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Maximum likelihood estimation of generalized linear models with covariate measurement error

Sophia Rabe-Hesketh
Graduate School of Education
University of California
Berkeley, CA

Anders Skrondal
Division of Epidemiology
Norwegian Institute of
Public Health, Oslo

Andrew Pickles
School of Epidemiology
and Health Science & CCSR
The University of Manchester

Abstract. Generalized linear models with covariate measurement error can be estimated by maximum likelihood using gllamm, a program that fits a large class of multilevel latent variable models (Rabe-Hesketh, Skrondal, and Pickles 2004). The program uses adaptive quadrature to evaluate the log likelihood, producing more reliable results than many other methods (Rabe-Hesketh, Skrondal, and Pickles 2002). For a single covariate measured with error (assuming a classical measurement model), we describe a "wrapper" command, cme, that calls gllamm to estimate the model. The wrapper makes life easy for the user by accepting a simple syntax and data structure and producing extended and easily interpretable output. The commands for preparing the data and running gllamm can also be obtained from cme. We first discuss the case where several measurements are available and subsequently consider estimation when the measurement error variance is instead assumed known. The latter approach is useful for sensitivity analysis assessing the impact of assuming perfectly measured covariates in generalized linear models. An advantage of using gllamm directly is that the classical covariate measurement error model can be extended in various ways. For instance, we can use nonparametric maximum likelihood estimation (NPMLE) to relax the normality assumption for the true covariate. We can also specify a congeneric measurement model which relaxes the assumption that the measurements for a unit are exchangeable replicates by allowing for different measurement scales and error variances.

Keywords: st0052, covariate measurement error, measurement model, congeneric measurement model, factor model, adaptive quadrature, nonparametric maximum likelihood, NPMLE, latent class model, empirical Bayes, simulation, wrapper, sensitivity analysis, gllamm, cme

1 Introduction

Covariates are often measured with error, their true values being unobservable or latent. For simplicity, we assume in this paper that this is only the case for one covariate u_i, whereas the other covariates $\boldsymbol{z}_i$ are perfectly measured or observed. The problem, then, is to estimate a generalized linear model for a response or outcome variable y_i with link function $g(\cdot)$,

$$g(\mu_i) \;=\; \boldsymbol{z}_i'\boldsymbol{\beta} + u_i\beta_u \qquad (1)$$

We will call this model the *outcome model* (*disease model* in epidemiology).

It is well known that substituting an error-prone measured covariate w_i for the true covariate u_i will generally lead to biased estimates of both β_u and $\boldsymbol{\beta}$. We can attempt to correct the bias if further information is available, such as the true covariate values in a validation (sub)sample, instrumental variables, replicate measurements (at least in subsample), or knowledge of the measurement properties (e.g., measurement error variance).

In this paper, we describe maximum likelihood estimation of generalized linear models with covariate measurement error, making use of either replicate measurements, instrumental variables, or known measurement error variance. Remarkably, the maximum likelihood approach has received relatively scant attention in the literature, probably because it is perceived as complicated to implement and is not available in standard software. We hope that the `cme` (covariate measurement error) command introduced here will remedy this. This wrapper command uses the reliable adaptive quadrature method (Rabe-Hesketh, Skrondal, and Pickles 2002) implemented in the general `gllamm` command but is easier to use than `gllamm` because of its tailor-made syntax and output. Alternative methods, such as regression calibration, instrumental variables estimation, and simulation extrapolation are discussed in the companion papers by Hardin and Carroll (2003) and Hardin, Schmiediche, and Carroll (2003a,b,c).

The covariate measurement error model consists of three submodels (e.g., Clayton 1992): the *outcome model* in (1); a *measurement model*, specifying the relationship between the true covariate and its measurements; and a *true covariate model*, specifying a regression of the true covariate on observed covariates. Section 2.1 describes the classical covariate measurement error model. Although the outcome submodel of this classical model is very general, the measurement and true covariate submodels are rather restrictive. One limitation is that a normal distribution is assumed for the true covariate (given the observed covariates), raising concerns about robustness. In section 2.2, we therefore relax this assumption by using nonparametric maximum likelihood estimation. Another limitation is the implicit assumption of identical measurement properties for the fallible measures of the true covariate. We relax this assumption by introducing the general congeneric measurement model in section 2.3. Maximum likelihood estimation of the classical model and its extensions using the `cme` and `gllamm` commands is described in section 3.

2 Covariate measurement error models

2.1 Classical model

We first consider the situation where the true covariate has been measured n_i times for unit i, giving fallible measures w_{ij}, $j = 1, \ldots, n_i$, $n_i \leq k$. Sometimes replicate measurements are available only on a subsample, all other units being measured once.

The *classical measurement model* can be written as

$$w_{ij} \;=\; u_i + \epsilon_{ij}, \qquad \epsilon_{ij} \sim \mathrm{N}(0, \sigma^2) \tag{2}$$

The measurement errors ϵ_{ij} are independently normally distributed with zero mean and constant measurement error variance σ^2 and are independent of the true covariate u_i. This implies that the measurements are conditionally independent given the true covariate. Furthermore, the repeated measurements for a unit have mean equal to the true covariate; i.e., they are unbiased for the true covariate. In Carroll, Ruppert, and Stefanski (1995), lack of bias is a requirement for a measurement to be called a *replicate* measurement, but here we use the term for any repeated measurement.

To complete specification of the covariate measurement error model, we need to define a *true covariate model* (*exposure model* in epidemiology),

$$u_i \;=\; \boldsymbol{z}_i'\boldsymbol{\gamma} + \zeta_i, \qquad \zeta_i \sim \mathrm{N}(0, \tau^2) \tag{3}$$

where $\boldsymbol{\gamma}$ are regression parameters and ζ_i are disturbances or residuals, assumed to be independent of the covariates $\boldsymbol{z}_i$. The model includes $\boldsymbol{z}_i$ because it would be unrealistic to assume that the true covariate is independent of the other (observed) covariates in the outcome model.

The joint model, comprising the three submodels in (1) to (3), is illustrated in figure 1 for the case of a single observed covariate z_i and up to $k = 2$ measurements of the true covariate. Here, circles represent latent variables, and rectangles represent observed variables. Long arrows represent linear relations in the linear predictor, and short arrows represent residual variability. For the true covariate and measurement models, this residual variability is an additive error term, but for the outcome y_i it could be, for instance, binomial or Poisson variability, depending on the specified distribution. It is apparent from the diagram that the measurements are conditionally independent of the outcome y_i given the true covariate, a property known as *nondifferential measurement error*.

We see that the covariate z_i has an *indirect effect* $\gamma_1\beta_u$ on the outcome mediated by the true covariate in addition to the *direct effect* β_1. The total effect is simply the sum of these effects. This can also be seen by substituting the true covariate model (3) into the outcome model (1), giving the *reduced-form* outcome model

$$\begin{aligned} g(\mu_i) &= \boldsymbol{z}_i'\boldsymbol{\beta} + (\boldsymbol{z}_i'\boldsymbol{\gamma} + \zeta_i)\beta_u \\ &= \boldsymbol{z}_i'\underbrace{(\boldsymbol{\beta} + \boldsymbol{\gamma}\beta_u)}_{\boldsymbol{\alpha}} + \zeta_i\beta_u \end{aligned}$$

The reduced-form measurement model becomes

$$w_{ij} = \boldsymbol{z}_i'\boldsymbol{\gamma} + \zeta_i + \epsilon_{ij}$$

Incidentally, when all direct and indirect effects of covariates are included in the model, it is easier to estimate the reduced-form parameters $\boldsymbol{\alpha} = \boldsymbol{\beta} + \boldsymbol{\gamma}\beta_u$, β_u and $\boldsymbol{\gamma}$ (e.g., Aitkin and Rocci 2002) from which the parameters of primary interest, the *structural parameters* $\boldsymbol{\beta}$, $\boldsymbol{\gamma}$, and β_u, can be derived. However, removing (at least two of) the direct effects requires nonlinear constraints of the form $\alpha_p = \gamma_p \beta_u$ for the reduced-form parameters. Our programs, therefore, estimate the structural parameters directly.

