-press.com/data/r19/sat
```

(Fictional SAT data)

```
. tabulate class method
```

Class ID	Five methods of teaching algebra					Total
	1	2	3	4	5	
1	5	0	0	0	0	5
2	5	0	0	0	0	5
3	5	0	0	0	0	5
4	0	5	0	0	0	5
5	0	5	0	0	0	5
6	0	5	0	0	0	5
7	0	0	5	0	0	5
8	0	0	5	0	0	5
9	0	0	5	0	0	5
10	0	0	0	5	0	5
11	0	0	0	5	0	5
12	0	0	0	5	0	5
13	0	0	0	0	5	5
14	0	0	0	0	5	5
15	0	0	0	0	5	5
Total	15	15	15	15	15	75

We will consider method as fixed and class nested in method as random. To use class nested in method as the error term for method, we can specify the following anova model:

```
. anova score method / class|method /
```

	Number of obs =	75	R-squared =	0.7599	
	Root MSE =	71.8517	Adj R-squared =	0.7039	
Source	Partial SS	df	MS	F	Prob>F
Model	980312	14	70022.286	13.56	0.0000
method	905872	4	226468	30.42	0.0000
class method	74440	10	7444		
class method	74440	10	7444	1.44	0.1845
Residual	309760	60	5162.6667		
Total	1290072	74	17433.405		

Like anova, contrast allows the | operator, which specifies that one variable is nested in the levels of another. We can use contrast to test the main effects of method and the simple effects of class within method.

```
. contrast method class|method
```

Contrasts of marginal linear predictions

Margins: asbalanced

	df	F	P>F
method	(not testable)		
class method			
1	2	2.80	0.0687
2	2	0.91	0.4089
3	2	1.10	0.3390
4	2	0.22	0.8025
5	2	2.18	0.1221
Joint	10	1.44	0.1845
Denominator	60		

Although `contrast` was able to perform the individual tests for the simple effects of `class` within `method`, empty cells in the interaction between `method` and `class` prevented `contrast` from testing for a main effect of `method`. Here we add the `emptycells(reweight)` option so that `contrast` can take the empty cells into account when computing the marginal means for `method`.

```
. contrast method class|method, emptycells(reweight)
Contrasts of marginal linear predictions
Margins:      asbalanced
Empty cells: reweight
```

	df	F	P>F
method	4	43.87	0.0000
class method			
1	2	2.80	0.0687
2	2	0.91	0.4089
3	2	1.10	0.3390
4	2	0.22	0.8025
5	2	2.18	0.1221
Joint	10	1.44	0.1845
Denominator	60		

Now, `contrast` does report a test for the main effects of `method`. However, if we compare this with the `anova` results, we will see that the results are different. They are different because `contrast` uses the residual error term to compute the F test by default. Using notation similar to `anova`, we can use the `/` operator to specify a different error term for the test. Therefore, we can reproduce the test of main effects from our `anova` command by typing

```
. contrast method / class|method /, emptycells(reweight)
Contrasts of marginal linear predictions
Margins:      asbalanced
Empty cells: reweight
```

	df	F	P>F
method	4	30.42	0.0000
class method	10 (denominator)		
class method			
1	2	2.80	0.0687
2	2	0.91	0.4089
3	2	1.10	0.3390
4	2	0.22	0.8025
5	2	2.18	0.1221
Joint	10	1.44	0.1845
Denominator	60		

Multiple comparisons

We have seen that `contrast` can report the individual linear combinations that make up the requested effects. Depending upon the specified option, `contrast` will report confidence intervals, p -values, or both in the effects table. By default, the reported confidence intervals and p -values are not adjusted for multiple comparisons. Use the `mcompare()` option to adjust the confidence intervals and p -values for multiple comparisons of the individual effects.

Let's compute the grand mean effects of `race` using the `g.` operator. We also specify the `mcompare(bonferroni)` option to compute p -values and confidence intervals using Bonferroni's adjustment.

```
. use https://www.stata-press.com/data/r19/cholesterol
(Artificial cholesterol data)
. anova chol race##agegrp
(output omitted)
. contrast g.race, mcompare(bonferroni)
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	Bonferroni P>F	P>F
race				
(Black vs mean)	1	7.07	0.0100	0.0301
(White vs mean)	1	2.82	0.0982	0.2947
(Other vs mean)	1	0.96	0.3312	0.9936
Joint	2	3.62	0.0329	
Denominator	60			

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

	Number of comparisons
race	3

	Contrast	Std. err.	Bonferroni [95% conf. interval]
race			
(Black vs mean)	4.17666	1.570588	.3083743 8.044945
(White vs mean)	-2.638058	1.570588	-6.506343 1.230227
(Other vs mean)	-1.538602	1.570588	-5.406887 2.329684

The last table reports a Bonferroni-adjusted confidence interval for each individual contrast. (Use the `effects` option to add p -values to the last table.) The first table includes a Bonferroni-adjusted p -value for each test that is not a joint test.

Joint tests are never adjusted for multiple comparisons. For example,

```
. contrast race@agegrp, mcompare(bonferroni)
```

Contrasts of marginal linear predictions

Margins: asbalanced

	df	F	P>F
race@agegrp			
10-19	2	1.37	0.2620
20-29	2	2.44	0.0958
30-39	2	3.12	0.0512
40-59	2	0.53	0.5889
60-79	2	2.90	0.0628
Joint	10	2.07	0.0409
Denominator	60		

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

	Number of comparisons
race@agegrp	10

	Contrast	Std. err.	Bonferroni [95% conf. interval]	
race@agegrp				
(White vs base) 10-19	6.841855	6.082862	-10.88697	24.57068
(White vs base) 20-29	-11.80631	6.082862	-29.53513	5.922513
(White vs base) 30-39	-14.40607	6.082862	-32.13489	3.322751
(White vs base) 40-59	-4.101691	6.082862	-21.83051	13.62713
(White vs base) 60-79	-10.60137	6.082862	-28.33019	7.127448
(Other vs base) 10-19	-2.975244	6.082862	-20.70407	14.75358
(Other vs base) 20-29	-11.45679	6.082862	-29.18561	6.272031
(Other vs base) 30-39	-11.41958	6.082862	-29.1484	6.309244
(Other vs base) 40-59	-6.17807	6.082862	-23.90689	11.55075
(Other vs base) 60-79	3.453375	6.082862	-14.27545	21.1822

Here we have five tests of simple effects with two degrees of freedom each. No Bonferroni-adjusted p -values are available for these tests, but the confidence intervals for the individual contrasts are adjusted.

Unbalanced data

By default, `contrast` treats all factors as balanced when computing marginal means. By balanced, we mean that `contrast` assumes an equal number of observations in each level of each factor and an equal number of observations in each cell of each interaction. If our data are balanced, there is no issue. If, however, our data are not balanced, we might prefer that `contrast` use the actual cell frequencies from our data in computing marginal means. We instruct `contrast` to use observed frequencies by adding the `asobserved` option.

