Example 49g — Multiple-group Weibull survival model

Description

Below we demonstrate `gsem`'s `group()` option, which allows us to fit models in which coefficients, intercepts, and other types of parameters differ across groups of the data. We will fit a Weibull model to the following survival data

```
. use https://www.stata-press.com/data/r16/gsem_cancer
(Patient Survival in Drug Trial)
. describe
Contains data from https://www.stata-press.com/data/r16/gsem_cancer.dta
obs: 48 Patient Survival in Drug Trial
vars: 4 16 Jan 2019 15:41
(_dta has notes)

 storage display value
  variable name type format label variable label
 studytime byte %8.0g Months to death or end of exp.
died byte %8.0g 1 if patient died
drug byte %8.0g Drug type (1=placebo)
age byte %8.0g Patient's age at start of exp.
```

Sorted by:

. notes
_dta:
1. Artificial data on cancer patient survival.
2. Drug 1 is a placebo. Drugs 2 and 3 are alternative treatments.

See [SEM] Example 47g and [SEM] Example 48g for how to fit survival models using `gsem`. In this example, we focus on fitting multiple-group models using `gsem`'s `group()` and `ginvariant()` options. See [SEM] Intro 6 for background on these options.

Remarks and examples

Remarks are presented under the following headings:

Fitting the multiple-group model
Fitting the model with the Builder
Fitting the multiple-group model

We want to fit the model

\[
\text{studytime} \sim \text{Weibull} (\log \text{age})
\]

If we do not allow for group differences, we can fit this model by typing

\[
\texttt{. gsem (studytime <- age, family(weibull, failure(died)))}
\]

However, this study used one placebo and two drugs. We want to allow the intercept and auxiliary parameter to vary across the levels of \textit{drug} but constrain the coefficient on \textit{age} to be equal across the levels of \textit{drug}. In other words, we want to fit a stratified Weibull model. We add the \texttt{group(drug)} and \texttt{ginvariant(coef)} options to our \texttt{gsem} command to specify that \textit{drug} is the group identifier and that coefficients should not vary across groups.

\[
\texttt{. gsem (studytime <- age, family(weibull, failure(died))), g}
\]

\[
\texttt{roup(drug) ginvariant(coef)}
\]

\[
(\text{iteration log omitted})
\]

\[
\text{Generalized structural equation model} \quad \text{Number of obs} = 48
\]

\[
\text{Grouping variable} = \text{drug} \quad \text{Number of groups} = 3
\]

\[
\text{Log likelihood} = -109.28976
\]

\[
(1) \quad [\text{studytime}]_1\text{bn.drug}\#c\text{.age} - [\text{studytime}]_3\text{.drug}\#c\text{.age} = 0
\]

\[
(2) \quad [\text{studytime}]_2\text{.drug}\#c\text{.age} - [\text{studytime}]_3\text{.drug}\#c\text{.age} = 0
\]

\[
\text{Group} : 1 \quad \text{Number of obs} = 20
\]

\[
\text{Response} : \text{studytime} \quad \text{No. of failures} = 19
\]

\[
\text{Family} : \text{Weibull} \quad \text{Time at risk} = 180
\]

\[
\text{Form} : \text{proportional hazards}
\]

\[
\text{Link} : \log
\]

| Coef.     | Std. Err. | z      | P>|z|     | [95% Conf. Interval] |
|-----------|-----------|--------|---------|--------------------|
| studytime age | .1212332  | .0367538 | 3.30   | 0.001   | .049197  | .1932694 |
|           _cons | -10.36921 | 2.341022 | -4.43  | 0.000   | -14.95753 | -5.780896 |

\[
[/\text{studytime} ln_p]
\]

| Coef.     | Std. Err. | z      | P>|z|     | [95% Conf. Interval] |
|-----------|-----------|--------|---------|--------------------|
| studytime age | .1212332  | .0367538 | 3.30   | 0.001   | .049197  | .1932694 |
|           _cons | -14.93039 | 3.445179 | -4.33  | 0.000   | -21.68282 | -8.177965 |

\[
[/\text{studytime} ln_p]
\]

| Coef.     | Std. Err. | z      | P>|z|     | [95% Conf. Interval] |
|-----------|-----------|--------|---------|--------------------|
| studytime age | .9413477  | .2943728 | 3.12   | 0.002   | .3643876 | 1.518308 |
|           _cons | -14.93039 | 3.445179 | -4.33  | 0.000   | -21.68282 | -8.177965 |
Notes:

1. In [SEM] Intro 6, we wrote that \texttt{gsem} classifies each parameter into one of seven classes, which are the following:

<table>
<thead>
<tr>
<th>Class description</th>
<th>Class name</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. intercepts and cutpoints</td>
<td>\texttt{cons}</td>
</tr>
<tr>
<td>2. fixed coefficients</td>
<td>\texttt{coef}</td>
</tr>
<tr>
<td>3. latent variable coefficients</td>
<td>\texttt{loading}</td>
</tr>
<tr>
<td>4. covariances of errors</td>
<td>\texttt{errvar}</td>
</tr>
<tr>
<td>5. scaling parameters</td>
<td>\texttt{scale}</td>
</tr>
<tr>
<td>6. means of exogenous variables</td>
<td>\texttt{means}</td>
</tr>
<tr>
<td>7. covariances of exogenous latent variables</td>
<td>\texttt{covex}</td>
</tr>
<tr>
<td>8. all the above</td>
<td>\texttt{all}</td>
</tr>
<tr>
<td>9. none of the above</td>
<td>\texttt{none}</td>
</tr>
</tbody>
</table>

By default, classes 1, 2, and 3 are constrained to be equal, and the others are allowed to vary.

