

Practical 6:

Longitudinal data II

Data

- The Beta-blocker trial continued

Questions

8. Now allow the slope to vary between patients:

```
. mixed dbp time treat c_pre || id: time, var cov(un) reml
```

9. Check again the distribution of the predicted residuals. Remember to list two variable names when using the option **reffects**:

```
. predict r_slope r_inter, reffects
```

10. Keeping the fixed effects the same, test whether this model fits better than the random intercepts one.
11. Test whether the slopes vary with treatment.
12. Calculate some of the estimated correlations among repeated observations on the same individual, as predicted by the random intercept and random slope model and compare them with those calculated from the data in question 3. For example calculate the predicted correlation between the first and second observation and between the first and sixth.

Recall that, for two observations from the same individual but taken at times t_i and $t_{i'}$,

$$\text{Cov}(Y_{ij}, Y_{i'j}) = \text{cov}(u_{0j} + t_i u_{1j}, u_{0j} + t_{i'} u_{1j}) = \sigma_{u00}^2 + (t_i + t_{i'})\sigma_{u01} + t_i t_{i'} \sigma_{u11}^2$$

while the variance of an observation Y_{ij} is

$$\text{Var}(Y_{ij}) = \sigma_{u00}^2 + 2t_i \sigma_{u01} + t_i^2 \sigma_{u11}^2 + \sigma_e^2$$

.

13. Calculate the predicted mean profiles in the two treatment arms with:

```
. predict yhat, fitted
. preserve
. keep yhat time id pre treat
. reshape wide yhat,i(id) j(time)
. collapse pre yhat1-yhat6,by(treat)
. rename pre yhat0
. reshape long yhat, i(treat) j(time)
. gen yhat_act=yhat if treat==1
. gen yhat_pl=yhat if treat==0
. twoway (line yhat_act time,sort) (line yhat_pl time, lpat(dash)sort)
. restore
```

Compare the plot with the observed profiles.

14. Plot the predicted individual profiles for a selection of patients.

```
.qui mixed dbp time treat c_pre || id: time, var cov(un)
. predict r_inter, fitted
. twoway (line r_inter time, sort) (scatter dbp time) if id<23 & id>1 & id!=13, ///
  xtitle("Time (years)") ytitle("DBP (mmHg)") by(id) ///
  yscale(range(80 100)) ylabel(80(5)100, angle(h))
```

15. Extract standard errors for individual random intercepts and plot estimates with approximate 95% confidence intervals as follows:

```
.drop r_*
.qui mixed dbp time treat c_pre || id: time, var cov(un)
. predict r_slope r_inter, reffects reses(r_slope_se r_inter_se)
. gen low=r_inter-1.96*r_inter_se
. gen high=r_inter+1.96*r_inter_se
. sort r_inter
. drop if pickone==0
. gen individual=_n
. twoway (scatter r_inter individual, mcolor(navy) msize(small)) ///
  (rspike low high individual, lcolor(navy)) if pickone, ///
  xtitle("Individual") ytitle("DBP (mmHg)")
```