MULTILEVEL MIXED-EFFECTS MODELS

Whether the groupings in your data arise in a nested fashion (students nested in schools and schools nested in districts) or in a nonnested fashion (regions crossed with occupations), you can fit a multilevel model to account for the lack of independence within these groups.

Fit models for continuous, binary, count, ordinal, and survival outcomes. Fit linear, generalized linear, and nonlinear models.

Estimate variances of random intercepts and random coefficients. Compute intraclass correlations. Predict random effects. Estimate relationships that are population averaged over the random effects. Perform Bayesian analysis. And much more.

Models for
- Continuous outcomes
- Binary outcomes
- Count outcomes
- Categorical outcomes
- Ordinal outcomes
- Survival-time outcomes

Types of models
- Linear, generalized linear, and nonlinear
- Two-, three-, and higher-level models
- Nested (hierarchical) models
- Crossed models
- Mixed models
- Balanced and unbalanced designs

Estimated effects
- Random intercepts
- Random coefficients (slopes)
- Variances of random effects (variance components)
- Fixed effects (regression coefficients)

Covariance structures
- Identity
- Independent
- Exchangeable
- Unstructured

Error (residual) structures
- Independent
- Exchangeable
- Autoregressive
- Moving average
- Exponential
- Banded
- Toeplitz
- Unstructured

Estimation methods
- Maximum likelihood (ML)
- Restricted maximum likelihood (REML)
- Mean-variance or mode-curvature adaptive Gauss-Hermite quadrature
- Nonadaptive Gauss-Hermite quadrature
- Laplacian approximation

Inferences
- Expected means, probabilities, counts
- Marginal effects
- Conditional or population averaged
- Tests, contrasts, and pairwise comparisons

Adjustments for small-sample inference
- Kenward–Roger
- Satterthwaite
- ANOVA
- Repeated-measures ANOVA
- Residual

Account for survey design
- Weights at each level
- Clustering
- Stratification

Estimates of random effects
- BLUPs for linear models
- Empirical Bayes posterior means
- Empirical Bayes posterior modes
- With standard errors

Bayesian analysis
- Incorporate prior knowledge
- Estimate distributions of random effects
- Compute probability for any hypothesis of interest
LINEAR MODELS

When you are modeling continuous outcomes—weight, log of income, test scores, and the like—the `mixed` command can fit a variety of multilevel mixed-effects linear models.

**Fit your model**
You can fit a two-level model (observations nested in `id`) with random intercepts for `id` and with fixed coefficients for continuous variables `x1` and `x2` and categorical variable `a`.

```stata
mixed y x1 x2 i.a || id: x1
```

Unstructured covariance for random slopes and random intercepts
```stata
mixed y x1 x2 i.a || id: x1, covariance(unstructured)
```

Autoregressive residual variance structure
```stata
mixed y x1 x2 i.a || id:, residuals(ar 1, t(time))
```

REML estimation
```stata
mixed y x1 x2 i.a || id:, reml
```

Kenward–Roger adjustment for small-sample inference
```stata
mixed y x1 x2 i.a || id:, reml dfmethod(kroger)
```

**Explore the results**
Predict random effects (BLUPs) and their standard errors
```stata
predict re, reffects rese(re_se)
```

Estimate intraclass correlations
```stata
estat icc
```

Perform Wald tests of coefficients
```stata
test x1=1
```

Compare models
```stata
lrtest model1 model2
```

Estimate and plot marginal means
```stata
margins a
```

**Bayesian estimation**
Bayesian two-level model with random intercepts
```stata
bayes: mixed y x1 x2 i.a || id:
```

Bayesian multilevel linear models
```stata
bayes, priors ...: mixed ... bayesgraph histogram ...
```

Crossed effects for `grp1` and `grp2`
```stata
mixed y x1 x2 i.a || _all: R.grp1 || grp2:
```
GENERALIZED LINEAR MODELS

When your outcome is not continuous—pass or fail a test, number of doctor visits, survival time, etc—the `me` commands can fit logit, probit, Poisson, ordinal logit, Weibull, and many other multilevel mixed-effects models using syntax similar to that for `mixed` with linear models.

Binary outcomes

You can use `melogit`, `meprobit`, and `mecloglog` to fit multilevel logit, probit, and complementary log-log models.

Two-level logit model with random intercepts
```
.melogit y x1 x2 i.a || id:
```

Three-level model
```
.melogit y x1 x2 i.a || group: || id:
```

Random coefficients
```
.melogit y x1 x2 i.a || group: x1 || id: x2
```

You can easily modify this syntax, just as with `mixed`, to incorporate different covariance structures and fit four- and higher-level nested models and crossed-effects models. Replace `melogit` with `meprobit` or `mecloglog` to fit a probit or complementary log-log model.

Ordinal outcomes

Use `meologit` and `meprobit` to fit multilevel ordinal logit and ordinal probit models.

