

Models In Epidemiology And Biostatistics

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Conditional Models With Repeated Measures

In considering the dental data, the asthma data and the pain data, we have identified a number of issues that need to be addressed.

1) Repeated measurements from the same individual are not independent. For example:

```
. use pott.dta
. reshape wide
. corr dist1 dist2 dist3 dist4
(obs=27)
```

		dist1	dist2	dist3	dist4
dist1		1.0000			
dist2		0.6256	1.0000		
dist3		0.7108	0.6349	1.0000	
dist4		0.5998	0.7593	0.7950	1.0000

2) Regression analyses adjusting for subjects has an analog with viewing subjects like confounders but subjects are not 'populations'. Rather they might be viewed as a sample from a population. We tried:

$E(y) = \beta_0 + \sum_{j=2}^{27} \beta_j \delta_j + \beta_{28} \text{age} + \beta_{29} \text{age} * \text{sex}$ where δ_j is the indicator for the j th subject. The first 27 β_j attempt to 'adjust' for subjects. A more realistic plan conceives of u_j instead of β_j where the u_j are a sample from a population of such children.

3) We need to consider data that have varying numbers of repeated measurements per individual.

4) We need to consider data with varying values for the covariates. For example, in the dental data, we should use the child's actual age when each distance measurement was recorded.

5) The regression analyses considered so far have not enabled the separation of key between subjects comparisons. In the asthma data, we could not consider order modification in our regression approach.

6) So far, we have seen that the data could be placed in either wide format or in long format. In long format, a covariate of interest [age in the dental data] is recorded as a column with multiple rows per individual. In wide format, the covariate is implicitly a part of the outcome variable name. This would be acceptable with the data recorded in 'waves' [as in ages 8, 10 12, 14] but would not be practical if we recorded the child's actual age.

7) We would like to have methods that extend these matters to dichotomous outcomes [logistic regression and others], ordinal outcomes [proportional odds models and others], count outcomes [poisson, negative binomial and variants] and interval 'measured' outcomes [linear regression and its many extensions]

8) We need to identify other settings in which a lack of independence is crucial [matching, blocking, clustering; for example] and then anticipate that our methods extend to these settings.

We can write our models in vector/matrix notation:

$$y = X\beta + \epsilon \quad [\text{linear}]$$

$$\log\left(\frac{p}{1-p}\right) = X\beta \quad [\text{logistic: } p = \text{Pr}(y=1)]$$

$$\log \lambda = X\beta + \log e \quad [\text{poisson or negative binomial with exposure } e; \quad E(y) = \lambda]$$

$$\log\left(\frac{p_j}{1-p_j}\right) = X\beta - \kappa_j \quad [\text{proportional odds model}] \quad p_j = \text{Pr}(y > \text{cut } j)$$

All our models use the assumption that y are statistically independent.

If y is normally distributed, statistical independence is the same as $\text{VAR } y$ being a diagonal matrix. In many circumstances, we restrict this assumption even more and say that $\text{VAR } y = \sigma^2 I$

Let us now consider the 'simplest' conditional model:

$$y = X\beta + Z\mathbf{u} + \epsilon \quad \text{or} \quad E(y:\mathbf{u}) = X\beta + Z\mathbf{u} \quad \text{and, for now, we will assume that } \text{VAR } \epsilon = \sigma^2 I$$

and let us return to the dental data:

y will be a 108 x 1 column vector; X will be a 108x4 matrix; β will be a 4x1 column vector; \mathbf{u} will be a 27x1 column vector; Z will be 108x27 matrix and ϵ will be a 108x1 column vector.

The columns of Z are the indicators for each of the 27 subjects. The \mathbf{u} vector is something new. They are not regression coefficients in the sense we seen before. They are unknown values from a probability distribution with mean zero and $\text{VAR } \mathbf{u} = \sigma_u^2 I$. Also, it is standard here to require that

$$\mathbf{1}'\mathbf{u} = 0 \quad . \text{ This constraint ensures the correct interpretation of } \beta$$

With this model and our data, we will have estimates for the regression coefficients and σ^2 as before. Now we will get an estimate for σ_u^2 and predictions for the \mathbf{u} .

We then get different sets of quantities to study. We get estimates of $X\beta$ like before but we now also get estimates of $E(y:\mathbf{u}) = X\beta + Z\mathbf{u}$

. mixed dist age sex as || subject:

Performing EM optimization:

Performing gradient-based optimization:

Iteration 0: log likelihood = -214.31953

Iteration 1: log likelihood = -214.31953

Computing standard errors:

Mixed-effects ML regression	Number of obs	=	108
Group variable: subject	Number of groups	=	27
	Obs per group: min	=	4
	avg	=	4.0
	max	=	4
	Wald chi2(3)	=	142.05
Log likelihood = -214.31953	Prob > chi2	=	0.0000

dist	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
age	.784375	.0765383	10.25	0.000	.6343626 .9343874