2. In the output, we have a separate table of parameter estimates for each level of \texttt{drug}. The coefficient on \texttt{age} is 0.12 in all groups, but, as expected, the other parameters differ across groups.

We can replay the results with the \texttt{byparm} option to request that results be sorted by parameter rather than by groups. This output makes it easy to compare estimates across the groups. Alternatively, we could have added the \texttt{byparm} option when we fit the model.
Example 49g — Multiple-group Weibull survival model

<table>
<thead>
<tr>
<th>Group</th>
<th>Response</th>
<th>Family</th>
<th>Log likelihood</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>studytime</td>
<td>Weibull</td>
<td>-109.28976</td>
</tr>
</tbody>
</table>

Number of obs = 14
No. of failures = 6
Time at risk = 355

Form: proportional hazards
Link: log

| Coef. Std. Err. z P>|z| [95% Conf. Interval] |
|------------------------|------------------------|--------|------------------------|
| studytime              |                        |        |                        |
| age                    | 1                      | .1212332 | .0367538 | 3.30 | 0.001 | .049197 | .1932694 |
|                        | 2                      | .1212332 | .0367538 | 3.30 | 0.001 | .049197 | .1932694 |
|                        | 3                      | .1212332 | .0367538 | 3.30 | 0.001 | .049197 | .1932694 |
| _cons                  |                        |        |                        |
|                        | 1                      | -10.36921 | 2.341022 | -4.43 | 0.000 | -14.95753 | -5.780896 |
|                        | 2                      | -14.93039 | 3.445179 | -4.33 | 0.000 | -21.68282 | -8.177965 |
|                        | 3                      | -14.08495 | 3.242463 | -4.34 | 0.000 | -20.44006 | -7.72984 |

/studytime ln_p

| Coef. Std. Err. z P>|z| [95% Conf. Interval] |
|------------------------|------------------------|--------|------------------------|
|                        | 1                      | .4541282 | .1715663 | .1178645 | .7903919 |
|                        | 2                      | .9413477 | .2943728 | .3643876 | 1.518308 |
|                        | 3                      | .6735495 | .369625 | -.0509022 | 1.398001 |

The estimated intercepts, labeled _cons in the first section of the table, do not vary much across groups. We can perform a Wald test of whether these coefficients are the same using the test command. If we replay the results by typing gsem, coelegend, we find that we can refer to the three intercepts as _b[studytime:1.drug], _b[studytime:2.drug], and _b[studytime:3.drug]. Therefore, our test command is:

```
```

( 1) [studytime]1bn.drug - [studytime]2.drug = 0
( 2) [studytime]1bn.drug - [studytime]3.drug = 0

chi2( 2) = 5.49
Prob > chi2 = 0.0641

Using a 5% significance level, we fail to reject the null hypothesis that the intercepts are equal. If we wanted to refit the model based on these findings, we could include cons in the ginvariant() option as follows and constrain both the coefficients and the intercepts across groups.

```
gsem (studytime <- age, family(weibull, failure(died))), group(drug) ginvariant(coef cons)
```

Fitting the model with the Builder

Use the diagram in *Fitting the multiple-group model* above for reference.

1. Open the dataset.

   In the Command window, type

   ```
   use https://www.stata-press.com/data/r16/gsem_cancer
   ```
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 button.

4. Create the Weibull regression component for studytime.

   Select the Add regression component tool, , and then click in the diagram about one-third of the way in from the left and halfway down.

   In the resulting dialog box,
   a. select studytime in the **Dependent variable** control;
   b. check **Make response generalized**;
   c. select Weibull, Log in the **Family/Link** control;
   d. select the **Select variables** radio button (it may already be selected);
   e. use the **Independent variables** control to select the variable age;
   f. select Left in the **Independent variables’ direction** control;
   g. click on OK.

   If you wish, move the component by clicking on any variable and dragging it.

5. Specify the censoring variable.

   a. Choose the Select tool, .
   b. Click on the box for studytime.
   c. In the Contextual Toolbar, click on the **Properties...** button.
   d. In the resulting Variable properties dialog box, click on the **Failure and truncation...** button in the Variable tab.
   e. In the resulting Failure and truncation dialog box, select died in the Failure variable control. Click on OK.
   f. Click on OK in the Variables properties dialog box.

6. Clean up.

   The box for _t is created closer to the independent variables than it is in the example diagram. Use the Select tool, , and click on the box for _t. Drag it to the right to allow more space for results along the paths.

7. Estimate.

   Click on the Estimate button, , in the Standard Toolbar.

   In the resulting dialog box, do the following:
   a. Select the **Group** tab.
   b. Select the **Group analysis** radio button. Select the variable drug in the **Group variable** control.
   c. Select **Fixed coefficients** in the **Parameters that are equal across groups** control.
   d. Click on OK.
e. In the Standard Toolbar, use the Group control to toggle between results for group 1 and group 2.

You can open a completed diagram in the Builder by typing

   . webgetsem gsem.grp

Also see

[SEM] Example 47g — Exponential survival model
[SEM] Example 48g — Loglogistic survival model with censored and truncated data
[SEM] Intro 5 — Tour of models
[SEM] Intro 6 — Comparing groups
[SEM] gsem — Generalized structural equation model estimation command