# Homework 2

Leah Schultz
9/28/2017

### Chapter 3: Growth Curves

```
library(dplyr)
library(tidyr)
library(lme4)
library(ggplot2)
library(broom)
library(merTools)
purpose <- read.csv("~/Dropbox/Lab & Research/OYSUP Project/oysup_self.csv")

First, restructuring data:
purpose_long <- tbl_df(purpose) %>%
    gather(-c(FAMID, SEX2, MEDUC2, MPEDUC2), key = "grade", value = "value") %>%
    separate(grade, into = c("variable", "grade"), sep = "_", convert = T) %>%
    spread(variable, value)

purpose_long_elem <- purpose_long %>%
    filter(grade != 21)
```

1. Run linear models on all of your subjects (a basic regression). What is the average intercept, the average slope?

```
model1 <- lm(cbmom ~ grade, data = purpose_long)</pre>
summary(model1)
##
## Call:
## lm(formula = cbmom ~ grade, data = purpose_long)
##
## Residuals:
##
      Min
               1Q Median
                               ЗQ
## -1.6754 -1.3599 -0.4388 0.6401 5.4035
##
## Coefficients:
##
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.28108 0.07657 16.731 < 2e-16 ***
## grade
              0.07886
                          0.01987 3.969 7.4e-05 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.38 on 3032 degrees of freedom
    (3410 observations deleted due to missingness)
## Multiple R-squared: 0.005167, Adjusted R-squared: 0.004839
## F-statistic: 15.75 on 1 and 3032 DF, p-value: 7.4e-05
```

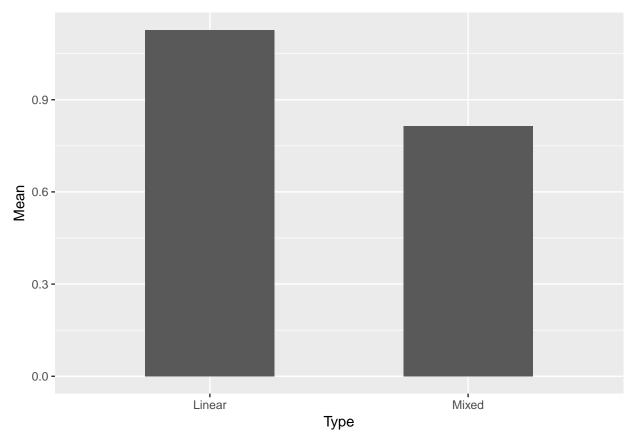
```
Average intercept = 1.28
Average slope = .08
```

#### 2. Now run a mlm/lmer model with only a random intercept.

```
model2 <- lmer(cbmom ~ 1 + (1 | FAMID), data = purpose_long)</pre>
summary(model2)
## Linear mixed model fit by REML ['lmerMod']
## Formula: cbmom ~ 1 + (1 | FAMID)
##
     Data: purpose_long
## REML criterion at convergence: 10280.8
##
## Scaled residuals:
      Min
             1Q Median
                               3Q
                                      Max
## -2.4057 -0.6586 -0.0506 0.5544 4.0774
##
## Random effects:
## Groups Name
                        Variance Std.Dev.
## FAMID
          (Intercept) 0.6328 0.7955
                                1.1375
                        1.2939
## Residual
## Number of obs: 3034, groups: FAMID, 1063
##
## Fixed effects:
##
              Estimate Std. Error t value
## (Intercept) 1.60288
                        0.03302
                                   48.54
3. What is the ICC?
```

```
ICC = \% between- vs. within-person variance
variance by ID / variance by ID + residual variance
.64 / (.64 + 1.30) = .33
```

What does residual variance look like compared to linear model? Create a graph to show this effect.



Absolute value of the average residual variance is lower in the mixed model, since we're accounting for individual-level, random effects.

3. Introduce a fixed slope term. What is the difference in terms of the fixed effects estimates between this estimate and the previous? Of the residual standard error? Create a graph to show both fixed effects estimates and the CIs around them.

```
model3 <- lmer(cbmom ~ grade + (1 | FAMID), data = purpose_long)</pre>
summary(model3)
## Linear mixed model fit by REML ['lmerMod']
## Formula: cbmom ~ grade + (1 | FAMID)
##
     Data: purpose_long
##
## REML criterion at convergence: 10269.4
##
## Scaled residuals:
           1Q Median
      Min
                                3Q
                                       Max
## -2.4634 -0.6873 -0.1045 0.5563 4.0622
##
## Random effects:
  Groups Name
                        Variance Std.Dev.
  FAMID
            (Intercept) 0.6296
                                0.7935
                                  1.1343
## Residual
                        1.2867
```

Fixed effect estimate for intercept decreased from 1.60 to 1.32.

# 4. Run an additional model with a random slope. How does this change compare to the previous model? Should you keep the random slope or not?

```
model4 <- lmer(cbmom ~ grade + (1 + grade | FAMID), data = purpose_long)</pre>
summary(model4)
## Linear mixed model fit by REML ['lmerMod']
## Formula: cbmom ~ grade + (1 + grade | FAMID)
##
      Data: purpose_long
## REML criterion at convergence: 10243.6
##
## Scaled residuals:
      Min
               1Q Median
                                3Q
                                       Max
## -2.7435 -0.6404 -0.0741 0.5636 4.0278
##
## Random effects:
## Groups
                         Variance Std.Dev. Corr
             Name
## FAMID
             (Intercept) 0.65308 0.8081
             grade
##
                         0.04358 0.2087
                                           -0.48
                         1.19431 1.0928
## Number of obs: 3034, groups: FAMID, 1063
## Fixed effects:
               Estimate Std. Error t value
## (Intercept) 1.30324
                           0.07316 17.813
## grade
                0.07852
                           0.01844
                                     4.257
##
## Correlation of Fixed Effects:
         (Intr)
## grade -0.894
```

### 5. Interpret the correlation between the slope and the intercept.

Correlation between slope and intercept = -.89.

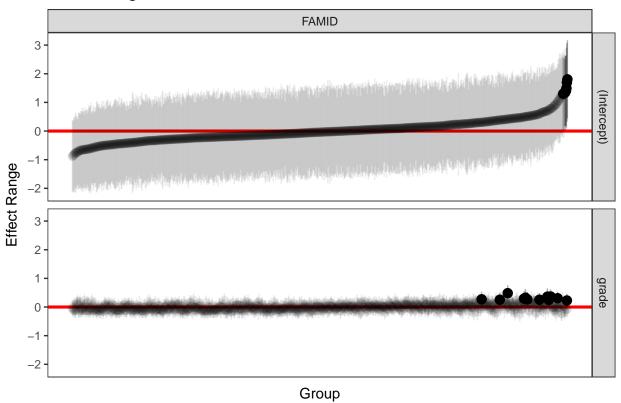
6. Create a density plot of the random effects from your final model.

```
random_params <- tidy(model4, effect = "ran_modes")</pre>
raneff_plot <- ggplot(random_params, aes(x = estimate, color = term)) +</pre>
  geom_density()
raneff_plot
    4 -
    3 -
                                                                                       term
density 2 -
                                                                                           (Intercept)
                                                                                           grade
    1 -
    0 -
                                                      2
                                        estimate
```

7. Create a caterpillar plot of the random effects. Is there any person that seems odd in terms of a large standard errors around intercept and slope estimates?

```
re.sim <- REsim(model4)
plotREsim(re.sim)</pre>
```

## **Effect Ranges**



8. Create a plot of the trajectory, along with a spaghetti plot of each person's individual slope. Set the alpha level (transparency) on the individual slopes to make them easier to see.