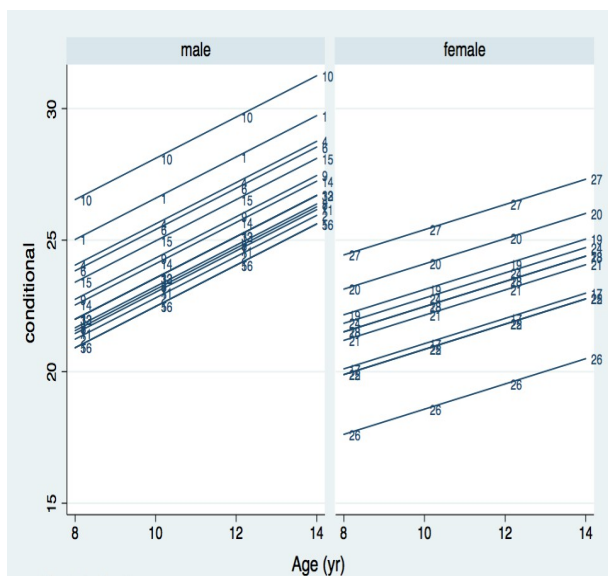
sex		1.032102	1.508864	0.68	0.494	-1.925217	3.989422
as		-.3048295	.1199125	-2.54	0.011	-.5398537	-.0698054
_cons		16.34062	.9630849	16.97	0.000	14.45301	18.22824

Random-effects Parameters		Estimate	Std. Err.	[95% Conf. Interval]
subject: Identity				
var(_cons)		3.030561	.9552074	1.633923 5.621014
var(Residual)		1.874597	.2945645	1.377699 2.550711

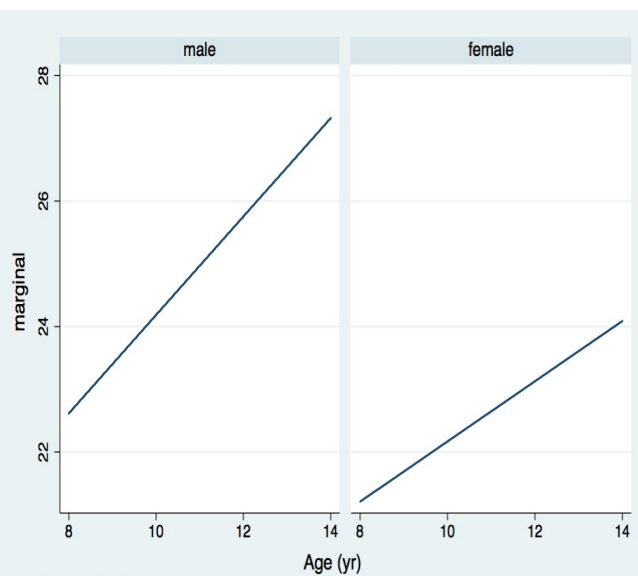
LR test vs. linear regression: chibar2(01) = 49.60 Prob >= chibar2 = 0.0000

```
. predict yhm,xb
. predict yhc,fitted
. predict u, reffects
. predict res,res
. scatter yhc age,connect(ascending) msymbol(i) mlabel(subject) by(sex)
ytitle("conditional")

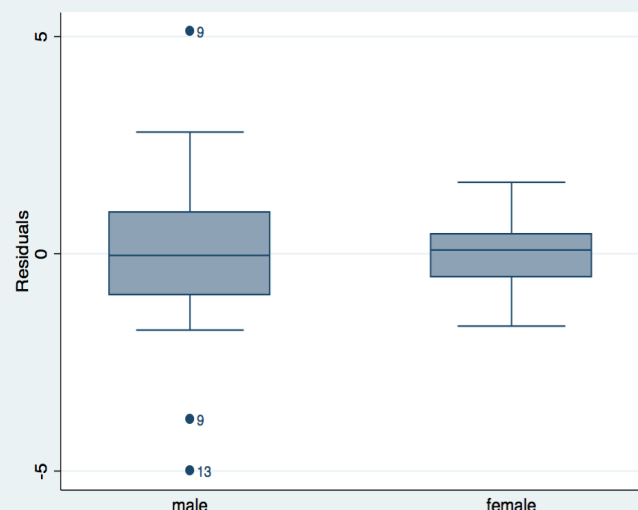
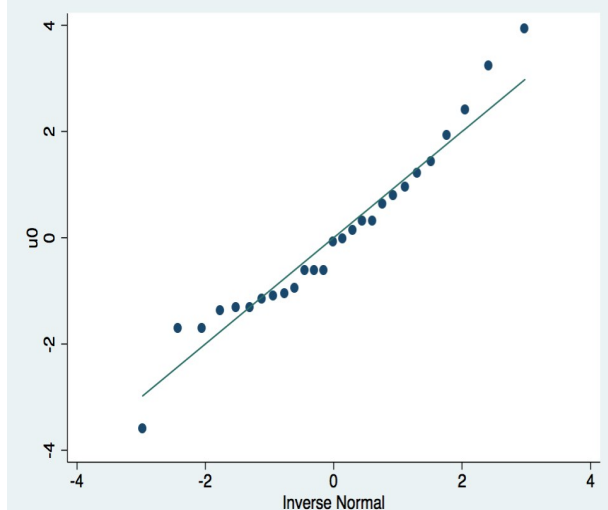
. scatter yhm age,connect(ascending) msymbol(i) by(sex) ytitle("marginal")
. gen u0=u
. by subject: replace u0=. if _n!=1
. qnorm u,ytitle("sorted observed")
. graph box res, over(sex) marker(1,mlabel(subject))
```



