Review & Intro to GH Notation

Daniel Anderson

Week 4

Agenda

- Review Homework 1
- Review the most important parts of Week 3 content
- Discuss Gelman and Hill notation – contrast with Raudenbush and Bryk
- Unstructured VCV Matrices and alternatives

Learning Objectives

- Understand at least the basics of the GH notation and why I view it as preferable
- Gain a deeper understanding of how the residual structure is different in multilevel models
- Understand that there are methods for changing the residual structure, and understand when and why this might be preferable
- Have a basic understanding of implementing alternative methods

Review Homework 1

Review Week 3 content

Data and model

```r
library(tidyverse)
library(lme4)

popular <- read_csv(here::here("data", "popularity.csv"))

m <- lmer(popular ~ extrav + (extrav|class), popular,
          control = lmerControl(optimizer = "bobyqa"))
```

`extrav` is a measure of extraversion.

What is this model fitting, in plain English?

Model summary

```r
arm::display(m)
```

```
## lmer(formula = popular ~ extrav + (extrav | class), data = popular,
##     control = lmerControl(optimizer = "bobyqa"))
##             coef.est coef.se
## (Intercept) 2.46     0.20
## extrav      0.49     0.03
##
## Error terms:
##  Groups   Name        Std.Dev. Corr
##  class    (Intercept) 1.73
##           extrav      0.16     -0.97
##  Residual             0.95
## ---
## number of obs: 2000, groups: class, 100
## AIC = 5791.4, DIC = 5762
## deviance = 5770.7
```

Let's walk through

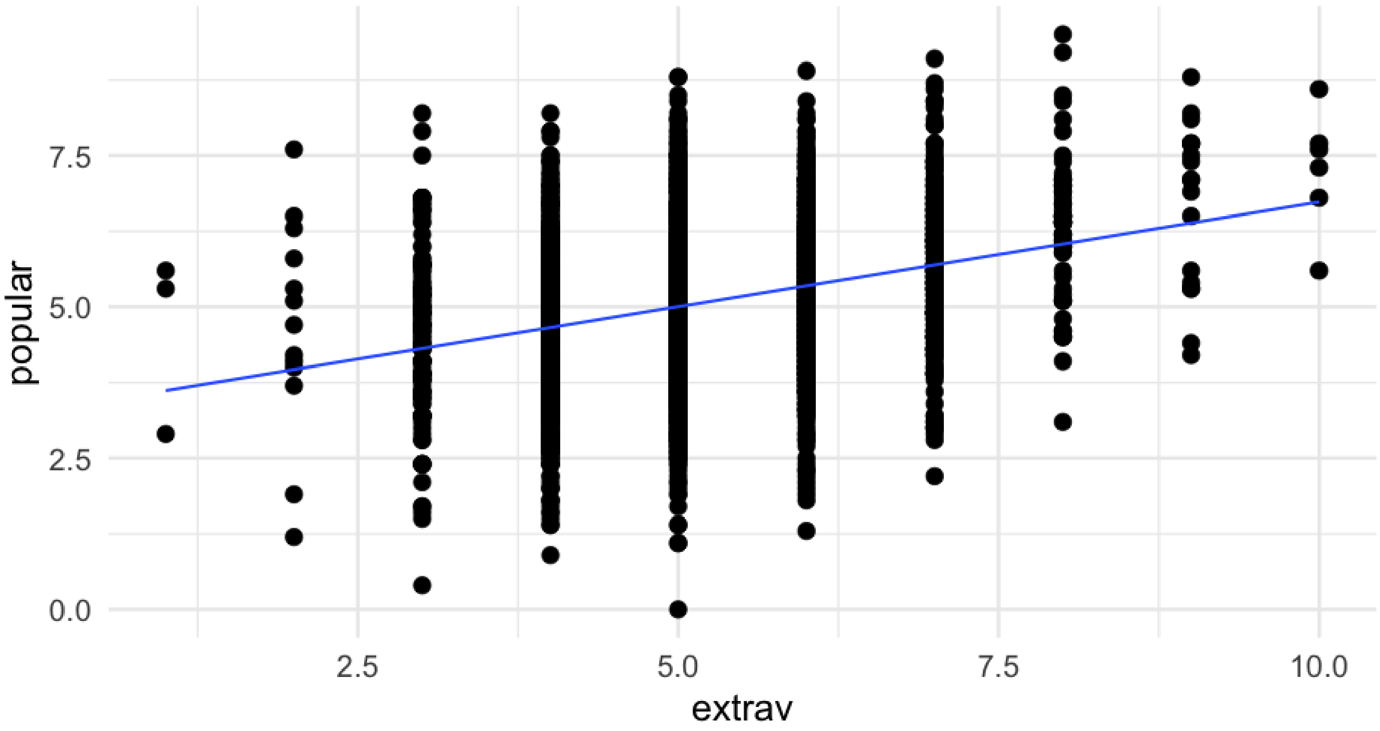
- By way of thinking through it, let's compare to simple linear regression

```r
slr <- lm(popular ~ extrav, popular)
arm::display(slr)
```

```
## lm(formula = popular ~ extrav, data = popular)
##             coef.est coef.se
## (Intercept) 3.27     0.12   
## extrav      0.35     0.02   
## ---
## n = 2000, k = 2
## residual sd = 1.31, R-Squared = 0.10
```

Visually

```
ggplot(popular, aes(extrav, popular)) +
  geom_point() +
  geom_smooth(se = FALSE, method = "lm")
```



Making predictions

$$\widehat{\text{popular}} = 3.27 + 0.35(\text{extrav})$$

Scores of 0 to 5

$$\widehat{\text{popular}} = 3.27 + 0.35 \times 0 = 3.27$$

$$\widehat{\text{popular}} = 3.27 + 0.35 \times 1 = 3.62$$

$$\widehat{\text{popular}} = 3.27 + 0.35 \times 2 = 3.97$$

$$\widehat{\text{popular}} = 3.27 + 0.35 \times 3 = 4.32$$

$$\widehat{\text{popular}} = 3.27 + 0.35 \times 4 = 4.67$$

$$\widehat{\text{popular}} = 3.27 + 0.35 \times 5 = 5.02$$

Now for the mlm

It's more complicated now for a couple of reasons

- Each `class` has their own intercept and slope. Which class is the student in?