Even if our data are unbalanced, we might still want `contrast` to compute balanced marginal means. It depends on what we want to test and what our data represent. If we have data from a designed experiment that started with an equal number of males and females but the data became unbalanced because the data from a few males were unusable, we might still want our margins computed as though the data were balanced. If, however, we have a representative sample of individuals from Los Angeles with 40% of European descent, 34% African-American, 25% Hispanic, and 1% Australian, we probably want our margins computed using these representative frequencies. We do not want Australians receiving the same weight as Europeans.

The following examples will use an unbalanced version of our dataset.

```
. use https://www.stata-press.com/data/r19/cholesterol3
(Artificial cholesterol data, unbalanced)
. tab race agegrp
```

Race	Age group					Total
	10-19	20-29	30-39	40-59	60-79	
Black	1	5	5	4	3	18
White	4	5	7	4	4	24
Other	3	7	6	5	4	25
Total	8	17	18	13	11	67

The row labeled `Total` gives observed cell frequencies for age group. These can be obtained by summing frequencies from the cells in the corresponding column. In this respect, we can also refer to them as marginal frequencies. We use the terms marginal frequencies and cell frequencies interchangeably below.

We begin by fitting the two-factor model with an interaction.

```
. anova chol race##agegrp
```

		Number of obs =	67	R-squared =	0.8179
		Root MSE =	8.37496	Adj R-squared =	0.7689
Source	Partial SS	df	MS	F	Prob>F
Model	16379.993	14	1169.9995	16.68	0.0000
race	230.7544	2	115.3772	1.64	0.2029
agegrp	13857.988	4	3464.4969	49.39	0.0000
race#agegrp	857.81521	8	107.2269	1.53	0.1701
Residual	3647.2774	52	70.13995		
Total	20027.27	66	303.44349		

Using observed cell frequencies

Recall that the marginal means are computed from the cell means. Treating the factors as balanced yields the following marginal means for race:

$$\eta_{1.} = \frac{1}{5}(\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15})$$

$$\eta_{2.} = \frac{1}{5}(\mu_{21} + \mu_{22} + \mu_{23} + \mu_{24} + \mu_{25})$$

$$\eta_{3.} = \frac{1}{5}(\mu_{31} + \mu_{32} + \mu_{33} + \mu_{34} + \mu_{35})$$

If we have a fixed population and unbalanced cells, then the $\eta_{i.}$ do not represent population means. If, however, our data are representative of the population, we can use the frequencies from our estimation sample to estimate the population marginal means, denoted $\mu_{i.}$.

Here are the results of testing for a main effect of race, treating all the factors as balanced.

```
. contrast r.race
```

```
Contrasts of marginal linear predictions
```

```
Margins: asbalanced
```

	df	F	P>F
race			
(White vs Black)	1	3.28	0.0757
(Other vs Black)	1	1.50	0.2263
Joint	2	1.64	0.2029
Denominator	52		

	Contrast	Std. err.	[95% conf. interval]	
race				
(White vs Black)	-5.324254	2.93778	-11.21934	.5708338
(Other vs Black)	-3.596867	2.93778	-9.491955	2.298221

The row labeled (White vs Black) is the test for $\eta_{2.} = \eta_{1.}$. The row labeled (Other vs Black) is the test for $\eta_{3.} = \eta_{1.}$.

If the observed marginal frequencies are representative of the distribution of the levels of agegrp, we can use them to form the marginal means of cho1 for each of the levels of race from the cell means.

$$\mu_{1.} = \frac{1}{67}(8\mu_{11} + 17\mu_{12} + 18\mu_{13} + 13\mu_{14} + 11\mu_{15})$$

$$\mu_{2.} = \frac{1}{67}(8\mu_{21} + 17\mu_{22} + 18\mu_{23} + 13\mu_{24} + 11\mu_{25})$$

$$\mu_{3.} = \frac{1}{67}(8\mu_{31} + 17\mu_{32} + 18\mu_{33} + 13\mu_{34} + 11\mu_{35})$$

Here are the results of testing for the main effects of race, using the observed marginal frequencies:

```
. contrast r.race, asobserved
```

```
Contrasts of marginal linear predictions
```

```
Margins: asobserved
```

	df	F	P>F
race			
(White vs Black)	1	7.25	0.0095
(Other vs Black)	1	3.89	0.0538
Joint	2	3.74	0.0304
Denominator	52		

	Contrast	Std. err.	[95% conf. interval]	
race				
(White vs Black)	-7.232433	2.686089	-12.62246	-1.842402
(Other vs Black)	-5.231198	2.651203	-10.55123	.0888295

The row labeled (White vs Black) is the test for $\mu_{2.} = \mu_{1.}$. The row labeled (Other vs Black) is the test for $\mu_{3.} = \mu_{1.}$. Both tests were insignificant when we tested the cell means resulting from balanced frequencies; however, when we tested the cell means from observed frequencies, the first test is significant beyond the 5% level (and the second test is nearly so).

Here we reproduce the results of the `asobserved` option with custom contrasts. Because we are modifying the way that the marginal means are constructed from the cell means, we will specify the contrasts on the predicted cell means. We use macro expansion, `=exp`, to evaluate the fractions instead of approximating them with decimals. Macro expansion guarantees that the contrast coefficients sum to zero. For more information, see [Macro expansion operators and function](#) in [P] [macro](#).

```
. contrast {race#agegrp -'=8/67' -'=17/67' -'=18/67' -'=13/67' -'=11/67'
>                  '=8/67'  '=17/67'  '=18/67'  '=13/67'  '=11/67'}
>          {race#agegrp -'=8/67' -'=17/67' -'=18/67' -'=13/67' -'=11/67'
>                  0          0          0          0          0
>                  '=8/67'  '=17/67'  '=18/67'  '=13/67'  '=11/67'}
```

Contrasts of marginal linear predictions

Margins: asbalanced

	df	F	P>F
race#agegrp			
(1) (1)	1	7.25	0.0095
(2) (2)	1	3.89	0.0538
Joint	2	3.74	0.0304
Denominator	52		

	Contrast	Std. err.	[95% conf. interval]	
race#agegrp				
(1) (1)	-7.232433	2.686089	-12.62246	-1.842402
(2) (2)	-5.231198	2.651203	-10.55123	.0888295

Weighted contrast operators

`contrast` provides observation-weighted versions of five of the contrast operators—`gw.`, `hw.`, `jw.`, `pw.`, and `qw.`. The first three of these operators perform comparisons of means across cells, and like the marginal means just discussed, these means can be computed in two ways: 1) as though the cell frequencies were equal or 2) using the observed cell frequencies from the estimation sample. The weighted operators provide versions of the standard (as balanced) operators that weight these means by their cell frequencies. The two orthogonal polynomial operators involve similar adjustments for weighting.

Let's examine what this means by using the `gw.` operator. The `gw.` operator is a weighted version of the `g.` operator. The `gw.` operator computes the grand mean using the cell frequencies for race obtained from the model fit.