Graphs by Gender



Graphs by Gender



There are many ways to extend the above model. Lets try:

$E(\mathbf{y}:\mathbf{u}_0\mathbf{u}_1)=X\boldsymbol{\beta}+Z_0\mathbf{u}_0+Z_1\mathbf{u}_1$ where Z_0 contains the indicators for the subjects as before and Z_1 is again a 108x27 matrix that contains the ages for each child. Each row of $[\mathbf{u}_0\mathbf{u}_1]$ then provides intercept and slope adjustment of each child. Further it fairly standard to model

$VAR\mathbf{u}_0=\sigma_{u0}^2I$ and $VAR\mathbf{u}_1=\sigma_{u1}^2I$ and to allow for a covariance σ_{u0u1} . It is known that intercept and slope are typically correlated.

```
. mixed dist age sex as || subject: age,covariance(unstr)
```

Performing EM optimization:

Performing gradient-based optimization:

```
Iteration 0:  log likelihood = -213.92903
Iteration 1:  log likelihood = -213.90624
Iteration 2:  log likelihood = -213.90298
Iteration 3:  log likelihood = -213.90298
```

Computing standard errors:

Mixed-effects ML regression	Number of obs	=	108
Group variable: subject	Number of groups	=	27
	Obs per group: min	=	4
	avg	=	4.0
	max	=	4
	Wald chi2(3)	=	121.59
Log likelihood = -213.90298	Prob > chi2	=	0.0000

dist	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
age	.784375	.0827532	9.48	0.000	.6221818 .9465682
sex	1.032102	1.535496	0.67	0.501	-1.977414 4.041618
as	-.3048295	.1296493	-2.35	0.019	-.5589375 -.0507216
_cons	16.34062	.9800834	16.67	0.000	14.4197 18.26155

Random-effects Parameters	Estimate	Std. Err.	[95% Conf. Interval]
subject: Unstructured			
var(age)	.0237593	.0340875	.0014276 .3954176
var(_cons)	4.556941	4.671805	.610965 33.98839
cov(age,_cons)	-.1982569	.3790498	-.9411809 .5446671
var(Residual)	1.716202	.3302811	1.176944 2.502541

LR test vs. linear regression: chi2(3) = 50.44 Prob > chi2 = 0.0000

Note: LR test is conservative and provided only for reference.

The four graphs in the first example should be repeated.

```
. drop yhm yhc u u0 res
. predict yhm,xb
. predict yhc,fitted
. predict u1 u0, reffects
. predict res,res
. scatter yhc age,connect(ascending) msymbol(i) mlabel(subject) by(sex)
ytittle("conditional")
```

```
. scatter yhm age,connect(ascending) msymbol(i) by(sex) ytitle("marginal")
. by subject: replace u0=. if _n!=1
. by subject: replace u1=. if _n!=1
. qnorm u0,ytitle("sorted observed")
. qnorm u1,ytitle("sorted observed")
. scatter u1 u0
. graph box res, over(sex) marker(1,mlabel(subject))
```

Next, lets briefly look at the asthma data:

```
use forsal.dta
reshape long
gen ord =tr
replace ord =1-ord if grp==1
mixed pef tr ord grp ||id:
```

```
Mixed-effects ML regression      Number of obs      =      24
Group variable: id              Number of groups   =      12

                                Obs per group: min =      2
                                avg =      2.0
                                max =      2

                                Wald chi2(3)      =      19.11
                                Prob > chi2       =      0.0003

Log likelihood = -121.55306
```

	pef	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
tr		-38.33333	9.084224	-4.22	0.000	-56.13808 -20.52858
ord		3.333333	9.084224	0.37	0.714	-14.47142 21.13808
grp		-29.16667	26.93013	-1.08	0.279	-81.94875 23.61541
_cons		364.1667	20.0967	18.12	0.000	324.7779 403.5555

Random-effects Parameters		Estimate	Std. Err.	[95% Conf. Interval]
id: Identity				
	var(_cons)	1928.126	893.9558	777.1136 4783.946
	var(Residual)	495.1387	202.1395	222.4464 1102.119

```
LR test vs. linear regression: chibar2(01) = 12.03 Prob >= chibar2 = 0.0003
```

Notice the resemblance [closeness] to the three t-tests considered earlier. Not exactly the same. The three t-tests perhaps get the edge [for this little study] since they correctly use the t-distribution for the p-values and confidence intervals. Our new conditional model uses approximate z values. On the other hand our conditional model approach is quite general and extensions to a wide range of cross over type studies are available.