- What if we want to make a prediction for someone outside our sample? Let's walk through 4 predictions

Sample preds

```r
sample_preds <- popular %>%
  group_by(class) %>%
  slice(1) %>%
  ungroup() %>%
  slice(1:4)

sample_preds
```

```
## # A tibble: 4 x 7
##   pupil class extrav sex    texp  popular popteach
##   <dbl> <dbl>  <dbl> <chr> <dbl>    <dbl>    <dbl>
## 1     1     1      5 girl     24 6.3             6
## 2     1     2      8 girl     14 6.4             6
## 3     1     3      5 boy      13 4.2             4
## 4     1     4      3 girl     20 4.100000        4
```

Coefficients

$$
\begin{aligned}
\widehat{\text{popular}}_i &\sim N\left(\mu, 0.95\right) \\
\mu &= 2.46_{\alpha_{j[i]}} + 0.49_{\beta_{1j[i]}}(\text{extrav}) \\
\left(\begin{array}{c} \alpha_j \\ \beta_{1j} \end{array}\right) &\sim N\left(\left(\begin{array}{c} 0 \\ 0 \end{array}\right), \left(\begin{array}{cc} 1.73 & -0.97 \\ -0.97 & 0.16 \end{array}\right)\right), \text{ for class j} = 1, \dots, \text{J}
\end{aligned}
$$

Grab params

Fixed effects

```
f <- fixef(m)
f
```

```
## (Intercept)      extrav
##   2.4610234   0.4928571
```

classroom deviations

```
r <- ranef(m)
r
```

```
## $class
##     (Intercept)       extrav
## 1    0.34095954 -0.027014677
## 2   -1.17798954  0.096974668
## 3   -0.62937002  0.057097182
## 4    1.08529708 -0.099953042
## 5   -0.19489641  0.021601800
## 6   -0.98339230  0.083762531
## 7   -1.00065422  0.064825024
```

Predictions depend on classroom

Fixed effect part

Works just like simple linear regression

```
sample_preds[1, ]
```

```
## # A tibble: 1 x 7
##   pupil class extrav sex    texp popular popteach
##   <dbl> <dbl>  <dbl> <chr> <dbl>   <dbl>    <dbl>
## 1     1     1      5 girl     24     6.3        6
```

$$\widehat{\textbf{popular}} = 2.46 + 0.49 \times 5 = 4.91$$

```
f[1] + f[2]*5
```

```
## (Intercept)
##    4.925309
```

Random effects

We now have to add in the random effects *for the corresponding classroom*.

```
head(r$class)
```

```
##   (Intercept)      extrav
## 1   0.3409595 -0.02701468
## 2  -1.1779895  0.09697467
## 3  -0.6293700  0.05709718
## 4   1.0852971 -0.09995304
## 5  -0.1948964  0.02160180
## 6  -0.9833923  0.08376253
```

$$\widehat{\mathbf{popular}} = (\mathbf{2.46} + \mathbf{0.34}) + (\mathbf{0.49} + -\mathbf{0.03}) \times \mathbf{5} = \mathbf{5.10}$$

In code

```r
class1 <- r$class[1, ]
class1
```

```
##   (Intercept)      extrav
## 1   0.3409595 -0.02701468
```

```r
(f[1] + class1[1]) + (f[2] + class1[2])*5
```

```
##   (Intercept)
## 1    5.131195
```

Predictions

```r
sample_preds
```

```
## # A tibble: 4 x 7
##   pupil class extrav sex    texp  popular popteach
##   <dbl> <dbl>  <dbl> <chr> <dbl>    <dbl>    <dbl>
## 1     1     1      5 girl     24 6.3                6
## 2     1     2      8 girl     14 6.4                6
## 3     1     3      5 boy      13 4.2                4
## 4     1     4      3 girl     20 4.100000           4
```

```r
head(r$class, n = 4)
```

```
##    (Intercept)      extrav
## 1   0.3409595 -0.02701468
## 2  -1.1779895  0.09697467
## 3  -0.6293700  0.05709718
## 4   1.0852971 -0.09995304
```

```r
fixef(m)
```

```
## (Intercept)      extrav
##   2.4610234   0.4928571
```

$$\widehat{\text{popular}} = (2.46 + 0.34) + (0.49 + -0.03) \times 5 = 5.10$$

$$\widehat{\text{popular}} = (2.46 + -1.18) + (0.49 + 0.10) \times 8 = 6.00$$

$$\widehat{\text{popular}} = (2.46 + -0.63) + (0.49 + 0.06) \times 5 = 4.58$$

$$\widehat{\text{popular}} = (2.46 + 1.09) + (0.49 + -0.10) \times 3 = 4.72$$

```r
predict(m, newdata = sample_preds)
```

```
##        1        2        3        4 
## 5.131195 6.001688 4.581425 4.725033
```

What if we want to make a prediction outside of our classrooms?