Here we test the effects of race, comparing each level with the weighted grand mean but otherwise treating the factors as balanced in the marginal mean calculations.

```
. contrast gw.race
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
race			
(Black vs mean)	1	2.78	0.1014
(White vs mean)	1	2.06	0.1573
(Other vs mean)	1	0.06	0.8068
Joint	2	1.64	0.2029
Denominator	52		

	Contrast	Std. err.	[95% conf. interval]	
race				
(Black vs mean)	3.24931	1.948468	-.6605779	7.159198
(White vs mean)	-2.074944	1.44618	-4.976915	.8270276
(Other vs mean)	-.347557	1.414182	-3.18532	2.490206

The **observed marginal frequencies** of race are 18, 24, and 25. Thus, the row labeled (Black vs Mean) tests $\eta_1 = (18\eta_1 + 24\eta_2 + 25\eta_3)/67$; the row labeled (White vs Mean) tests $\eta_2 = (18\eta_1 + 24\eta_2 + 25\eta_3)/67$; and the row labeled (Other vs Mean) tests $\eta_3 = (18\eta_1 + 24\eta_2 + 25\eta_3)/67$.

Now, we reproduce the above results using custom contrasts. We are weighting the calculation of the grand mean from the marginal means for each of the races, but we are not weighting the calculation of the marginal means themselves. Therefore, we can specify the custom contrast on the marginal means for race instead of on the cell means.

```
. contrast {race '49/67' -'24/67' -'25/67'}
> {race -'18/67' '43/67' -'25/67'}
> {race -'18/67' -'24/67' '42/67'}
```

```
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
race			
(1)	1	2.78	0.1014
(2)	1	2.06	0.1573
(3)	1	0.06	0.8068
Joint	2	1.64	0.2029
Denominator	52		

	Contrast	Std. err.	[95% conf. interval]	
race				
(1)	3.24931	1.948468	-.6605779	7.159198
(2)	-2.074944	1.44618	-4.976915	.8270276
(3)	-.347557	1.414182	-3.18532	2.490206

Now, we will test for each race the difference between the marginal mean and the weighted grand mean, treating the factors as observed in the marginal mean calculations.

```
. contrast gw.race, asobserved wald ci
Contrasts of marginal linear predictions
Margins: asobserved
```

	df	F	P>F
race			
(Black vs mean)	1	6.81	0.0118
(White vs mean)	1	3.74	0.0587
(Other vs mean)	1	0.26	0.6099
Joint	2	3.74	0.0304
Denominator	52		

	Contrast	Std. err.	[95% conf. interval]	
race				
(Black vs mean)	4.542662	1.740331	1.050432	8.034891
(White vs mean)	-2.689771	1.39142	-5.481859	.1023172
(Other vs mean)	-.6885363	1.341261	-3.379973	2.002901

The row labeled (Black vs Mean) tests $\mu_1. = (18\mu_1. + 24\mu_2. + 25\mu_3.)/67$; the row labeled (White vs Mean) tests $\mu_2. = (18\mu_1. + 24\mu_2. + 25\mu_3.)/67$; and the row labeled (Other vs Mean) tests $\mu_3. = (18\mu_1. + 24\mu_2. + 25\mu_3.)/67$.

Here we use a custom contrast to reproduce the above result testing $\mu_1. = (18\mu_1. + 24\mu_2. + 25\mu_3.)/67$. Because both the calculation of the marginal means and the calculation of the grand mean are adjusted, we specify the custom contrast on the cell means.

```
. contrast {race#agegrp ' =49/67*8/67' ' =49/67*17/67' ' =49/67*18/67'
> ' =49/67*13/67' ' =49/67*11/67'
> ' =24/67*8/67' -' =24/67*17/67' -' =24/67*18/67'
> -' =24/67*13/67' -' =24/67*11/67'
> -' =25/67*8/67' -' =25/67*17/67' -' =25/67*18/67'
> -' =25/67*13/67' -' =25/67*11/67' }, nowald
```

```
Contrasts of marginal linear predictions
Margins: asbalanced
```

	Contrast	Std. err.	[95% conf. interval]	
race#agegrp (1) (1)	4.542662	1.740331	1.050432	8.034891

The Helmert and reverse Helmert contrasts also involve calculating averages of the marginal means; therefore, weighted versions of these parameters are available as well. The `hw.` operator is a weighted version of the `h.` operator that computes the mean of the subsequent levels using the cell frequencies obtained from the model fit. The `jw.` operator is a weighted version of the `j.` operator that computes the mean of the previous levels using the cell frequencies obtained from the model fit.

For orthogonal polynomials, we can use the `pw.` and `qw.` operators, which are the weighted versions of the `p.` and `q.` operators. In this case, the cell frequencies from the model fit are used in the calculation of the orthogonal polynomial contrast coefficients.

Testing factor effects on slopes

For linear models where the independent variables are all factor variables, the linear prediction at fixed levels of the factor variables turns out to be a cell mean. With these models, `contrast` computes and tests the effects of the factor variables on the expected mean of the dependent variable. When factor variables are interacted with continuous variables, `contrast` distinguishes factor effects on the intercept from factor effects on the slope.

Here we have 1980 census data including information on the birthrate (`brate`), the median age (`medage`), and the region of the country (`region`) for each of the 50 states. We can fit an ANCOVA model for `brate` using main effects of the factor variable `region` and the continuous variable `medage`.

```
. use https://www.stata-press.com/data/r19/census3
(1980 Census data by state)

. label list cenreg
cenreg:
      1 NE
      2 NCentral
      3 South
      4 West

. anova brate i.region c.medage
```

	Number of obs =	50	R-squared =	0.8264	
	Root MSE =	12.7575	Adj R-squared =	0.8110	
Source	Partial SS	df	MS	F	Prob>F
Model	34872.859	4	8718.2147	53.57	0.0000
region	2197.7545	3	732.58484	4.50	0.0076
medage	15327.423	1	15327.423	94.18	0.0000
Residual	7323.9611	45	162.75469		
Total	42196.82	49	861.15959		

For those more comfortable with linear regression, this is equivalent to the regression model

```
. regress brate i.region c.medage
```

You may use either.

We can use contrast to compute reference category effects for region. These contrasts compare the adjusted means of NCentral, South, and West regions with the adjusted mean of the NE region.

```
. contrast r.region
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
region			
(NCentral vs NE)	1	2.24	0.1417
(South vs NE)	1	0.78	0.3805
(West vs NE)	1	10.33	0.0024
Joint	3	4.50	0.0076
Denominator	45		

	Contrast	Std. err.	[95% conf. interval]	
region				
(NCentral vs NE)	9.061063	6.057484	-3.139337	21.26146
(South vs NE)	5.06991	5.72396	-6.458738	16.59856
(West vs NE)	21.71328	6.755616	8.106774	35.31979

Let's add the interaction between region and medage to the model.

