example 21 — Group-level goodness of fit

Description

Below we demonstrate the `estat ggof` command, which may be used after `sem` with the `group()` option. `estat ggof` displays group-by-group goodness-of-fit statistics.

We pick up where [SEM] example 20 left off:

```
. use http://www.stata-press.com/data/r15/sem_2fmmby
. sem (Peer -> peerrel1 peerrel2 peerrel3 peerrel4) ///
    (Par  -> parrel1 parrel2 parrel3 parrel4), group(grade)
```

Remarks and examples

```
. estat ggof
```

Group-level fit statistics

<table>
<thead>
<tr>
<th>grade</th>
<th>N</th>
<th>SRMR</th>
<th>CD</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>134</td>
<td>0.063</td>
<td>0.969</td>
</tr>
<tr>
<td>2</td>
<td>251</td>
<td>0.047</td>
<td>0.955</td>
</tr>
</tbody>
</table>

Note: Group-level chi-squared statistics are not reported because of constraints between groups.

Notes:

1. Reported are the goodness-of-fit tests that `estat gof, stats(residuals)` would report. The difference is that they are reported for each group rather than overall.

2. If the fit is good, then SRMR (standardized root mean squared residual) will be close to 0 and CD (the coefficient of determination) will be near 1.

It is also appropriate to run `estat gof` to obtain overall results:

```
. estat gof, stats(residuals)
```

<table>
<thead>
<tr>
<th>Fit statistic</th>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Size of residuals</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SRMR</td>
<td>0.056</td>
<td>Standardized root mean squared residual</td>
</tr>
<tr>
<td>CD</td>
<td>0.958</td>
<td>Coefficient of determination</td>
</tr>
</tbody>
</table>

Also see

- [SEM] example 20 — Two-factor measurement model by group
- [SEM] example 4 — Goodness-of-fit statistics
- [SEM] estat ggof — Group-level goodness-of-fit statistics
- [SEM] estat gof — Goodness-of-fit statistics