Now lets revisit the pain study with conditional models:

$\text{logit}(p:u) = X\beta + Zu$ where $p = \Pr(y=1:u)$

The regression coefficients now have interpretations in terms of conditional log odds [conditional on u]. We have adjusted for subject specific components.

We can construct estimates assuming $u=0$ but these are not marginal log odds. We can construct predictions of the conditional log odds and the u . Assessment of the u can be limited if there are only a fixed small set of possible outcomes and explanatory variables.

```

use pain.dta
replace grp=grp-1
gen trg=tr*grp
melogit imp tr grp trg || id:

```

```

Mixed-effects logistic regression      Number of obs      =      168
Group variable:      id                Number of groups   =      84

Obs per group: min =      2
                  avg =      2.0
                  max =      2

```

```

Integration method: mvaghermite      Integration points =      7

```

```

Log likelihood = -105.41698           Wald chi2(3)       =      14.57
                                      Prob > chi2         =      0.0022

```

	imp	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
tr		.3327301	.4738805	0.70	0.483	-.5960587	1.261519
grp		-1.530021	.5735093	-2.67	0.008	-2.654079	-.4059636
trg		1.891031	.752978	2.51	0.012	.4152214	3.366841
_cons		.2166222	.3527853	0.61	0.539	-.4748242	.9080687

	id	var(_cons)		
		.6153444	.7999041	.0481522 7.863574

```

LR test vs. logistic regression: chibar2(01) =      0.91 Prob>=chibar2 = 0.1704

```

For proportional odds, we now have:

$$\text{logit}(p_j; u) = X\beta - \kappa_j + Z'u \quad \text{where} \quad p_j = \Pr(y > \text{cut}_j; u)$$

Again, the regression coefficients are in terms of conditional log odds

```

. meologit ove tr grp trg || id:

```

```

Mixed-effects ologit regression      Number of obs      =      168
Group variable:      id                Number of groups   =      84

Obs per group: min =      2
                  avg =      2.0
                  max =      2

```

```

Integration method: mvaghermite      Integration points =      7

```

```

Log likelihood = -251.87999           Wald chi2(3)       =      24.12
                                      Prob > chi2         =      0.0000

```

	ove	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
tr		.0601627	.4147691	0.15	0.885	-.7527698	.8730952
grp		-1.528548	.525087	-2.91	0.004	-2.557699	-.4993961
trg		2.206275	.6230285	3.54	0.000	.9851615	3.427388
/cut1		-5.220747	.7941854	-6.57	0.000	-6.777322	-3.664173
/cut2		-1.396146	.4046063	-3.45	0.001	-2.18916	-.6031321
/cut3		-.3287973	.380997	-0.86	0.388	-1.075538	.4179431
/cut4		.5194378	.3821936	1.36	0.174	-.2296478	1.268523
/cut5		2.978362	.511053	5.83	0.000	1.976716	3.980007

	id	var(_cons)		
		1.498867	.7778412	.5420376 4.144733

```

LR test vs. ologit regression:  chibar2(01) =      7.33 Prob>=chibar2 = 0.0034

```

melogit provides the conditional model for repeated dichotomous outcomes and the logit link.

meologit provides the conditional model for repeated ordinal outcomes, the logit link and the proportional odds assumption.

Now let us consider a study of count outcomes.

$$\log(\lambda:u) = X\beta + Z u \quad \text{where } y \sim \text{poisson}(\lambda:u)$$

The details are given in the paper by Breslow and Clayton (1993)

```
use epilepsy.dta
gen ls1=log(seizures+1)
sort subject vs
lab def trl 0 placebo 1 active
lab val treat trl
scatter ls1 vs,connect(ascending) by(treat) mlabel(subject)
table treat,c(mean lbas sd lbas)
table treat vs,c(mean ls1 sd ls1)
gen trv=treat*vs
mepoisson seizures treat vs trv || subject:
```

Mixed-effects Poisson regression	Number of obs	=	236
Group variable: subject	Number of groups	=	59

Obs per group: min	=	4
avg	=	4.0
max	=	4

Integration method: mvaghermite	Integration points	=	7
---------------------------------	--------------------	---	---

Log likelihood = -695.90821	Wald chi2(3)	=	10.26
	Prob > chi2	=	0.0164

seizures	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
treat	-.2126636	.2713048	-0.78	0.433	-.7444113 .3190841
vs	-.0428052	.028845	-1.48	0.138	-.0993403 .0137299
trv	-.0314748	.0405755	-0.78	0.438	-.1110014 .0480518
_cons	1.878152	.1953233	9.62	0.000	1.495326 2.260979

subject					
var(_cons)	.8788584	.1788546			.5897836 1.309619

LR test vs. Poisson regression: chibar2(01) = 1884.04 Prob>=chibar2 = 0.0000
 . mepoisson seizures treat vs trv || subject: vs ,cov(unstr)

