Title

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example 39g — Three-level model (multilevel, generalized response)

Description Remarks and examples References Also see

Description

To demonstrate three-level models, we use the following data:

```
. use http://www.stata-press.com/data/r15/gsem_melanoma
(Skin cancer (melanoma) data)
. describe
Contains data from http://www.stata-press.com/data/r15/gsem_melanoma.dta
  obs:           354                          Skin cancer (melanoma) data
 vars:             6                          25 Mar 2016 15:28
 size:         4,956                          (_dta has notes)
-------------------------------------------------------------------------------
              storage   display    value
variable name   type    format     label      variable label
-------------------------------------------------------------------------------
nation          byte    %12.0g     nation     Nation ID
region          byte    %9.0g                 Region ID: EEC level-I areas
county          int     %9.0g                 County ID: EEC level-II/level-III
                                                areas
deaths          int     %9.0g                 No. deaths during 1971-1980
expected        float   %9.0g                 No. expected deaths
uv              float   %9.0g                 UV dose, mean-centered
-------------------------------------------------------------------------------
Sorted by: nation  region  county
. notes
_dta:
  1.  Smans, M., C. S. Muir, and P. Boyle. 1992. _Atlas of Cancer Mortality in
      the European Economic Community_.  Lyon, France: IARC Scientific
      Publications
  2.  Data on 7 nations, 3-95 regions w/i nation, 1-13 counties w/i region.
  3.  Variable deaths is # of deaths among males due to malignant melanoma,
      1971-1980.
  4.  Variable expected contains # of expected male deaths based on crude rates
      for the combined counties.
```

Rabe-Hesketh and Skrondal (2012, exercise 13.7) describe data from the *Atlas of Cancer Mortality in the European Economic Community* (EEC) (Smans, Mair, and Boyle 1993). The data were analyzed in Langford, Bentham, and McDonald (1998) and record the number of deaths among males due to malignant melanoma during 1971–1980.

Data are stored in the long form. Observations are counties within regions within nation. These data and some of the models fit below are also demonstrated in [ME] **menbreg**.

See *Structural models 4: Count models* and *Multilevel mixed-effects models* in [SEM] **intro 5** for background.

Remarks and examples

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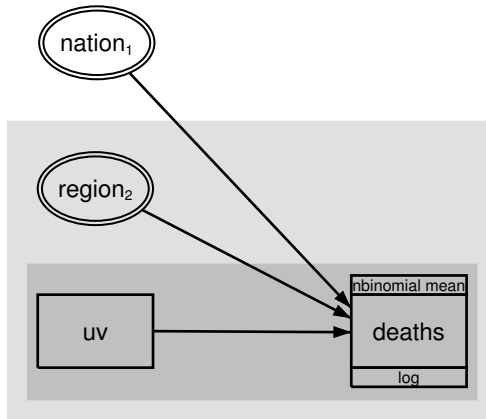
Remarks are presented under the following headings:

Three-level negative binomial model

The model we wish to fit is



Deaths due to malignant melanoma at the county level are modeled as being affected by ultraviolet exposure with random region and nation effects.

