Description

xtcloglog fits population-averaged and random-effects complementary log-log (cloglog) models for a binary dependent variable. Complementary log-log models are typically used when one of the outcomes is rare relative to the other.

Quick start

Random-effects complementary log-log regression of \( y \) on \( x_1 \) and \( x_2 \) using \texttt{xtset} data
\[
\texttt{xtcloglog \ y \ x1 \ x2}
\]
Add indicators for levels of categorical variable \( a \) and interact \( x_1 \) with \( x_2 \)
\[
\texttt{xtcloglog \ y \ x1 \ x2 \ c.x1#c.x2 \ i.a}
\]
As above, but suppress iteration log
\[
\texttt{xtcloglog \ y \ x1 \ x2 \ c.x1#c.x2 \ i.a, nolog}
\]
Population-averaged model with an exchangeable correlation structure
\[
\texttt{xtcloglog \ y \ x1 \ x2 \ c.x1#c.x2 \ i.a, pa}
\]
Random-effects model with bootstrap standard errors
\[
\texttt{xtcloglog \ y \ x1 \ x2 \ c.x1#c.x2 \ i.a, vce(bootstrap)}
\]
Population-averaged model with an autoregressive correlation structure of order 1
\[
\texttt{xtcloglog \ y \ x1 \ x2 \ c.x1#c.x2 \ i.a, pa corr(ar 1)}
\]

Menu

Statistics > Longitudinal/panel data > Binary outcomes > Complementary log-log regression (RE, PA)
## Syntax

### Random-effects (RE) model

```plaintext
xtcloglog  depvar  [ indepvars ]  [ if ]  [ in ]  [ weight ]  [ , re  RE_options ]
```

### Population-averaged (PA) model

```plaintext
xtcloglog  depvar  [ indepvars ]  [ if ]  [ in ]  [ weight ]  ,  pa  [ PA_options ]
```

<table>
<thead>
<tr>
<th><strong>RE_options</strong></th>
<th><strong>Description</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td><code>noconstant</code></td>
<td>suppress constant term</td>
</tr>
<tr>
<td><code>re</code></td>
<td>use random-effects estimator; the default</td>
</tr>
<tr>
<td><code>offset(varname)</code></td>
<td>include <code>varname</code> in model with coefficient constrained to 1</td>
</tr>
<tr>
<td><code>constraints(constraints)</code></td>
<td>apply specified linear constraints</td>
</tr>
<tr>
<td><code>asis</code></td>
<td>retain perfect predictor variables</td>
</tr>
<tr>
<td><code>vce(vcetype)</code></td>
<td><code>vcetype</code> may be <code>oim</code>, <code>robust</code>, <code>cluster clustvar</code>, <code>bootstrap</code>, or <code>jackknife</code></td>
</tr>
<tr>
<td><code>level(#)</code></td>
<td>set confidence level; default is <code>level(95)</code></td>
</tr>
<tr>
<td><code>lrmodel</code></td>
<td>perform the likelihood-ratio model test instead of the default Wald test</td>
</tr>
<tr>
<td><code>eform</code></td>
<td>report exponentiated coefficients</td>
</tr>
<tr>
<td><code>nocnsreport</code></td>
<td>do not display constraints</td>
</tr>
<tr>
<td><code>display_options</code></td>
<td>control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling</td>
</tr>
</tbody>
</table>

### Integration

| `intmethod(intmethod)`        | integration method; `intmethod` may be `mvaghermite` (the default) or `ghermite` |
| `intpoints(#)`                | use `#` quadrature points; default is `intpoints(12)`                           |

### Maximization

| `maximize_options`           | control the maximization process; seldom used                                   |
| `collinear`                   | keep collinear variables                                                       |
| `coeflegend`                  | display legend instead of statistics                                            |
| **xtcloglog** — Random-effects and population-averaged cloglog models |
|------------------------|-----------------------------|

### PA_options

#### Model
- **noconstant**  
  suppress constant term
- **pa**  
  use population-averaged estimator
- **offset(varname)**  
  include varname in model with coefficient constrained to 1
- **asis**  
  retain perfect predictor variables

#### Correlation
- **corr(correlation)**  
  within-panel correlation structure
- **force**  
  estimate even if observations unequally spaced in time