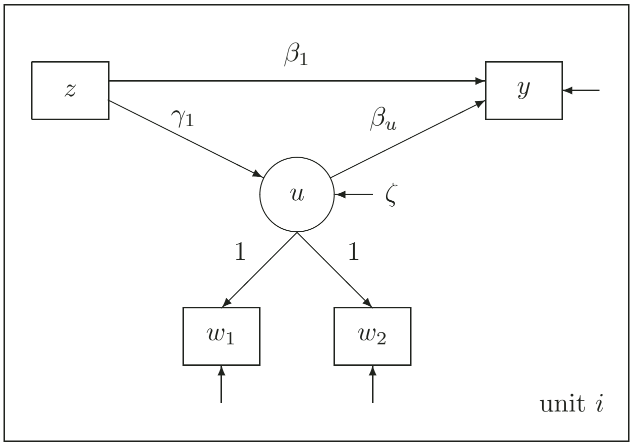


Figure 1: Path diagram with direct and indirect effects of z on y

The model is not identified if there are no replicate measurements, i.e., $k = 1$. In this case, a parameter constraint is required to estimate the model, for instance, setting the measurement error variance σ^2 to a known non-negative constant, typically an estimate from another study. Transporting a parameter estimate this way requires that the parameter not vary between populations, an assumption that is reasonable for the measurement error variance. By contrast, the reliability (to be defined in (5)) depends on the true covariate variance, a characteristic of the population. A major problem with treating unknown parameters as known is that estimation uncertainty is not taken into account. We therefore consider this "plugging in" approach most useful as a sensitivity analysis to investigate how the parameter estimates change for different values of the assumed measurement error variance. Importantly, this allows us to assess the impact of the implicit assumption of perfectly measured covariates in generalized linear models.

2.2 Nonparametric distribution of the true covariate

Instead of assuming a normal distribution for the true covariate u_i or for the residual ζ_i when there are observed covariates $\boldsymbol{z}_i$, we can leave the distribution unspecified. The nonparametric maximum likelihood estimator (NPMLE) of the distribution is discrete (Laird 1978; Heckman and Singer 1984) with masses π_c at a finite number of locations $\zeta_i = e_c$, $c = 1, \ldots, C$. The number of masses is determined to achieve the largest possible likelihood. Attempts to estimate the model with $C + 1$ masses would result either in one mass having an estimated probability approaching zero or in two masses nearly sharing the same estimated location. This model is also sometimes referred to as a semiparametric mixture model.

Our approach to finding the NPMLE (Rabe-Hesketh, Pickles, and Skrondal 2003) is to start with a small number of masses and estimate both locations and masses by maximum likelihood, along with all the other parameters. We then use the idea of directional derivative, referred to as *gateaux derivative* in Heckman and Singer (1984), to decide if another mass should be added. Here, a very small new mass is moved across a wide range of locations, keeping all parameters at their current estimates. If the log likelihood increases at any location, a new mass is introduced. It is helpful to use the location resulting in the greatest increase in log likelihood as a starting value for the new masspoint. NPMLE for covariate measurement error models has been discussed by Roeder, Carroll, and Lindsay (1996); Schafer (2001); Aitkin and Rocci (2002); and Rabe-Hesketh, Pickles, and Skrondal (2003). General references include Lindsay (1995) and Böhning (2000).

2.3 Congeneric measurement model

The classical measurement model in (2) assumes that the fallible measures have the same mean (no relative bias) and measurement error variance. This is reasonable if the measures are essentially exchangeable replicates. However, if the measurements are separated in time, there may be a drift in the mean measurement (e.g., Carroll, Ruppert, and Stefanski 1995). More importantly, if the fallible measures are obtained by different methods, such as different instruments or different raters, we should allow the measures to have different means, scales, and measurement error variances. We can therefore extend the classical measurement model to a *congeneric measurement model* (Jöreskog 1971) or one-factor model of the form

$$w_{ij} \;=\; \delta_j + \lambda_j u_i + \epsilon_{ij}, \quad \epsilon_{ij} \sim \mathrm{N}(0, \sigma_j^2) \tag{4}$$

where $\delta_1 = 0$ and $\lambda_1 = 1$ for identification. Here, δ_j represents the *bias* of measure j, λ_j the *scale* or factor loading, and σ_j^2 the *measurement error variance*. We interpret $\lambda_j u_i$ as the *true score* for unit i expressed in the scale of instrument or rater j.

Note that this general model can also be used for instrumental variables w_{ij}, that is, any variables that are correlated with u_i (not necessarily direct measures of u_i), independent of the measurement errors of the other measures and independent of the outcome y_i given $\boldsymbol{z}_i$ and u_i (e.g., Carroll, Ruppert, and Stefanski 1995).

The following hierarchy of increasingly restrictive versions of the congeneric measurement models is often considered (Jöreskog 1971; Lord and Novick 1968):

1. *Essentially tau-equivalent* model.

   The true scores have identical scales; i.e., all factor loadings are set equal across raters or instruments j, $\lambda_j = \lambda = 1$.

2. *Tau-equivalent* model.

   The true scores have identical locations and scales; i.e., the intercepts are also set equal, $\delta_j = \delta = 0$.

3. *Parallel* or *classical measurement* model in (2).

   The measurement properties of raters or instruments are identical; i.e., the measurement error variances are also set equal, $\sigma_j^2 = \sigma^2$.

The measures can have different *reliabilities*, defined as the proportion of the total variance that is due to variability between the units' true scores (true covariate values)

$$R_j \;=\; \frac{\lambda_j^2 \tau^2}{\lambda_j^2 \tau^2 + \sigma_j^2} \tag{5}$$

If the true covariate model includes covariates, the reliability is interpreted as conditional on these covariates. This conditional reliability could be substantially lower than the unconditional one if the covariates explain a substantial portion of the between-subject variance in the true covariate. We refer to Dunn (1992, 2004) and Dunn and Roberts (1999) for useful treatments of reliability and measurement models.

The congeneric measurement model can be further generalized by specifying a generalized linear factor model as

$$g(\mu_{ij}) = \delta_j + \lambda_j u_i$$

If the responses are dichotomous, this is a two-parameter item response model (Birnbaum 1968). If the true covariate is categorical, a latent class model (e.g., Clogg 1995) can be specified where u_i is categorical and the true covariate model becomes a multinomial logit model. We refer to Bartholomew and Knott (1999) and Skrondal and Rabe-Hesketh (2004) for theory and applications of generalized linear models with latent variables.