```
. anova brate region##c.medage
```

	Number of obs =	50	R-squared =	0.9000	
	Root MSE =	10.0244	Adj R-squared =	0.8833	
Source	Partial SS	df	MS	F	Prob>F
Model	37976.315	7	5425.1878	53.99	0.0000
region	3405.0704	3	1135.0235	11.30	0.0000
medage	5279.7145	1	5279.7145	52.54	0.0000
region#medage	3103.456	3	1034.4853	10.29	0.0000
Residual	4220.5051	42	100.48822		
Total	42196.82	49	861.15959		

The parameterization for the expected value of brate as a function of region and medage is given by

$$E(\text{brate} | \text{region} = i, \text{medage}) = \alpha_0 + \alpha_i + \beta_0 \text{medage} + \beta_i \text{medage}$$

where α_0 is the intercept and β_0 is the slope of medage. We are modeling the effects of region in two different ways. The α_i parameters measure the effect of region on the intercept, and the β_i parameters measure the effect of region on the slope of medage.

contrast computes and tests effects on slopes separately from effects on intercepts. First, we will compute the reference category effects of region on the intercept:

```
. contrast r.region
```

Contrasts of marginal linear predictions

Margins: asbalanced

	df	F	P>F
region			
(NCentral vs NE)	1	0.09	0.7691
(South vs NE)	1	0.01	0.9389
(West vs NE)	1	8.50	0.0057
Joint	3	11.30	0.0000
Denominator	42		

	Contrast	Std. err.	[95% conf. interval]	
region				
(NCentral vs NE)	-49.38396	167.1281	-386.6622	287.8942
(South vs NE)	-9.058983	117.424	-246.0302	227.9123
(West vs NE)	343.0024	117.6547	105.5656	580.4393

Now, we will compute the reference category effects of region on the slope of medage:

```
. contrast r.region#c.medage
```

Contrasts of marginal linear predictions

Margins: asbalanced

	df	F	P>F
region#c.medage			
(NCentral vs NE)	1	0.16	0.6917
(South vs NE)	1	0.03	0.8558
(West vs NE)	1	8.18	0.0066
Joint	3	10.29	0.0000
Denominator	42		

	Contrast	Std. err.	[95% conf. interval]	
region#c.medage				
(NCentral vs NE)	2.208539	5.530981	-8.953432	13.37051
(South vs NE)	.6928008	3.788735	-6.953175	8.338777
(West vs NE)	-10.94649	3.827357	-18.67041	-3.22257

At the 5% level, the slope of medage for the West region differs from that of the NE region, but at that level of significance, we cannot say that the slope for the NCentral or the South region differs from that of the NE region.

This model is simple enough that the reference category contrasts reproduce the coefficients for region and for the interactions in an equivalent model fit by regress.

```
. regress brate region##c.medage
```

Source	SS	df	MS	Number of obs	=	50
Model	37976.3149	7	5425.18784	F(7, 42)	=	53.99
Residual	4220.5051	42	100.488217	Prob > F	=	0.0000
				R-squared	=	0.9000
				Adj R-squared	=	0.8833
Total	42196.82	49	861.159592	Root MSE	=	10.024

brate	Coefficient	Std. err.	t	P> t	[95% conf. interval]	
region						
NCentral	-49.38396	167.1281	-0.30	0.769	-386.6622	287.8942
South	-9.058983	117.424	-0.08	0.939	-246.0302	227.9123
West	343.0024	117.6547	2.92	0.006	105.5656	580.4393
medage	-8.802707	3.462865	-2.54	0.015	-15.79105	-1.814362
region#c.medage						
NCentral	2.208539	5.530981	0.40	0.692	-8.953432	13.37051
South	.6928008	3.788735	0.18	0.856	-6.953175	8.338777
West	-10.94649	3.827357	-2.86	0.007	-18.67041	-3.22257
_cons	411.8268	108.2084	3.81	0.000	193.4533	630.2002

This will not be the case for models that are more complicated.

Chow tests

Now, let's suppose we are fitting a model for birthrates on median age and marriage rate. We are also interested in whether the regression coefficients differ for states in the east versus states in the west. We use census divisions to create a new variable, `west`, that indicates which states are in the western half of the United States.

```
. generate west = inlist(division, 4, 7, 8, 9)
```

We fit a model that includes a separate intercept for west as well as an interaction between west and each of the other variables in our model.

```
. regress brate i.west#c.medage i.west#c.mrgrate
```

Source	SS	df	MS	Number of obs	=	50
Model	38516.2172	5	7703.24344	F(5, 44)	=	92.09
Residual	3680.60281	44	83.6500639	Prob > F	=	0.0000
				R-squared	=	0.9128
				Adj R-squared	=	0.9029
Total	42196.82	49	861.159592	Root MSE	=	9.146

brate	Coefficient	Std. err.	t	P> t	[95% conf. interval]	
1.west	327.8733	58.71793	5.58	0.000	209.5351	446.2115
medage	-7.532304	1.387624	-5.43	0.000	-10.32888	-4.735731
west#c.medage						
1	-10.11443	1.849103	-5.47	0.000	-13.84105	-6.387808
mrgrate	828.6813	643.3443	1.29	0.204	-467.8939	2125.257
west#c.mrgrate						
1	-800.8036	645.488	-1.24	0.221	-2101.699	500.092
_cons	366.5325	47.08904	7.78	0.000	271.6308	461.4343

We can test the effects of west on the intercept and on the slopes of medage and mrgrate. We will specify all of these effects in a single contrast command and include the overall option to obtain a joint test of effects, that is, a test that the coefficients for eastern states and for western states are equal.

```
. contrast west west#c.medage west#c.mrgrate, overall
```

```
Contrasts of marginal linear predictions
```

```
Margins: asbalanced
```

	df	F	P>F
west	1	31.18	0.0000
west#c.medage	1	29.92	0.0000
west#c.mrgrate	1	1.54	0.2213
Overall	3	22.82	0.0000
Denominator	44		

This overall test is referred to as a Chow test in econometrics ([Chow 1960](#)).

Beyond linear models

`contrast` may be used after almost any estimation command, with the added benefit that `contrast` provides direct support for testing main and interaction effects that is not available in most estimation commands. To illustrate, we will use `contrast` with results from a logistic regression. Stata's `logit` command fits logistic regression models, reporting the fitted regression coefficients. The `logistic` command fits the same models but reports odds ratios. Although `contrast` can report odds ratios for the computed effects, the tests are all computed from linear combinations of the model coefficients regardless of which estimation command we used.

Suppose we have data on patient satisfaction for three hospitals in a city. Let's begin by fitting a model for satisfied, whether the patient was satisfied with his or her treatment, using the main effects of hospital:

```
. use https://www.stata-press.com/data/r19/hospital, clear
(Artificial hospital satisfaction data)
. logit satisfied i.hospital
Iteration 0:  Log likelihood = -393.72216
Iteration 1:  Log likelihood = -387.55736
Iteration 2:  Log likelihood = -387.4768
Iteration 3:  Log likelihood = -387.47679

Logistic regression
Log likelihood = -387.47679
```

Number of obs =	802
LR chi2(2) =	12.49
Prob > chi2 =	0.0019
Pseudo R2 =	0.0159

satisfied	Coefficient	Std. err.	z	P> z	[95% conf. interval]	
hospital						
2	.5348129	.2136021	2.50	0.012	.1161604	.9534654
3	.7354519	.2221929	3.31	0.001	.2999618	1.170942
_cons	1.034708	.1391469	7.44	0.000	.7619855	1.307431

Because there are no other independent variables in this model, the reference category effects of hospital computed by `contrast` will match the fitted model coefficients, assuming a common reference level.

