11th UK Stata Users Group Meeting

Centre for Econometric Analysis, London

Applications of gllamm in health evaluation studies

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with material from

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and

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GLLAMM and gllamm

- GLLAMM is a modelling framework most fully elaborated in the book

  Skrondal, A. and Rabe-Hesketh, S. (2004). *Generalized Latent Variable Modeling: Multilevel, Longitudinal and Structural Equation Models*. Chapman & Hall/CRC Press. Boca Raton, FL.

- gllamm is a software implementation that is capable of fitting very many of the models with the GLLAMM framework.

  - Rabe-Hesketh, S., Pickles, A. and Taylor, C. (2000). sg129: Generalized linear latent and mixed models. *Stata Technical Bulletin* **53**, 47-57.

  - Rabe-Hesketh, S., Skrondal, A. and Pickles, A. (2002). Reliable estimation of generalized linear mixed models using adaptive quadrature. *The Stata Journal* **2**, 1-21.

- gllamm now consists of a model fitting program, and post-estimation and simulation programs gllapred and gllasim.

- gllamm and gllamm manual, datasets and other information are available from *www.gllamm.org*

GLLAMM and gllamm

What do GLLAMM and gllamm let you do?

GLLAMM helps you to understand and gllamm allows you to analyse the effects of covariates and the structure of covariance (multivariate normal and discrete mixture) among sets of measures that may be of different kinds (continuous, count, nominal, ordered, ranked, censored)

GLLAMM and gllamm

This includes for any response type:

- variance components (including frailty models)
- random coefficient and growth curve models
- factor analysis
- structural equation models
- latent class models
- selection models
- non-ignorable non-response
- multilevel versions of the above

GLLAMM and gllamm

This generality is gained at some expense.

Speed: for any 'standard' analysis a specialist program will run more quickly.

Speed is improving as the result of the efforts of StataCorp, the gllamm team (Sophia Rabe-Hesketh, Andrew Pickles and Anders Skrondal) and as computers improve.

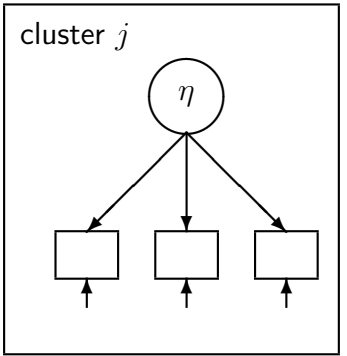
Model set-up: some more complex models can require careful prior data manipulation. The writing of wrapper programs that do this for you for particular model types is in progress.

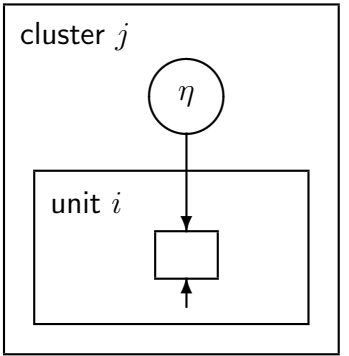
Generalized linear mixed models

We can add random effects into any GLM

- Clustered or 'two-level' data: level-1 units i nested in level-2 clusters j
  - Repeated measurements on patients
  - Twins in families
- Unobserved between-cluster covariates (or unobserved heterogeneity)
  $\Longrightarrow$ Dependence between units ij and $i'j$ in the same cluster j
- Include a cluster-specific random intercept η_j in the linear predictor

$$\nu_{ij} = \mathbf{x}'_{ij}\boldsymbol{\beta} + \eta_j$$





Note:

☞ frames indicate 'level'

☞ ◯ encloses latent variables

☞ □ surrounds observed var.

☞ $\longrightarrow$ represents a regression

Random coefficient models in GLLAMM

- One covariate multiplies each latent variable,

$$\eta_m^{(l)} z_{m1}^{(l)} \quad (\lambda_{m1}^{(l)} = 1)$$

- e.g. Latent growth curve model for individuals j (level 2) observed at times t_{ij}, $i = 1, \cdots, n_j$ (level 1)

$$\text{Linear predictor: } \nu_{ij} = \beta_1 + \beta_2 t_{ij} + \eta_{1j}^{(2)} + \eta_{2j}^{(2)} t_{ij}$$

β_1, β_2 : mean intercept and slope

$\eta_{1j}^{(2)}$, $\eta_{2j}^{(2)}$: random deviations of unit-specific intercepts and slopes from their means

Generalized random coeff. model in GLLAMM

$$\nu = \mathbf{x}'\boldsymbol{\beta} + \sum_{l=2}^{L}\sum_{m=1}^{M_l} \eta_m^{(l)} \mathbf{z}_m^{(l)\prime} \boldsymbol{\lambda}_m^{(l)}$$

For identification, $\lambda_{m1}^{(l)} = 1$

- Fixed part: $\mathbf{x}'\boldsymbol{\beta}$ as usual
- Random part:
  - $\eta_m^{(l)}$ is mth latent variable at level l, $m = 1, \cdots, M_l$, $l = 2, \cdots, L$
    Can be a factor or a random coefficient
  - $\mathbf{z}_m^{(l)}$ are variables and $\boldsymbol{\lambda}_m^{(l)}$ are parameters
  - Unless regressions for the latent variables are specified, latent variables at different levels are independent whereas latent variables at the same level may be dependent

gllamm syntax for estimating GLMMs

gllamm [*varlist*] [if *exp*] [in *range*] , i(*varlist*) [nrf(*numlist*)
eqs(*eqnames*) offset(*varname*) family(*family*) link(*link*) eform
nip(*numlist*) adapt from(*matrix*) ...]

i(*varlist*) $L-1$ variables identifying the hierarchical, nested clusters, from level 2 to L, e.g., `i(pupil class school)`.

nrf(*numlist*) $L-1$ numbers specifying the numbers of latent variables M_l at each level.

eqs(*eqnames*) $M = \sum M_l$ equations for the $\mathbf{z}_m^{(l)\prime}\boldsymbol{\lambda}_m^{(l)}$ multiplying each latent variable. Constants must be explicitly included in the equation definition.

family(*family*), link(*link*) and eform as for glm.

offset(*varname*) variable in fixed part with regression coefficient set to 1.

nip(*numlist*) numbers of quadrature points for each latent variable (total M), a single number meaning that all values are the same.

adapt adaptive quadrature will be used.

from(*matrix*) passes starting values to gllamm – use skip if matrix contains extra parameters and copy if column and equation names not right.

Syntax examples: linear predictor

- Two-level growth curve model (occasions in subjects)

$$\text{Linear predictor: } \nu_{ij} = \beta_1 + \beta_2 t_{ij} + \eta_{1j}^{(2)} + \eta_{2j}^{(2)} t_{ij}$$

```
gen cons=1
eq int: cons
eq slope: time
gllamm y time, i(subject) nrf(2) eqs(int slope) ...
```

- Three-level growth curve model (occasions in subjects in centres)

$$\text{Linear predictor: } \nu_{ijk} = \beta_1 + \beta_2 t_{ijk} + \eta_{1jk}^{(2)} + \eta_{2jk}^{(2)} t_{ijk} + \eta_{1k}^{(3)} + \eta_{2k}^{(3)} t_{ijk}$$

```
gllamm y time, i(subject centre) nrf(2 2) /*
   */ eqs(int slope int slope) ...
```

gllapred syntax for prediction

gllapred *varname* [if *exp*] [in *range*] [, xb u linpred mu
marginal us(*varname*) outcome(#) above(#) ···]

xb fixed part of linear predictor returned in *varname*.

u posterior means and standard deviations of latent variables returned in *varname*m1, *varname*s1, *varname*m2, etc.

ustd same as u but divided by approximate sampling standard deviation.

linpred linear predictor (with posterior means of latent variables) returned in *varname*.

mu mean response $\mathrm{E}[g^{-1}(\nu)]$ returned in *varname*. By default expectation w.r.t. posterior distribution.

marginal marginal or population average mean (expectation w.r.t. prior distribution).

us(*varname*) expectation conditional on latent variables being equal to the values in *varname*1, *varname*2, etc.

outcome(#) with mlogit link, probability that the response equals #.

above(#) with ordinal links, probability that response exceeds #.

gllasim syntax for simulation

gllasim *varname* [if *exp*] [in *range*] [, u us(*varname*) from(*matrix*) ⋯]

By default, responses are simulated for the model just estimated and returned in *varname*.

u latent variables are simulated and returned in *varname*p1, *varname*p2, etc.

us(*varname*) response variables are simulated for latent variables equal to *varname*1, *varname*2, etc.

from(*matrix*) causes responses/latent variables to be simulated from the model just estimated in gllamm but with parameter values in matrix.