3 Estimation using cme and gllamm

3.1 Classical covariate measurement error model

We will illustrate covariate measurement error modeling using data from Morris, Marr, and Clayton (1977). This study investigated the relationship between diet and coronary heart disease (CHD). At the time of recruitment, 337 middle-aged men weighed their food intake over a 7-day period, allowing food constituents to be derived. A subsample of 76 of the men repeated this 6 months later, and all the men were then followed up for CHD. We will estimate the effect of dietary fiber intake on CHD, controlling for occupation. The relevant variables are

- `chd`: dummy for coronary heart disease, CHD (1: present, 0: absent)
- `fiber1` and `fiber2`: dietary fiber intake (grams/day) at first and second occasions
- `bus`: dummy for man working for London Transport (1: London Transport, 0: bank staff)
- `id`: subject identifier

Since fiber intake has a skewed distribution, we will analyze log-fiber. We also subtract 2.8, approximately the mean log-fiber, to reduce correlations among the estimates $\widehat{\beta}_u$ and $\widehat{\beta}_0$, giving variables `lfiber1` and `lfiber2`. Subtracting the mean is advisable and will only affect the estimates of the constants $\widehat{\beta}_0$ and $\widehat{\gamma}_0$ in the measurement and outcome models, which are rarely of interest.

We specify a classical measurement model for log-fiber of the form of (2) and a logistic regression model for CHD as in (1) with observed covariate `bus` (corresponding to z_i) and true log-fiber intake u_i, where $g(\cdot)$ is the logit link. True log-fiber intake is regressed on `bus` as in (3).

cme command

The classical covariate measurement error model can be estimated using the `cme` command, which is a wrapper for `gllamm`. The syntax is the same as for the Stata command `glm`, except that the measurement model for the true covariate is specified as `(`*label*`:` *measure1 measure2 . . . measurek*`)`. Note that the variables *measure1 measure2 . . . measurek* can contain missing values if not all units have been measured on all occasions, as is the case here. All subjects with at least one nonmissing value will contribute to the analysis, the assumption being that the data are missing at random (MAR). For the present example, we obtain

```
. cme chd bus (lfib: lfiber1 lfiber2), l(logit) f(binom) nolog
gllamm covariate measurement error model           No. of obs      = 333

log likelihood = -186.93042

OUTCOME MODEL
------------------------------------------------------------------------------
         chd |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
chd          |
         bus |  -.1890801   .3396132    -0.56   0.578    -.8547097    .4765496
        lfib |  -1.956459   .7261552    -2.69   0.007    -3.379698   -.5332214
       _cons |  -1.852415   .2459018    -7.53   0.000    -2.334374   -1.370457
------------------------------------------------------------------------------

TRUE COVARIATE MODEL
------------------------------------------------------------------------------
        lfib |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
lfib         |
         bus |  -.1208526   .0327975    -3.68   0.000    -.1851344   -.0565707
       _cons |   .0637085   .0238865     2.67   0.008     .0168919    .1105252
-------------+----------------------------------------------------------------
    res. var. |   .0701975   .0075798                       .0561274    .0858397
------------------------------------------------------------------------------

MEASUREMENT MODEL
------------------------------------------------------------------------------
  error var. |   .0217326   .0035269                       .0158115    .0298711
 reliability |   .7635967   .0412876                       .6756077    .8365528
------------------------------------------------------------------------------
```

There are three tables in the output: the generalized linear outcome model of primary interest, followed by the true covariate model and the measurement model. In the *outcome model*, the coefficient -1.96 of `lfib` represents the estimated effect $\widehat{\beta}_u$ of true log-fiber. The corresponding odds ratio, $\exp(-1.956459) = 0.14$, can be obtained along with the odds ratio for `bus` using the `eform` option. This extremely large estimated protective effect of log-fiber is probably due to omitting important confounding variables, such as exercise, which is protective of heart disease and increases food intake, including fiber. Occupation does not appear to have an important direct effect on CHD. In the *true covariate model*, we see that London transport staff consume less fiber than bank staff. The residual variance (i.e., the within-occupation variance) of true log-fiber is estimated as $\widehat{\tau}^2 = 0.07$. In the *measurement model*, the measurement error variance is estimated as $\widehat{\sigma}^2 = 0.02$. The estimated reliability, conditional on occupation, is $\widehat{R} = \widehat{\tau}^2/(\widehat{\tau}^2 + \widehat{\sigma}^2) = 0.76$.

The estimates are also shown under "Classical model" in table 1. Note that, by default, 8-point adaptive quadrature was used to obtain these estimates. To ensure that integration is accurate (see Rabe-Hesketh, Skrondal, and Pickles 2002), these estimates should be compared with estimates using a larger number of points, for instance 12 using the `nip(12)` option.

Table 1: Estimates of different models for diet and CHD data

	Classical model		Only indirect effect		NPMLE (dir. & indir.)	
	Est	(SE)	Est	(SE)	Est	(SE)
Outcome model						
β_0 [Cons]	-1.852	(0.246)	-1.951	(0.176)	-1.855	(0.246)
β_1 [Bus]	-0.189	(0.340)	–		-0.183	(0.338)
β_u	-1.956	(0.726)	-1.860	(0.702)	-1.928	(0.702)
True covariate model						
γ_0 [Cons]	0.064	(0.024)	0.063	(0.024)	0.061	(0.024)
γ_1 [Bus]	-0.121	(0.033)	-0.120	(0.033)	-0.115	(0.033)
τ^2	0.070	(0.008)	0.070	(0.008)	0.073	(–)
Measurement model						
σ^2	0.022	(0.004)	0.022	(0.004)	0.019	(0.003)
Log likelihood	-186.93		-187.09		-177.87	

We can use the `total` and `indirect` options to obtain estimates of total and indirect effects of `bus`, in terms of odds ratios if the `eform` option is used

```
. cme, eform indirect total
gllamm covariate measurement error model          No. of obs      = 333

log likelihood = -186.93044

OUTCOME MODEL
------------------------------------------------------------------------------
         chd |     exp(b)   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
chd          |
         bus |   .8270867   .2809421    -0.56   0.576     .4250281    1.609475
        lfib |    .140508   .1020968    -2.70   0.007     .0338217    .5837223
------------------------------------------------------------------------------

      Indirect effects of covariates via true covariate
------------------------------------------------------------------------------
         bus |   1.267658   .1378737    2.18    0.029     1.024291    1.568848
------------------------------------------------------------------------------

      Total effects of covariates
------------------------------------------------------------------------------
         bus |   1.048463   .3490437    0.14    0.887     .5459838    2.013384
------------------------------------------------------------------------------
```

(output for true covariate model and measurement model not shown)

The indirect effect of reduced fiber intake among transport staff is to increase the odds of CHD (estimated odds ratio of 1.27). The protective direct effect of being transport staff (estimated odds ratio of 0.83) counteracts this, giving a negligible total effect (estimated odds ratio of 1.27×0.83=1.05). However, there is not much evidence for a direct effect, and we may therefore wish to estimate a more parsimonious model omitting this effect (possibly to perform a likelihood-ratio test):

```
. cme chd (lfib: lfiber1 lfiber2), l(logit) f(binom) tcovmod(bus)
```

(output omitted)

Here, `bus` has been omitted after `chd`, whereas the `tcovmod()` option specifies `bus` as a covariate for the `t`rue `cov`ariate `mod`el. The estimates are shown under "Only indirect effect" in table 1. The odds ratio for the total effect of `bus` is now estimated as 1.25 with a 95% confidence interval from 1.02 to 1.53.

