**Description**

`estat residuals` is for use after `sem` but not `gsem`.

`estat residuals` displays the mean and covariance residuals. Normalized and standardized residuals are available.

Both mean and covariance residuals are reported unless `sem`’s option `nomeans` was specified or implied at the time the model was fit, in which case mean residuals are not reported.

`estat residuals` usually does not work following `sem` models fit with `method(mlmv)`. It also does not work if there are any missing values, which after all is the whole point of using `method(mlmv)`.

**Menu**

Statistics > SEM (structural equation modeling) > Goodness of fit > Matrices of residuals

**Syntax**

```
estat residuals [, options]
```

<table>
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<th>options</th>
<th>Description</th>
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<td><code>normalized</code></td>
<td>report normalized residuals</td>
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<tr>
<td><code>standardized</code></td>
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<tr>
<td><code>sample</code></td>
<td>use sample covariances in residual variance calculations</td>
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<td><code>zerotolerance(tol)</code></td>
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**Options**

`normalized` and `standardized` are alternatives. If neither is specified, raw residuals are reported.

Normalized residuals and standardized residuals attempt to adjust the residuals in the same way, but they go about it differently. The normalized residuals are always valid, but they do not follow a standard normal distribution. The standardized residuals do follow a standard normal distribution but only if they can be calculated; otherwise, they will equal missing values. When both can be calculated (equivalent to both being appropriate), the normalized residuals will be a little smaller than the standardized residuals. See Jöreskog and Sörbom (1986).
`estat residuals` — Display mean and covariance residuals

Sample specifies that the sample variance and covariances be used in variance formulas to compute normalized and standardized residuals. The default uses fitted variance and covariance values as described by Bollen (1989).

`nm1` specifies that the variances be computed using $N - 1$ in the denominator rather than using sample size $N$.

`zerotolerance(tol)` treats residuals within $tol$ of 0 as if they were 0. $tol$ must be a numeric value less than 1. The default is `zerotolerance(0)`, meaning that no tolerance is applied. When standardized residuals cannot be calculated, it is because a variance calculated by the Hausman (1978) theorem turns negative. Applying a tolerance to the residuals turns some residuals into 0 and then division by the negative variance becomes irrelevant, and that may be enough to solve the calculation problem.

`format(%)fmt)` specifies the display format. The default is `format(%9.3f)`.

Remarks and examples

See `[SEM] Example 10`.

Stored results

`estat residuals` stores the following in `r()`: Scalars

- `r(N_groups)` number of groups

Macros

- `r(sample)` empty or `sample`, if `sample` was specified
- `r(nm1)` empty or `nm1`, if `nm1` was specified

Matrices

- `r(nobs)` sample size for each group
- `r(res_mean[#,])` raw mean residuals (for group #) (*)
- `r(res_cov[#,])` raw covariance residuals (for group #)
- `r(nres_mean[#,])` normalized mean residuals (for group #) (*)
- `r(nres_cov[#,])` normalized covariance residuals (for group #)
- `r(sres_mean[#,])` standardized mean residuals (for group #) (*)
- `r(sres_cov[#,])` standardized covariance residuals (for group #)

(*) If there are no estimated means or intercepts in the `sem` model, these matrices are not returned.

References


Also see

[SEM] `sem` — Structural equation model estimation command

[SEM] `sem postestimation` — Postestimation tools for sem

[SEM] `estat eqgof` — Equation-level goodness-of-fit statistics

[SEM] `estat ggof` — Group-level goodness-of-fit statistics

[SEM] `estat gof` — Goodness-of-fit statistics

[SEM] Example 10 — MIMIC model

[SEM] Methods and formulas for sem — Methods and formulas for sem