```
. contrast r.hospital
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	chi2	P>chi2
hospital			
(2 vs 1)	1	6.27	0.0123
(3 vs 1)	1	10.96	0.0009
Joint	2	12.55	0.0019

	Contrast	Std. err.	[95% conf. interval]	
hospital				
(2 vs 1)	.5348129	.2136021	.1161604	.9534654
(3 vs 1)	.7354519	.2221929	.2999618	1.170942

We see that the reference category effects are equal to the fitted coefficients. They also have the same interpretation, the difference in log odds from the reference category. The top table also provides a joint test of these effects, a test of the main effects of hospital.

We also have information on the condition for which each patient is being treated in the variable `illness`. Here we fit a logistic regression using a two-way crossed model of `hospital` and `illness`.

```
. label list illness
illness:
      1 Heart attack
      2 Stroke
      3 Pneumonia
      4 Lung disease
      5 Kidney failure

. logistic satisfied hospital##illness
Logistic regression                                Number of obs =    802
                                                    LR chi2(14)    =   38.51
                                                    Prob > chi2    =  0.0004
                                                    Pseudo R2     =  0.0489

Log likelihood = -374.46865
```

satisfied	Odds ratio	Std. err.	z	P> z	[95% conf. interval]	
hospital						
2	1.226496	.5492177	0.46	0.648	.509921	2.950049
3	1.711111	.8061016	1.14	0.254	.6796395	4.308021
illness						
Stroke	1.328704	.6044214	0.62	0.532	.544779	3.240678
Pneumonia	.7993827	.3408305	-0.53	0.599	.3466015	1.843653
Lung dise..	1.231481	.5627958	0.46	0.649	.5028318	3.016012
Kidney fa..	1.25	.5489438	0.51	0.611	.5285676	2.956102
hospital#illness						
2#Stroke	2.434061	1.768427	1.22	0.221	.5860099	10.11016
2#Pneumonia	4.045805	2.868559	1.97	0.049	1.008058	16.23769
2 #Lung dise..	.54713	.3469342	-0.95	0.342	.1578866	1.89599
2 #Kidney fa..	1.594425	1.081104	0.69	0.491	.4221288	6.022312
3#Stroke	.5416535	.3590089	-0.93	0.355	.1477555	1.985635
3#Pneumonia	1.579502	1.042504	0.69	0.489	.4332209	5.758783
3 #Lung dise..	3.137388	2.595748	1.38	0.167	.6198955	15.87881
3 #Kidney fa..	1.672727	1.226149	0.70	0.483	.3976256	7.036812
_cons	2.571429	.8099239	3.00	0.003	1.386983	4.767358

Note: **_cons** estimates baseline odds.

Using contrast, we can obtain an ANOVA-style table of tests for the main effects and interaction effects of hospital and illness.

```
. contrast hospital##illness
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	chi2	P>chi2
hospital	2	14.92	0.0006
illness	4	4.09	0.3937
hospital#illness	8	20.45	0.0088

Our interaction effect is significant, so we decide to evaluate the simple reference category effects of hospital within illness. We are particularly interested in patient satisfaction when being treated for a heart attack or stroke, so we will use the `i.` operator to limit our output to simple effects within the first two illnesses.

```
. contrast r.hospital@i(1 2).illness, nowald
Contrasts of marginal linear predictions
Margins: asbalanced
```

	Contrast	Std. err.	[95% conf. interval]	
hospital@illness				
(2 vs 1) Heart attack	.2041611	.4477942	-.6734995	1.081822
(2 vs 1) Stroke	1.093722	.5721288	-.0276296	2.215074
(3 vs 1) Heart attack	.5371429	.4710983	-.3861928	1.460479
(3 vs 1) Stroke	-.0759859	.4662325	-.9897847	.8378129

The row labeled (2 vs 1) heart attack estimates simple effects on the log odds when comparing hospital 2 with hospital 1 for patients having heart attacks. These effects are differences in the cell means of the linear predictions.

We can add the `or` option to report an odds ratio for each of these simple effects:

```
. contrast r.hospital@i(1 2).illness, nowald or
Contrasts of marginal linear predictions
Margins: asbalanced
```

	Odds ratio	Std. err.	[95% conf. interval]	
hospital@illness				
(2 vs 1) Heart attack	1.226496	.5492177	.509921	2.950049
(2 vs 1) Stroke	2.985366	1.708014	.9727486	9.162089
(3 vs 1) Heart attack	1.711111	.8061016	.6796395	4.308021
(3 vs 1) Stroke	.9268293	.4321179	.3716567	2.311306

These odds ratios are just the exponentiated version of the contrasts in the previous table.

For contrasts of the margins of nonlinear predictions, such as predicted probabilities, see [\[R\] margins, contrast](#).

Multiple equations

`contrast` works with models containing multiple equations. Commands such as `intreg` and `gnbreg` allow their ancillary parameters to be modeled as functions of independent variables, and `contrast` can compute and test effects within these equations. In addition, `contrast` allows a special pseudofactor for equation—called `_eqns`—when working with results from `manova`, `mvreg`, `mlogit`, and `mprobit`.

In [example 4](#) of [\[MV\] manova](#), we fit a two-way MANOVA model using data from [Woodard \(1931\)](#). Here we will fit this model using `mvreg`. The data represent patients with jaw fractures. `y1` is the patient's age, `y2` is blood lymphocytes, and `y3` is blood polymorphonuclears. Two factor variables, `gender` and `fracture`, are used as independent variables.