We can estimate these models with the measurement error variance σ^2 constrained at a particular value using the `mevar(#)` option. As discussed in section 2.1, such a constraint is necessary for model identification if there are no replicate measurements. We will pretend that we only had the first log-fiber measurement `lfiber1` and explore how the estimates of β_u and β_1 change for a range of values of σ^2 from 0 to 0.05:

```
. gen beta_u = .
. gen beta_1 = .
. gen variance = (_n-1)/200 in 1/11
. glm chd bus lfiber1, l(logit) f(binom)
. replace beta_u = [chd]lfiber1 in 1
. replace beta_1 = [chd]bus in 1
. forvalues s=2/11 {
.     local var=(`s´-1)/200
.     cme chd bus (lfib: lfiber1), l(logit) f(binom) mevar(`var´)
.     replace beta_u = [chd]lfib in `s´
.     replace beta_1 = [chd]bus in `s´
. }
. twoway connect beta_u variance, ytitle(Log odds ratio for true log-fiber) /*
.  */ xtitle(Measurement error variance)
. twoway connect beta_u variance, ytitle(Log odds ratio for bus) /*
.  */ xtitle(Measurement error variance)
```

Here, the estimate for $\sigma^2 = 0$ is obtained using `glm`, whereas `cme` is used within a `forvalues` loop for variances $\sigma^{2(s)} = (s-1)/200,\ s = 2, \ldots, 11$. The corresponding estimates $\widehat{\beta}_u^{(s)}$ and $\widehat{\beta}_1^{(s)}$ are accessed using the equation name `chd` (outcome variable) and the column names `lfib` (the label for the true covariate specified in the `cme` command) and `bus`. The resulting graphs of $\widehat{\beta}_u^{(s)}$ and $\widehat{\beta}_1^{(s)}$ versus $\sigma^{2(s)} = (s-1)/200$ are shown in figure 2.

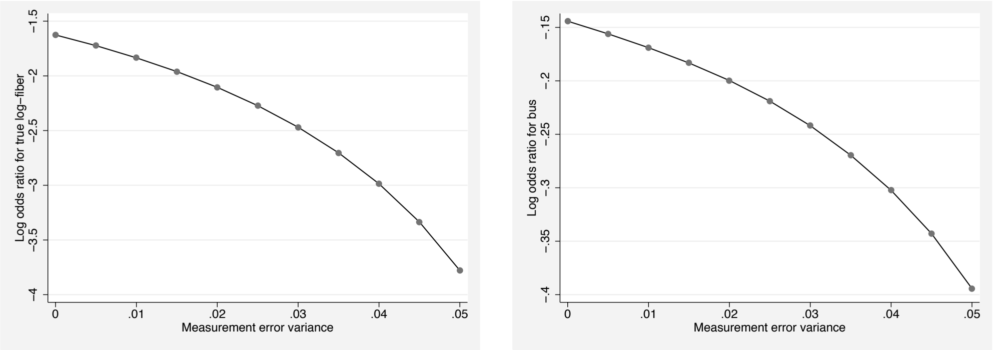


Figure 2: Sensitivity analysis for β_u and β_1.

Such graphs are useful for assessing the sensitivity of the parameter estimates to the implicit assumption in generalized linear models that there is no covariate measurement error.

The `cme` command allows a wide range of generalized linear models for the outcome as well as ordinal logit and probit models (see *Appendix: Syntax for cme* for all the options), but the classical measurement model and a normally distributed true covariate are always assumed. To relax these assumptions, `gllamm` has to be used directly. As we will see, the `commands` option of `cme` is very useful for this purpose since it creates commands for estimating the model in `gllamm`, including all the necessary data manipulation.

GLLAMM framework

Here, we briefly describe the GLLAMM (generalized linear latent and mixed model) framework confining ourselves to the special case of two-level models with a single latent variable (the general framework is described in Rabe-Hesketh, Skrondal, and Pickles (2004) and Skrondal and Rabe-Hesketh (2004)). All response variables, the outcome y_i (CHD), and the repeated measurements w_{ij} of the true covariate are stacked in a single response vector $\boldsymbol{y}$ with elements indexed ij, where $j=1$ if the element corresponds to the outcome for unit i and $j=2,\ldots,k+1$ for the fallible measurements. The linear predictor then has the form

$$g_{ij}(\mu_{ij}) \;=\; \boldsymbol{x}'_{ij}\boldsymbol{\beta} + u_i\boldsymbol{v}'_{ij}\boldsymbol{\lambda}, \quad \lambda_1 = 1$$

where $\boldsymbol{x}_{ij}$ and $\boldsymbol{v}_{ij}$ are variables, $\boldsymbol{\beta}$ and $\boldsymbol{\lambda}$ parameters and u_i is a latent variable. The ij subscript for the link implies that different link functions can apply to different responses, for example, the logit link for the outcome and the identity link for the fallible measurements. The fixed part $\boldsymbol{x}'_{ij}\boldsymbol{\beta}$ allows inclusion of observed covariates in the model. To include the observed covariates $\boldsymbol{z}_i$ in the outcome model only, we must multiply these covariates by a dummy variable for CHD

$$d_{1ij} \;=\; \begin{cases} 1 & \text{if } j=1 \\ 0 & \text{if } j>1 \end{cases}$$

so that $\boldsymbol{x}_{ij}=d_{1ij}\boldsymbol{z}_i$.

The variables $\boldsymbol{v}_{ij}$ are typically dummy variables, allowing the regressions for different response variables on the latent variable u_i to have different regression coefficients λ_p. In the present example, using the dummy variables $v_{1ij}=d_{mij}$,

$$d_{mij} = 1 - d_{1ij} \;=\; \begin{cases} 0 & \text{if } j=1 \\ 1 & \text{if } j>1 \end{cases}$$

and $v_{2ij}=d_{1ij}$ results in the following model:

$$\begin{aligned} g_{ij}(\mu_{ij}) &= d_{1ij}\boldsymbol{z}'_i\boldsymbol{\beta} + u_i(\lambda_1 d_{mij} + \lambda_2 d_{1ij}), \quad \lambda_1 = 1 \\ &= \begin{cases} \boldsymbol{z}'_i\boldsymbol{\beta} + u_i\lambda_2 & \text{if } j=1 \\ u_i & \text{if } j>1 \end{cases} \end{aligned} \tag{6}$$

Here, λ_2 corresponds to β_u in (1). Note that we only required a single dummy variable for both log-fiber measurements since the regressions on u_i share the same regression coefficient $\lambda_1=1$.

Finally, we specify the true covariate model, called the *structural model* in the GLLAMM framework, as

$$u_i = \boldsymbol{z}'_i\boldsymbol{\gamma} + \zeta_i, \quad \zeta_i \sim \mathrm{N}(0,\tau^2)$$

We assume here that the first observed covariate z_{1i} is a constant so that the true covariate model and outcome model both contain intercepts, γ_0 and β_0, respectively.