#### SE/Robust
- **vce(vcetype)**  
  vcetype may be conventional, robust, bootstrap, or jackknife
- **ncmp**  
  use divisor \(N - P\) instead of the default \(N\)
- **scale(parm)**  
  overrides the default scale parameter; \(parm\) may be \(x^2\), dev, phi, or #

#### Reporting
- **level(#)**  
  set confidence level; default is level(95)
- **eform**  
  report exponentiated coefficients
- **display_options**  
  control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling

#### Optimization
- **optimize_options**  
  control the optimization process; seldom used
- **coeflegend**  
  display legend instead of statistics

### correlation

- **exchangeable**  
  exchangeable; the default
- **independent**  
  independent
- **unstructured**  
  unstructured
- **fixed matname**  
  user-specified
- **ar #**  
  autoregressive of order #
- **stationary #**  
  stationary of order #
- **nonstationary #**  
  nonstationary of order #

A panel variable must be specified. For xtcloglog, pa, correlation structures other than exchangeable and independent require that a time variable also be specified. Use xtset; see [XT] xtset.

indepvars may contain factor variables; see [U] 11.4.3 Factor variables.

by, mi estimate, and statsby are allowed; see [U] 11.1.10 Prefix commands. fp is allowed for the random-effects model.

vce(bootstrap) and vce(jackknife) are not allowed with the mi estimate prefix; see [MI] mi estimate. iwights, fweights, and pweights are allowed for the population-averaged model, and iwights are allowed for the random-effects model; see [U] 11.1.6 weight. Weights must be constant within panel.

collinear and coeflegend do not appear in the dialog box.

See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.
Options for RE model

- **noconstant**: see [R] Estimation options.
- **re** requests the random-effects estimator, which is the default.
- **offset(varname)**, **constraints(constraints)**: see [R] Estimation options.
- **asis** forces retention of perfect predictor variables and their associated, perfectly predicted observations and may produce instabilities in maximization; see [R] probit.

---

**SE/Robust**

- **vce(vcetype)** specifies the type of standard error reported, which includes types that are derived from asymptotic theory (oim), that are robust to some kinds of misspecification (robust), that allow for intragroup correlation (cluster clustvar), and that use bootstrap or jackknife methods (bootstrap, jackknife); see [XT] vce_options.

Specifying vce(robust) is equivalent to specifying vce(cluster panelvar); see xtcloglog, re and the robust VCE estimator in Methods and formulas.

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**Reporting**

- **level(#)**, **lrmodel**: see [R] Estimation options.
- **eform** displays the exponentiated coefficients and corresponding standard errors and confidence intervals.
- **nocnsreport**: see [R] Estimation options.
- **display_options**: noci, noprvalues, nomitted, vsquish, noemptycells, baselevels, allbaselevels, nofvlabel, fvwrap(#), fvwrapon(style), cformat(%fmt), pformat(%fmt), sformat(%fmt), and nolstretch; see [R] Estimation options.

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**Integration**

- **intmethod(intmethod)**, **intpoints(#)**: see [R] Estimation options.

---

**Maximization**

- **maximize_options**: difficult, technique(algorithm_spec), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(init_specs); see [R] Maximize. These options are seldom used.

The following options are available with xtcloglog but are not shown in the dialog box:
- **collinear**, **coeflegend**: see [R] Estimation options.

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Options for PA model

- **noconstant**: see [R] Estimation options.
- **pa** requests the population-averaged estimator.
- **offset(varname)**: see [R] Estimation options
asis forces retention of perfect predictor variables and their associated, perfectly predicted observations and may produce instabilities in maximization; see [R] probit.

**Correlation**

`corr(correlation)` specifies the within-panel correlation structure; the default corresponds to the equal-correlation model, `corr(exchangeable)`.

When you specify a correlation structure that requires a lag, you indicate the lag after the structure’s name with or without a blank; for example, `corr(ar 1)` or `corr(ar1)`.

If you specify the fixed correlation structure, you specify the name of the matrix containing the assumed correlations following the word `fixed`, for example, `corr(fixed myr)`.

**SE/Robust**

`vce(vcetype)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory (`conventional`), that are robust to some kinds of misspecification (`robust`), and that use bootstrap or jackknife methods (`bootstrap`, `jackknife`); see [XT] `vce_options`.

`vce(conventional)`, the default, uses the conventionally derived variance estimator for generalized least-squares regression.