Fixed effects only

$$\widehat{\text{popular}} = 2.46 + 0.49 \times \text{extraversion}$$

Plotting

We can use the `expand.grid()` function to create different conditions. Let's compare slopes across the first five classrooms

```r
conditions <- expand.grid(extrav = 1:10, class = 1:5)
```

```r
head(conditions)
```

```
##   extrav class
## 1      1     1
## 2      2     1
## 3      3     1
## 4      4     1
## 5      5     1
## 6      6     1
```

```r
tail(conditions)
```

```
##    extrav class
## 45      5     5
## 46      6     5
## 47      7     5
## 48      8     5
## 49      9     5
## 50     10     5
```

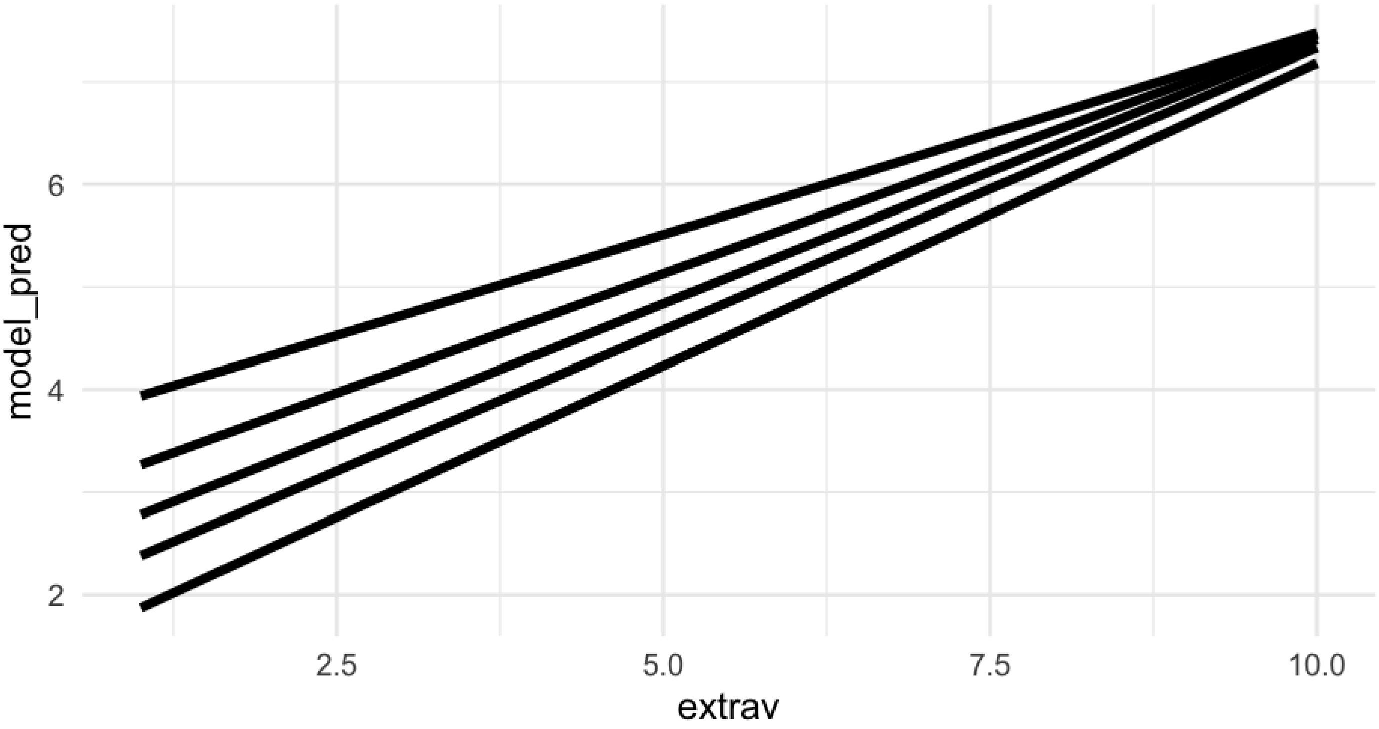
Make predictions

```
conditions %>%
  mutate(model_pred = predict(m, newdata = conditions))
```

```
##    extrav class model_pred
## 1       1     1   3.267825
## 2       2     1   3.733668
## 3       3     1   4.199510
## 4       4     1   4.665353
## 5       5     1   5.131195
## 6       6     1   5.597038
## 7       7     1   6.062880
## 8       8     1   6.528722
## 9       9     1   6.994565
## 10     10     1   7.460407
## 11      1     2   1.872866
## 12      2     2   2.462697
## 13      3     2   3.052529
## 14      4     2   3.642361
## 15      5     2   4.232193
## 16      6     2   4.822025
## 17      7     2   5.411856
## 18      8     2   6.001688
## 19      9     2   6.591520
## 20     10     2   7.181352
## 21      1     3   2.381608
```

Plot

```
conditions %>%
  mutate(model_pred = predict(m, newdata = conditions)) %>%
  ggplot(aes(extrav, model_pred)) +
  geom_line(aes(group = class))
```



One more quick example

Model an interaction

```
m2 <- lmer(popular ~ extrav*sex + (extrav|class), popular,
           control = lmerControl(optimizer = "bobyqa"))
```

Model summary

```r
arm::display(m2)
```

```
## lmer(formula = popular ~ extrav * sex + (extrav | class), data = popular
##     control = lmerControl(optimizer = "bobyqa"))
##                  coef.est coef.se
## (Intercept)      2.23     0.20
## extrav           0.41     0.03
## sexgirl          0.95     0.16
## extrav:sexgirl 0.06     0.03
##
## Error terms:
##  Groups   Name        Std.Dev. Corr
##  class    (Intercept) 1.63
##           extrav      0.18     -0.94
##  Residual             0.74
## ---
## number of obs: 2000, groups: class, 100
## AIC = 4890.7, DIC = 4836.6
## deviance = 4855.7
```

