

[Description](#)[Options for RE model](#)[Methods and formulas](#)[Quick start](#)[Options for PA model](#)[References](#)[Menu](#)[Remarks and examples](#)[Also see](#)[Syntax](#)[Stored results](#)

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 `x1` and `x2` using `xtset` data

```
xtcloglog y x1 x2
```

Add [indicators](#) for levels of categorical variable `a` and interact `x1` with `x2`

```
xtcloglog y x1 x2 c.x1#c.x2 i.a
```

Same as above, but suppress iteration log

```
xtcloglog y x1 x2 c.x1#c.x2 i.a, nolog
```

Population-averaged model with an exchangeable correlation structure

```
xtcloglog y x1 x2 c.x1#c.x2 i.a, pa
```

Random-effects model with bootstrap standard errors

```
xtcloglog y x1 x2 c.x1#c.x2 i.a, vce(bootstrap)
```

Population-averaged model with an autoregressive correlation structure of order 1

```
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

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

Population-averaged (PA) model

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

RE_options

Description

Model

<u>noconstant</u>	suppress constant term
<u>re</u>	use random-effects estimator; the default
<u>offset</u> (<i>varname</i>)	include <i>varname</i> in model with coefficient constrained to 1
<u>constraints</u> (<i>constraints</i>)	apply specified linear constraints
<u>asis</u>	retain perfect predictor variables

SE/Robust

<u>vce</u> (<i>vcetype</i>)	<i>vcetype</i> may be <u>oim</u> , <u>robust</u> , <u>cluster</u> <i>clustvar</i> , <u>bootstrap</u> , or <u>jackknife</u>
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Reporting

<u>level</u> (#)	set confidence level; default is <u>level</u> (95)
<u>lrmodel</u>	perform the likelihood-ratio model test instead of the default Wald test
<u>eform</u>	report exponentiated coefficients
<u>nocnsreport</u>	do not display constraints
<u>display_options</u>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling

Integration

<u>intmethod</u> (<i>intmethod</i>)	integration method; <i>intmethod</i> may be <u>mvaghermite</u> (the default) or <u>ghermite</u>
<u>intpoints</u> (#)	use # quadrature points; default is <u>intpoints</u> (12)

Maximization

<u>maximize_options</u>	control the maximization process; seldom used
<u>collinear</u>	keep collinear variables
<u>coeflegend</u>	display legend instead of statistics

<i>PA_options</i>	Description
Model	
<code>noconstant</code>	suppress constant term
<code>pa</code>	use population-averaged estimator
<code>offset(<i>varname</i>)</code>	include <i>varname</i> in model with coefficient constrained to 1
<code>asis</code>	retain perfect predictor variables
Correlation	
<code>corr(<i>correlation</i>)</code>	within-panel correlation structure
<code>force</code>	estimate even if observations unequally spaced in time
SE/Robust	
<code>vce(<i>vcetype</i>)</code>	<i>vcetype</i> may be conventional, <code>robust</code> , <code>bootstrap</code> , or <code>jackknife</code>
<code>nmp</code>	use divisor $N - P$ instead of the default N
<code>scale(<i>parm</i>)</code>	overrides the default scale parameter; <i>parm</i> may be x2, dev, phi, or #
Reporting	
<code>level(#)</code>	set confidence level; default is level(95)
<code>eform</code>	report exponentiated coefficients
<code>display_options</code>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Optimization	
<code>optimize_options</code>	control the optimization process; seldom used
<code>coeflegend</code>	display legend instead of statistics

<i>correlation</i>	Description
<code>exchangeable</code>	exchangeable; the default
<code>independent</code>	independent
<code>unstructured</code>	unstructured
<code>fixed <i>matname</i></code>	user-specified
<code>ar #</code>	autoregressive of order #
<code>stationary #</code>	stationary of order #
<code>nonstationary #</code>	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](#).

indepvvars may contain factor variables; see [U] [11.4.3 Factor variables](#).

`by`, `collect`, `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](#).

`iweights`, `fweights`, and `pweights` are allowed for the population-averaged model, and `iweights` 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

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*.

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

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](#).

Options for PA model

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)`.

`force` specifies that estimation be forced even though the time variable is not equally spaced. This is relevant only for correlation structures that require knowledge of the time variable. These correlation structures require that observations be equally spaced so that calculations based on lags correspond to a constant time change. If you specify a time variable indicating that observations are not equally spaced, the (time dependent) model will not be fit. If you also specify `force`, the model will be fit, and it will be assumed that the lags based on the data ordered by the time variable are appropriate.

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

Optimization

`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

$$\Pr(y_{it} \neq 0 | \mathbf{x}_{it}) = P(\mathbf{x}_{it}\boldsymbol{\beta} + \nu_i)$$

for $i = 1, \dots, n$ panels, where $t = 1, \dots, n_i$, ν_i are i.i.d., $N(0, \sigma_\nu^2)$, and $P(z) = 1 - \exp\{-\exp(z)\}$.

Underlying this model is the variance-components model

$$y_{it} \neq 0 \iff \mathbf{x}_{it}\boldsymbol{\beta} + \nu_i + \epsilon_{it} > 0$$

where ϵ_{it} are i.i.d. extreme-value (Gumbel) distributed with the mean equal to Euler's constant and variance $\sigma_\epsilon^2 = \pi^2/6$, independently of ν_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/r19/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
Prob > chi2 = 0.0000
Log likelihood = -10535.928
```