Mixed-effects Poisson regression	Number of obs	=	236
Group variable: subject	Number of groups	=	59

Obs per group: min	=	4
avg	=	4.0
max	=	4

Integration method: mvaghermite	Integration points	=	7
---------------------------------	--------------------	---	---

Log likelihood = -686.33683	Wald chi2(3)	=	3.30
	Prob > chi2	=	0.3470

seizures	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
treat	-.2509616	.2987855	-0.84	0.401	-.8365704 .3346471
vs	-.0434861	.045908	-0.95	0.344	-.133464 .0464918
trv	-.0138791	.0627282	-0.22	0.825	-.1368241 .1090658
_cons	1.864557	.2166208	8.61	0.000	1.439987 2.289126

subject					
var(vs)	.0211017	.0091714			.0090024 .0494622

```

      var(_cons) |    1.032918    .243383                                .650879    1.639199
-----+-----
subject      |
cov(_cons,vs) |   -.0573591    .0381642    -1.50    0.133    -.1321596    .0174414
-----+-----
LR test vs. Poisson regression:      chi2(3) = 1903.18    Prob > chi2 = 0.0000

```

Note: LR test is conservative and provided only for reference.

$\log(\lambda:u) = X\beta + Z'u$ where $y:u \sim \text{NB}(\lambda)$ with $E(y:u) = \lambda$ and $\text{VAR}(y:u) = \text{diag}[\lambda(1 + \alpha\lambda)]$
 . menbreg seizures treat vs trv || subject:

```

Mixed-effects nbinomial regression      Number of obs      =      236
Overdispersion:      mean
Group variable:      subject      Number of groups      =      59

Obs per group: min =      4
               avg  =     4.0
               max  =      4

Integration method: mvaghermite      Integration points =      7

Wald chi2(3)      =      3.97
Log likelihood = -655.11664      Prob > chi2      =      0.2649

```

```

-----+-----
      seizures |      Coef.   Std. Err.      z    P>|z|      [95% Conf. Interval]
-----+-----
      treat |   -.2438501   .3021013    -0.81   0.420    -.8359577    .3482575
      vs |   -.0447497   .0465564    -0.96   0.336    -.1359985    .0464991
      trv |   -.0184578   .0667353    -0.28   0.782    -.1492566    .112341
      _cons |    1.89958    .2157934     8.80   0.000     1.476633    2.322528
-----+-----
      /lnalpha |  -2.008753   .2353817    -8.53   0.000    -2.470092   -1.547413
-----+-----
subject      |
      var(_cons) |   .8447953   .1788146                .5579315    1.279152
-----+-----
LR test vs. nbinomial regression:chibar2(01) = 183.61 Prob>=chibar2 = 0.0000

```

Mean dispersion is the default. Constant dispersion is an option.

Breslow & Clayton provide one analysis and discussion. The following is a close version of their results.

. mepoisson seizures lbas treat lbas_trt lage v4 vs || subject: vs ,cov(unstr)

```

Mixed-effects Poisson regression      Number of obs      =      236
Group variable:      subject      Number of groups      =      59

Obs per group: min =      4
               avg  =     4.0
               max  =      4

Integration method: mvaghermite      Integration points =      7

Wald chi2(6)      =     118.18
Log likelihood = -654.32718      Prob > chi2      =      0.0000

```

```

-----+-----
      seizures |      Coef.   Std. Err.      z    P>|z|      [95% Conf. Interval]
-----+-----
      lbas |   .8850952   .1312167     6.75   0.000     .6279152    1.142275
      treat |  -.9281649   .4020194    -2.31   0.021    -1.716108   -.1402214
      lbas_trt | .3378666   .2043677     1.65   0.098    -.0626867    .7384199
      lage |   .4760858   .353526     1.35   0.178    -.2168124    1.168984
      v4 |  -.1392905   .0845376    -1.65   0.099    -.3049812    .0264001

```


vs		-.0131428	.0415294	-0.32	0.752	-.0945388	.0682532
_cons		2.165474	.2410654	8.98	0.000	1.692995	2.637954

subject							
var(vs)		.0230964	.0098286			.0100304	.0531828
var(_cons)		.3929233	.1249306			.2107011	.7327381

subject							
cov(_cons,vs)		-.0571615	.0308857	-1.85	0.064	-.1176965	.0033734

LR test vs. Poisson regression: chi2(3) = 325.78 Prob > chi2 = 0.0000

Note: LR test is conservative and provided only for reference.