Marginal effect

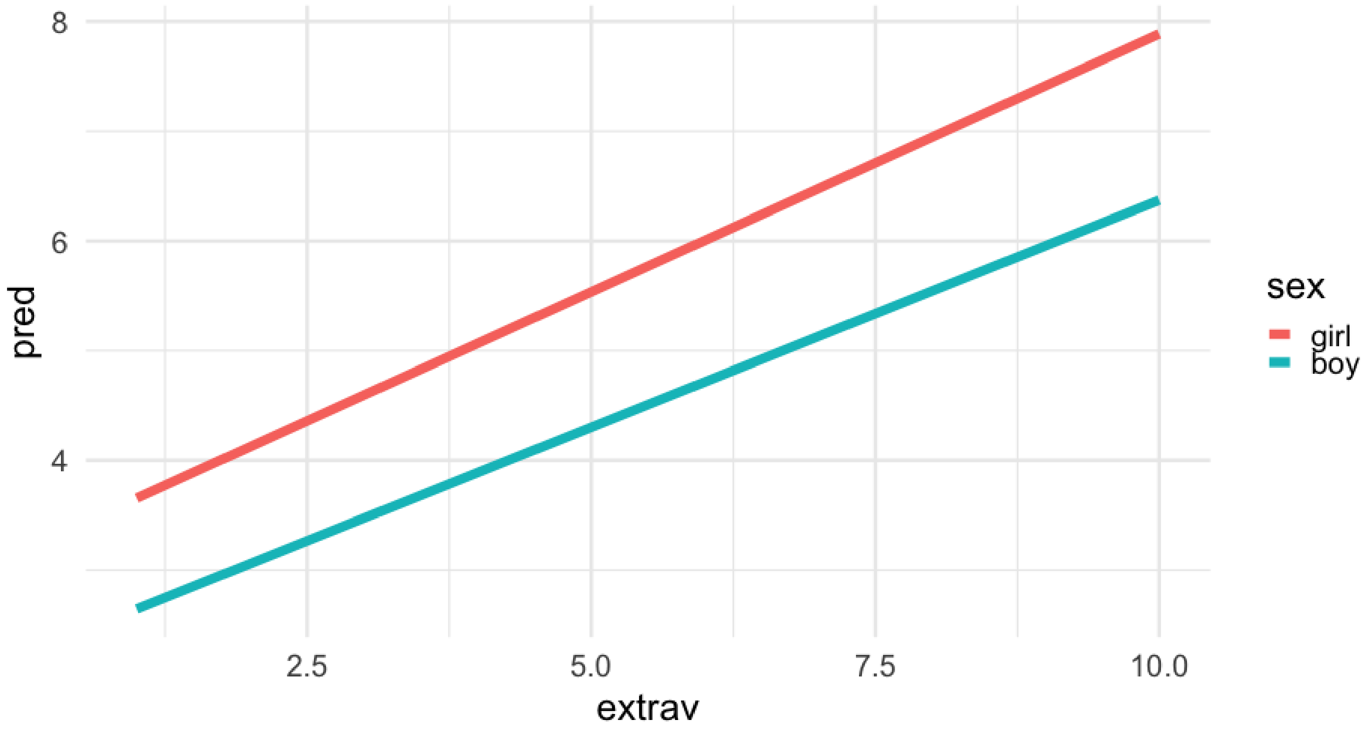
Let's look at the interaction between extraversion and sex

```
conditions2 <- expand.grid(extrav = 1:10,
                           sex = c("girl", "boy"),
                           class = 0) %>%
  mutate(pred = predict(m2,
                        newdata = .,
                        allow.new.levels = TRUE))
conditions2
```

```
##    extrav  sex class     pred
## 1       1 girl     0 3.654686
## 2       2 girl     0 4.124926
## 3       3 girl     0 4.595165
## 4       4 girl     0 5.065404
## 5       5 girl     0 5.535643
## 6       6 girl     0 6.005883
## 7       7 girl     0 6.476122
## 8       8 girl     0 6.946361
## 9       9 girl     0 7.416600
## 10     10 girl     0 7.886840
## 11      1  boy     0 2.645470
## 12      2  boy     0 3.059526
## 13      3  boy     0 3.473583
```

Plot

```
ggplot(conditions2, aes(extrav, pred)) +
  geom_line(aes(color = sex))
```



Questions?

Notation

Introducing the Gelman and Hill notation

Standard regression

Imagine we have a model like this

```r
m <- lm(mpg ~ disp + hp + drat, data = mtcars)
```

We would probably display this model like this

$$\mathbf{mpg} = \alpha + \beta_1(\mathbf{disp}) + \beta_2(\mathbf{hp}) + \beta_3(\mathbf{drat}) + \epsilon$$

What we often don't show, is the distributional assumption of the residuals

$$\epsilon \sim N\left(0, \sigma\right)$$

A different view

The model on the previous slide could also be displayed like this

$$\begin{aligned} \hat{y} &= \alpha + \beta_1(\mathbf{disp}) + \beta_2(\mathbf{hp}) + \beta_3(\mathbf{drat}) \\ \mathbf{mpg} &\sim N\left(\hat{y}, \sigma\right) \end{aligned}$$

This makes the distributional assumptions clearer

Each `mpg` value is assumed generated from a normal distribution, with a mean structure according to $\hat{y}$, and an unknown standard deviation, σ.

Simulate

I'm not expecting you to follow along here

If we have a solid understanding of the distributional properties, we can simulate new data from the model

First let's set some population parameters

```r
n <- 1000
intercept <- 100
b1 <- 5
b2 <- -3
b3 <- 0.5
sigma <- 4.5
```

Simulate

Next create some variables. The standard deviations relate to the standard errors – more variance in the predictor leads to lower standard errors.

```r
set.seed(123)
x1 <- rnorm(n, sd = 1)
x2 <- rnorm(n, sd = 2)
x3 <- rnorm(n, sd = 4)
```

Create y–hat

```r
yhat <- intercept + b1*x1 + b2*x2 + b3*x3
```

Generate data & test

```
sim <- rnorm(n, yhat, sigma)
summary(lm(sim ~ x1 + x2 + x3))
```

```
## 
## Call:
## lm(formula = sim ~ x1 + x2 + x3)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -13.7528  -2.8505   0.0021   3.0387  13.0151 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 99.96508    0.14141  706.92   <2e-16 ***
## x1           4.99415    0.14306   34.91   <2e-16 ***
## x2          -3.01827    0.07027  -42.95   <2e-16 ***
## x3           0.55792    0.03613   15.44   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 4.466 on 996 degrees of freedom
## Multiple R-squared:  0.7514,    Adjusted R-squared:  0.7506 
## F-statistic:  1003 on 3 and 996 DF,  p-value: < 2.2e-16
```

Generalizing

We can generalize this same basic approach to multilevel models

This is helpful because the error structure is more complicated

Using this approach helps us better understand the distributional assumptions of our model

Simple example

I know we hate the HSB data but bear with me for a minute.

