

ATCR Lab Repeated Measures 2 – Lab Key

1. The estimates of the pilltype differences are exactly the same as are the standard errors. The p-values for the individual differences are slightly different because REGRESS uses t-tests (correcting for small sample size) whereas MIXED does not. Correspondingly, for the overall test REGRESS uses an F-test (which corrects for small sample sizes) whereas MIXED uses a chi-square test which does not. But, since results for z- and t-tests (and F- and chi-square tests) usually aren't very different, the results are very similar. Why not just use REGRESS all the time? First, one cannot use REGRESS to get a test of the gender effect (i.e., between cluster effects). Second, with more complicated situations (unbalanced data, continuous predictors, or more complicated studies) REGRESS (or ANOVA) does not give comparable or correct results. The purpose of this lab exercise (beyond getting practice on mixed) was to reinforce that MIXED does make a type of "adjustment" for patient effects.

2. All estimates noted below are for average WOMAC pain score

```

2.sex | .2110945 Estimated difference between the sexes at baseline
visit |
      12 | -.3676323 Estimated difference between baseline (reference) and 12
months for males (reference sex group)
      18 | -.1990016 Estimated difference between baseline (reference) and 12
months for males (reference sex group)
sex#visit |
      2 12 | .1954676 Estimated difference between sexes in the difference between
baseline and 12 months
      2 18 | .5527628 Estimated difference between sexes in the difference between
baseline and 18 months
      _cons | 2.19869 Estimated mean value for reference group (male, baseline)

```

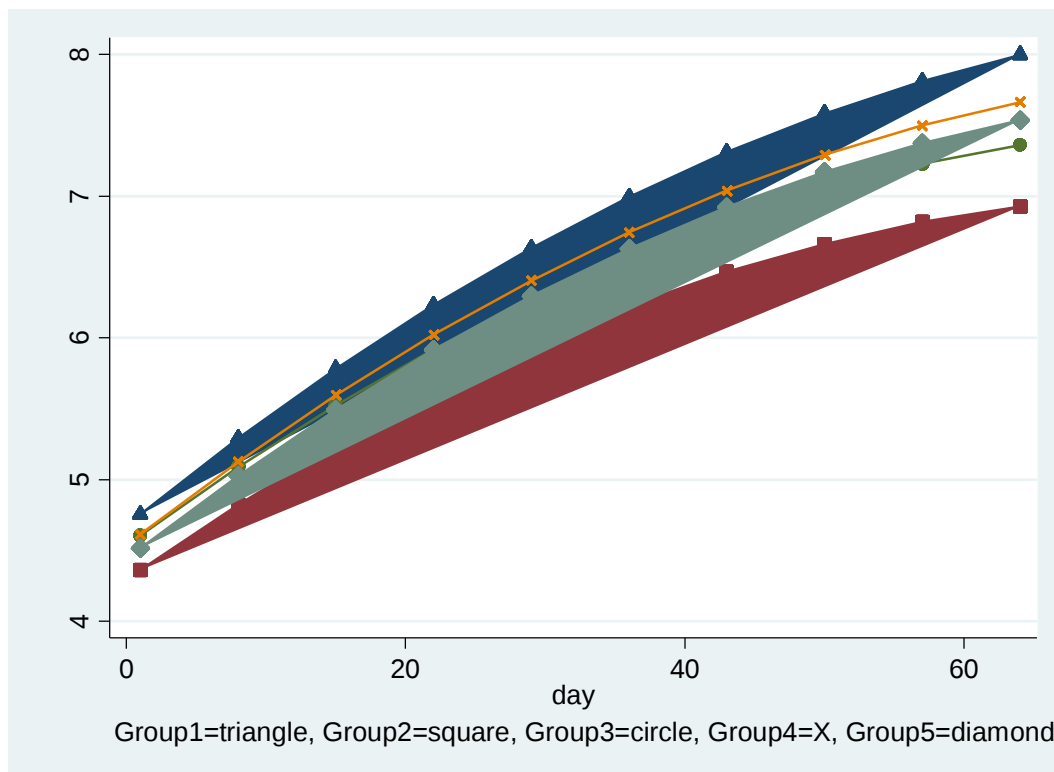
The formal test confirms the impression from the graph. The lines for males and females are roughly parallel. There is not sufficient evidence to conclude that the changes over time are different for men and women.

3. The residual plots look largely OK. No significant outliers, dropping all the points with absolute standardized residuals > 3 makes almost no difference.
4. The plots show a monotonic upward trend in weight for each group, with perhaps slight differences in growth trajectories. All of the trajectories seem to be leveling off slightly. So we'll need something like a quadratic term to model the curved relationship.
5. For the model with random intercepts (just "mouse:") the group by day interaction (testing if the linear slopes are different between the groups) is highly stat significant, with a p-value of almost 0. When the random slopes are added to the model the result is *not* statistically significant. This occurs because there is evident variation in the slopes from animal to animal that we ignored in the first analysis. This directly and dramatically affects a comparison of slopes across the groups (it assumes away a significant portion of the variability). We could have checked the original (incorrect) model either by running XTGEE with the robust option (see below) or a bootstrap. To run the bootstrap you have to let Stata know to resample *mice* not individual data points through the cluster option:

```
bootstrap, reps(200) cluster(mouseid): mixed logw i.group##c.day day2 || mouse:
```

Both XTGEE with robust and the bootstrap give p-values very similar to the analysis with random slopes. So there isn't strong evidence of an incorrect model as long as we've included random slopes. But did you try adding group-specific curvature terms?

6. Going with the random slopes model the plot looks like:



So all the groups increase and with the same degree of leveling off (forced by the model since they all have the same curvature) with group 1 having the highest trajectory (as it happens that is the control group and their tumors are growing fastest). Group 5 has the lowest growth rate.

Note: Stata is pretty good at generating simple plots quickly but tidying them up takes a lot of fiddling. The command for the above was:

```
. twoway (conn prd day if gr==1, msymbol(triangle)) (conn prd day if gr==2,
msymbol(square)) (conn prd day if gr==3, msymbol(circle)) (conn prd day if gr==4,
msymbol(X)) (conn prd day if gr==5, msymbol(diamond)), caption("Group1=triangle,
Group2=square, Group3=circle, Group4=X, Group5=diamond") legend(off) ytitle("Predicted
values")
```

5. XTGEE without the robust option gives p-values that are incorrect. But with the robust option, it gives p-values very similar to the random slopes and intercepts model. The random slopes and intercepts model is essentially just a fancy correlation structure, which the robust option accommodates.