Note that GLLAMMs also allow more general structural models, regressing latent variables at different levels on same or higher-level latent and observed variables.

gllamm command

We will now show how all commands necessary for estimating the classical covariate measurement error model for the diet and CHD example can be generated using the `commands` option in `cme` (we have added the line numbers for ease of reference):

```
. cme chd bus (lfib: lfiber1 lfiber2), l(logit) f(binom) nolog commands
                              begin do-file
1 * starting values
2 matrix startv = ( -.1474, -1.853, -1.458, -1.54, .3555, -.1237, .06659)
3 gen _id = _n
4 * collapse data to make gllamm faster
5 gen _one = 1
6 collapse (sum) _wt2 = _one, by(chd lfiber1 lfiber2 _id bus bus)
7 * give response variable and replicate measurements same prefix
8 rename chd _r1
9 rename lfiber1 _r2
10 rename lfiber2 _r3
11 * reshape data to long
12 reshape long _r, i(_id) j(_var)
13 * create dummy variables and interactions
14 gen byte cons = 1
15 gen byte _d1 = _var == 1
16 gen byte _dmeas = 1-_d1
17 gen _type = _d1 + 2*_dmeas /* response type */
18 gen _bus_d1 = bus*_d1
19 * define equations
20 eq load: _dmeas _d1
21 eq f1: bus cons

22 * call gllamm
23 gllamm _r  _bus_d1 _d1, /*
24  */ i(_id) nocons eqs(load) link(logit ident) family(binom gauss) /*
25  */ lv(_type) fv(_type)  geqs(f1)  from(startv) copy adapt  /*
26  */  weightf(_wt)     nolog
                               end do-file
```

Note that running this do-file will change the data irreversibly, so users may wish to save their data first. The variables generated by the do-file start with "_" to distinguish them from other variables in the dataset. If the variables `_id` or `_one` already exist, the do-file will stop running, and the user must make changes to the do-file or data. In line 2, the starting values generated by `cme` are placed into a matrix `startv` for later use. In lines 5 and 6, the data are collapsed to reduce the number of observations if several units share the same values on all variables contributing to the analysis (this is not the case in this example). Since the two repeated log-fiber measurements and CHD are all response variables, these variables need to be stacked into a single variable `_r`. In lines 8 to 10, the variables are therefore first renamed to `_r1`, `_r2` and `_r3` and in line 12 the `reshape` command is used to stack these responses into `_r` and create a variable `_var` taking on the values 1,2,3 for responses originally in `_r1`, `_r2` and `_r3`, respectively.

A constant is generated in line 14. Two response models will need to be specified, one for CHD and one for log-fiber. Lines 15 to 17 therefore create dummy variables `_d1`

(d_{1ij}) for CHD and dmeas $(d_{mj} = 1 - d_{1ij})$ for log-fiber and a variable _type taking on values 1 and 2 for these two response-types, respectively. In line 18, the explanatory variable bus in the CHD model is multiplied by _d1 to pick out the values of bus for responses corresponding to CHD.

The data manipulation is now complete and the model can be specified. In line 20, the linear combination of variables $\boldsymbol{v}'_{ij}\boldsymbol{\lambda}$ multiplying the latent variable is specified using the equation command eq load: _dmeas _d1. To include the effect of bus on true log-fiber, line 21 defines an equation for the structural model. Since there could be several latent variables, the second character of the equation name must be a number, here 1 for the first (and only) latent variable. In the gllamm command, the response variable and the variables for the fixed part $\boldsymbol{x}'_{ij}\boldsymbol{\beta}$ are first listed in line 23. In line 24, the i() option declares _id as the unit-identifier i, and the nocons option specifies that the overall constant should be omitted. The eqs() option passes the equation for $\boldsymbol{v}'_{ij}\boldsymbol{\lambda}$ to gllamm. The link() and family() options list the links and families needed. In line 25, lv() and fv() specify that the first link and family should apply when _type equals 1 and the second when it equals 2. The equation for the structural model for the true covariate is passed to gllamm using the geqs() option.

The from(startv) and copy options specify that starting values are in the matrix startv and should be copied in the order in which they appear (not according to column and equation names). The adapt option causes gllamm to use adaptive quadrature. In line 26, weightf(_wt) declares that unit-specific frequency weights can be found in _wt2, whereas any response-specific weights would be in _wt1. Since _wt1 does not exist, the latter are assumed to be 1. For further explanations of these options, see help gllamm, the gllamm manual (Rabe-Hesketh, Pickles, and Skrondal 2001) and book (Rabe-Hesketh, Pickles, and Skrondal 2004).

Running this do-file gives the following gllamm output:

```
number of level 1 units = 742
number of level 2 units = 333

Condition Number = 56.335474

gllamm model

log likelihood = -186.93042

------------------------------------------------------------------------------
          _r |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     _bus_d1 |  -.1892767   .3396128    -0.56   0.577    -.8549055    .4763522
         _d1 |  -1.852311   .2458932    -7.53   0.000    -2.334253   -1.370369
------------------------------------------------------------------------------

Variance at level 1
------------------------------------------------------------------------------

  .02173286 (.00352703)
```

```
Variances and covariances of random effects
------------------------------------------------------------------------------


***level 2 (_id)

    var(1): .07019567 (.00757967)

    loadings for random effect 1
    _dmeas: 1 (fixed)
    _d1: -1.9565293 (.72616402)


Regressions of latent variables on covariates
------------------------------------------------------------------------------

    random effect 1 has 2 covariates:
    bus: -.12085325 (.03279718)
    cons: .06370884 (.02388626)
------------------------------------------------------------------------------
```

Here ζ_i (and u_i) are referred to as random effects. The estimated residual variance τ^2 and loadings $\boldsymbol{\lambda}$ are listed under `Variances and covariances of random effects`. The coefficient $\beta_u \equiv \lambda_2$ is therefore somewhat hidden. The measurement error variance is referred to as `Variance at level 1` since it represents the variance between different level-1 units ij within the same level-2 unit i. The estimated effect $\widehat{\gamma}_1$ of `bus` on true log-fiber and the estimated intercept $\widehat{\gamma}_0$ are listed under `Regressions of latent variables on covariates`.

An important advantage of understanding how `gllamm` works is that many of the assumptions of the classical covariate measurement error model can be relaxed and the model extended in many ways, some of which will be discussed in the following sections. Another advantage is that we can make use of `gllamm`'s post-estimation commands to obtain predictions and simulate from the model. For example, to predict the true covariate values by empirical Bayes, use

```
. gllapred resfib, u            /* predict $\zeta_i$ */
. gllapred truefib, fac         /* predict $u_i = \mathbf{z}_i'\widehat{\boldsymbol{\gamma}} + \zeta_i$ */
```

To simulate responses from the model (including measurements for the second occasion that were missing), use

```
. gllasim resp, fsample
```

3.2 Nonparametric true covariate distribution

We now relax the normality assumption for true log-fiber intake on which the previous analyses have relied. Assuming the data are still as we left them in the previous section, we can estimate a discrete true covariate distribution with three masses using `gllamm` with the `ip(f)` and `nip(3)` options:

```
. eq load: _dmeas _d1
. eq f1: _bus cons
. gllamm _r _bus_d1 _d1, /*
>    */ i(_id) nocons eqs(load) link(logit ident) family(binom gauss) /*
>    */ fv(_type) lv(_type) geqs(f1) ip(f) nip(3)
  (output omitted)
```