Consider this simple model

```r
library(lme4)
library(equatiomatic)
hsb_m0 <- lmer(math ~ ses + (1|sch.id), data = hsb)
```

R&B

In Raudenbush and Bryk notation, the model on the prior slide would look like this

$$
\begin{aligned}
\textbf{math}_{ij} &= \beta_{0j} + \beta_{1j}(\textbf{ses}) + e_{ij} \\
\beta_{0j} &= \gamma_{00} + u_{0j} \\
\beta_{1j} &= \gamma_{10}
\end{aligned}
$$

Generally, the distributional part is omitted, which in this case is

$$
\begin{aligned}
E\left(e_{ij}\right) = 0, \text{Var}\left(e_{ij}\right) = \sigma^2 \\
E\left(u_{0j}\right) = 0, \text{Var}\left(u_{0j}\right) = \tau_{00}
\end{aligned}
$$

Put differently

$$
\begin{aligned}
e_{ij} &\sim N\left(0, \sigma^2\right) \\
u_{0j} &\sim N\left(0, \tau_{00}\right)
\end{aligned}
$$

G&H

In Gelman & Hill notation, this same model can be communicated as

$$
\begin{aligned}
\textbf{math}_i &\sim N\left(\alpha_{j[i]} + \beta_1(\textbf{ses}), \sigma^2\right) \\
\alpha_j &\sim N\left(\mu_{\alpha_j}, \sigma^2_{\alpha_j}\right) \text{, for sch.id j} = 1, \dots \text{,J}
\end{aligned}
$$

This notation communicates the distributional assumptions

We can also still easily see what levels the predictors are at

It does look a little more complex, but it's not hiding anything

If you properly understand the notation, you can simultate data assuming this data generating process (which we'll do later)

Bonus

It works really well to communicate model results

$$
\begin{aligned}
\widehat{\operatorname{math}}_{i} &\sim N \left(12.66_{\alpha_{j[i]}} + 2.39_{\beta_{1}}(\operatorname{ses}), 6.09 \right) \\
\alpha_{j} &\sim N \left(0, 2.18 \right) \text{, for sch.id j = 1,} \dots \text{,J}
\end{aligned}
$$

Extra bonus!

You can use equatiomatic to give you the model formula. The above was generated with `extract_eq(hsb_m0, use_coef = TRUE)`

Quick simulation

We'll go over this in more detail later, but I want to give you the general idea.

First, set some parameters

```r
j <- 30 # 30 schools
nj <- 50 # 50 students per school
```

Next, simulate the school distribution

```r
# School distribution
a_j <- rnorm(j, 0, 2.18)
```

For each school, simulate nj obs from the level 1 model, adding in the school deviation

There are lots of ways to do this – I'm using a `for()` loop here in an effort to be transparent

```r
school_scores <- vector("list", j)
ses <- vector("list", j)

for(i in 1:j) {
  ses[[i]] <- rnorm(nj)
  school_scores[[i]] <- rnorm(nj,
                              12.66 + 2.39*ses[[i]] + a_j[i],
                              6.09)
}
```

Put in a df

```
sim_df <- data.frame(
  scid = rep(1:j, each = nj),
  ses = unlist(ses),
  score = unlist(school_scores)
)
head(sim_df)
```

```
##   scid        ses     score
## 1    1 -0.9529766  9.789073
## 2    1  0.4057701 12.820300
## 3    1 -0.9839385 20.956667
## 4    1 -1.6101230 15.884079
## 5    1 -0.4301688  1.363627
## 6    1 -1.2242106  7.820335
```

Test it out

```r
sim_m0 <- lmer(score ~ ses + (1|scid), data = sim_df)
summary(sim_m0)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: score ~ ses + (1 | scid)
##    Data: sim_df
##
## REML criterion at convergence: 9704.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.1418 -0.6848  0.0030  0.6552  3.5886
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  scid     (Intercept)  5.685   2.384
##  Residual             36.187   6.016
## Number of obs: 1500, groups:  scid, 30
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  12.3901     0.4622   26.81
## ses           2.4682     0.1562   15.80
##
## Correlation of Fixed Effects:
```

Expanding the model

Let's add a school–level predictor

```r
hsb_m1 <- lmer(math ~ ses + sector + (1|sch.id), data = hsb)
```

```r
extract_eq(hsb_m1)
```

$$
\begin{aligned}
\operatorname{math}_{i} &\sim N \left(\alpha_{j[i]} + \beta_{1}(\operatorname{ses}), \sigma^2 \right) \\
\alpha_{j} &\sim N \left(\gamma_{0}^{\alpha} + \gamma_{1}^{\alpha}(\operatorname{sector}), \sigma^2_{\alpha_{j}} \right) \text{, for sch.id j = 1,} \dots \text{,J}
\end{aligned}
$$