**nmp, scale(x2 | dev | phi | #); see [XT] `vce_options`**.

**Reporting**

`level(#); see [R] Estimation options.`

eform displays the exponentiated coefficients and corresponding standard errors and confidence intervals.

`display_options: noci, nopvalues, noomitted, vsquish, noemptycells, baselevels, allbaselevels, nofvlabel, fvwrap(#), fvwrapon(style), cformat(%fmt), pformat(%fmt), sformat(%fmt), and nolstretch; see [R] Estimation options.`

**Optimize**

`optimize_options` control the iterative optimization process. These options are seldom used.

`iterate(#)` specifies the maximum number of iterations. When the number of iterations equals #, the optimization stops and presents the current results, even if convergence has not been reached. The default is `iterate(100)`.

`tolerance(#)` specifies the tolerance for the coefficient vector. When the relative change in the coefficient vector from one iteration to the next is less than or equal to #, the optimization process is stopped. `tolerance(1e-6)` is the default.

`log` and `nolog` specify whether to display the iteration log. The iteration log is displayed by default unless you used `set iterlog off` to suppress it; see `set iterlog in [R] set iter`.

`trace` specifies that the current estimates be printed at each iteration.
The following option is available with `xtcloglog` but is not shown in the dialog box: `coeflegend`; see [R] Estimation options.

**Remarks and examples**

`xtcloglog` may be used to fit a population-averaged model or a random-effects complementary log-log (cloglog) model. There is no command for a conditional fixed-effects model, as there does not exist a sufficient statistic allowing the fixed effects to be conditioned out of the likelihood. Unconditional fixed-effects cloglog models may be fit with `cloglog` with indicator variables for the panels. However, unconditional fixed-effects estimates are biased. We do not discuss fixed-effects further in this entry.

By default, the population-averaged model is an equal-correlation model; that is, `xtcloglog`, `pa` assumes `corr(exchangeable)`. Thus, `xtcloglog`, `pa` is a shortcut command for fitting the population-averaged model using `xtgee`; see [XT] `xtgee`. Typing

```
  . xtcloglog ..., pa ...
```

is equivalent to typing

```
  . xtgee ..., ... family(binomial) link(cloglog) corr(exchangeable)
```

Also see [XT] `xtgee` for information about `xtcloglog`.

By default or when `re` is specified, `xtcloglog` fits, via maximum likelihood, the random-effects model

\[
Pr(y_{it} \neq 0|x_{it}) = P(x_{it}\beta + \nu_i)
\]

for \(i = 1, \ldots, n\) panels, where \(t = 1, \ldots, n_i\), \(\nu_i\) are i.i.d., \(N(0, \sigma^2_{\nu})\), and \(P(z) = 1 - \exp\{-\exp(z)\}\).

Underlying this model is the variance-components model

\[
y_{it} \neq 0 \iff x_{it}\beta + \nu_i + \epsilon_{it} > 0
\]

where \(\epsilon_{it}\) are i.i.d. extreme-value (Gumbel) distributed with the mean equal to Euler’s constant and variance \(\sigma^2_{\epsilon} = \pi^2/6\), independently of \(\nu_i\). The nonsymmetric error distribution is an alternative to logit and probit analysis and is typically used when the positive (or negative) outcome is rare.
Example 1

Suppose that we are studying unionization of women in the United States and are using the union dataset; see [XT] xt. We wish to fit a random-effects model of union membership:

```
. use https://www.stata-press.com/data/r16/union
(NLS Women 14–24 in 1968)
. xtcloglog union age grade not_smsa south##c.year
(output omitted)
```

Random-effects complementary log-log model  Number of obs = 26,200
Group variable: idcode  Number of groups = 4,434
Random effects u_i ~ Gaussian  Obs per group:
min = 1  avg = 5.9  max = 12
Integration method: mvaghermite  Integration pts. = 12
Wald chi2(6) = 248.58
Log likelihood = -10535.928  Prob > chi2 = 0.0000

| union          | Coef. | Std. Err. | z    | P>|z| | [95% Conf. Interval] |
|---------------|-------|-----------|------|-----|----------------------|
| age           | .0128659 | .0119004 | 1.08 | 0.280 | -.0104586 to .0361903 |
| grade         | .06985 | .0138135 | 5.06 | 0.000 | .0427776 to .096924 |
| not_smsa      | -.198416 | .0647943 | -3.06 | 0.002 | -.3254104 to -.0714215 |
| i.south       | -2.047645 | .488965 | -4.19 | 0.000 | -.3.005999 to -1.089291 |
| year          | -.0006432 | .0123569 | -0.05 | 0.958 | -.0248623 to .0235759 |
| south#c.year  |       |           |      |       |                      |
| 1             | .0164259 | .006065 | 2.71 | 0.007 | .0045387 to .0283132 |
| _cons         | -3.269158 | .659029 | -4.96 | 0.000 | -4.560831 to -1.977485 |