To see if a fourth mass can be added, we next specify `nip(4)` and use the `gateaux()` and `lf0()` options. In the `gateaux()` option, we specify the minimum, maximum, and number of steps for the search for a new mass location. In the `lf0()` option, we specify the number of parameters and log likelihood of the three-mass model. The latter is necessary so that `gllamm` can check whether the log likelihood increases when a tiny fourth mass is placed at any of the locations tried in the search. The necessary commands are

```
. local k = e(k)
. local ll = e(ll)
. gllamm _r _bus_d1 _d1, /*
>    */ i(_id) nocons eqs(load) link(logit ident) family(binom gauss) /*
>    */ fv(_type) lv(_type) geqs(f1) ip(f) nip(4) lf0(‘k’ ‘ll’)      /*
>    */ gateaux(-2 2 1000)
  (output omitted)
```

At the end of the search, `gllamm` prints

```
maximum gateaux derivative is 1.9500323
```

and starts estimating the four-mass model using the location with the greatest increase in log likelihood as the starting value for the new location. Increasing the number of masses this way one by one, the maximum gateaux derivative remains positive until the eight-mass solution is reached, giving the following output:

```
number of level 1 units = 742
number of level 2 units = 333

Condition Number = 148.23236


gllamm model                                      Number of obs   =        333
                                                  LR chi2(2)      =       0.79
Log likelihood = -177.87417                       Prob > chi2     =     0.6751

------------------------------------------------------------------------------
          _r |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     _bus_d1 |  -.1832445   .3382886    -0.54   0.588     -.846278     .479789
         _d1 |  -1.855017   .2460202    -7.54   0.000    -2.337208   -1.372827
------------------------------------------------------------------------------

Variance at level 1
-------------------------------------------------------------------------------

  .01902727 (.00306924)
```

```
Probabilities and locations of random effects
------------------------------------------------------------------------------


***level 2 (_id)

    loc1: -.74544, .01391, .40077, .68476, 1.0856, -.53297, .20197, -.2587
  var(1): .07299487

    loadings for random effect 1
    _dmeas: 1 (fixed)
    _d1: -1.9278901 (.70234087)

    prob: 0.0216, 0.4474, 0.0982, 0.0146, 0.0062, 0.0341, 0.1515, 0.2264

Regressions of latent variables on covariates
------------------------------------------------------------------------------


    random effect 1 has 2 covariates:
    bus: -.11507202 (.03271296)
    cons: .06066323 (.0239785)
------------------------------------------------------------------------------
```

Up to `Probabilities and locations of random effects` and from `Regressions of latent variables on covariates`, the output has the same format as for a normally distributed true covariate (see the previous section). In between, the estimated locations $\widehat{e}_c$, $c = 1, \ldots, 8$ of the eight masses are listed to the right of `loc1:`, followed by the variance of the estimated discrete distribution to the right of `var(1):`. This variance is not a model parameter but is derived from the estimated locations and probabilities using

$$\texttt{var(1)} = \sum_{c=1}^{8} \widehat{\pi}_c \widehat{e}_c^2$$

since the mean of the discrete distribution is set to 0, $\sum_{c=1}^{8} \widehat{\pi}_c \widehat{e}_c = 0$ (only 7 locations were independently estimated). The estimated factor loading $\widehat{\beta}_u$ is then given as for a continuous true covariate, followed by the estimated probabilities $\widehat{\pi}_c$, $c = 1, \ldots, 8$ to the right of `prob:` (to obtain the corresponding log-odds parameters with their standard errors, as well as standard errors for the location parameters, use `gllamm, allc`).

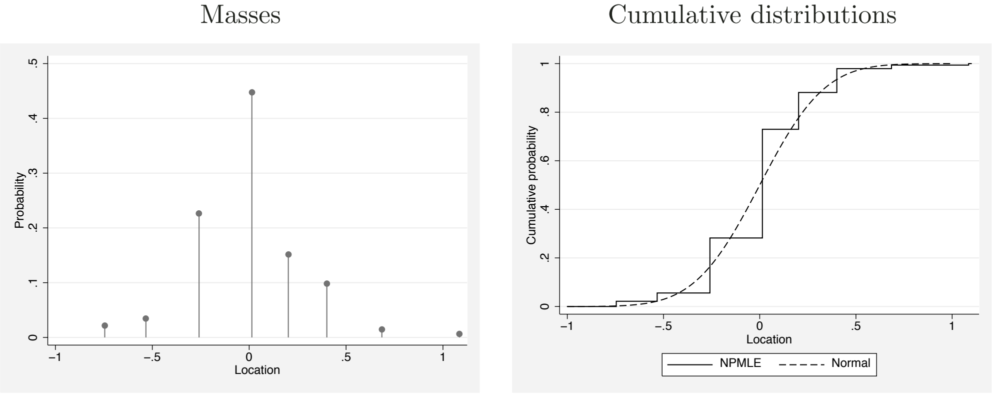
The parameter estimates (except for the locations and probabilities) are given under “NPMLE” in table 1. It is remarkable how close the estimates are to those obtained by assuming a normally distributed true covariate (see “Direct and indirect effects” in table 1).

The discrete distribution can be displayed graphically using the following sequence of commands:

```
. * save locations and log probabilities as variables
. matrix locs = e(zlc2)'
. matrix lp = e(zps2)'
. svmat locs
. svmat lp
. * calculate probabilities
. gen p=exp(lp1)

. * plot masses
. twoway (dropline p locs1), xtitle(Location) ytitle(Probability)
```

giving the graph in the left panel of figure 3. Here, we have used matrices of locations and log probabilities stored in the first (and only) rows of `zlcs2` and `zps2`, respectively. After transposing these matrices so that the estimates are in the first (and only) columns, we place the values into new variables `locs1` and `lp1` using the `svmat` command. We then convert the log probabilities to probabilities `p` and plot the masses using the `twoway dropline` command.


Masses

Cumulative distributions

Figure 3: Nonparametric true covariate distribution

It is also useful to plot the corresponding cumulative distribution together with that of the normal distribution with zero mean and variance $\widehat{\tau}^2 = 0.0702$ estimated in section 3.1:

```
. * set end-points for cumulative probabilities
. replace locs1 = -1 in 9
. replace p = 0 in 9
. replace locs1 = 1.1 in 10
. replace p = 0 in 10

. * calculate cumulative probabilities
. sort locs1
. gen cump = sum(p)

. * plot cumulative probabilities
. twoway (line cump locs1, connect(stairstep))              /*
>    */   (function y=norm(x/sqrt(.0702)), range(-1 1)),     /*
>    */   xtitle(Location) ytitle(Cumulative probability)    /*
>    */   legend(order(1 "NPMLE" 2 "Normal"))
```

giving the graph in the right panel of figure 3. Here, we first create two artificial masses at -1 and 1.1 with zero probabilities so that the cumulative distribution will start at 0 and finish at 1. We then sort the locations and calculate the cumulative probabilities using the `sum()` function. The `twoway line` command with the `connect(stairstep)` option creates the stair-shaped plot for the discrete cumulative distribution, and the `twoway function` command combined with the `norm()` function produces a smooth curve for the normal cumulative distribution function with the required variance.

The estimated discrete distribution resembles the normal distribution. This may be the reason why the NPML estimates so closely resemble those assuming normality. In Rabe-Hesketh, Pickles, and Skrondal (2003), raw fiber was also analyzed, giving a skewed nonparametric distribution for true fiber and greater differences between the NPML estimates and those assuming normality. Rabe-Hesketh, Pickles, and Skrondal (2003) also carried out simulations to investigate the performance of parameter estimates and empirical Bayes predictions for both NPMLE and assuming normality when the true covariate distribution is either normal or skewed.