```
. use https://www.stata-press.com/data/r19/jaw
(Table 4.6. Two-way unbalanced data for fractures of the jaw, Rencher (1998))
```

```
. mvreg y1 y2 y3 = gender##fracture, vsquish nofvlabel
```

Equation	Obs	Parms	RMSE	"R-sq"	F	P>F
y1	27	6	10.21777	0.4086	2.902124	0.0382
y2	27	6	5.268768	0.4743	3.78967	0.0133
y3	27	6	4.993647	0.4518	3.460938	0.0195

	Coefficient	Std. err.	t	P> t	[95% conf. interval]	
y1						
2.gender	-17.5	11.03645	-1.59	0.128	-40.45156	5.451555
fracture						
2	-12.625	5.518225	-2.29	0.033	-24.10078	-1.149222
3	5.666667	5.899231	0.96	0.348	-6.601456	17.93479
gender#						
fracture						
2 2	21.375	12.68678	1.68	0.107	-5.008595	47.75859
2 3	8.833333	13.83492	0.64	0.530	-19.93796	37.60463
_cons	39.5	4.171386	9.47	0.000	30.82513	48.17487
y2						
2.gender	20.5	5.69092	3.60	0.002	8.665083	32.33492
fracture						
2	-3.125	2.84546	-1.10	0.285	-9.042458	2.792458
3	.6666667	3.041925	0.22	0.829	-5.659362	6.992696
gender#						
fracture						
2 2	-19.625	6.541907	-3.00	0.007	-33.22964	-6.02036
2 3	-23.66667	7.133946	-3.32	0.003	-38.50252	-8.830813
_cons	35.5	2.150966	16.50	0.000	31.02682	39.97318
y3						
2.gender	-18.16667	5.393755	-3.37	0.003	-29.38359	-6.949739
fracture						
2	1.083333	2.696877	0.40	0.692	-4.52513	6.691797
3	-3	2.883083	-1.04	0.310	-8.9957	2.9957
gender#						
fracture						
2 2	19.91667	6.200305	3.21	0.004	7.022426	32.81091
2 3	23.5	6.76143	3.48	0.002	9.438837	37.56116
_cons	61.16667	2.038648	30.00	0.000	56.92707	65.40627

contrast computes Wald tests using the coefficients from the first equation by default.

```
. contrast gender##fracture
Contrasts of marginal linear predictions
Margins: asbalanced
```

		df	F	P>F
y1	gender	1	2.16	0.1569
	fracture	2	2.74	0.0880
	gender#fracture	2	1.69	0.2085
	Denominator	21		

Here we use the equation() option to compute the Wald tests in the y2 equation:

```
. contrast gender##fracture, equation(y2)
Contrasts of marginal linear predictions
Margins: asbalanced
```

		df	F	P>F
y2	gender	1	5.41	0.0301
	fracture	2	7.97	0.0027
	gender#fracture	2	5.97	0.0088
	Denominator	21		

Here we use the equation index to compute the Wald tests in the third equation:

```
. contrast gender##fracture, equation(#3)
Contrasts of marginal linear predictions
Margins: asbalanced
```

		df	F	P>F
y3	gender	1	2.23	0.1502
	fracture	2	6.36	0.0069
	gender#fracture	2	6.66	0.0058
	Denominator	21		

Here we use the `atequations` option to compute Wald tests for each equation in the model. We also use the `vsquish` option to suppress the extra blank lines between terms.

```
. contrast gender##fracture, atequations vsquish
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
y1			
gender	1	2.16	0.1569
fracture	2	2.74	0.0880
gender#fracture	2	1.69	0.2085
y2			
gender	1	5.41	0.0301
fracture	2	7.97	0.0027
gender#fracture	2	5.97	0.0088
y3			
gender	1	2.23	0.1502
fracture	2	6.36	0.0069
gender#fracture	2	6.66	0.0058
Denominator	21		

Because we are investigating the results from `mvreg`, we can use the special `_eqns` factor to test for a marginal effect on the means among the dependent variables:

```
. contrast _eqns
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
_eqns	2	49.19	0.0000
Denominator	21		

Here we test whether the main effects of `gender` differ among the dependent variables:

```
. contrast gender#_eqns
Contrasts of marginal linear predictions
Margins: asbalanced
```

	df	F	P>F
gender#_eqns	2	3.61	0.0448
Denominator	21		

Although it is not terribly interesting in this case, we can even calculate contrasts across equations:

```
. contrast gender#r._eqns
```

Contrasts of marginal linear predictions

Margins: asbalanced

	df	F	P>F
gender#_eqns			
(joint) (2 vs 1)	1	5.82	0.0251
(joint) (3 vs 1)	1	0.40	0.5352
Joint	2	3.61	0.0448
Denominator	21		

Video example

[Introduction to contrasts in Stata: One-way ANOVA](#)

Stored results

`contrast` stores the following in `r()`:

Scalars

<code>r(df_r)</code>	variance degrees of freedom
<code>r(k_terms)</code>	number of terms in <i>termlist</i>
<code>r(level)</code>	confidence level of confidence intervals

Macros

<code>r(cmd)</code>	<code>contrast</code>
<code>r(cmdline)</code>	command as typed
<code>r(est_cmd)</code>	<code>e(cmd)</code> from original estimation results
<code>r(est_cmdline)</code>	<code>e(cmdline)</code> from original estimation results
<code>r(title)</code>	title in output
<code>r(overall)</code>	overall or empty
<code>r(emptycells)</code>	<i>empspec</i> from <code>emptycells()</code>
<code>r(mcmethod)</code>	<i>method</i> from <code>mcompare()</code>
<code>r(mctitle)</code>	title for <i>method</i> from <code>mcompare()</code>
<code>r(mcadjustall)</code>	<code>adjustall</code> or empty
<code>r(margin_method)</code>	<code>asbalanced</code> or <code>asobserved</code>

Matrices

<code>r(b)</code>	contrast estimates
<code>r(V)</code>	variance-covariance matrix of the contrast estimates
<code>r(error)</code>	contrast estimability codes; 0 means estimable, 8 means not estimable
<code>r(L)</code>	matrix of contrasts applied to the model coefficients
<code>r(table)</code>	matrix containing the contrasts with their standard errors, test statistics, <i>p</i> -values, and confidence intervals
<code>r(F)</code>	vector of <i>F</i> statistics; <code>r(df_r)</code> present
<code>r(chi2)</code>	vector of χ^2 statistics; <code>r(df_r)</code> not present
<code>r(p)</code>	vector of <i>p</i> -values corresponding to <code>r(F)</code> or <code>r(chi2)</code>
<code>r(df)</code>	vector of degrees of freedom corresponding to <code>r(p)</code>
<code>r(df2)</code>	vector of denominator degrees of freedom corresponding to <code>r(F)</code>

contrast with the post option stores the following in `e()`:

Scalars

<code>e(df_r)</code>	variance degrees of freedom
<code>e(k_terms)</code>	number of terms in <i>term</i> list

Macros

<code>e(cmd)</code>	contrast
<code>e(cmdline)</code>	command as typed
<code>e(properties)</code>	b V
<code>e(est_cmd)</code>	<code>e(cmd)</code> from original estimation results
<code>e(est_cmdline)</code>	<code>e(cmdline)</code> from original estimation results
<code>e(title)</code>	title in output
<code>e(overall)</code>	overall or empty
<code>e(emptycells)</code>	<i>empspec</i> from <code>emptycells()</code>
<code>e(margin_method)</code>	asbalanced or asobserved
<code>e(asbalanced)</code>	factor variables fvset as asbalanced
<code>e(asobserved)</code>	factor variables fvset as asobserved

Matrices

<code>e(b)</code>	contrast estimates
<code>e(V)</code>	variance–covariance matrix of the contrast estimates
<code>e(error)</code>	contrast estimability codes; 0 means estimable, 8 means not estimable
<code>e(L)</code>	matrix of contrasts applied to the model coefficients
<code>e(F)</code>	vector of unadjusted <i>F</i> statistics; <code>e(df_r)</code> present
<code>e(chi2)</code>	vector of χ^2 statistics; <code>e(df_r)</code> not present
<code>e(p)</code>	vector of unadjusted <i>p</i> -values corresponding to <code>e(F)</code> or <code>e(chi2)</code>
<code>e(df)</code>	vector of degrees of freedom corresponding to <code>e(p)</code>
<code>e(df2)</code>	vector of denominator degrees of freedom corresponding to <code>e(F)</code>

Methods and formulas

Methods and formulas are presented under the following headings:

Marginal linear predictions

Contrast operators

Reference level contrasts

Adjacent contrasts

Grand mean contrasts

Helmert contrasts

Reverse Helmert contrasts

Orthogonal polynomial contrasts

Contrasts within interactions

Multiple comparisons

Marginal linear predictions

`contrast` treats intercept effects separately from slope effects. To illustrate, consider the following parameterization for a quadratic regression of y on x that also models the effects of two factor variables A and B , where the levels of A are indexed by $i = 1, \dots, k_a$ and the levels of B are indexed by $j = 1, \dots, k_b$.

$$\begin{aligned} E(y|A = i, B = j, x) &= \eta_{0ij} + \eta_{1ij}x + \eta_{2ij}x^2 \\ \eta_{0ij} &= \eta_0 + \alpha_{0i} + \beta_{0j} + (\alpha\beta)_{0ij} \\ \eta_{1ij} &= \eta_1 + \alpha_{1i} + \beta_{1j} + (\alpha\beta)_{1ij} \\ \eta_{2ij} &= \eta_2 + \alpha_{2i} + \beta_{2j} + (\alpha\beta)_{2ij} \end{aligned}$$

We have partitioned the coefficients into three groups of parameters: η_{0ij} is a cell prediction for the intercept, η_{1ij} is a cell prediction for the slope on x , and η_{2ij} is a cell prediction for the slope on x^2 . For the intercept parameters, η_0 is the intercept, α_{0i} represents a main effect for factor A at its i th level, β_{0j} represents a main effect for factor B at its j th level, and $(\alpha\beta)_{0ij}$ represents an effect for the interaction of A and B at the ij th level. The individual coefficients in η_{1ij} and η_{2ij} have similar interpretations, but the effects are on the slopes of x and x^2 , respectively.

The marginal intercepts for A are given by

$$\eta_{0i.} = \sum_{j=1}^{k_b} f_{ij} \eta_{0ij}$$

where f_{ij} is a marginal relative frequency of the j th level of B and is controlled by the `asobserved` and `emptycells(reweight)` options according to

$$f_{ij} = \begin{cases} 1/k_b, & \text{default} \\ w_{.j}/w_{..}, & \text{asobserved} \\ 1/(k_b - e_{i.}), & \text{emptycells(reweight)} \\ w_{ij}/w_{i.}, & \text{emptycells(reweight) and asobserved} \end{cases}$$

Above, w_{ij} is the number of individuals with A at its i th level and B at its j th,

$$\begin{aligned} w_{i.} &= \sum_{j=1}^{k_b} w_{ij} \\ w_{.j} &= \sum_{i=1}^{k_a} w_{ij} \\ w_{..} &= \sum_{i=1}^{k_a} \sum_{j=1}^{k_b} w_{ij} \end{aligned}$$

and $e_{i.}$ is the number of empty cells where A is at its i th level. The marginal intercepts for B and marginal slopes on x and x^2 are similarly defined.

Estimates for the cell intercepts and slopes are computed using the corresponding linear combination of the coefficients from the fitted model. For example, the estimated cell intercepts are computed using

$$\hat{\eta}_{0ij} = \hat{\eta}_0 + \hat{\alpha}_{0i} + \hat{\beta}_{0j} + (\widehat{\alpha\beta})_{0ij}$$

and the estimated marginal intercepts for A are computed as

$$\hat{\eta}_{0i.} = \sum_{j=1}^{k_b} f_{ij} \hat{\eta}_{0ij}$$

Contrast operators

`contrast` performs Wald tests using linear combinations of marginal linear predictions. For example, the following linear combination can be used to test for a specific effect of factor A on the marginal intercepts.

$$\sum_{i=1}^{k_a} c_i \eta_{0i.}$$

If the c_i elements sum to zero, the linear combination is called a contrast. If the factor A is represented by a variable named A , then we specify this contrast using the following syntax:

$$\{A \ c_1 \ c_2 \ \dots \ c_{k_a}\}$$

Similarly, the following linear combination can be used to test for a specific interaction effect of factors A and B on the marginal slope of x .

$$\sum_{i=1}^{k_a} \sum_{j=1}^{k_b} c_{ij} \eta_{1ij}$$

If the factor B is represented by a variable named B , then we specify this contrast using the following syntax:

$$\{A\#B \ c_{11} \ c_{12} \ \dots \ c_{1k_b} \ c_{21} \ \dots \ c_{k_a k_b}\}$$