Growth and trajectory models: treatment of depression

Postnatal depression example

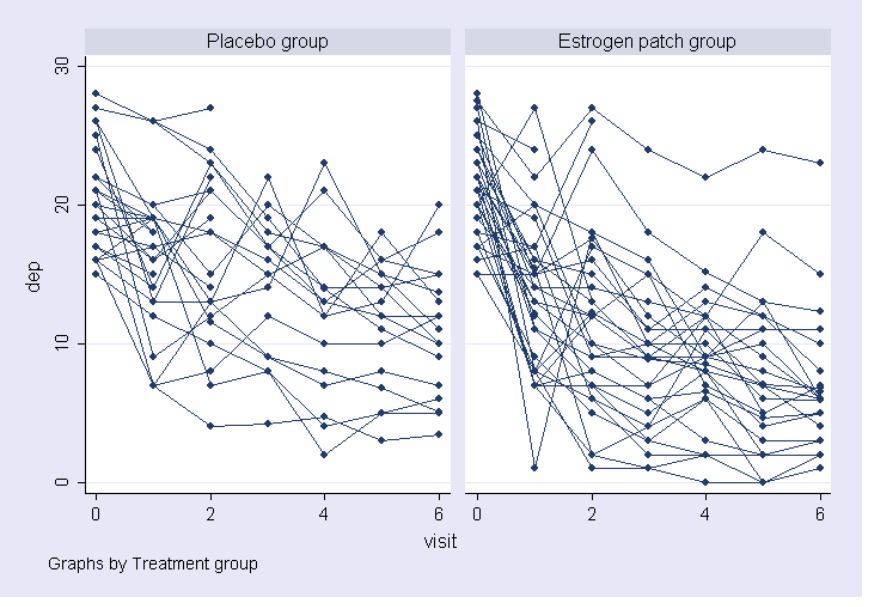
The data look like

```
use depress7.dta, clear
list, clean
```

	subj	visit	group	dep
1.	1	0	Placebo group	18
2.	1	1	Placebo group	17
3.	1	2	Placebo group	18
4.	1	3	Placebo group	15
5.	1	4	Placebo group	17
6.	1	5	Placebo group	14
7.	1	6	Placebo group	15
8.	2	0	Placebo group	27
9.	2	1	Placebo group	26
10.	2	2	Placebo group	23
...				
349.	59	0	Estrogen patch group	17
350.	59	1	Estrogen patch group	15
351.	60	0	Estrogen patch group	22
352.	60	1	Estrogen patch group	7
353.	60	2	Estrogen patch group	12
354.	60	3	Estrogen patch group	15
355.	61	0	Estrogen patch group	26
356.	61	1	Estrogen patch group	24

Postnatal depression example

```
sort group subj visit
twoway (connected dep visit, connect(ascending)), by(group)
```



Depression example: growth curve model

Response at time t of individual i, y_{it}, is given by:

$$y_{it} = \underbrace{\alpha + \beta t}_{\text{fixed part}} + \underbrace{\eta_{it}}_{\substack{\text{random} \\ \text{effects}}} + \underbrace{e_{it}}_{\substack{\text{occasion} \\ \text{specific error}}}$$

where

$$\eta_{it} = u_{1i} + u_{2i}t$$

and $(u_{1i}, u_{2i}) \sim$ bivariate normal.

In the standard growth curve model the random effects for slope and intercept are allowed to be correlated.

Postnatal depression example

Bivariate random effects model

```
gen con=1
eq int: con
eq slope: visit
xi: gllamm dep i.group*visit, i(subj) nrf(2) eqs(int slope) adapt
```

```
...
number of level 1 units = 356
number of level 2 units = 61

Condition Number = 28.96942

gllamm model

log likelihood = -1041.133
```

dep	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_Igroup_1	-1.653089	1.035749	-1.60	0.110	-3.683121	.3769425
visit	-1.526425	.2091052	-7.30	0.000	-1.936264	-1.116587
_IgroXvisi~1	-.5464383	.2660811	-2.05	0.040	-1.067948	-.0249289
_cons	19.2888	.7769387	24.83	0.000	17.76603	20.81157

```
Variance at level 1
------------------------------------------------------------------------------
14.4725 (1.2985379)

Variances and covariances of random effects
------------------------------------------------------------------------------
***level 2 (subj)

    var(1): 8.9642528 (2.9576111)
    cov(2,1): .38745363 (.54299217) cor(2,1): .25252183

    var(2): .26261984 (.16961806)
------------------------------------------------------------------------------
```

Postnatal depression example

Compare random intercept model with random coefficient model by using Likelihood Ratio Test

Model 1: random intercept model

```
xi: gllamm dep i.group*visit, i(subj) adapt
    ... log likelihood = -1045.7117

estimates store model1          /* store estimates in model1 */
```

Model 2: Random coefficient model

```
xi: gllamm dep i.group*visit, i(subj) nrf(2) eqs(int slope) adapt
    ... log likelihood = -1041.133
```

Likelihood ratio test:

```
lrtest model1 .          /* compare model1 with current */
    (log-likelihoods of null models cannot be compared)

    likelihood-ratio test                          LR chi2(2)  =      9.16
    (Assumption: model1 nested in .)               Prob > chi2 =    0.0103
```

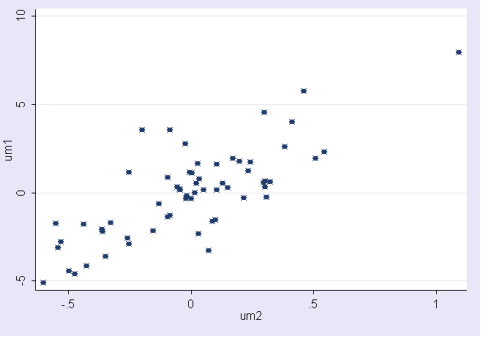
Note:

- ☞ Likelihood ratio test not valid since null hypothesis on boundary of parameter space
- ☞ Snijders and Bosker (1999) and others suggest dividing p-value by 2

Postnatal depression example

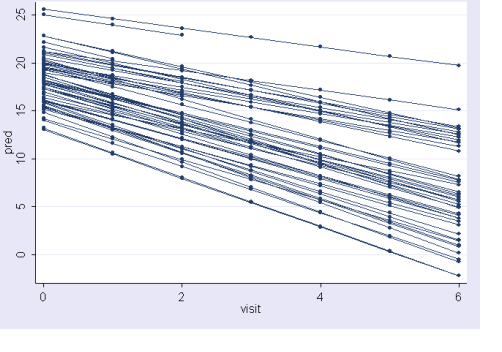
- Obtaining estimates of the random effects for individual deviations for intercepts and slopes

```
gllapred u, u
twoway (scatter um1 um2)
```



- Obtaining estimates of individual predicted values (trajectories)

```
gllapred pred, mu
sort subj visit
twoway (connected pred visit, msymbol(smcircle) /*
    */ connect(ascending))
```



bmatrix option in gllamm

bmatrix(*matrix*) specifies a matrix B of regression coefficients for the dependence of the latent variables on other latent variables. The matrix must be upper diagonal and have number of rows and columns equal to the total number of random effects.