union	Coefficient	Std. err.	z	P> z	[95% conf. interval]	
age	.0128659	.0119004	1.08	0.280	-.0104586	.0361903
grade	.06985	.0138135	5.06	0.000	.042776	.096924
not_smsa	-.198416	.0647943	-3.06	0.002	-.3254104	-.0714215
1.south	-2.047645	.488965	-4.19	0.000	-3.005999	-1.089291
year	-.0006432	.0123569	-0.05	0.958	-.0248623	.0235759
south#c.year						
1	.0164259	.006065	2.71	0.007	.0045387	.0283132
_cons	-3.269158	.659029	-4.96	0.000	-4.560831	-1.977485
/lnsig2u	1.24128	.0461705			1.150787	1.331772
sigma_u	1.860118	.0429413			1.77783	1.946214
rho	.677778	.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 σ_ν is also included in the output, labeled `sigma_u`, together with ρ (labeled `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 = 1.661e-06
Iteration 6: Tolerance = 8.308e-08

GEE population-averaged model
Group variable: idcode
Family: Binomial
Link: Complementary log-log
Correlation: exchangeable

Number of obs    = 26,200
Number of groups = 4,434
Obs per group:
    min = 1
    avg = 5.9
    max = 12
Wald chi2(6)    = 234.66
Prob > chi2     = 0.0000

Scale parameter = 1
```

union	Coefficient	Std. err.	z	P> z	[95% conf. interval]	
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          Number of obs   = 26,200
Group variable: idcode                 Number of groups  = 4,434
Family: Binomial                      Obs per group:
Link: Complementary log-log              min = 1
Correlation: exchangeable                avg = 5.9
                                           max = 12
                                           Wald chi2(6)      = 157.24
                                           Prob > chi2       = 0.0000

Scale parameter = 1
                                   (Std. err. adjusted for clustering on idcode)
```

union	Semirobust		z	P> z	[95% conf. interval]	
	Coefficient	std. err.				
age	.0153737	.0079446	1.94	0.053	-.0001974	.0309448
grade	.0549518	.0117258	4.69	0.000	.0319697	.077934
not_smsa	-.1045232	.0548598	-1.91	0.057	-.2120465	.0030001
1.south	-1.714868	.4864999	-3.52	0.000	-2.66839	-.7613455
year	-.0115881	.0085742	-1.35	0.177	-.0283932	.005217
south#c.year						
1	.0149796	.0060548	2.47	0.013	.0031124	.0268468
_cons	-1.488278	.4924738	-3.02	0.003	-2.453509	-.5230472

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 [\[XT\] xtprobit](#) 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.