Add in a random slope

```
hsb_m2 <- lmer(math ~ ses + sector + (ses|sch.id), data = hsb)
extract_eq(hsb_m2)
```

$$
\begin{aligned}
  \operatorname{math}_{i} &\sim N \left(\alpha_{j[i]} + \beta_{1j[i]}(\operatorname{ses}), \sigma^2 \right) \\
    \left(
      \begin{array}{c}
        \begin{aligned}
          &\alpha_{j} \\
          &\beta_{1j}
        \end{aligned}
      \end{array}
    \right)
      &\sim N \left(
    \left(
      \begin{array}{c}
        \begin{aligned}
          &\gamma_{0}^{\alpha} + \gamma_{1}^{\alpha}(\operatorname{sector}) \\
          &\mu_{\beta_{1j}}
        \end{aligned}
      \end{array}
    \right)
  ,
    \left(
      \begin{array}{cc}
         \sigma^2_{\alpha_{j}} & \rho_{\alpha_{j}\beta_{1j}} \\
         \rho_{\beta_{1j}\alpha_{j}} & \sigma^2_{\beta_{1j}}
      \end{array}
    \right)
   \right)
    \text{, for sch.id j = 1,} \dots \text{,J}
\end{aligned}
$$

Include interaction

Include `sector` as a predictor of the relation between `ses` and `math`

```r
hsb_m3 <- lmer(math ~ ses * sector + (ses|sch.id), data = hsb,
               control = lmerControl(optimizer = "nmkbw"))
extract_eq(hsb_m3)
```

$$
\begin{aligned}
  \operatorname{math}_{i} &\sim N \left(\alpha_{j[i]} + \beta_{1j[i]}(\operatorname{ses}), \sigma^2 \right) \\
    \left(
      \begin{array}{c}
        \begin{aligned}
          &\alpha_{j} \\
          &\beta_{1j}
        \end{aligned}
      \end{array}
    \right)
      &\sim N \left(
    \left(
      \begin{array}{c}
        \begin{aligned}
          &\gamma_{0}^{\alpha} + \gamma_{1}^{\alpha}(\operatorname{sector}) \\
          &\gamma^{\beta_{1}}_{0} + \gamma^{\beta_{1}}_{1}(\operatorname{sector})
        \end{aligned}
      \end{array}
    \right)
  ,
    \left(
      \begin{array}{cc}
         \sigma^2_{\alpha_{j}} & \rho_{\alpha_{j}\beta_{1j}} \\
         \rho_{\beta_{1j}\alpha_{j}} & \sigma^2_{\beta_{1j}}
      \end{array}
    \right)
   \right)
    \text{, for sch.id j = 1,} \dots \text{,J}
\end{aligned}
$$

Even more complicated

This model doesn't actually fit well – I omitted some convergence warnings

```
hsb_m4 <- lmer(
  math ~ ses * sector + minority + female + meanses + size +
    (ses + minority + female|sch.id),
  data = hsb
)

extract_eq(hsb_m4)
```

$$
\begin{aligned}
\operatorname{math}_{i} &\sim N \left(\mu, \sigma^2 \right) \\
\mu &= \alpha_{j[i]} + \beta_{1j[i]}(\operatorname{ses}) + \beta_{2j[i]}(\operatorname{minority}) + \beta_{3j[i]}(\operatorname{female}) \\
\left(
\begin{array}{c}
\alpha_{j} \\
\beta_{1j} \\
\beta_{2j} \\
\beta_{3j}
\end{array}
\right)
&\sim N \left(
\left(
\begin{array}{c}
\gamma_{0}^{\alpha} + \gamma_{1}^{\alpha}(\operatorname{sector}) + \gamma_{2}^{\alpha}(\operatorname{meanses}) + \gamma_{3}^{\alpha}(\operatorname{size}) \\
\gamma^{\beta_{1}}_{0} + \gamma^{\beta_{1}}_{1}(\operatorname{sector}) \\
\mu_{\beta_{2j}} \\
\mu_{\beta_{3j}}
\end{array}
\right)
,
\left(
\begin{array}{cccc}
\sigma^2_{\alpha_{j}} & \rho_{\alpha_{j}\beta_{1j}} & \rho_{\alpha_{j}\beta_{2j}} & \rho_{\alpha_{j}\beta_{3j}} \\
\rho_{\beta_{1j}\alpha_{j}} & \sigma^2_{\beta_{1j}} & \rho_{\beta_{1j}\beta_{2j}} & \rho_{\beta_{1j}\beta_{3j}} \\
\rho_{\beta_{2j}\alpha_{j}} & \rho_{\beta_{2j}\beta_{1j}} & \sigma^2_{\beta_{2j}} & \rho_{\beta_{2j}\beta_{3j}} \\
\rho_{\beta_{3j}\alpha_{j}} & \rho_{\beta_{3j}\beta_{1j}} & \rho_{\beta_{3j}\beta_{2j}} & \sigma^2_{\beta_{3j}}
\end{array}
\right)
\right)
\text{, for sch.id j = 1,} \dots \text{,J}
\end{aligned}
$$

Multiple levels

Let's go to a different dataset from equatiomatic

```r
head(sim_longitudinal)
```

```
## # A tibble: 6 x 8
## # Groups:   school [1]
##     sid school district group  treatment  prop_low  wave    score
##   <int>  <int>    <int> <chr>  <fct>         <dbl> <dbl>    <dbl>
## 1     1      1        1 medium 1         0.1428571     0 102.2686
## 2     1      1        1 medium 1         0.1428571     1 102.0135
## 3     1      1        1 medium 1         0.1428571     2 102.5216
## 4     1      1        1 medium 1         0.1428571     3 102.2792
## 5     1      1        1 medium 1         0.1428571     4 102.2834
## 6     1      1        1 medium 1         0.1428571     5 102.7963
```