Depression example by using bmatrix

An alternative setup is to let one of the random effects be regressed upon the other:

$$\begin{aligned} \eta_1 &= 0\eta_1 + \beta\eta_2 + \zeta_1 \\ \eta_2 &= 0\eta_1 + 0\eta_2 + \zeta_2 \end{aligned}$$

where ζ_1 and ζ_2 are uncorrelated.

```
constraint 1 [sub1_2_1]_cons=0

matrix b=(0,1 \ 0,0)

xi: gllamm dep i.group*visit, i(subj) nrf(2) nip(8) eqs(int slope) /*
       */ bmatrix(b) nocorrel adapt
```

Depression example by using bmatrix

Output

```
...
log likelihood = -1041.133021837493
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_Igroup_1	-1.653089	1.035749	-1.60	0.110	-3.68312	.3769416
visit	-1.526425	.2091052	-7.30	0.000	-1.936264	-1.116587
_IgroXvisi~1	-.5464382	.2660812	-2.05	0.040	-1.067948	-.0249287
_cons	19.2888	.7769384	24.83	0.000	17.76603	20.81157

```
 Variance at level 1
------------------------------------------------------------------------------
  14.472499 (1.2985371)

Variances and covariances of random effects
------------------------------------------------------------------------------
***level 2 (subj)
    var(1): 8.392612 (4.101821)
    cov(2,1): 0 (0) cor(2,1): 0
    var(2): .26262034 (.16961689)

 B-matrix:
------------------------------------------------------------------------------
    B(1,2): 1.4753391 (2.6476786)
------------------------------------------------------------------------------
```

☞ This gives the same likelihood, fixed effects estimates. The variance of the slope is 0.2626 as before, but the variance of the intercept is now given by $Var(\zeta_1) + b^2 Var(\zeta_2) = 8.3926 + 1.4753^2 * 0.2626 = 8.964$ (the same value as before).

Latent trajectory models

Response at time t of individual i, y_{it}, is given by a **growth model**:

$$y_{it} = \underbrace{\alpha + \beta t}_{\text{fixed part}} + \underbrace{\eta_{it}}_{\substack{\text{random} \\ \text{effects}}} + \underbrace{e_{it}}_{\substack{\text{occasion} \\ \text{specific error}}}$$

The η_{it}'s are represented by discrete trajectory classes c with probability π_c:

$$(\eta_{it} \mid c) = e_{1c} + e_{2c}t,$$

where

- e_{1c} is the trajectory origin or intercept for class c
- e_{2c} is the trajectory slope for class c
- Prevalence of trajectory class c is π_c
- $\sum_{k=1}^{C} \pi_k e_{1k} = 0$ and $\sum_{k=1}^{C} \pi_k e_{2k} = 0$

Latent trajectory models

We will hereafter consider three models:

Model 1: *unconditional trajectory classes and unconditional class probabilities*

Model 2: *unconditional trajectory classes and conditional class probabilities*

☞ *We allow probability* π_{ic} *that subject* i *belongs to latent class* c *to depend on covariates* $\boldsymbol{x_i}$ *through a multinomial logit model. For example, if we consider just one covariate* x_i*:*

$$\pi_{ic} = \frac{\exp(\gamma_{0c} + \gamma_{1c} x_i)}{\sum_{k=1}^{C} \exp(\gamma_{0k} + \gamma_{1k} x_i)},$$

where the γ_{0k}*'s and the* γ_{1k}*'s are parameters.*

Model 3: *conditional trajectory classes and unconditional class probabilities:*

$$y_{it} = \alpha + \beta x_i + \beta x_i t + \eta_{it} + e_{it}$$

☞ *Covariate effects included in fixed part of the model*

☞ *Classes now represent groups having accounted for covariate differences*

Postnatal depression example

- **Latent trajectory model (1)**: unconditional trajectory classes and unconditional class probabilities

```
gen cons=1
eq int: cons
eq slope: visit
gllamm dep visit, i(subj) nrf(2) eq(int slope) ip(f) trace nip(2)
```

```
...
```

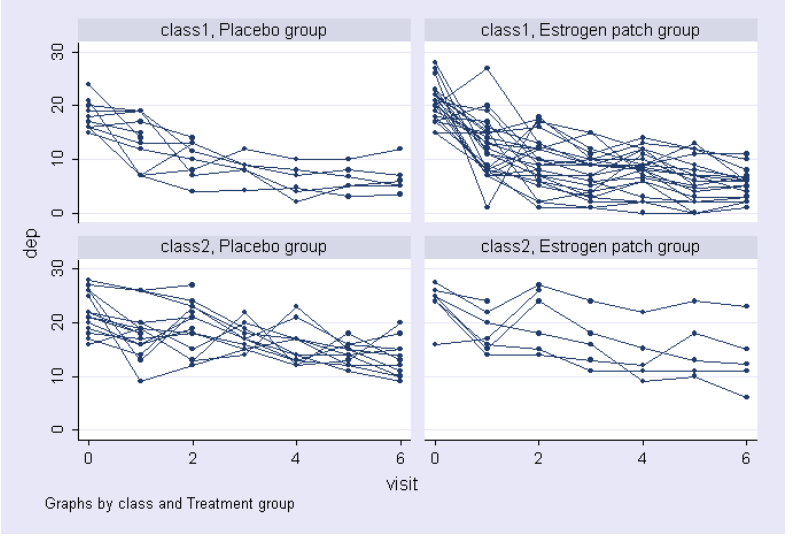
dep	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
visit	-1.898491	.1363647	-13.92	0.000	-2.165761	-1.631221
_cons	18.38703	.4981955	36.91	0.000	17.41058	19.36347

```
Variance at level 1
------------------------------------------------------------------------------
  19.139691 (1.4643147)

Probabilities and locations of random effects
------------------------------------------------------------------------------
***level 2 (subj)

    loc1: -1.9586, 2.933
  var(1): 5.7444392

    loc2: -.31928, .47814
cov(2,1): .9364582
  var(2): .15266137
    prob: 0.5996, 0.4004

    log odds parameters
    class 1
    _cons: .40381744 (.31445191)
------------------------------------------------------------------------------
```

Postnatal depression example

Now assign women to classes and look at what distinguishes one class from another.

```
preserve
gllapred prob, p
gen class=cond(prob1>prob2,1,2)
label define classl 1 "class1"  2 "class2"
label values class classl
sort class subj visit
twoway (connected dep visit, msymbol(smcircle) connect(ascending)), by(class group)
```



Postnatal depression example

Test for association of class assignment with treatment:

```
tab class group if visit == 0, chi2
```

class	Treatment group: Placebo g	Estrogen	Total
class1	11	27	38
class2	16	7	23
Total	27	34	61

```
Pearson chi2(1) =   9.5815   Pr = 0.002
```

```
restore
```

☞ **Note**: we reject the null hypothesis that `class` and `group` are independent.

Postnatal depression example

Let's model treatment differences in latent class probabilities directly.

➠ **Latent trajectory model (2)**: unconditional trajectory classes and conditional class probabilities

```
eq clprob: group
gllamm dep visit, i(subj) nrf(2) eq(int slope) peqs(clprob) ip(f) trace nip(2)
...
```

dep	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
visit	-1.639986	.176207	-9.31	0.000	-1.985345	-1.294626
_cons	19.66	.6530511	30.10	0.000	18.38004	20.93996

```
Variance at level 1
------------------------------------------------------------------------------
19.192753 (1.4748225)

Probabilities and locations of random effects
------------------------------------------------------------------------------
***level 2 (subj)

    loc1: -3.1888, 1.6681
  var(1): 5.3192671

    loc2: -.54866, .28701
cov(2,1): .91522481
  var(2): .15747215
    prob: 0.3435, 0.6565

    log odds parameters
    class 1
    group: 2.1258399 (.70207624)
    _cons: -.64795694 (.46781989)
```

☞ treatment effect on class assignment

Postnatal depression example

- **Latent trajectory model (3)**: conditional trajectory classes and unconditional class probabilities