| /lnsig2u      | 1.24128 | .0461705 | 1.150787 | 1.331772 |
| sigma_u       | 1.860118 | .0429413 | 1.77783 | 1.946214 |
| rho           | .6777778 | .0100834 | .6577057 | .6972152 |

LR test of rho=0: chibar2(01) = 6009.36  Prob >= chibar2 = 0.000

The output includes the additional panel-level variance component, which is parameterized as the log of the standard deviation, \( \ln \sigma_\nu \) (labeled \( \lnsig2u \) in the output). The standard deviation \( \sigma_\nu \) is also included in the output, labeled \( \sigma_u \), together with \( \rho \) (labeled \( \text{rho} \)),

\[
\rho = \frac{\sigma_\nu^2}{\sigma_\nu^2 + \sigma_\epsilon^2}
\]

which is the proportion of the total variance contributed by the panel-level variance component.

When \( \rho \) is zero, the panel-level variance component is not important, and the panel estimator is no different from the pooled estimator (cloglog). A likelihood-ratio test of this is included at the bottom of the output, which formally compares the pooled estimator with the panel estimator.
As an alternative to the random-effects specification, you might want to fit an equal-correlation population-averaged cloglog model by typing

```
.xtcloglog union age grade not_smsa south##c.year, pa
```

```
Iteration 1:  tolerance =  .11878399
Iteration 2:  tolerance =  .01424628
Iteration 3:  tolerance =  .00075278
Iteration 4:  tolerance =  .00003195
Iteration 5:  tolerance =  1.66e-06
Iteration 6:  tolerance =  8.308e-08
```

GEE population-averaged model

<table>
<thead>
<tr>
<th>Number of obs</th>
<th>26,200</th>
</tr>
</thead>
<tbody>
<tr>
<td>Group variable:</td>
<td>idcode</td>
</tr>
<tr>
<td>Number of groups</td>
<td>4,434</td>
</tr>
<tr>
<td>Link:</td>
<td>cloglog</td>
</tr>
<tr>
<td>Family:</td>
<td>binomial</td>
</tr>
<tr>
<td>Correlation:</td>
<td>exchangeable</td>
</tr>
<tr>
<td>Wald chi2(6)</td>
<td>234.66</td>
</tr>
</tbody>
</table>

Scale parameter: 1

```
| Coef. | Std. Err. | z   | P>|z|  | [95% Conf. Interval] |
|-------|-----------|-----|------|-----------------------|
| union |           |     |      |                       |
| age   | .0153737  | .0081156 | 1.89 | 0.058 | -.0005326 .03128 |
| grade | .0549518  | .0095093 | 5.78 | 0.000 | .0363139 .0735897 |
| not_smsa | -.1045232 | .0431082 | -2.42 | 0.015 | -.1890138 -.0200326 |
| 1.south | -1.714868 | .3384558 | -5.07 | 0.000 | -2.378229 -1.051507 |
| year   | -.0115881 | .0084125 | -1.38 | 0.168 | -.0280763 .0049001 |
| south#c.year | 1 | .0149796 | .0041687 | 3.59 | 0.000 | .0068091 .0231501 |
| _cons  | -1.488278 | .4468005 | -3.33 | 0.001 | -2.363991 -.6125652 |
```

Example 2

In [R] **cloglog**, we showed these results and compared them with cloglog, vce(cluster id). **xtcloglog** with the **pa** option allows a **vce(robust)** option so we can obtain the population-averaged cloglog estimator with the robust variance calculation by typing
. xtcloglog union age grade not_smsa south##c.year, pa vce(robust)

(output omitted)

GEE population-averaged model

<table>
<thead>
<tr>
<th></th>
<th>Number of obs = 26,200</th>
</tr>
</thead>
<tbody>
<tr>
<td>Group variable:</td>
<td>idcode</td>
</tr>
<tr>
<td>Number of groups</td>
<td>4,434</td>
</tr>
</tbody>
</table>

| Family: | binomial |
| Correlation: | exchangeable |
| min = | 1 |
| max = | 12 |