To fit this model, we type

```
. gsem (deaths <- uv M1[nation] M2[nation>region]), nbreg exposure(expected)
Fitting fixed-effects model:
Iteration 0:   log likelihood =  -1361.855
Iteration 1:   log likelihood = -1230.0211
Iteration 2:   log likelihood =  -1211.049
Iteration 3:   log likelihood = -1202.5641
Iteration 4:   log likelihood = -1202.5329
Iteration 5:   log likelihood = -1202.5329
Refining starting values:
Grid node 0:   log likelihood = -1209.6951
Fitting full model:
Iteration 0:   log likelihood = -1209.6951  (not concave)
Iteration 1:   log likelihood = -1195.0761  (not concave)
Iteration 2:   log likelihood = -1189.7235  (not concave)
Iteration 3:   log likelihood =   -1167.58  (not concave)
Iteration 4:   log likelihood = -1145.4325  (not concave)
Iteration 5:   log likelihood = -1138.4471
Iteration 6:   log likelihood = -1088.3882
Iteration 7:   log likelihood = -1086.7992
Iteration 8:   log likelihood = -1086.4085
Iteration 9:   log likelihood = -1086.3903
Iteration 10:  log likelihood = -1086.3902
Iteration 11:  log likelihood = -1086.3902
Generalized structural equation model           Number of obs     =        354
Response       : deaths
Family         : nbinomial
Dispersion     : mean
Link           : log
Log likelihood = -1086.3902
 ( 1)  [deaths]M1[nation] = 1
 ( 2)  [deaths]M2[nation>region] = 1
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
deaths						
uv	-.0335933	.0113725	-2.95	0.003	-.055883	-.0113035
M1[nation]	1	(constrained)				
M2[nation>region]	1	(constrained)				
_cons	-.0790606	.1295931	-0.61	0.542	-.3330583	.1749372
ln(expected)	1	(exposure)				
/deaths						
lnalpha	-4.182603	.3415036			-4.851937	-3.513268
var(M1[nation])	.1283614	.0678971			.0455187	.3619758
var(M2[nation>region])	.0401818	.0104855			.0240938	.067012

Notes:

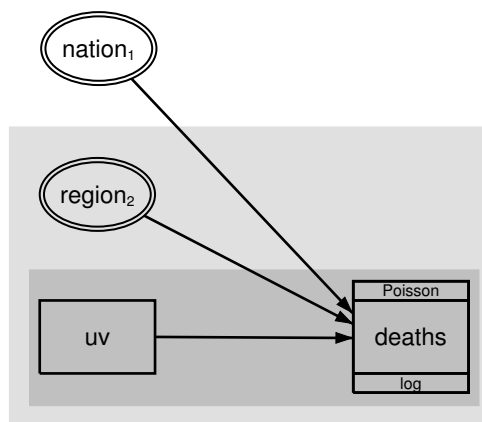
1. This is a three-level model of counties nested within region nested within nation, so we specified the latent variables as `M1[nation] M2[nation>region]`. Actually, we did the same thing in the diagram when we used the SEM Builder to define the latent variables, but the nesting information does not show in the double rings.
2. We fit this model by using negative binomial regression, also known as a mean-dispersion model. In the command, we typed `nbreg`, which is shorthand for `family(nbinomial mean) link(log)`.
3. A negative binomial distribution can be regarded as a gamma mixture of Poisson random variables, where said gamma distribution has mean 1 and variance α. The estimated $\ln(\alpha)$ is -4.183, which is small; α is estimated as 0.0153. The reported test statistic of -12.25 is significant at better than the 1% level for $\ln(\alpha) = 0$, but this is a test for $\alpha = 1$, not 0.
4. Zero does not mean lack of overdispersion, because we are including random effects that also allow for extra dispersion. For a discussion on these issues, see [ME] **menbreg**.
5. Notice that we specified `exposure(expected)`, where variable `expected` contains the expected number of deaths based on crude rates.

   The `exposure()` option is allowed with Poisson and negative binomial models. If we specify `exposure(`*varname*`)`, we are usually saying that each observation's time at risk is recorded in variable *varname*. When we omit the option, we are saying that each observation has the same time at risk. Obviously, if one observation had twice the time at risk of another observation, but was otherwise identical, we would expect twice the number of events in the first observation.

   In this case, however, we are using `exposure()` differently. We have a variable called `expected` containing the expected number of deaths from crude rates, and we are claiming `exposure(expected)`. What this is doing is saying that in two otherwise identical observations, if the number of expected deaths differed, we would expect the number of deaths due to melanoma to differ, too, and by the same proportion. See [SEM] **gsem family-and-link options**.

Three-level Poisson model

The same model, fit with Poisson, is



To fit the model in the command language, we type

```
. gsem (deaths <- uv  M1[nation] M2[nation>region]), poisson exposure(expected)
Fitting fixed-effects model:
Iteration 0:   log likelihood = -2136.5847
Iteration 1:   log likelihood = -1723.8955
Iteration 2:   log likelihood = -1723.7727
Iteration 3:   log likelihood = -1723.7727
Refining starting values:
Grid node 0:   log likelihood = -1166.6536
Refining starting values (unscaled likelihoods):
Grid node 0:   log likelihood = -1166.6536
Fitting full model:
Iteration 0:   log likelihood = -1166.6536  (not concave)
Iteration 1:   log likelihood = -1152.2741  (not concave)
Iteration 2:   log likelihood = -1146.3094  (not concave)
Iteration 3:   log likelihood = -1119.8479  (not concave)
Iteration 4:   log likelihood = -1108.0129  (not concave)
Iteration 5:   log likelihood = -1098.8067
Iteration 6:   log likelihood = -1095.7563
Iteration 7:   log likelihood = -1095.3164
Iteration 8:   log likelihood =   -1095.31
Iteration 9:   log likelihood =   -1095.31
Generalized structural equation model           Number of obs     =        354
Response       : deaths
Family         : Poisson
Link           : log
Log likelihood =   -1095.31
 ( 1)  [deaths]M1[nation] = 1
 ( 2)  [deaths]M2[nation>region] = 1
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
deaths						
uv	-.0282041	.0113998	-2.47	0.013	-.0505473	-.0058608
M1[nation]	1	(constrained)				
M2[nation>region]	1	(constrained)				
_cons	-.0639672	.1335515	-0.48	0.632	-.3257234	.197789
ln(expected)	1	(exposure)				
var(M1[nation])	.1371732	.0723303			.048802	.3855676
var(M2[nation>region])	.0483483	.0109079			.0310699	.0752353