It is worth noting that a syntax very similar to that used in this section would be used to specify a *latent class model* with two classes when the true covariate, as well as the measurements, are dichotomous:

```
. gllamm _r _bus_d1 _d1, i(_id) nocons eqs(load) /*
>  */ link(logit) family(binom) peqs(f1) ip(f) nip(2)
```

3.3 Congeneric measurement model

Returning to a normally distributed true covariate, we now extend the measurement model to the congeneric measurement model in (4) and estimate this model using `gllamm`. However, the congeneric model is not identified with only two measurements of log-fiber, and we will therefore simulate data resembling the CHD data but with three measures of log-fiber. Defining dummy variables d_{2ij} to d_{4ij} for the measures of log-fiber, the model can be written as

$$\begin{aligned} g(\mu_{ij}) &= d_{1ij}\beta_0 + d_{mij}\mu + d_{3ij}\alpha_2 + d_{4ij}\alpha_3 \\ &\quad + u_i(\lambda_1 d_{2ij} + \lambda_2 d_{3ij} + \lambda_3 d_{4ij} + \lambda_4 d_{1ij}), \quad \lambda_1 = 1 \\ &= \begin{cases} \beta_0 + u_i\lambda_4 & \text{if } j=1 \text{ (CHD)} \\ \mu + u_i & \text{if } j=2 \text{ (measure 1)} \\ \mu + \alpha_2 + u_i\lambda_2 & \text{if } j=3 \text{ (measure 2)} \\ \mu + \alpha_3 + u_i\lambda_3 & \text{if } j=4 \text{ (measure 3)} \end{cases} \end{aligned} \tag{7}$$

Here, a constant μ is now included in the measurement model, and we must therefore omit the constant γ_0 in the true covariate model:

```
. eq f1: bus
```

Note that it is advisable to include constants in the response model instead of the structural model when no starting values are provided for `gllamm`.

To allow for different measurement error variances σ_j^2, we model the log of the level 1 standard deviation as

$$\ln(\mathrm{sd}(\epsilon_{ij})) \;=\; \delta_1 d_{2ij} + \delta_2 d_{3ij} + \delta_3 d_{4ij}, \quad \sigma_j^2 = \exp(2\delta_j)$$

To simulate the data, we first create new observations for the third measurement of log-fiber by replicating the records representing the second measurement (`_var=3`).

```
. expand 2 if _var==3
```

We need separate dummy variables `d2`, `d3`, and `d4` for the three measures:

```
. qui tab _var, gen(d)
. bysort _id _var: gen d4 = _n==2
. replace d3=0 if d4==1
```

The first command only generates three dummy variables `d1` to `d3` since `_var` equals 3 for both the second and third measures. Each subject, therefore, has two observations with `d3`=1. In the second and third commands, we set `d4` to 1 and `d3` to 0 for one of these observations.

We can now specify the model we wish to simulate from using the `gllamm` command, preventing `gllamm` from estimating the model using the `eval` option, which instructs `gllamm` to merely evaluate the log likelihood.

First, we specify the linear predictor $d_{2ij} + \lambda_2 d_{3ij} + \lambda_3 d_{4ij} + \lambda_4 d_{1ij}$ multiplying u_i using

```
. eq load: d2 d3 d4 d1
```

where `d2` is given first since the first factor loading λ_1 equals 1. Then, we specify the linear predictor $\delta_1 d_{2ij} + \delta_2 d_{3ij} + \delta_3 d_{4ij}$ for the log standard deviation using

```
. eq het: d2 d3 d4
```

The latter is passed to `gllamm` using the `s()` option:

```
. matrix a=J(1,12,0) /* matrix with 12 columns, all elements equal to 0 */
. qui gllamm _r d1 _dmeas d3 d4, /*
>   */ i(_id) nocons eqs(load) link(logit ident) family(binom gauss) /*
>   */ fv(_type) lv(_type) geqs(u1) s(het) from(a) copy eval
```

Although no model has been estimated, estimates have been stored, and the parameter matrix with values as specified in the `from()` option can be obtained using

```
. matrix a=e(b)

. matrix list a

a[1,12]
          _r:       _r:       _r:       _r:     lns1:     lns1:     lns1:
          d1    _dmeas        d3        d4        d2        d3        d4
y1         0         0         0         0         0         0         0

          _id1_1l:  _id1_1l:  _id1_1l:   _id1_1:     u1:
               d3        d4        d1        d2     bus
y1              0         0         0         0       0
```

We can now specify the parameter values of the model from which we wish to simulate in the order required by the simulation command gllasim (same order as for gllamm):

```
. * Intercept for CHD: $\beta_0$
. matrix a[1,1] = -2

. * Mean of measure 1: $\mu$
. matrix a[1,2] = 3

. * Bias parameters: $\alpha_j$
. matrix a[1,3] = 1       /* measure 2 */
. matrix a[1,4] = -1      /* measure 3 */

. * Log(sd) parameters: $\delta_j$
. matrix a[1,5] = -2      /* measure 1 */
. matrix a[1,6] = -2      /* measure 2 */
. matrix a[1,7] = -1      /* measure 3 */

. * Factor loadings: $\lambda_j$
. matrix a[1,8] = 1.5     /* measure 2 */
. matrix a[1,9] = 2       /* measure 3 */
. matrix a[1,10] = -2     /* $\beta_u$ */

. * True covariate sd: $\tau$
. matrix a[1,11] = 0.3

. * Effect of bus on true covariate: $\gamma_1$
. matrix a[1,12] = -0.2
```

We now set the random number seed (to allow replication) and simulate responses for the full sample (instead of the previous estimation sample) from the model specified in the previous gllamm command but with parameters from a using

```
. set seed 131123
. gllasim r, fsample from(a)
```

The parameters can then be estimated using the same gllamm command as before:

```
. gllamm r _d1 _dmeas d3 d4, /*
>   */ i(_id) nocons eqs(load) link(logit ident) family(binom gauss) /*
>   */ fv(_type) lv(_type) geqs(u1) s(het) adapt

Running adaptive quadrature
Iteration 1:    log likelihood = -677.30613
Iteration 2:    log likelihood = -458.65378
Iteration 3:    log likelihood = -419.96371
Iteration 4:    log likelihood = -410.83011
Iteration 5:    log likelihood = -410.55348
Iteration 6:    log likelihood = -410.55324

Adaptive quadrature has converged, running Newton-Raphson
Iteration 0:   log likelihood = -410.55324
Iteration 1:   log likelihood = -410.55324

number of level 1 units = 1332
number of level 2 units = 333

Condition Number = 46.814881
```

```
gllamm model

log likelihood = -410.55324

------------------------------------------------------------------------------
           r |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         _d1 |  -1.997545   .2007127    -9.95   0.000    -2.390935   -1.604155
      _dmeas |   3.043896    .026312   115.68   0.000     2.992325    3.095467
          d3 |     1.0229   .0176837    57.84   0.000     .9882403    1.057559
          d4 |  -.9608751   .0352518   -27.26   0.000    -1.029967   -.8917829
------------------------------------------------------------------------------

Variance at level 1
------------------------------------------------------------------------------

    equation for log standard deviation:

    d2: -1.9827443 (.06099411)
    d3: -1.8834334 (.09502256)
    d4: -1.0093654 (.04794215)

Variances and covariances of random effects
------------------------------------------------------------------------------

***level 2 (_id)

    var(1): .09123715 (.00840143)

    loadings for random effect 1
    d2: 1 (fixed)
    d3: 1.5103875 (.04910599)
    d4: 2.0653678 (.08170733)
    d1: -1.5363324 (.51209769)

Regressions of latent variables on covariates
------------------------------------------------------------------------------

    random effect 1 has 1 covariates:
    bus: -.24193129 (.03478306)
------------------------------------------------------------------------------
```

The estimates are quite close to the true values and stay the same (to about four decimal places) when 12-point quadrature is used. Assuming equal measurement error variances and factor loadings but retaining the bias parameters α_j, the log likelihood decreases substantially from -410.55 to -686.85 (12-point adaptive quadrature), and the estimate $\widehat{\beta}_u$ of the effect of the true covariate is attenuated from -1.54 (0.51) to -1.04 (0.35), the true value being -2.