Wald chi2(6) = 157.24

Scale parameter: 1

(Std. Err. adjusted for clustering on idcode)

<table>
<thead>
<tr>
<th></th>
<th>Coef.</th>
<th>Std. Err.</th>
<th>z</th>
<th>P&gt;z</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>union</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>age</td>
<td>0.0153737</td>
<td>0.0079446</td>
<td>1.94</td>
<td>0.053</td>
<td>-0.0001974 to 0.0309448</td>
</tr>
<tr>
<td>grade</td>
<td>0.0549518</td>
<td>0.0117258</td>
<td>4.69</td>
<td>0.000</td>
<td>0.0319697 to 0.077934</td>
</tr>
<tr>
<td>not_smsa</td>
<td>-0.1045232</td>
<td>0.0548598</td>
<td>-1.91</td>
<td>0.057</td>
<td>-0.2120465 to 0.0030001</td>
</tr>
<tr>
<td>1.south</td>
<td>-1.714868</td>
<td>0.4864999</td>
<td>-3.52</td>
<td>0.000</td>
<td>-2.66839 to -0.7613455</td>
</tr>
<tr>
<td>year</td>
<td>-0.0115881</td>
<td>0.0085742</td>
<td>-1.35</td>
<td>0.177</td>
<td>-0.0283932 to 0.005217</td>
</tr>
<tr>
<td>south#c.year</td>
<td>1</td>
<td>0.0149796</td>
<td>2.47</td>
<td>0.013</td>
<td>0.0031124 to 0.0268468</td>
</tr>
<tr>
<td>_cons</td>
<td>-1.488278</td>
<td>0.4924738</td>
<td>-3.02</td>
<td>0.003</td>
<td>-2.453509 to -0.5230472</td>
</tr>
</tbody>
</table>

These standard errors are similar to those shown for cloglog, vce(cluster id) in [R] cloglog.

Technical note

The random-effects model is calculated using quadrature, which is an approximation whose accuracy depends partially on the number of integration points used. We can use the quadchk command to see if changing the number of integration points affects the results. If the results change, the quadrature approximation is not accurate given the number of integration points. Try increasing the number of integration points using the intpoints() option and run quadchk again. Do not attempt to interpret the results of estimates when the coefficients reported by quadchk differ substantially. See [XT] quadchk for details and [XT] xtpoisson for an example.

Because the xtcloglog likelihood function is calculated by Gauss–Hermite quadrature, on large problems the computations can be slow. Computation time is roughly proportional to the number of points used for the quadrature.
xtcloglog, re stores the following in e():

Scalars

- \( e(N) \) number of observations
- \( e(N_g) \) number of groups
- \( e(k) \) number of parameters
- \( e(k_{aux}) \) number of auxiliary parameters
- \( e(k_{eq}) \) number of equations in \( e(b) \)
- \( e(k_{eq_model}) \) number of equations in overall model test
- \( e(k_dv) \) number of dependent variables
- \( e(ll) \) log likelihood
- \( e(ll_0) \) log likelihood, constant-only model
- \( e(ll_c) \) log likelihood, comparison model
- \( e(chi2) \) \( \chi^2 \)
- \( e(chi2_c) \) \( \chi^2 \) for comparison test
- \( e(N_clust) \) number of clusters
- \( e(rho) \) \( \rho \)
- \( e(sigma_u) \) panel-level standard deviation
- \( e(n_quad) \) number of quadrature points
- \( e(g_min) \) smallest group size
- \( e(g_avg) \) average group size
- \( e(g_max) \) largest group size
- \( e(p) \) \( p \)-value for model test
- \( e(rank) \) rank of \( e(V) \)
- \( e(rank0) \) rank of \( e(V) \) for constant-only model
- \( e(ic) \) number of iterations
- \( e(rc) \) return code
- \( e(converged) \) 1 if converged, 0 otherwise