Four levels

Model doesn't really fit again

```
sl_m <- lmer(
  score ~ wave*treatment + group + prop_low +
    (wave|sid) + (wave + treatment| school) + (1|district),
  data = sim_longitudinal
)
extract_eq(sl_m)
```

$$
\begin{aligned}
  \operatorname{score}_{i} &\sim N \left(\alpha_{j[i],k[i],l[i]} + \beta_{1j[i],k[i]}(\operatorname{wave}), \sigma^2 \right) \\
    \left(
      \begin{array}{c}
        \begin{aligned}
          &\alpha_{j} \\
          &\beta_{1j}
        \end{aligned}
      \end{array}
    \right)
      &\sim N \left(
    \left(
      \begin{array}{c}
        \begin{aligned}
          &\gamma_{0}^{\alpha} + \gamma_{1k[i]}^{\alpha}(\operatorname{treatment}_{\operatorname{1}}) + \gamma_{2}^{\alpha}(\operatorname{group}_{\operatorname{low}}) + \gamma_{3}^{\alpha}(\operatorname{group}_{\operatorname{medium}}) \\
          &\gamma^{\beta_{1}}_{0} + \gamma^{\beta_{1}}_{1}(\operatorname{treatment}_{\operatorname{1}})
        \end{aligned}
      \end{array}
    \right)
  ,
    \left(
      \begin{array}{cc}
         \sigma^2_{\alpha_{j}} & \rho_{\alpha_{j}\beta_{1j}} \\
         \rho_{\beta_{1j}\alpha_{j}} & \sigma^2_{\beta_{1j}}
      \end{array}
    \right)
   \right)
    \text{, for sid j = 1,} \dots \\
    \left(
      \begin{array}{c}
        \begin{aligned}
          &\alpha_{k} \\
          &\beta_{1k} \\
          &\gamma_{1k}
        \end{aligned}
      \end{array}
    \right)
      &\sim N \left(
    \left(
      \begin{array}{c}
        \begin{aligned}
          &\gamma_{0}^{\alpha} + \gamma_{1}^{\alpha}(\operatorname{prop\_low}) \\
          &\mu_{\beta_{1k}} \\
          &\mu_{\gamma_{1k}}
        \end{aligned}
      \end{array}
    \right)
  ,
    \left(
      \begin{array}{ccc}
         \sigma^2_{\alpha_{k}} & \rho_{\alpha_{k}\beta_{1k}} & \rho_{\alpha_{k}\gamma_{1k}} \\
         \rho_{\beta_{1k}\alpha_{k}} & \sigma^2_{\beta_{1k}} & \rho_{\beta_{1k}\gamma_{1k}} \\
         \rho_{\gamma_{1k}\alpha_{k}} & \rho_{\gamma_{1k}\beta_{1k}} & \sigma^2_{\gamma_{1k}}
      \end{array}
    \right)
   \right)
    \text{, for school k = 1,} \dots \text{,K} \\
    \alpha_{l} &\sim N \left(\mu_{\alpha_{l}}, \sigma^2_{\alpha_{l}} \right)
    \text{, for district l = 1,} \dots \text{,L}
\end{aligned}
$$

Residual structures

Data

Willett, 1988

- n = 35 people
- Each completed a cognitive inventory on "opposites naming"
- At first time point, participants also completed a general cognitive measure

Read in data

```
willett <- read_csv(here::here("data", "willett-1988.csv"))
willett
```

```
## # A tibble: 140 x 4
##       id  time   opp   cog
##    <dbl> <dbl> <dbl> <dbl>
##  1     1     0   205   137
##  2     1     1   217   137
##  3     1     2   268   137
##  4     1     3   302   137
##  5     2     0   219   123
##  6     2     1   243   123
##  7     2     2   279   123
##  8     2     3   302   123
##  9     3     0   142   129
## 10     3     1   212   129
## # … with 130 more rows
```

Standard OLS

- We have four observations per participant.
- If we fit a standard OLS model, it would look like this

```
bad <- lm(opp ~ time, data = willett)
summary(bad)
```

```
##
## Call:
## lm(formula = opp ~ time, data = willett)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -88.374 -25.584   1.186  28.926  64.746
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  164.374      5.035   32.65   <2e-16 ***
## time          26.960      2.691   10.02   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 35.6 on 138 degrees of freedom
```

Assumptions

As we discussed previously, this model looks like this

$$\mathbf{opp} = \alpha + \beta_1(\mathbf{time}) + \epsilon$$

where

$$\epsilon \sim (0, \sigma)$$

Individual level residuals

We can expand our notation, so it looks like a multivariate normal distribution

$$\begin{pmatrix} \epsilon_1 \\ \epsilon_2 \\ \epsilon_3 \\ \vdots \\ \epsilon_n \end{pmatrix} \sim MVN\left(\begin{bmatrix} 0 \\ 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma_\epsilon & 0 & 0 & \dots & 0 \\ 0 & \sigma_\epsilon & 0 & 0 & 0 \\ 0 & 0 & \sigma_\epsilon & 0 & 0 \\ \vdots & 0 & 0 & \ddots & \vdots \\ 0 & 0 & 0 & \dots & \sigma_\epsilon \end{bmatrix} \right)$$

This is where the $\boldsymbol{i.i.d.}$ part comes in. The residuals are assumed $\boldsymbol{i}$ndependent and $\boldsymbol{i}$dentically $\boldsymbol{d}$istributed.

Multilevel model

Very regularly, there are reasons to believe the $\boldsymbol{i.i.d.}$ assumption is violated. Consider our current case, with 4 time points for each individual.

- Is an observation for one time point for one individual *independent* from the other observations for that individual?