Stored results

`xtcloglog`, `re` stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(N_g)</code>	number of groups
<code>e(k)</code>	number of parameters
<code>e(k_aux)</code>	number of auxiliary parameters
<code>e(k_eq)</code>	number of equations in <code>e(b)</code>
<code>e(k_eq_model)</code>	number of equations in overall model test
<code>e(k_dv)</code>	number of dependent variables
<code>e(df_m)</code>	model degrees of freedom
<code>e(ll)</code>	log likelihood
<code>e(ll_0)</code>	log likelihood, constant-only model
<code>e(ll_c)</code>	log likelihood, comparison model
<code>e(chi2)</code>	χ^2
<code>e(chi2_c)</code>	χ^2 for comparison test
<code>e(N_clust)</code>	number of clusters
<code>e(rho)</code>	ρ
<code>e(sigma_u)</code>	panel-level standard deviation
<code>e(n_quad)</code>	number of quadrature points
<code>e(g_min)</code>	smallest group size
<code>e(g_avg)</code>	average group size
<code>e(g_max)</code>	largest group size
<code>e(p)</code>	p -value for model test
<code>e(rank)</code>	rank of <code>e(V)</code>
<code>e(rank0)</code>	rank of <code>e(V)</code> for constant-only model
<code>e(ic)</code>	number of iterations
<code>e(rc)</code>	return code
<code>e(converged)</code>	1 if converged, 0 otherwise

Macros

<code>e(cmd)</code>	<code>xtcloglog</code>
<code>e(cmdline)</code>	command as typed
<code>e(depvar)</code>	name of dependent variable
<code>e(ivar)</code>	variable denoting groups
<code>e(model)</code>	<code>re</code>
<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(clustvar)</code>	name of cluster variable
<code>e(offset)</code>	linear offset variable
<code>e(chi2type)</code>	Wald or LR; type of model χ^2 test
<code>e(chi2_ct)</code>	Wald or LR; type of model χ^2 test corresponding to <code>e(chi2_c)</code>
<code>e(vce)</code>	<i>vcetype</i> specified in <code>vce()</code>
<code>e(vctype)</code>	title used to label Std. err.
<code>e(intmethod)</code>	integration method
<code>e(distrib)</code>	Gaussian; the distribution of the random effect
<code>e(opt)</code>	type of optimization
<code>e(which)</code>	max or min; whether optimizer is to perform maximization or minimization
<code>e(ml_method)</code>	type of <code>ml</code> method
<code>e(user)</code>	name of likelihood-evaluator program
<code>e(technique)</code>	maximization technique
<code>e(properties)</code>	<code>b V</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(marginsdefault)</code>	default <code>predict()</code> specification for <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>

Matrices	
e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance
Functions	
e(sample)	marks estimation sample

In addition to the above, the following is stored in `r()`:

Matrices	
r(table)	matrix containing the coefficients with their standard errors, test statistics, <i>p</i> -values, and confidence intervals

Note that results stored in `r()` are updated when the command is replayed and will be replaced when any `r`-class command is run after the estimation command.

`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)	χ^2
e(p)	<i>p</i> -value for model test
e(df_pear)	degrees of freedom for Pearson χ^2
e(chi2_dev)	χ^2 test of deviance
e(chi2_dis)	χ^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 <code>e(V)</code>
e(tol)	target tolerance
e(dif)	achieved tolerance
e(rc)	return code

Macros	
e(cmd)	<code>xtgee</code>
e(cmd2)	<code>xtcloglog</code>
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)	<code>pa</code>
e(family)	binomial
e(link)	<code>cloglog</code> ; link function
e(corr)	correlation structure
e(scale)	<code>x2</code> , <code>dev</code> , <code>phi</code> , or <code>#</code> ; scale parameter
e(wtype)	weight type
e(wexp)	weight expression
e(offset)	linear offset variable
e(chi2type)	Wald; type of model χ^2 test
e(vce)	<code>vcetype</code> specified in <code>vce()</code>

e(vcetype)	title used to label Std. err.
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

In addition to the above, the following is stored in `r()`:

Matrices	
r(table)	matrix containing the coefficients with their standard errors, test statistics, p -values, and confidence intervals

Note that results stored in `r()` are updated when the command is replayed and will be replaced when any `r-class` command is run after the estimation command.