```
gen gpvisit=group*visit
gllamm dep visit gpvisit, i(subj) nrf(2) eq(int slope) ip(f) trace nip(2)
...
```

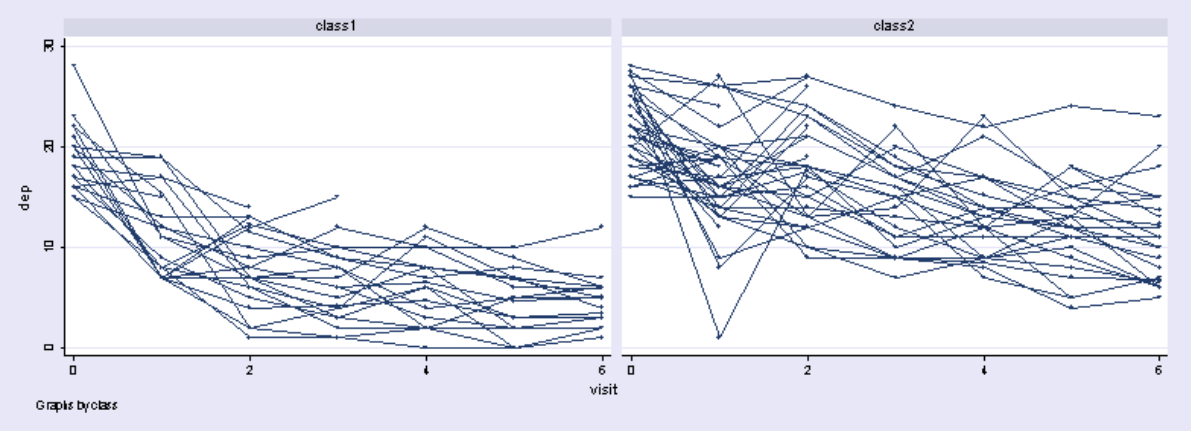
dep	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
visit	-1.424514	.1655199	-8.61	0.000	-1.748927	-1.100101
gpvisit	-.7501039	.1692819	-4.43	0.000	-1.08189	-.4183175
_cons	18.36341	.4986261	36.83	0.000	17.38612	19.3407

```
Variance at level 1
------------------------------------------------------------------------------
  18.927176 (1.4531254)

Probabilities and locations of random effects
------------------------------------------------------------------------------
***level 2 (subj)

    loc1: -3.0379, 1.9312
  var(1): 5.8667044

    loc2: -.31252, .19867
cov(2,1): .60354323
  var(2): .06209013
    prob: 0.3886, 0.6114

    log odds parameters
    class 1
    _cons: -.45301726 (.32825506)
------------------------------------------------------------------------------
```

Postnatal depression example

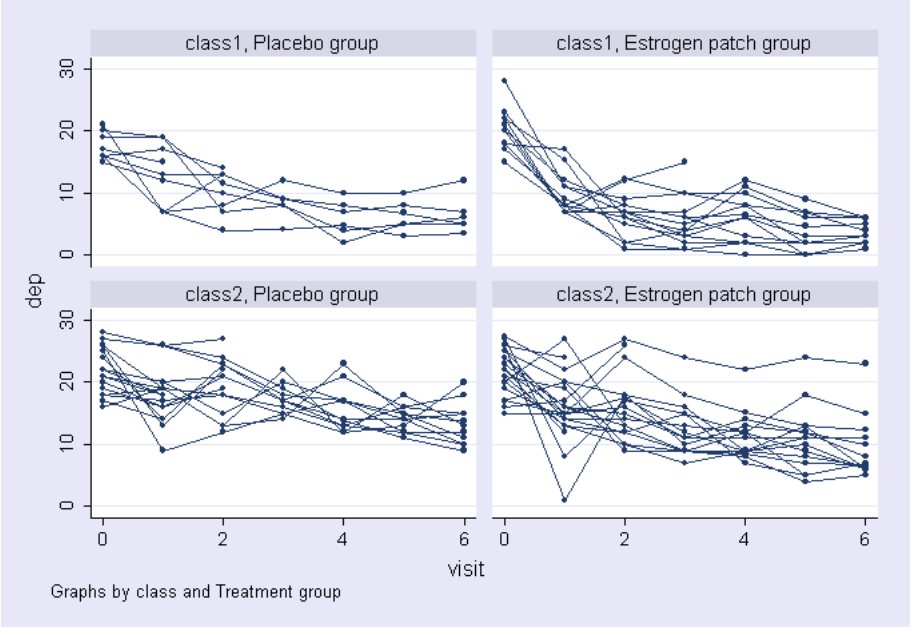
Posterior probabilities:

```
gllapred prob, p
gen class=cond(prob1>prob2,1,2)
label define classl 1 "class1"  2 "class2"
label values class classl
sort class subj visit
twoway (connected dep visit, msymbol(smcircle) connect(ascending)), /*
    */ by(class) ysize(8) xsize(20)
```



Postnatal depression example

```
twoway (connected dep visit, msymbol(smcircle) connect(ascending)), /*
     */ by(class group)
```



Postnatal depression example

Test for association of class assignment with treatment:

```
tab class group if visit == 0, chi2
```

class	Treatment group: Placebo g	Estrogen	Total
class1	9	14	23
class2	18	20	38
Total	27	34	61

```
Pearson chi2(1) =   0.3941   Pr = 0.530
```

☞ **Note:** As expected, we accept the null hypothesis of independence since the treatment effect has already been accounted for in the fixed part and the latent classes relate to variation around the fixed part.

Instrumental variables and CACE estimation

Trials that go wrong

- In many trials treatment assignment does not fully determine treatment exposure. Non-compliance results in other factors also influencing exposure.

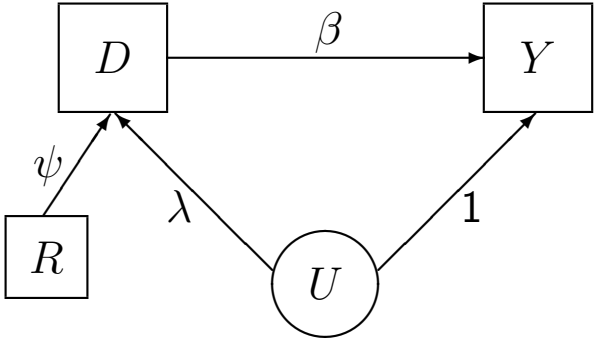
- It cannot be assumed that those other factors are not selective. In other words some aspects of exposure may be associated with confounders.

- Nonetheless can exploit random assignment as an instrumental variable, to identify part of the variation in exposure that is uncorrelated with confounders.

IV modelling with gllamm

Endogenous treatment as a factor model:

D causes Y, with unmeasured confounder U
and instrumental variable R



U is a random effect/latent variable with factor loading λ.

The ODIN study

The data:

R is the randomization indicator (`rgroup`: 0,1).

D is the number of sessions of psychotherapy attended (`sessions`: from 0 to 8).

Y is the BDI score at 6 months (`bdi6`).

U (the unmeasured confounder) is a random effect; it's a latent variable with loading λ.

Remember that there are missing outcome data (assumed to be ignorable)

Model:

$$\begin{aligned} \texttt{bdi6} &= \alpha + \beta\ \texttt{sessions} + U + \varepsilon \\ \texttt{sessions} &= \gamma + \psi\ \texttt{rgroup} + \lambda U + \delta \end{aligned}$$

where $corr(\delta, \varepsilon) = 0$.

Using the two-stage ATR method (Nagelekerke *et al.*) produces $\hat{\beta} = -0.496$ (s.e. 0.312).

Preparing the ODIN data

```
summarize
```

Variable	Obs	Mean	Std. Dev.	Min	Max
rgroup	427	.5526932	.4977989	0	1
sessions	427	2.058548	2.890626	0	8
bdi6	317	14.11356	10.13733	0	46
id	427	214	123.4085	1	427

```
list id rgroup sessions bdi6 in 1/10, clean
```

	id	rgroup	sessions	bdi6
1.	1	1	3	.
2.	2	1	5	0
3.	3	1	6	.
4.	4	0	0	.
5.	5	0	0	.
6.	6	1	0	.
7.	7	1	2	40
8.	8	0	0	18
9.	9	0	0	5
10.	10	1	6	7

Preparing the ODIN data (continued)

```
gen resp1=bdi6
gen resp2=sessions

reshape long resp, i(id) j(type)
```

```
(note: j = 1 2)

Data                               wide   ->   long
-----------------------------------------------------------------------------
Number of obs.                      427   ->      854
Number of variables                   6   ->        6
j variable (2 values)                     ->     type
xij variables:
                              resp1 resp2   ->     resp
-----------------------------------------------------------------------------
```