Two-level ordinal logit model with random intercepts
```
.melogit y x1 x2 i.a || id:
```

Again, the same syntax modifications allow for random coefficients, different covariance structures, more levels, and crossed effects.

Count outcomes

Use `mepoisson` and `menbreg` to fit multilevel Poisson and negative binomial models. And the syntax is the same.
```
.mepoisson y x1 x2 i.a || ...  
membreg y x1 x2 i.a || ...
```

Censored outcomes

When your outcome is continuous but censored, fit a multilevel interval-censored or tobit model.
```
melintreg ylower yupper x1 x2 i.a || ...  
melobit y x1 x2 i.a || ..., l1(0)
```

Survival-time outcomes

Use `mestreg` to fit multilevel exponential, Weibull, lognormal, loglogistic, or gamma models.

Specify the time and failure variables
```
.stset time, failure(fail)
```

Two-level Weibull model with random intercepts
```
mestreg x1 x2 i.a || id:, distribution(weibull)
```

Additional multilevel parametric survival models
```
mestreg x1 x2 i.a || ..., distribution(...)
```

More

You can use `meglm` to specify any family and link functions for fitting multilevel generalized linear models.
```
meglm y x1 x2 i.a || ... , family(...) link(...)
```

Account for complex survey design

Specify the survey design—weights at each level, clustering, stratification, and more.
```
.svset cluster, weight(wvar2) strata(stvar) || _n, weight(wvar1)
```

Fit two-level logit model with random intercepts
```
.svy: melogit y x1 x2 i.a || id:
```

Fit any `me` model
```
.svy: mecmd ...
```

Explore the results

Predict random effects (empirical Bayes means or modes) and their standard errors
```
.predict re, reflect re
```

Predict probabilities, counts, incidence rates, survival times, and more
```
.predict mypred
```

Estimate intraclass correlations
```
.estat icc
```

Perform Wald tests of coefficients
```
.test x1=1
```

Compare models via a likelihood-ratio test
```
lrtest modell modell2
```

Estimate and plot marginal predictions—expected probabilities, counts, survival times, and more
```
margins a, at(x1=5 7 9 11)
marginsplot ...
```

Bayesian estimation

Bayesian two-level logit model with random intercepts
```
bayes: melogit y x1 x2 i.a || id:
```

Bayesian multilevel models
```
bayes, priors ...: mecmd ...
```
NONLINEAR MODELS

When your model is not linear in the parameters, the **`menl`** command can fit nonlinear multilevel mixed-effects models.

### Random-intercept model

Say you are modeling growth in the weight of plant leaves with random intercepts $U$ for plots:

$$weight = \phi_i / [1 + \exp(-\text{time} - \beta_j U_j)] + \epsilon$$

$$\phi_i = \phi_0 + \beta_i + U_j$$

You can type your command almost the same way you wrote your model:

```stata
. menl weight = (phi1: / (1+exp(-(time - {b2})/b3))), define(phi: (b1)+(U(plot)))
```

You can also fit the model using restricted maximum likelihood instead of the default maximum likelihood:

```stata
. menl weight = (phi1: / (1+exp(-(time - {b2})/b3))), define(phi: (b1)+(U(plot))) reml
```

### Multilevel models

We can also extend the model to three or more levels.

If plots are nested within zones, we can fit a model with both zone-level and plot-level random intercepts by typing:

```stata
. menl weight = (phi1: / (1+exp(-(time - {b2})/b3))), define(phi: (b1)+(U[zone])+(U[plot]))
define(phi2: (b2)+(U2[zone])+(U2[plot]))
```

In the above, we allowed phi1 and phi2 to be zone and plot specific.

### Residual covariance structures

Sometimes, you need to model error heteroskedasticity and its within-group dependence, so **`menl`** allows flexible variance-covariance residual structures.

For instance, we model these drug concentration-time profiles and use a power-plus-constant function of the predicted mean to model the within-subject error variance:

$$\text{conc} = \text{dose} \times c_1 \times k_1 / \{c_2 (k_2 - k_1) \times \exp(-k_1 \times \text{time}) - \exp(-k_2 \times \text{time})\} + \epsilon$$

$$c_1 = c_0 + \exp(\beta_1 + U_1)$$

$$k_1 = k_2 + \exp(\beta_2 + U_2)$$

$$k_1 = \exp(\beta_2)$$

$$\text{Var}(\epsilon) = c^2 (a + \text{conch}^2)$$

To fit this model, we type:

```stata
. menl conc = (dose*(ke:*{ka:}/({c1:}*({ka:}-{ke:})*
  (exp(-ke:*time)-exp(-ka:*time))))
  define(c1: exp(b0)+(U0[subject])))
define(ka: exp(b1)+(U1[subject]))
define(ke: exp(b2)))
resvariance(power _yhat)
```

### Predictions

After fitting the model, we can predict parameters of interest by typing, for instance:

```stata
. predict double (c1 = {c1:})
```

We can also predict random effects at a specific level:

```stata
. predict u*, reffects relevel(subject)
```