Macros

- \( e(cmd) \) xtcloglog
- \( e(cmdline) \) command as typed
- \( e(depvar) \) name of dependent variable
- \( e(ivar) \) variable denoting groups
- \( e(model) \) re
- \( e(wtype) \) weight type
- \( e(wexp) \) weight expression
- \( e(title) \) title in estimation output
- \( e(clustvar) \) name of cluster variable
- \( e(offset) \) linear offset variable
- \( e(chi2type) \) Wald or LR; type of model \( \chi^2 \) test
- \( e(chi2_c) \) Wald or LR; type of model \( \chi^2 \) test corresponding to \( e(chi2_c) \)
- \( e(vcetype) \) vcetype specified in vce()
- \( e(vctype) \) title used to label Std. Err.
- \( e(intmethod) \) integration method
- \( e(distrib) \) Gaussian; the distribution of the random effect
- \( e(opt) \) type of optimization
- \( e(which) \) max or min: whether optimizer is to perform maximization or minimization
- \( e(ml_method) \) type of ml method
- \( e(user) \) name of likelihood-evaluator program
- \( e(technique) \) maximization technique
- \( e(properties) \) b V
- \( e(predict) \) program used to implement predict
- \( e(marginsdefault) \) default predict() specification for margins
- \( e(asbalanced) \) factor variables fvset as asbalanced
- \( e(asobserved) \) factor variables fvset as asobserved

Matrices

- \( e(b) \) coefficient vector
- \( e(Cns) \) constraints matrix
- \( e(ilog) \) iteration log
- \( e(gradient) \) gradient vector
xtcloglog, pa stores the following in e():

Scalars
- e(N) number of observations
- e(N_g) number of groups
- e(df_m) model degrees of freedom
- e(chi2) $\chi^2$
- e(p) $p$-value for model test
- e(df_pear) degrees of freedom for Pearson $\chi^2$
- e(chi2_dev) $\chi^2$ test of deviance
- e(chi2_dis) $\chi^2$ test of deviance dispersion
- e(deviance) deviance
- e(dispers) deviance dispersion
- e(phi) scale parameter
- e(g_min) smallest group size
- e(g_avg) average group size
- e(g_max) largest group size
- e(rank) rank of e(V)
- e(tol) target tolerance
- e(dif) achieved tolerance
- e(rc) return code

Macros
- e(cmd) xtgee
- e(cmd2) xtcloglog
- e(cmdline) command as typed
- e(depvar) name of dependent variable
- e(ivar) variable denoting groups
- e(tvar) variable denoting time within groups
- e(model) pa
- e(family) binomial
- e(link) cloglog; link function
- e(corr) correlation structure
- e(scale) x2, dev, phi, or #; scale parameter
- e(wtype) weight type
- e(wexp) weight expression
- e(offset) linear offset variable
- e(chi2type) Wald; type of model $\chi^2$ test
- e(vcetype) vcetype specified in vce()
- e(nmp) nmp, if specified
- e(properties) b V
- e(predict) program used to implement predict
- e(marginsnotok) predictions disallowed by margins
- e(asbalanced) factor variables fvset as asbalanced
- e(asobserved) factor variables fvset as asobserved

Matrices
- e(b) coefficient vector
- e(R) estimated working correlation matrix
- e(V) variance–covariance matrix of the estimators
- e(V_modelbased) model-based variance

Functions
- e(sample) marks estimation sample
xtcloglog, pa reports the population-averaged results obtained using xtgee, family(binomial) link(cloglog) to obtain estimates.

For the random-effects model, assume a normal distribution, \( N(0, \sigma^2) \), for the random effects \( \nu_i \),

\[
Pr(y_{i1}, \ldots, y_{in_i} | x_{i1}, \ldots, x_{in_i}) = \int_{-\infty}^{\infty} \frac{e^{-\nu_i^2/2\sigma^2}}{\sqrt{2\pi\sigma^2}} \left\{ \prod_{t=1}^{n_i} F(y_{it}, x_{it}\beta + \nu_i) \right\} d\nu_i
\]

where

\[
F(y, z) = \begin{cases} 
1 - \exp\{ - \exp(z)\} & \text{if } y \neq 0 \\
\exp\{ - \exp(z)\} & \text{otherwise}
\end{cases}
\]

The panel-level likelihood \( l_i \) is given by

\[
l_i = \int_{-\infty}^{\infty} \frac{e^{-\nu_i^2/2\sigma^2}}{\sqrt{2\pi\sigma^2}} \left\{ \prod_{t=1}^{n_i} F(y_{it}, x_{it}\beta + \nu_i) \right\} d\nu_i
\]

\[
\equiv \int_{-\infty}^{\infty} g(y_{it}, x_{it}, \nu_i) d\nu_i
\]

This integral can be approximated with \( M \)-point Gauss–Hermite quadrature

\[
\int_{-\infty}^{\infty} e^{-x^2} h(x) dx \approx \sum_{m=1}^{M} w^*_m h(a^*_m)
\]

This is equivalent to

\[
\int_{-\infty}^{\infty} f(x) dx \approx \sum_{m=1}^{M} w^*_m \exp\{ (a^*_m)^2 \} f(a^*_m)
\]

where the \( w^*_m \) denote the quadrature weights and the \( a^*_m \) denote the quadrature abscissas. The log likelihood, \( L \), is the sum of the logs of the panel-level likelihoods \( l_i \).