```
tab type, gen(d)
```

type	Freq.	Percent	Cum.
1	427	50.00	50.00
2	427	50.00	100.00
Total	854	100.00	

Preparing the ODIN data (continued)

```
list id rgroup type d1 d2 resp in 1/20, clean
```

	id	rgroup	type	d1	d2	resp
1.	1	1	1	1	0	.
2.	1	1	2	0	1	3
3.	2	1	1	1	0	0
4.	2	1	2	0	1	5
5.	3	1	1	1	0	.
6.	3	1	2	0	1	6
7.	4	0	1	1	0	.
8.	4	0	2	0	1	0
9.	5	0	1	1	0	.
10.	5	0	2	0	1	0
11.	6	1	1	1	0	.
12.	6	1	2	0	1	0
13.	7	1	1	1	0	40
14.	7	1	2	0	1	2
15.	8	0	1	1	0	18
16.	8	0	2	0	1	0
17.	9	0	1	1	0	5
18.	9	0	2	0	1	0
19.	10	1	1	1	0	7
20.	10	1	2	0	1	6

Preparing the ODIN data (continued)

```
gen d1_sessions=d1*sessions

gen d2_rgroup=d2*rgroup

eq fac: d1 d2

gllamm resp d1_sessions d1 d2 d2_rgroup, nocons i(id) /*
    */ family(gauss gauss) link(identity identity) fv(type) /*
    */ lv(type) eq(fac) adapt nip(15) trace
```

The gllamm command

```
eq fac: d1 d2
gllamm resp d1_sessions d1 d2 d2_rgroup, nocons i(id) family(gauss gauss) /*
    */ link(identity identity) fv(type) lv(type) eq(fac) adapt nip(15) trace
```

Explanation:

The fixed effects are d1, d1_sessions, d2, and d2_rgroup. The random effect (U) is fac loading from d1 and d2 (the binary indicators for Y and D, respectively).

nocons	suppresses the intercept term (represented, instead, by the effects for d1 and d2)
i(id)	identifies the participants (level 2 units)
family(gauss gauss)	probability distributions for the two outcomes
link(identity identity)	link functions for the two outcomes
fv(type)	variable whose values indicate which family applies to which observation
lv(type)	variable whose values indicate which link function applies to which observation
eq(fac)	equation for the latent variable
adapt nip(15)	specification for adaptive quadrature

The gllamm output (final part only)

```
...
number of level 1 units = 744
number of level 2 units = 427

gllamm model

log likelihood = -2127.6743
```

resp	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
d1_sessions	-.4958635	.3112457	-1.59	0.111	-1.105894	.1141668
d1	15.15714	.8550292	17.73	0.000	13.48132	16.83297
d2	2.44e-09	.1602771	0.00	1.000	-.3141374	.3141374
d2_rgroup	3.724576	.2155904	17.28	0.000	3.302027	4.147126

```
Variance at level 1

  4.853494 (.34316457)

Variances and covariances of random effects

***level 2 (id)

    var(1): 97.779296 (8.3379229)

    loadings for random effect 1
    d1: 1 (fixed)
    d2: .02329433 (.02173818)
```

gllamm with binary endogenous treatment effects

```
eq fac: d1 d2

gllamm resp d1_treat d1 d2 d2_rgroup, nocons i(id) family(gauss binom) /*
    */ link(identity probit) fv(type) lv(type) eq(fac) adapt nip(15) trace
```

Differences from the previous run:

- Replace `d1_sessions` with corresponding `d1_treat`
- `family(gauss binom)`
- `link (identity probit)`

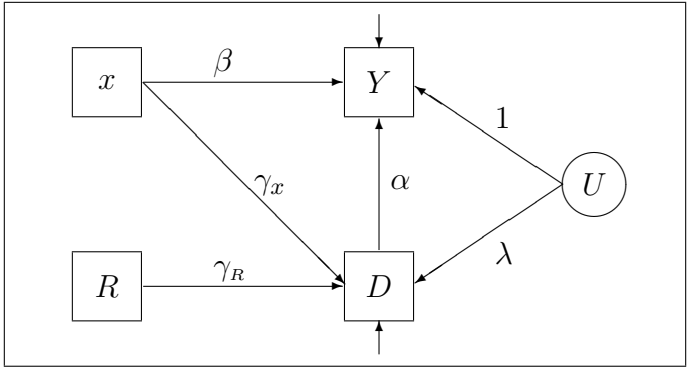
Binary endogenous treatment model: gllamm output

```
...
number of level 1 units = 744
number of level 2 units = 427

log likelihood = -1344.6925
```

resp	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
d1_treat	-4.259795	2.458733	-1.73	0.083	-9.078823	.5592327
d1	15.36503	.9200239	16.70	0.000	13.56182	17.16824
d2	-16.97098	419.7303	-0.04	0.968	-839.6273	805.6854
d2_rgroup	17.13592	419.732	0.04	0.967	-805.5237	839.7955

```
Variance at level 1
------------------------------------------------------------------------------
  89.246447 (133.98532)

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

***level 2 (id)

    var(1): 15.143656 (134.2019)

    loadings for random effect 1
    d1: 1 (fixed)
    d2: .31621095 (4.8864784)
```

Generalised IV factor model



with a model for Y from the GLM family

$$E(Y_j \mid D_j, x_j, U_j) = g_Y^{-1}(\alpha D_j + \beta x_j + U_j)$$

and similarly for D

$$E(D_j \mid R_j, x_j, U_j) = g_D^{-1}(\gamma_R R_j + \gamma_x x_j + \lambda U_j)$$

where g_Y^{-1} and g_D^{-1} are inverse link functions.

Estimation for non-identity link functions

For g_Y and g_D identity links we have a standard instrumental variable model for the treatment effect α. While incorrect choice of g_D does not lead to inconsistent estimates of the treatment effect α, this is not the case for incorrect choice of g_Y; see e.g. Ten Have *et al.* (2003).

Estimation of models with non-identity links is more complicated. The Stata routine `gllamm` allows an estimation of these models for any appropriate choice of the link function by the explicit integration over the distribution of U using Gaussian, adaptive or non-parametric methods.

Physician advice and drinking example

Kenkel and Terza (2001) analysed 2467 currently drinking males with hypertension.

Data description

- Data from the 1990 National Health Interview Survey.
- Count of alcohol units in last 2 weeks.
- Three dummy explanatory variables:

  `race` (0 = non-black, 1 = black)

  `educ` (high education; 0 if ≤ 12 years, 1 if > 12 years)

  `advice` (told by physician to drink less; 0 = no, 1 = yes)
- There is no randomization to receive advice – instead three IV's are selected on theoretical grounds, i.e.

  `hlthins` (covered by health insurance; 0 = no, 1 = yes)

  `regmed` (registered source of medical care; 0 = no, 1 = yes)

  `heart` (heart condition; 0 = no, 1 = yes)

Physician advice and drinking example

Modelling issues

- Analysed in `gllamm` by Skrondal and Rabe-Hesketh (2004).
- **Drink model**: over-dispersed poisson

$$\log(\mu_j) = \alpha D_j + \mathbf{x}_j'\boldsymbol{\beta} + u_j, \qquad \text{where } u_j \sim \mathcal{N}(0, \psi).$$

- **Advice model**:

$$\text{probit}(p_j) = \mathbf{z}_j'\boldsymbol{\gamma}_z + \mathbf{x}_j'\boldsymbol{\gamma}_x + \lambda u_j$$

☞ **Note**: the coefficients in the probit advice model are scale dependent and require rescaling by $\dfrac{1}{\sqrt{\lambda^2\psi + 1}}$.

Physician advice and drinking

Let a continuous, normally distributed latent variable, T, be explained by the following

$$T = \gamma_0 + \gamma_1 \texttt{black} + \gamma_2 \texttt{hieduc} + \gamma_3 \texttt{regmed} + \gamma_4 \texttt{heart} + \gamma_5 \texttt{hlthins} + \varepsilon$$

Let $\texttt{advice} = 1$ if $T > 0$ and $\texttt{advice} = 0$ otherwise. That is, advice is predicted through a linear probit model.

In addition,

$$\texttt{logdrinks} = \beta_0 + \beta_1 \texttt{advice} + \beta_2 \texttt{black} + \beta_3 \texttt{hieduc} + \delta$$

☞ **Note**: $Var(\delta) = \sigma^2$ (to be estimated) but $Var(\varepsilon) = 1$ (a constraint). The two residual terms, δ and ε, have correlation ρ (again, to be estimated from the data).

Physician advice and drinking example