`contrast` has variable operators for several commonly used contrasts. Each contrast operator specifies a matrix of linear combinations that yield the requested set of contrasts to be applied to the marginal linear predictions associated with the attached factor variable.

Reference level contrasts

The `r .` operator compares each level with a reference level. Let \mathbf{R} be the corresponding contrast matrix for factor A , and then \mathbf{R} is a $(k_a - 1) \times k_a$ matrix with elements

$$\mathbf{R}_{ij} = \begin{cases} -1, & \text{if } j \text{ is the reference level} \\ 1, & \text{if } i = j \text{ and } j \text{ is less than the reference level} \\ 1, & \text{if } i + 1 = j \text{ and } j \text{ is greater than the reference level} \\ 0, & \text{otherwise} \end{cases}$$

If $k_a = 5$ and the reference level is the third level of A (specified as `rb(#3) . A`), then

$$\mathbf{R} = \begin{pmatrix} 1 & 0 & -1 & 0 & 0 \\ 0 & 1 & -1 & 0 & 0 \\ 0 & 0 & -1 & 1 & 0 \\ 0 & 0 & -1 & 0 & 1 \end{pmatrix}$$

Adjacent contrasts

The `a .` operator compares each level with the next level. Let \mathbf{A} be the corresponding contrast matrix for factor A , and then \mathbf{A} is a $(k_a - 1) \times k_a$ matrix with elements

$$\mathbf{A}_{ij} = \begin{cases} 1, & \text{if } i = j \\ -1, & \text{if } i + 1 = j \\ 0, & \text{otherwise} \end{cases}$$

If $k_a = 5$, then

$$\mathbf{A} = \begin{pmatrix} 1 & -1 & 0 & 0 & 0 \\ 0 & 1 & -1 & 0 & 0 \\ 0 & 0 & 1 & -1 & 0 \\ 0 & 0 & 0 & 1 & -1 \end{pmatrix}$$

The `ar .` operator compares each level with the previous level. If \mathbf{A} is the contrast matrix for the `a .` operator, then $-\mathbf{A}$ is the corresponding contrast matrix for the `ar .` operator.

Grand mean contrasts

The $g.$ operator compares each level with the mean of all the levels. Let \mathbf{G} be the corresponding contrast matrix for factor A , and then \mathbf{G} is a $k_a \times k_a$ matrix with elements

$$\mathbf{G}_{ij} = \begin{cases} 1 - 1/k_a, & \text{if } i = j \\ -1/k_a, & \text{if } i \neq j \end{cases}$$

If $k_a = 5$, then

$$\mathbf{G} = \begin{pmatrix} 4/5 & -1/5 & -1/5 & -1/5 & -1/5 \\ -1/5 & 4/5 & -1/5 & -1/5 & -1/5 \\ -1/5 & -1/5 & 4/5 & -1/5 & -1/5 \\ -1/5 & -1/5 & -1/5 & 4/5 & -1/5 \\ -1/5 & -1/5 & -1/5 & -1/5 & 4/5 \end{pmatrix}$$

The $gw.$ operator compares each level with the weighted mean of all the levels. The weights are taken from the observed weighted cell frequencies in the estimation sample of the fitted model. Let \mathbf{G}_w be the corresponding contrast matrix for factor A , and then \mathbf{G}_w is a $k_a \times k_a$ matrix with elements

$$\mathbf{G}_{ij} = \begin{cases} 1 - w_i/w., & \text{if } i = j \\ -w_j/w., & \text{if } i \neq j \end{cases}$$

where w_i is a marginal weight representing the number of individuals with A at its i th level and $w. = \sum_i w_i$.

Helmert contrasts

The $h.$ operator compares each level with the mean of the subsequent levels. Let \mathbf{H} be the corresponding contrast matrix for factor A , and then \mathbf{H} is a $(k_a - 1) \times k_a$ matrix with elements

$$\mathbf{H}_{ij} = \begin{cases} 1, & \text{if } i = j \\ -1/(k_a - i), & \text{if } i < j \\ 0, & \text{otherwise} \end{cases}$$

If $k_a = 5$, then

$$\mathbf{H} = \begin{pmatrix} 1 & -1/4 & -1/4 & -1/4 & -1/4 \\ 0 & 1 & -1/3 & -1/3 & -1/3 \\ 0 & 0 & 1 & -1/2 & -1/2 \\ 0 & 0 & 0 & 1 & -1 \end{pmatrix}$$

The hw . operator compares each level with the weighted mean of the subsequent levels. Let \mathbf{H}_w be the corresponding contrast matrix for factor A , and then \mathbf{H}_w is a $(k_a - 1) \times k_a$ matrix with elements

$$\mathbf{H}_{wij} = \begin{cases} 1, & \text{if } i = j \\ -w_j / \sum_{l=j}^{k_a} w_l, & \text{if } i < j \\ 0, & \text{otherwise} \end{cases}$$

Reverse Helmert contrasts

The j . operator compares each level with the mean of the previous levels. Let \mathbf{J} be the corresponding contrast matrix for factor A , and then \mathbf{J} is a $(k_a - 1) \times k_a$ matrix with elements

$$\mathbf{J}_{ij} = \begin{cases} 1, & \text{if } i + 1 = j \\ -1/i, & \text{if } j \leq i \\ 0, & \text{otherwise} \end{cases}$$

If $k_a = 5$, then

$$\mathbf{H} = \begin{pmatrix} -1 & 1 & 0 & 0 & 0 \\ -1/2 & -1/2 & 1 & 0 & 0 \\ -1/3 & -1/3 & -1/3 & 1 & 0 \\ -1/4 & -1/4 & -1/4 & -1/4 & 1 \end{pmatrix}$$

The jw . operator compares each level with the weighted mean of the previous levels. Let \mathbf{J}_w be the corresponding contrast matrix for factor A , and then \mathbf{J}_w is a $(k_a - 1) \times k_a$ matrix with elements

$$\mathbf{J}_{wij} = \begin{cases} 1, & \text{if } i + 1 = j \\ -w_j / \sum_{l=1}^i w_l, & \text{if } i \leq j \\ 0, & \text{otherwise} \end{cases}$$

Orthogonal polynomial contrasts

The `p.` operator applies orthogonal polynomial contrasts using the level values of the attached factor variable. The `q.` operator applies orthogonal polynomial contrasts using the level indices of the attached factor variable. These two operators are equivalent when the level values of the attached factor are equally spaced. The `pw.` and `qw.` operators are weighted versions of `p.` and `q.`, where the weights are taken from the observed weighted cell frequencies in the estimation sample of the fitted model. `contrast` uses the Christoffel–Darboux recurrence formula for computing orthogonal polynomial contrasts ([Abramowitz and Stegun 1964](#)). The elements of the contrasts are normalized such that

$$\mathbf{Q}'\mathbf{W}\mathbf{Q} = \frac{1}{w.}\mathbf{I}$$

where \mathbf{W} is a diagonal matrix of the marginal cell weights w_1, w_2, \dots, w_k of the attached factor variable (all 1 for `p.` and `q.`), and $w.$ is the sum of the weights (the number of levels k for `p.` and `q.`).

Contrasts within interactions

Contrast operators are allowed to be specified on factor variables participating in interactions. In such cases, `contrast` applies the proper matrix product of the contrast matrices to the cell margins of the interacted factor variables.

For example, consider the contrasts implied by specifying `r . A#h . B`. Let \mathbf{M} be the matrix of estimated cell margins for the levels of A and B , where the rows of \mathbf{M} are indexed by the levels of A and the columns are indexed by the levels of B . `contrast` puts the estimated cell margins in the following vector form:

$$\mathbf{v} = \text{vec}(\mathbf{M}') = \begin{pmatrix} \mathbf{M}_{11} \\ \mathbf{M}_{12} \\ \vdots \\ \mathbf{M}_{1k_b} \\ \mathbf{M}_{21} \\ \mathbf{M}_{22} \\ \vdots \\ \mathbf{M}_{2k_b} \\ \vdots \\ \mathbf{M}_{k_a k_b} \end{pmatrix}$$

The individual contrasts are then given by the elements of

$$(\mathbf{R} \otimes \mathbf{H})\mathbf{v}$$

where \otimes denotes the Kronecker direct product.

Multiple comparisons

See [R] **pwcompare** for details on the methods and formulas used to adjust p -values and confidence intervals for multiple comparisons. The formulas for Bonferroni's method and Šidák's method are presented with $m = k(k - 1)/2$, the number of pairwise comparisons for a factor term with k levels. For contrasts, m is instead the number of contrasts being performed on the factor term; often, $m = k - 1$ for a term with k levels.

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Also see

- [R] **contrast postestimation** — Postestimation tools for contrast
- [R] **lincom** — Linear combinations of parameters
- [R] **margins** — Marginal means, predictive margins, and marginal effects
- [R] **margins, contrast** — Contrasts of margins
- [R] **pwcompare** — Pairwise comparisons
- [R] **test** — Test linear hypotheses after estimation

[U] 20 Estimation and postestimation commands

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