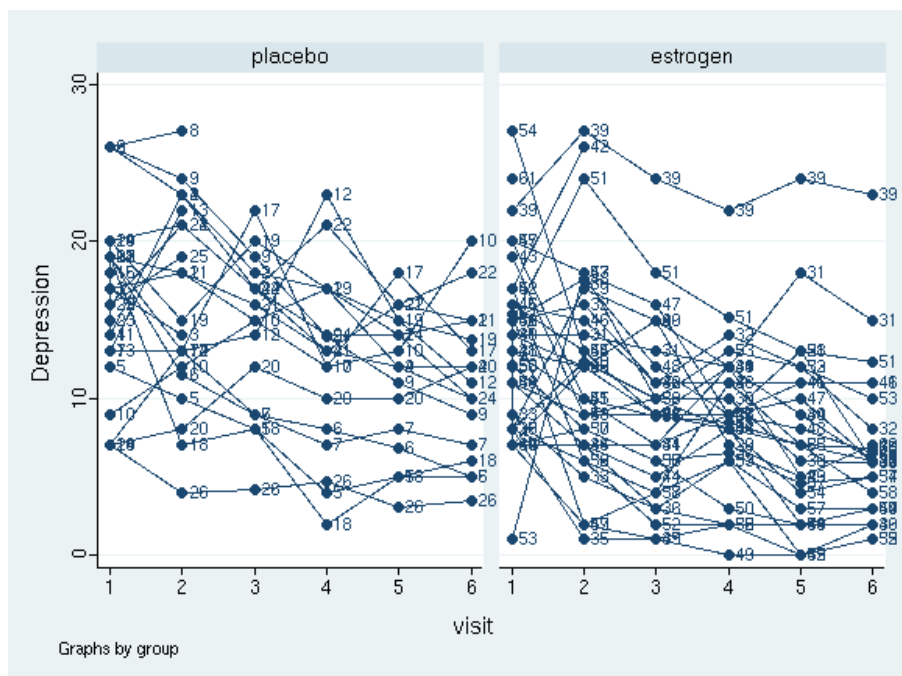
Lets now take a look at a study in Gregoire (1996). We can look at the data with:

```
use depress.dta
sort group subj visit
twoway connected dep visit,connect(ascending) by(group) ytitle(Depression) xlabel(1/6)
```

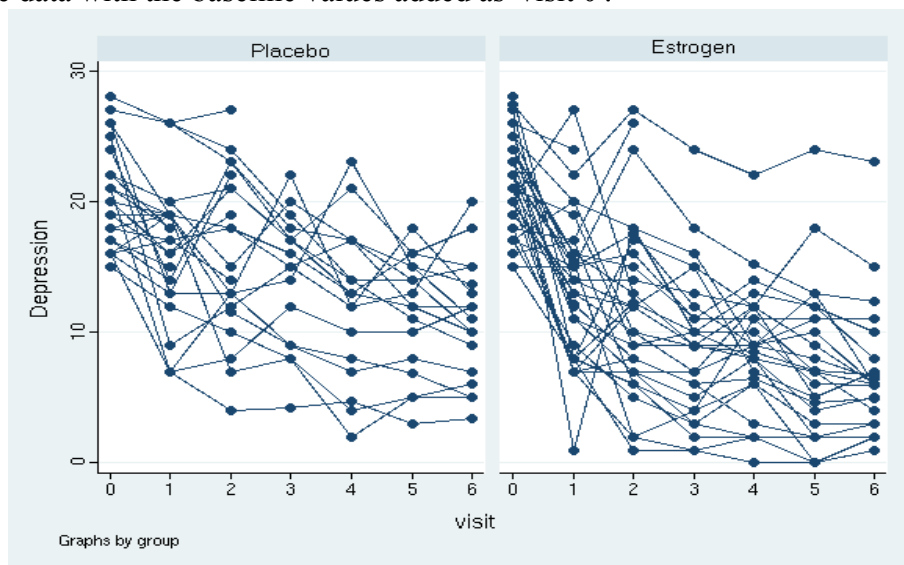
This data set display is probably too busy and we should, perhaps, regraph with about 10 subjects or so per display. Nevertheless, this display illustrates a whole range of issues that we did not see in the dental study. Some subjects have only one score after baseline (like subject #61) . Some subjects have only 2 scores (like subject #8). The majority of subjects completed all 6 visits. Subject #39 seems so different from the rest. Subject #53 appears to have an “impossibly” low score at visit #1 especially as this person's pre-assignment score was 26. Should we treat the 'completers' the same as the 'dropouts'? Also, there are ten dropouts in the placebo and six in the active group.

```
. table group visit,c(n dep)
```

group	visit					
	1	2	3	4	5	6
placebo	27	22	17	17	17	17
estrogen	34	31	29	28	28	28