The default approximation of the log likelihood is by adaptive Gauss–Hermite quadrature, which approximates the panel-level likelihood with

\[
l_i \approx \sqrt{2\hat{\sigma}_i} \sum_{m=1}^{M} w^*_m \exp\{ (a^*_m)^2 \} g(y_{it}, x_{it}, \sqrt{2\hat{\sigma}_i} a^*_m + \hat{\mu}_i)\]

where \( \hat{\sigma}_i \) and \( \hat{\mu}_i \) are the adaptive parameters for panel \( i \). Therefore, with the definition of \( g(y_{it}, x_{it}, \nu_i) \), the total log likelihood is approximated by
The log likelihood can also be calculated by nonadaptive Gauss–Hermite quadrature, the int-method(ghermite) option, where $\rho = \sigma_\nu^2 / (\sigma_\nu^2 + 1)$:

$$ L = \sum_{i=1}^{n} w_i \log \left\{ \Pr(y_{i1}, \ldots, y_{in_i} | x_{i1}, \ldots, x_{in_i}) \right\} $$

$$ \approx \sum_{i=1}^{n} w_i \log \left[ \frac{1}{\sqrt{\pi}} \sum_{m=1}^{M} w_m \prod_{t=1}^{n_i} F(y_{it}, x_{it}\beta + a_m^*(2\rho/(1-\rho))^{1/2}) \right] $$

Both quadrature formulas require that the integrated function be well approximated by a polynomial of degree equal to the number of quadrature points. The number of periods (panel size) can affect whether

$$ \prod_{t=1}^{n_i} F(y_{it}, x_{it}\beta + \nu) $$
is well approximated by a polynomial. As panel size and $\rho$ increase, the quadrature approximation can become less accurate. For large $\rho$, the random-effects model can also become unidentified. Adaptive quadrature gives better results for correlated data and large panels than nonadaptive quadrature; however, we recommend that you use the `quadchk` command (see [XT] `quadchk`) to verify the quadrature approximation used in this command, whichever approximation you choose.

**xtcloglog, re and the robust VCE estimator**

Specifying `vce(robust)` or `vce(cluster clustvar)` causes the Huber/White/sandwich VCE estimator to be calculated for the coefficients estimated in this regression. See [P] `_robust`, particularly Introduction and Methods and formulas. Wooldridge (2020) and Arellano (2003) discuss this application of the Huber/White/sandwich VCE estimator. As discussed by Wooldridge (2020), Stock and Watson (2008), and Arellano (2003), specifying `vce(robust)` is equivalent to specifying `vce(cluster panelvar)`, where `panelvar` is the variable that identifies the panels.

Clustering on the panel variable produces a consistent VCE estimator when the disturbances are not identically distributed over the panels or there is serial correlation in $\epsilon_{it}$.

The cluster–robust VCE estimator requires that there are many clusters and the disturbances are uncorrelated across the clusters. The panel variable must be nested within the cluster variable because of the within-panel correlation that is generally induced by the random-effects transform when there is heteroskedasticity or within-panel serial correlation in the idiosyncratic errors.

**References**


Also see

[XT] xtcloglog postestimation — Postestimation tools for xtcloglog
[XT] quadchk — Check sensitivity of quadrature approximation
[XT] xtgee — Fit population-averaged panel-data models by using GEE
[XT] xtlogit — Fixed-effects, random-effects, and population-averaged logit models
[XT] xtprobit — Random-effects and population-averaged probit models
[XT] xtset — Declare data to be panel data
[ME] mecloglog — Multilevel mixed-effects complementary log-log regression
[MI] Estimation — Estimation commands for use with mi estimate
[R] cloglog — Complementary log-log regression
[U] 20 Estimation and postestimation commands