```
use kenkel.dta, clear

sort id type

list in 1/10, clean noobs
```

id	type	advice	black	hlthins	regmed	heart	hieduc	wt2	cons	resp	d1	d2
1	1	0	0	0	0	0	0	7	1	0	1	0
1	2	0	0	0	0	0	0	7	1	0	0	1
2	1	1	0	0	0	0	0	3	1	0	1	0
2	2	1	0	0	0	0	0	3	1	1	0	1
3	1	0	0	0	0	0	0	1	1	1	1	0
3	2	0	0	0	0	0	0	1	1	0	0	1
4	1	1	0	0	0	0	0	1	1	1	1	0
4	2	1	0	0	0	0	0	1	1	1	0	1
5	1	0	0	0	0	0	0	2	1	2	1	0
5	2	0	0	0	0	0	0	2	1	0	0	1

Physician advice and drinking example

- Create interactions between `d1` and covariates in drinking model

```
gen d1_advice = d1*advice
gen d1_hieduc = d1*hieduc
gen d1_black = d1*black
```

- Create interactions between `d2` and covariates in advice model (use `foreach` to save typing)

```
foreach var in hieduc black hlthins regmed heart {
    gen d2_‘var’ = d2*‘var’
}
```

- Endogenous treatment:

```
eq fac: d2 d1
```

```
gllamm resp d1_advice d1 d1_hieduc d1_black d2 d2_hieduc /*
    */ d2_black d2_hlthins d2_regmed d2_heart, nocons i(id) /*
    */ weight(wt) family(poisson binom) link(log probit) /*
    */ fv(type) lv(type) eq(fac) adapt nip(15) trace
```

Physician advice and drinking example

Parameter	Poisson Est	Poisson (SE)	Overdisp. Poisson Est	Overdisp. Poisson (SE)	Probit Est	Probit (SE)	Endog. Treatment Est	Endog. Treatment (SE)
Fixed part								
Drinking model								
α [advice]	**0.47**	(0.01)	**0.59**	(0.08)			**−2.42**	(0.23)
β_0 [cons]	2.65	(0.01)	1.43	(0.06)			2.32	(0.09)
β_1 [hieduc]	−0.18	(0.01)	0.02	(0.07)			−0.29	(0.10)
β_2 [black]	−0.31	(0.02)	−0.29	(0.11)			0.20	(0.11)
Advice model								
γ_0 [cons]					−0.48	(0.08)	−1.13	(0.16)
γ_1 [hieduc]					−0.25	(0.06)	−0.40	(0.10)
γ_2 [black]					0.30	(0.08)	0.60	(0.15)
γ_3 [hlthins]					−0.27	(0.07)	−0.33	(0.10)
γ_4 [regmed]					0.18	(0.07)	0.39	(0.10)
γ_5 [heart]					0.17	(0.08)	0.51	(0.11)
Random part								
Variance								
ψ			2.90	(0.11)			2.50	(0.69)
Loading								
λ							1.43	(0.15)
Log likelihood	−32939.15		−8857.85		−1419.90		−10254.02	

JOB II trial: randomised job training study

- Aim: Estimate complier average causal effect of job training
- Data from Vinokur *et al.* (1995), analysed by Little and Yau (1998), Muthén (2002), Jo (2002) and Skrondal and Rabe-Hesketh (2004).
- People looking for a job randomised to receive either
  - Booklet with tips (control), $N = 167$
  - Five half-day sessions of job training plus booklet (new treatment), $N = 335$
- Outcome: Change in depression score from baseline
- Covariates for depression:

  `depbase`: baseline depression

  `risk`: baseline risk of depression (index based on poverty, etc.)

JOB II trial (continued)

- Non-attendance of job training (or noncompliance) a problem
- Aim of analysis is to compare those who attended the training with those in the control group who would have attended – this requires good covariates for compliance (at baseline):

  `age`: age in years

  `motivate`: motivation to attend training

  `educ`: school grade completed

  `assert`: assertiveness

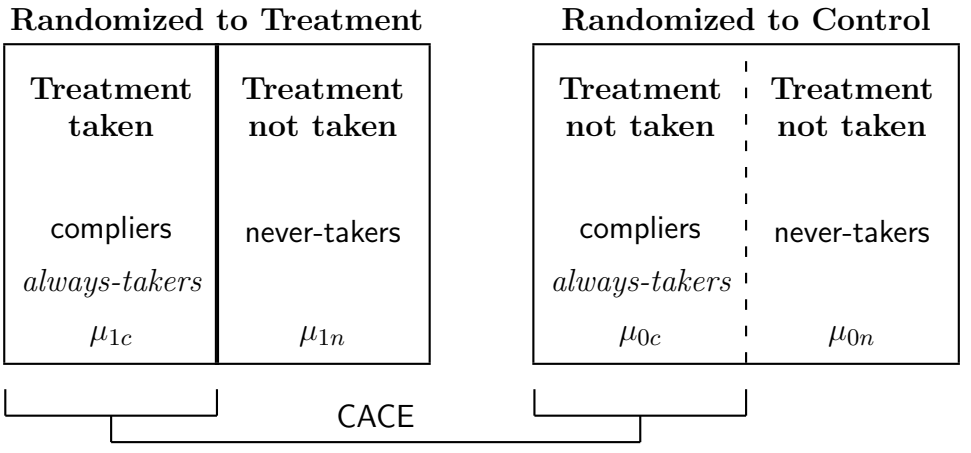
  `econ`: economic hardship

  `nonwhite`: dummy for not being white

Compliance Average Causal Effect (CACE)

- Imbens and Rubin (1997) consider four types of complier status
  - **Compliers:** take the assigned treatment
  - **Always-takers:** always take new treatment regardless of assigned treatment
  - **Never-takers:** never take new treatment (take control instead)
  - **Defiers:** take opposite of assigned treatment; assumed not to exist (monotonicity assumption)
- In JOB II, control group did not have access to treatment:
  - Treatment group
    - Participants:
      - Compliers
      - Always-takers
    - Non-participants:
      - Never-takers
  - Control group $\equiv$ Non-participants:
    - Compliers
    - Always-takers (not given opportunity to participate)
    - Never-takers

CACE (continued)



- CACE is treatment effect for compliers (and always-takers)

$$\delta_c = \mu_{1c} - \mu_{0c},$$

  μ_{1c} and μ_{0c} mean outcomes of compliers in treatment and control groups

- Exclusion restriction: mean outcome same among never-takers in both groups

$$\mu_{1n} = \mu_{0n}$$

Outcome model

- r_j is dummy for being randomized to treatment versus control
- c_j is dummy for compliers (or always-takers) versus never-takers
- Model for outcome if compliance were known for everyone:

$$y_j = \beta_0 + \beta_1 c_j(1 - r_j) + \beta_2 c_j r_j + \epsilon_j,$$

  - c_j observed only if $r_j = 1$, i.e. in third term
  - c_j in second term never observed: discrete latent variable $\eta_j = e_1, e_2$, where $e_1 = 1$, $e_2 = 0$:

$$\text{Depression model: } \; y_j = \beta_0 + \beta_1 \eta_j(1 - r_j) + \beta_2 c_j r_j + \epsilon_j$$

  - CACE:

$$\mu_{1n} = \mu_{0n} = \beta_0, \quad \mu_{0c} = \beta_0 + \beta_1, \quad \mu_{1c} = \beta_0 + \beta_2$$
$$\Longrightarrow \delta_c = \beta_2 - \beta_1$$

Compliance model

- Probability of being complier same in treatment and control groups (due to randomisation)

$$\Pr(c_j = 1 \mid r_j = 1) = \Pr(c_j = 1 \mid r_j = 0) = \Pr(\eta_j = e_1) = \pi_1$$

- Without covariates for compliance

$$\text{Compliance model: } \operatorname{logit}[\Pr(c_j = 1)] = \varrho = \operatorname{logit}(\pi_1)$$

CACE model in gllamm

- Model for depression and compliance with dummies d_{i1} and d_{i2}, respectively:

$$\textbf{Response model:} \quad \begin{aligned} \nu_{ij} &= d_{i1}[\beta_0 + \beta_1\eta_j(1-r_j) + \beta_2 c_j r_j] + d_{i2}[\varrho] \\ &= \beta_0 d_{i1} + \beta_1\eta_j(1-r_j)d_{i1} + \beta_2 c_j r_j d_{i1} + \varrho d_{i2} \end{aligned}$$

$$\textbf{Structural model:} \ \text{logit}[\pi_1] = \varrho.$$

- Data preparation:

```
infile depress risk r depbase age motivate educ /*
  */ assert single econ nonwhite x10 c c0 using wjobs.dat, clear
gen y1 = depress
gen y2 = c if r==1        /* missing in control group */
gen id=_n
reshape long y, i(id) j(var)
tab var, gen(d)           /*  create dummies d1 & d2  */
drop if y==.
list id var d1 d2 y r c if id==1|id==2|id==175|id==176, clean noobs
```

id	var	d1	d2	y	r	c
1	1	1	0	.45	0	1
2	1	1	0	-.72	0	1
175	1	1	0	-1.37	1	0
175	2	0	1	0	1	0
176	1	1	0	.54	1	1
176	2	0	1	1	1	1

CACE in gllamm (continued)

Response model: $\nu_{ij} = \beta_0 d_{i1} + \beta_1 \eta_j (1 - r_j) d_{i1} + \beta_2 c_j r_j d_{i1} + \varrho d_{i2}$

Structural model: $\text{logit}[\pi_1] = \varrho.$

- Interactions and equations:

```
gen c_r_d1 = c*r*d1          /* c_j r_j d_i1 */
gen nr_d1 = (1-r)*d1         /* (1 - r_j) d_i1 */
eq load: nr_d1               /* for β_1 (1 - r_j) d_j1 */
```

- Constraints:

```
cons def 1 [z2_1_1]nr_d1 = 1          /* e_1 = 1 */
cons def 2 [z2_1_2]nr_d1 = 0          /* e_2 = 0 */
cons def 3 [p2_1]_cons = [y]d2        /* constraint for ϱ */
```

- gllamm command:

```
gllamm y d1 c_r_d1 d2, i(id) eqs(load) l(ident logit) /*
  */ f(gauss binom) lv(var) fv(var) ip(fn) nip(2)     /*
  */ constr(1/3) frload(1) nocons    /* β_1 is 'freed' by frload(1) */
```

Output

```
...
log likelihood = -815.1493933028314
```

	Coef.	Std. Err.	z	P|z|	[95% Conf.	Interval]
d1	-.3909497	.0651724	-6.00	0.000	-.5186853	-.2632142
c_r_d1	-.1224929	.0867746	-1.41	0.158	-.292568	.0475822
d2	.1855983	.1097431	1.69	0.091	-.0294942	.4006908

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

  .60067675 (.03791846)

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

***level 2 (id)

    loc1: 1, 0
  var(1): .24785938

    loadings for random effect 1
    nr_d1: .01526939 (.17004299)

    prob: 0.5463, 0.4537

    log odds parameters
    class 1
    _cons: .18559831 (.10974308)
------------------------------------------------------------------------------
```

Estimates

- CACE $\delta_c = \beta_2 - \beta_1$:

```
lincom [y]c_r_d1 - [id1_1l]nr_d1
```

```
 ( 1)  [y]c_r_d1 - [id1_1l]nr_d1 = 0
```

y	Coef.	Std. Err.	z	P|z|	[95% Conf.	Interval]
(1)	-.1377623	.141096	-0.98	0.329	-.4143054	.1387808

Parameter	Est	SE
Depression model		
β_0	-0.39	(0.07)
β_1	0.02	(0.17)
β_2	-0.12	(0.09)
$\delta_c = \beta_2 - \beta_1$	-0.14	(0.14)
σ^2	0.60	(0.04)
Compliance model		
ϱ	0.19	(0.11)

- Exercise: obtain 95% confidence intervals for μ_{0c} and μ_{1c}

Exercise: Adding predictors

- Add predictors of depression with constant effects across compliance groups:

$$\text{Depression model: } y_j = \beta_0 + \mathbf{x}_j'\boldsymbol{\alpha} + \beta_1\eta_j(1-r_j) + \beta_2 c_j r_j + \epsilon_j$$

- Add predictors of compliance:

$$\text{Compliance model: } \text{logit}[\Pr(c_j=1)] = \mathbf{w}_j'\boldsymbol{\varrho} = \text{logit}[\pi_1]$$

- Use covariates listed in Slide 54.
  Start with `motivate` in compliance model:

```
eq p: motivate                              /* for latent compliance */
gen motivate_d2 = motivate*d2               /* for obs. comp. */
cons def 4 [p2_1]motivate = [y]motivate_d2
gllamm y d1 c_r_d1 motivate_d2 d2, ... peqs(p)
```

Estimates

Parameter	Est	SE
Depression model		
β_0	1.63	(0.28)
β_1	0.18	(0.13)
β_2	-0.13	(0.08)
$\delta_c = \beta_2 - \beta_1$	-0.31	(0.12)
α_1 [basedep]	-1.46	(0.18)
α_1 [risk]	0.91	(0.26)
σ^2	0.51	(0.03)
Compliance model		
ϱ_0	-8.74	(1.58)
ϱ_1 [age]	0.08	(0.01)
ϱ_2 [motivate]	0.67	(0.16)
ϱ_3 [educ]	0.30	(0.07)
ϱ_4 [assert]	-0.38	(0.15)
ϱ_5 [single]	0.54	(0.28)
ϱ_6 [econ]	-0.16	(0.16)
ϱ_6 [Nonwhite]	-0.50	(0.31)

Stated preference experiments

Random utility models

- Utility formulation useful:
  - Insight into logistic regression models (e.g. specification, identification)
  - Facilitates extension of conventional logistic regression for polytomous responses and rankings to MULTILEVEL designs
- Unobserved 'utility' U_i^a associated with each alternative $a = 1, ..., A$ for unit $i = 1, ..., N$
- Random utility models composed as

$$U_i^a = V_i^a + \epsilon_i^a$$

  - V_i^a is fixed linear predictor representing observed and shared unobserved heterogeneity
  - ϵ_i^a is random term representing unobserved heterogeneity (independent over i and a)

Polytomous responses as utility maximization

- Alternative f is chosen if

$$U_i^f > U_i^g \text{ for all } g \neq f$$

- ϵ_i^a independent (over i and a) **Gumbel** or extreme value distributed of type I:

$$g(\epsilon_i^a) \;=\; \exp\{-\epsilon_i^a - \exp(-\epsilon_i^a)\}$$

- McFadden (1973), Yellott (1977):

$$\epsilon_i^a \text{ independent Gumbel}$$

$$\Updownarrow$$

$$\Pr(f_i) \;=\; \frac{\exp(V_i^f)}{\sum_{a=1}^{A} \exp(V_i^a)}$$

[Conventional multinomial logit]

Polytomous responses

- Common special cases:

$$V_{ijk}^a = \mathbf{x}'_{ijk}\mathbf{g}^a \quad \text{[Statistics/Biostatistics]}$$

$$V_{ijk}^a = \mathbf{x}_{ijk}^{a\prime}\boldsymbol{b} \quad \text{[Econometrics/Psychometrics]}$$

- A general framework for multilevel modelling of polytomous data and rankings is described in Skrondal and Rabe-Hesketh (2003).

GHQoL example

Genital Herpes Quality of Life (GHQoL):

- Stated Preference Experiment (SPE)
- 192 respondents each presented with 8 pairs of scenarios.
- Scenarios represented hypothetical states of disease impairment in 6 different areas of life.
- Respondents were forced to state preferred alternative from each pair of alternatives presented.
- Explore preference heterogeneity.