Testing for overdispersion

The negative binomial model allows for overdispersion, or in a multilevel framework, allows for conditional overdispersion. The Poisson model has no overdispersion, or in a multilevel model, no overdispersion beyond that predicted by the latent variables. We can test whether there is dispersion beyond what Poisson would predict:

```
. gsem (deaths <- uv M1[nation] M2[nation>region]), nbreg exposure(expected)
(output omitted)
. estimates store nbreg
. gsem (deaths <- uv M1[nation] M2[nation>region]), poisson exposure(expected)
(output omitted)
. estimates store poisson
. lrtest nbreg poisson
Likelihood-ratio test                                 LR chi2(1)  =     17.84
(Assumption: poisson nested in nbreg)                 Prob > chi2 =    0.0000
```

We can reject at any reasonable level that the Poisson model adequately accounts for the dispersion in these data. Be aware that this test is conservative, because we are testing whether a variance goes to 0. `lrtest` usually issues a warning in such cases, but `lrtest` does not know that the relationship between negative binomial regression and Poisson regression involves a variance going to 0.

Fitting the models with the Builder

Use the diagram in *Three-level negative binomial model* above for reference.

1. Open the dataset.

   In the Command window, type

   ```
   . use http://www.stata-press.com/data/r15/gsem_melanoma
   ```

2. Open a new Builder diagram.

   Select menu item **Statistics > SEM (structural equation modeling) > Model building and estimation**.

3. Put the Builder in `gsem` mode by clicking on the GSEM button.

4. Create the generalized response variable.

   a. Select the Add generalized response variable tool, .

   b. Click in the diagram about one-third of the way in from the right and one-fourth of the way up from the bottom.

   c. In the Contextual Toolbar, select `Nbinomial mean, Log` in the *Family/Link* control.

   d. In the Contextual Toolbar, select `deaths` in the *Variable* control.

5. Create the observed exogenous variable.

   a. Select the Add observed variable tool, , and then click in the diagram about one-third of the way in from the right and one-fourth of the way up from the bottom.

   b. In the Contextual Toolbar, select `uv` with the *Variable* control.

6. Create the level-three latent variable.

   a. Select the Add multilevel latent variable tool, , and click above the rectangle for `uv` about one-fourth of the way down from the top.

   b. In the Contextual Toolbar, click on the ... button.

   c. Select the nesting level and nesting variable by selecting `2` from the *Nesting depth* control and selecting `nation` > *Observations* in the next line.

d. Specify `M1` as the *Base name*.

e. Click on **OK**.

7. Create the level-two latent variable.

a. Select the Add multilevel latent variable tool, , and click between the rectangle for `uv` and the double oval for $\texttt{nation}_1$.

b. In the Contextual Toolbar, click on the ... button.

c. Select the nesting level and nesting variable by selecting `3` from the *Nesting depth* control and selecting `nation` > `region` > *Observations* in the next control.

d. Specify `M2` as the *Base name*.

e. Click on **OK**.

8. Create the paths from the exogenous variables to `deaths`.

a. Select the Add path tool, .

b. Click in the right side of the `uv` rectangle (it will highlight when you hover over it), and drag a path to the left side of the `deaths` rectangle (it will highlight when you can release to connect the path).

c. Continuing with the tool, draw paths from the right side of the double ovals for $\texttt{nation}_1$ and $\texttt{region}_2$ to the left side of the `deaths` rectangle.

9. Specify the level of exposure.

Use the Select tool, , and double-click in the `deaths` rectangle. In the resulting dialog box, select `expected` in the *Exposure* control, and click on **OK**.

10. Clean up the location of the paths.

If you do not like where the paths have been connected to the rectangles or oval, use the Select tool, , to click on the path, and then simply click on where it connects to a rectangle or oval and drag the endpoint.

11. Estimate.

Click on the **Estimate** button, , in the Standard Toolbar, and then click on **OK** in the resulting *GSEM estimation options* dialog box.

You can open a completed diagram in the Builder by typing

```
. webgetsem gsem_3lev
```

References

Langford, I. H., G. Bentham, and A. McDonald. 1998. Multi-level modelling of geographically aggregated health data: A case study on malignant melanoma mortality and UV exposure in the European community. *Statistics in Medicine* 17: 41–57.

Rabe-Hesketh, S., and A. Skrondal. 2012. *Multilevel and Longitudinal Modeling Using Stata*. 3rd ed. College Station, TX: Stata Press.

Smans, M., C. S. Mair, and P. Boyle. 1993. *Atlas of Cancer Mortality in the European Economic Community*. Lyon, France: IARC Scientific Publications.

Also see

[SEM] **example 38g** — Random-intercept and random-slope models (multilevel)

[SEM] **example 34g** — Combined models (generalized responses)

[SEM] **gsem** — Generalized structural equation model estimation command

[SEM] **intro 5** — Tour of models