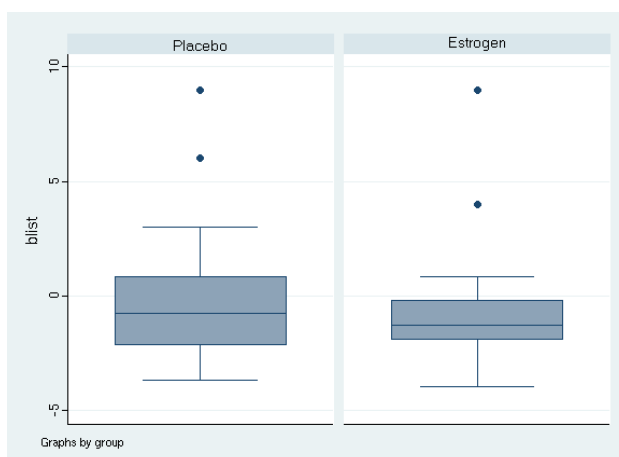


Here is the same data with the baseline values added as 'visit 0':



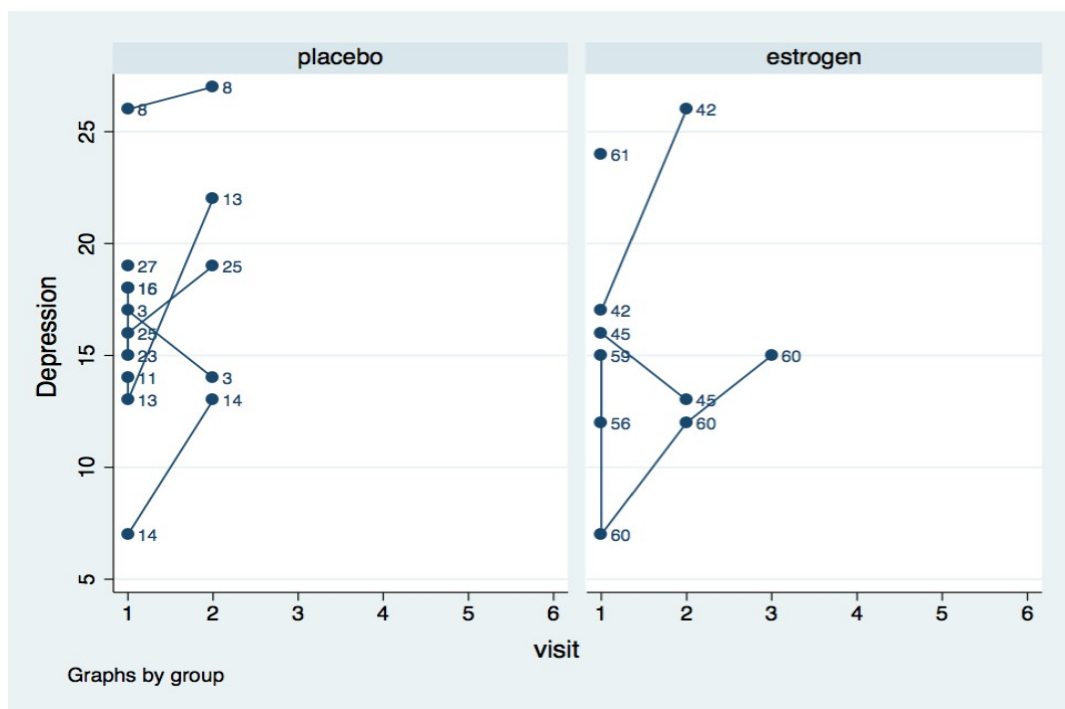
Notice that those receiving placebo seem to 'benefit' from being in this study. Placebos can be wonderful things :-). Let's further explore the idea of a post baseline slope as we did with the dental study. This is a bit trickier still in that we need to advise Stata to ignore those individuals with only one post baseline measurement. This requires use of the 'capture' command and the use of a system variable `_rc`. Have a look at the Stata Programming Manual for more on this valuable and powerful set of utilities.

```
quietly forval num = 1/61 {
  capture regr dep visit if subj==`num'
  if _rc==0 regr dep visit if subj==`num'
  if _rc==0 replace blist=_b[visit] if subj==`num'
}
by subj: replace blist=. if _n!=1
```



This display shows that median slope may be more negative for those receiving estrogen but there are serious outliers [that come from individuals with only 2 measurements]. Here is a display of the dropouts

```
twoway connected dep visit if drop==1, connect(ascending) by(group) ytitle(Depression)
xlabel(1/6) mlabel(subj)
```



The next two analyses enable us to consider dropout status as potential modifier/confounder.
 Completers: drop==0; dropouts: drop==1.

```
. mixed dep group drop dg || subj:
Mixed-effects ML regression
Group variable: subj
```

```
Number of obs      =      295
Number of groups   =       61

Obs per group: min =        1
                avg  =       4.8
                max  =        6
```

```
Log likelihood = -876.67365
Wald chi2(3)      =      26.94
Prob > chi2       =      0.0000
```

dep	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
group	-4.075945	1.308373	-3.12	0.002	-6.64031	-1.511581
drop	3.766207	1.934725	1.95	0.052	-.0257844	7.558199
dg	3.115024	2.957592	1.05	0.292	-2.681749	8.911798
_cons	13.37725	1.032059	12.96	0.000	11.35446	15.40005