Methods and formulas

`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, $N(0, \sigma_\nu^2)$, for the random effects ν_i ,

$$\Pr(y_{i1}, \dots, y_{in_i} | \mathbf{x}_{i1}, \dots, \mathbf{x}_{in_i}) = \int_{-\infty}^{\infty} \frac{e^{-\nu_i^2/2\sigma_\nu^2}}{\sqrt{2\pi}\sigma_\nu} \left\{ \prod_{t=1}^{n_i} F(y_{it}, \mathbf{x}_{it}\boldsymbol{\beta} + \nu_i) \right\} d\nu_i$$

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

$$\begin{aligned} l_i &= \int_{-\infty}^{\infty} \frac{e^{-\nu_i^2/2\sigma_\nu^2}}{\sqrt{2\pi}\sigma_\nu} \left\{ \prod_{t=1}^{n_i} F(y_{it}, \mathbf{x}_{it}\boldsymbol{\beta} + \nu_i) \right\} d\nu_i \\ &\equiv \int_{-\infty}^{\infty} g(y_{it}, x_{it}, \nu_i) d\nu_i \end{aligned}$$

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

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

where w_i is the user-specified weight for panel i ; if no weights are specified, $w_i = 1$.

The default method of adaptive Gauss–Hermite quadrature is to calculate the posterior mean and variance and use those parameters for $\hat{\mu}_i$ and $\hat{\sigma}_i$ by following the method of [Naylor and Smith \(1982\)](#), further discussed in [Skrondal and Rabe-Hesketh \(2004\)](#). We start with $\hat{\sigma}_{i,0} = 1$ and $\hat{\mu}_{i,0} = 0$, and the posterior means and variances are updated in the k th iteration. That is, at the k th iteration of the optimization for l_i , we use

$$l_{i,k} \approx \sum_{m=1}^M \sqrt{2}\hat{\sigma}_{i,k-1} w_m^* \exp\{(a_m^*)^2\} g(y_{it}, x_{it}, \sqrt{2}\hat{\sigma}_{i,k-1} a_m^* + \hat{\mu}_{i,k-1})$$

Letting

$$\tau_{i,m,k-1} = \sqrt{2}\hat{\sigma}_{i,k-1} a_m^* + \hat{\mu}_{i,k-1}$$

$$\hat{\mu}_{i,k} = \sum_{m=1}^M (\tau_{i,m,k-1}) \frac{\sqrt{2}\hat{\sigma}_{i,k-1} w_m^* \exp\{(a_m^*)^2\} g(y_{it}, x_{it}, \tau_{i,m,k-1})}{l_{i,k}}$$

and

$$\hat{\sigma}_{i,k} = \sum_{m=1}^M (\tau_{i,m,k-1})^2 \frac{\sqrt{2}\hat{\sigma}_{i,k-1} w_m^* \exp\{(a_m^*)^2\} g(y_{it}, x_{it}, \tau_{i,m,k-1})}{l_{i,k}} - (\hat{\mu}_{i,k})^2$$

and this is repeated until $\hat{\mu}_{i,k}$ and $\hat{\sigma}_{i,k}$ have converged for this iteration of the maximization algorithm. This adaptation is applied on every iteration until the log-likelihood change from the preceding iteration is less than a relative difference of $1e-6$; after this, the quadrature parameters are fixed.

The log likelihood can also be calculated by nonadaptive Gauss–Hermite quadrature, the `intmethod(ghermite)` option, where $\rho = \sigma_\nu^2/(\sigma_\nu^2 + 1)$:

$$L = \sum_{i=1}^n w_i \log \left\{ \Pr(y_{i1}, \dots, y_{in_i} | \mathbf{x}_{i1}, \dots, \mathbf{x}_{in_i}) \right\} \\ \approx \sum_{i=1}^n w_i \log \left[\frac{1}{\sqrt{\pi}} \sum_{m=1}^M w_m^* \prod_{t=1}^{n_i} F \left\{ y_{it}, \mathbf{x}_{it}\beta + a_m^* \left(\frac{2\rho}{1-\rho} \right)^{1/2} \right\} \right]$$

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

$$\prod_{t=1}^{n_i} F(y_{it}, \mathbf{x}_{it}\beta + \nu_i)$$

is well approximated by a polynomial. As panel size and ρ increase, the quadrature approximation can become less accurate. For large ρ , 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 ϵ_{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.

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Also see

- [XT] **xtcloglog postestimation** — Postestimation tools for xtcloglog
- [XT] **quadchk** — Check sensitivity of quadrature approximation
- [XT] **xtgee** — GEE population-averaged panel-data models
- [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**

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