4 Discussion

We have developed the `gllamm` wrapper `cme`, which makes estimation of an important class of generalized linear covariate measurement error models extremely easy while making use of the reliable adaptive quadrature method provided by `gllamm`. The wrapper will also produce the commands necessary to manipulate the data and estimate the model in `gllamm`, which should be useful for learning to use `gllamm`. The generated commands can subsequently be modified to extend the model or to use `gllamm`'s post-estimation commands `gllapred` and `gllasim` for prediction and simulation.

We have also extended the classical covariate measurement error model to relax the assumptions that the true covariate is normally distributed and that the fallible measurements of the true covariate are exchangeable replicates with the same measurement properties.

In addition to dichotomous outcomes and continuous measurements as discussed here, `gllamm` can handle continuous, censored, ordinal, and nominal responses and rankings (Skrondal and Rabe-Hesketh 2003), as well as continuous and discrete-time durations (Rabe-Hesketh, Yang, and Pickles 2001). Moreover, the measurements may be of mixed type.

We have discussed only the most common case of a single covariate measured with error. Models with several imperfectly measured covariates can easily be handled by `gllamm`; see also Rabe-Hesketh, Skrondal, and Pickles (2004). The NPMLE example showed how dichotomous true covariates and latent class modeling can be handled in `gllamm`. However, at present, it is not possible to have both continuous and categorical true covariates in the same model. When the true covariate is available in a validation sample, the model can also be estimated in `gllamm`; see Skrondal and Rabe-Hesketh (2004), chapter 14, for an example. `gllamm` can be used to estimate multilevel generalized linear mixed models with covariate measurement error. When the outcome has been measured several times, it can also be useful to construct models for a latent true outcome, see Rabe-Hesketh, Skrondal, and Pickles (2004), Skrondal and Rabe-Hesketh (2004), and Rabe-Hesketh, Pickles, and Skrondal (2004). Finally, we can allow measurement errors to be correlated (if the model is identified) using further latent variables.

The `gllamm` command is also useful for other problems involving latent variables, such as multilevel random effects models, multilevel structural equation models (including factor and item response models), latent class models, and multilevel selection and endogenous treatment models; see Skrondal and Rabe-Hesketh (2004).

Roberto G. Gutierrez at StataCorp achieved a considerable increase in the speed of `gllamm` in January 2003 by converting an important part of `gllamm` to internal code. As a result, `gllamm` is fairly quick for the models estimated in this paper. For models including many latent variables, `gllamm` can, however, still be slow, and we are working on further speed improvements.

5 Acknowledgment

We would like to thank David Clayton for kindly providing us with the data.

6 Appendix: Syntax for cme

`cme` *depvar* [*varlist*] `(`*label*`:` *varlist*`)` [*weight*] [`if` *exp*] [`in` *range*] [`,` `mevar(`*#*`)`
`family(`*familyname*`)` `link(`*linkname*`)` `denom(`*varname*`)` `noconstant`
`offset(`*varname*`)` `tcovmod(`*varlist*`)` `simple` `nip(`*#*`)` `noadapt` `robust`
`cluster(`*varname*`)` `commands` `indirect` `total` `eform` `level(`*#*`)` `nolog` `trace`
`from(`*matrix*`)`]

The outcome model is specified by *depvar* [*varlist*], `family(`*familyname*`)`, etc.

The classical measurement model for the true covariate is specified by `(`*label*`:` *varlist*`)`, where *label* is the name of the true covariate (it cannot have the same name as an existing variable in the dataset) and *varlist* are the fallible (continuous) measurements of the true covariate. At least two variables are required unless the `mevar(`*#*`)` option is used.

The true covariate model is a linear regression with explanatory variables (observed covariates) [*varlist*]unless the `tcovmod(`*varlist*`)` option is used to specify different explanatory variables.

families	links
`gaussian`	`identity`
`poisson`	`log`
`gamma`	`reciprocal`
`binomial`	`logit`
	`probit`
	`cll` (complementary log-log)
	`ologit` (`o` stands for ordinal)
	`oprobit`
	`ocll`

`fweight`s and `pweight`s are allowed; see [U] **14.1.6 weight**.

`cme` shares the features of all estimation commands; see [U] **23 Estimation and postestimation commands**.

6.1 Options

`mevar(`*#*`)` specifies the measurement error variance. This option is required if there are no replicate measurements.

`family(`*familyname*`)` specifies the distribution of *depvar*; `family(gaussian)` is the default.

`link(`*linkname*`)` specifies the link function; the default is the canonical link for the `family()` specified.

`denom(`*varname*`)` specifies the binomial denominator for the binomial link when *depvar* is the number of successes out of a fixed number of trials.

`noconstant` specifies that the linear predictor of the outcome model has no intercept term, thus forcing it through the origin on the scale defined by the link function.

`offset(`*varname*`)` specifies an offset to be added to the linear predictor of the outcome model.

`tcovmod(`*varlist*`)` specifies the observed covariates to be used in the true covariate model; a constant will automatically be estimated.

`simple` specifies that there are no observed covariates in the true covariate model.

`nip(`#`)` the number of quadrature points to be used.

`noadapt` uses ordinary quadrature instead of the default adaptive quadrature.

`robust` specifies that the Huber/White/sandwich estimator of variance is to be used.

`cluster(`*varname*`)` specifies that the observations are independent across groups (clusters) but not necessarily within groups.

`commands` displays the commands necessary to prepare the data and estimate the model in `gllamm` instead of estimating the model. Note that these commands change the data!

`indirect` displays the indirect effects of observed covariates on the outcome via the true covariate—this is shown for all covariates in the true covariate model.

`total` displays the total effects (indirect effects plus direct effects) of observed covariates on the outcome via the true covariate—this is shown for all covariates in the true covariate model.

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

`level(`#`)` specifies the confidence level, in percent, for confidence intervals (default 95).

`nolog` suppresses the iteration log.

`trace` requests that the estimated coefficient vector be printed at each iteration. In addition, all the output produced by `gllamm` with the `trace` option is also produced.

`from(`*matrix*`)` specifies a matrix of starting values. Elements must be in the order required by `cme`

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About the Authors

Sophia Rabe-Hesketh is Professor in the Graduate School of Education, University of California, Berkeley.

Anders Skrondal is Head of Biostatistics Group, Division of Epidemiology, Norwegian Institute of Public Health, Oslo.

Andrew Pickles is Professor of Epidemiological and Social Statistics at the School of Epidemiology and Health Science and CCSR, The University of Manchester.