GHQoL example

Attributes of scenarios

`plan`: herpes makes it hard to plan ahead

`forget`: it is difficult to forget that I have herpes

`sex`: herpes is affecting my sex life

`depress`: I get depressed about having herpes

`worry`: I worry about people I know finding out I have herpes

`tense`: I become tense when someone touches me

Each with 4 levels:
- yes, very difficult
- yes, quite difficult
- yes, a little difficult
- no, not at all

GHQoL example

	Scenario 1	Scenario 2
Herpes makes it difficult for me to plan ahead	Yes, quite difficult	No, not at all difficult
It is difficult to forget that I have herpes	Yes, it's a little difficult	Yes, it's a little difficult
Herpes is affecting my sex life	No, not at all difficult	Yes, it's a little difficult
...		

GHQoL example

```
list id pairid idn scenario plan forget sex depress worry tense alt /*
     */ ch in 1/10, clean noobs
```

id	pairid	idn	scenario	plan	forget	sex	depress	worry	tense	alt	ch
1	3	1	c1	3	2	1	1	3	4	1	1
1	3	1	c2	3	4	2	2	1	4	2	0
1	6	2	f1	1	3	1	4	1	4	1	0
1	6	2	f2	4	2	3	4	3	4	2	1
1	11	3	k1	2	1	1	2	3	3	1	1
1	11	3	k2	3	3	3	1	4	3	2	0
1	7	4	g1	1	1	1	3	4	4	1	1
1	7	4	g2	3	1	3	1	1	1	2	0
1	9	5	i1	4	1	2	1	2	4	1	0
1	9	5	i2	4	4	1	1	4	2	2	1

GHQoL example

Conditional logistic model

```
clogit ch plan forget sex depress worry tense, group(idn)
```

```
...

Log likelihood = -918.04928
```

ch	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
plan	-.1962345	.036957	-5.31	0.000	-.2686689	-.1238001
forget	-.2148092	.0460827	-4.66	0.000	-.3051297	-.1244887
sex	-.4131256	.0439349	-9.40	0.000	-.4992363	-.3270148
depress	-.2986656	.0417552	-7.15	0.000	-.3805042	-.216827
worry	-.0819647	.0307699	-2.66	0.008	-.1422726	-.0216568
tense	-.2390155	.0418356	-5.71	0.000	-.3210118	-.1570192

GHQoL example

Using `gllamm`

```
gllamm alt plan forget sex depress worry tense, i(id) nocons l(mlogit) /*
    */ f(bin) expand(idn ch o) init trace
```

```
...

log likelihood = -918.04928
```

alt	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
plan	-.1962345	.036957	-5.31	0.000	-.2686689	-.1238001
forget	-.2148092	.0460827	-4.66	0.000	-.3051297	-.1244887
sex	-.4131256	.0439349	-9.40	0.000	-.4992363	-.3270148
depress	-.2986656	.0417552	-7.15	0.000	-.3805042	-.216827
worry	-.0819647	.0307699	-2.66	0.008	-.1422726	-.0216568
tense	-.2390155	.0418356	-5.71	0.000	-.3210118	-.1570192

GHQoL example

Define 6 equations:

```
eq plan: plan
eq forget: forget
eq sex: sex
eq depress: depress
eq worry: worry
eq tense: tense
```

Specify a matrix to be used for initial values:

```
matrix input b=(0,0,0,0,0,0,-1,-1,-1,-1,-1,0)
```

GHQoL example

```
gllamm alt plan forget sex depress worry tense, i(id) nocons /*
        */ l(mlogit) f(bin) expand(idn ch o) nrf(6) /*
        */ eqs(plan forget sex depress worry tense) nip(2) /*
        */ ip(f) from(b) copy trace
```

➠ Output (fixed effects part)

```
...

log likelihood = -889.946
```

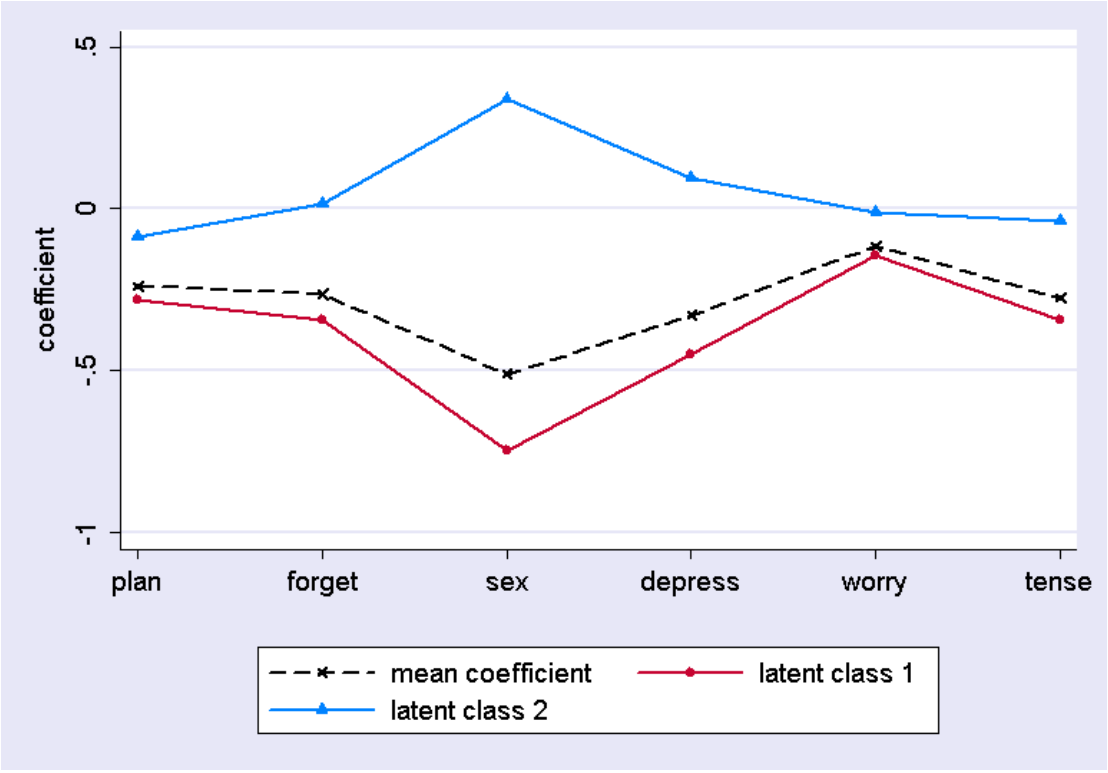
alt	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
plan	-.238834	.0411871	-5.80	0.000	-.3195593	-.1581087
forget	-.2645628	.0593709	-4.46	0.000	-.3809276	-.148198
sex	-.5113588	.0663416	-7.71	0.000	-.6413859	-.3813317
depress	-.3305231	.0546148	-6.05	0.000	-.437566	-.2234801
worry	-.1158108	.0351012	-3.30	0.001	-.184608	-.0470136
tense	-.2768218	.0499593	-5.54	0.000	-.3747403	-.1789032

GHQoL example

- Output (probabilities and locations of random effects)

```
    loc1: -.04222, .15115
  var(1): .0063817

    loc2: -.07841, .28072
cov(2,1): .01185207
  var(2): .0220116

    loc3: -.23677, .84769
cov(3,1): .03578927
cov(3,2): .06646764
  var(3): .20070996

    loc4: -.11827, .42341
cov(4,1): .01787628
cov(4,2): .03319973
cov(4,3): .10025206
  var(4): .05007462

    loc5: -.02923, .10465
cov(5,1): .00441842
cov(5,2): .00820586
cov(5,3): .02477894
cov(5,4): .01237676
  var(5): .00305912

    loc6: -.066, .23628
cov(6,1): .00997581
cov(6,2): .01852702
cov(6,3): .05594538
cov(6,4): .027944
cov(6,5): .00690682
  var(6): .01559407

    prob: 0.7817, 0.2183
```

GHQoL example



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