Random-effects Parameters	Estimate	Std. Err.	[95% Conf. Interval]	
subj: Identity				
var(_cons)	15.46552	3.469955	9.96283	24.00746
var(Residual)	15.8517	1.453268	13.24459	18.972

```
LR test vs. linear regression: chibar2(01) = 104.98 Prob >= chibar2 = 0.0000
```

```

. mixed dep group drop || subj:
Mixed-effects ML regression
Group variable: subj

Number of obs      =      295
Number of groups   =       61

Obs per group: min =       1
                avg  =      4.8
                max  =       6

Wald chi2(2)       =      25.54
Prob > chi2        =      0.0000

Log likelihood = -877.22587

```

dep	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
group	-3.464283	1.180574	-2.93	0.003	-5.778165	-1.1504
drop	5.100048	1.470863	3.47	0.001	2.217209	7.982886
_cons	12.99666	.9732443	13.35	0.000	11.08914	14.90419

Random-effects Parameters		Estimate	Std. Err.	[95% Conf. Interval]	
subj: Identity					
	var(_cons)	15.69568	3.529713	10.10086	24.38945
	var(Residual)	15.87724	1.45723	13.26328	19.00637

LR test vs. linear regression: chibar2(01) = 105.01 Prob >= chibar2 = 0.0000

Now we can consider the distribution of the residuals ϵ conditional on the subject specific components u . The default is to assume [conditional] independence and constant variance. There are a very wide range of possible forms for this distribution. We do continue to assume independence between the residuals from different subjects.

As a couple of examples, we can allow for possibly different variances, say, between treatment groups or allow for the Toeplitz form of covariances.

```

. mixed dep group drop || subj:,res(,by(group))

Mixed-effects ML regression
Group variable: subj

Number of obs      =      295
Number of groups   =       61

Obs per group: min =       1
                avg  =      4.8
                max  =       6

Wald chi2(2)       =      25.57
Prob > chi2        =      0.0000

Log likelihood = -877.22

```

dep	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
group	-3.464819	1.180137	-2.94	0.003	-5.777845	-1.151792
drop	5.094085	1.469908	3.47	0.001	2.213119	7.975051
_cons	12.99742	.9723903	13.37	0.000	11.09157	14.90327

Random-effects Parameters		Estimate	Std. Err.	[95% Conf. Interval]	
subj: Identity					
	var(_cons)	15.6917	3.528878	10.09822	24.38345

Residual: Independent,					
by group					
placebo: var(e)	15.68204	2.291416	11.7768	20.88227	
estrogen: var(e)	16.00389	1.884266	12.70594	20.15785	

LR test vs. linear regression: chi2(2) = 105.02 Prob > chi2 = 0.0000

Note: LR test is conservative and provided only for reference.

. mixed dep group drop || subj:,res(toeplitz 1,t(visit))

Mixed-effects ML regression	Number of obs	=	295
Group variable: subj	Number of groups	=	61
	Obs per group: min	=	1
	avg	=	4.8
	max	=	6

	Wald chi2(2)	=	25.94
Log likelihood = -856.75753	Prob > chi2	=	0.0000

dep	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
group	-3.504549	1.145759	-3.06	0.002	-5.750195	-1.258903
drop	5.004422	1.460866	3.43	0.001	2.141178	7.867666
_cons	13.08391	.9416329	13.89	0.000	11.23834	14.92948

Random-effects Parameters	Estimate	Std. Err.	[95% Conf. Interval]	
subj: Identity				
var(_cons)	12.20801	3.39303	7.080542	21.04861
Residual: Toeplitz(1)				
cov1	6.957426	1.199411	4.606623	9.308229
var(e)	18.07575	1.922631	14.67432	22.26561

LR test vs. linear regression: chi2(2) = 145.95 Prob > chi2 = 0.0000

Note: LR test is conservative and provided only for reference.

. estat wcorr

Standard deviations and correlations for subj = 1:

Standard deviations:

visit	1	2	3	4	5	6
sd	5.503	5.503	5.503	5.503	5.503	5.503

Correlations:

visit	1	2	3	4	5	6
1	1.000					
2	0.633	1.000				
3	0.403	0.633	1.000			
4	0.403	0.403	0.633	1.000		
5	0.403	0.403	0.403	0.633	1.000	
6	0.403	0.403	0.403	0.403	0.633	1.000

```
. estat wcorr,cov
```

```
Covariances for subj = 1:
```

visit	1	2	3	4	5	6
1	30.284					
2	19.165	30.284				
3	12.208	19.165	30.284			
4	12.208	12.208	19.165	30.284		
5	12.208	12.208	12.208	19.165	30.284	
6	12.208	12.208	12.208	12.208	19.165	30.284