- Rather than estimating a single residual variance, we estimate an additional components associated with individuals, leading to a *block* diagonal structure

Block diagonal

$$
\begin{pmatrix} \epsilon_{11} \\ \epsilon_{12} \\ \epsilon_{13} \\ \epsilon_{14} \\ \epsilon_{21} \\ \epsilon_{22} \\ \epsilon_{23} \\ \epsilon_{24} \\ \vdots \\ \epsilon_{n1} \\ \epsilon_{n2} \\ \epsilon_{n3} \\ \epsilon_{n4} \end{pmatrix} \sim \left(\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ \vdots \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix}
\sigma_{11} & \sigma_{12} & \sigma_{13} & \sigma_{14} & 0 & 0 & 0 & 0 & \dots & 0 & 0 & 0 & 0 \\
\sigma_{21} & \sigma_{22} & \sigma_{23} & \sigma_{24} & 0 & 0 & 0 & 0 & \dots & 0 & 0 & 0 & 0 \\
\sigma_{31} & \sigma_{32} & \sigma_{33} & \sigma_{34} & 0 & 0 & 0 & 0 & \dots & 0 & 0 & 0 & 0 \\
\sigma_{41} & \sigma_{42} & \sigma_{43} & \sigma_{44} & 0 & 0 & 0 & 0 & \dots & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \sigma_{11} & \sigma_{12} & \sigma_{13} & \sigma_{14} & \dots & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \sigma_{21} & \sigma_{22} & \sigma_{23} & \sigma_{24} & \dots & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \sigma_{31} & \sigma_{32} & \sigma_{33} & \sigma_{34} & \dots & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \sigma_{41} & \sigma_{42} & \sigma_{43} & \sigma_{44} & \dots & 0 & 0 & 0 & 0 \\
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \vdots \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \dots & \sigma_{11} & \sigma_{12} & \sigma_{13} & \sigma_{14} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \dots & \sigma_{21} & \sigma_{22} & \sigma_{23} & \sigma_{24} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \dots & \sigma_{31} & \sigma_{32} & \sigma_{33} & \sigma_{34} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \dots & \sigma_{41} & \sigma_{42} & \sigma_{43} & \sigma_{44}
\end{bmatrix} \right)
$$

Correlations for off–diagonals estimated

Same variance components for all blocks

Out–of–block diagonals are still zero

Homogeneity of variance

As mentioned on the previous slide, we assume the same variance components across all student

This is referred to as the homogeneity of variance assumption – although the block (often referred to as the composite residual) may be heteroscedastic and dependent **within** a grouping factor (i.e., people) the entire error structure is repeated identically across units (i.e., people)

Block diagonal

Because of the homogeneity of variance assumption, we can re–express our block diagonal design as follows

$$\boldsymbol{r} \sim N\left(\mathbf{0}, \begin{bmatrix} \boldsymbol{\Sigma_r} & \mathbf{0} & \mathbf{0} & \dots & \mathbf{0} \\ \mathbf{0} & \boldsymbol{\Sigma_r} & \mathbf{0} & \dots & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \boldsymbol{\Sigma_r} & \dots & \mathbf{0} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \dots & \boldsymbol{\Sigma_r} \end{bmatrix}\right)$$

Composite residual

We then define the composite residual, which is common across units

$$\boldsymbol{\Sigma_r} = \begin{bmatrix} \sigma_{11} & \sigma_{12} & \sigma_{13} & \sigma_{14} \\ \sigma_{21} & \sigma_{22} & \sigma_{23} & \sigma_{24} \\ \sigma_{31} & \sigma_{32} & \sigma_{33} & \sigma_{34} \\ \sigma_{41} & \sigma_{42} & \sigma_{43} & \sigma_{44} \end{bmatrix}$$

Let's try!

Let's fit a parallel slopes model with the Willett data. You try first.

```r
w0 <- lmer(opp ~ time + (1|id), willett)
```

What does the residual variance–covariance look like? Let's use **sundry** to pull it

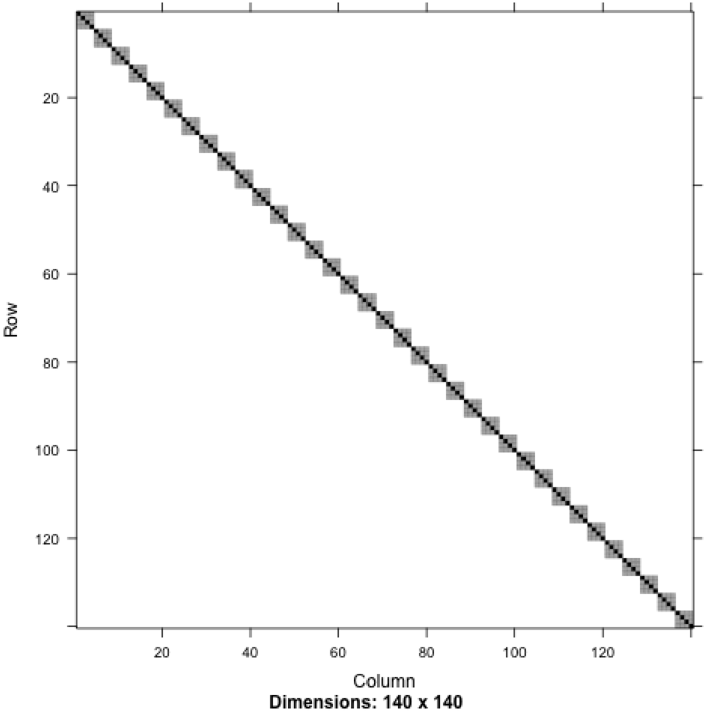
```r
library(sundry)
w0_rvcv <- pull_residual_vcov(w0)
```

02:00

Image

Sparse matrix – we can view it with `image()`

```
image(w0_rvcv)
```



Pull first few rows/cols

```r
w0_rvcv[1:8, 1:8]
```

```
## 8 x 8 sparse Matrix of class "dgCMatrix"
##           1         2         3         4         5         6         7
## 1 1280.7065  904.8054  904.8054  904.8054    .         .         .
## 2  904.8054 1280.7065  904.8054  904.8054    .         .         .
## 3  904.8054  904.8054 1280.7065  904.8054    .         .         .
## 4  904.8054  904.8054  904.8054 1280.7065    .         .         .
## 5    .         .         .         .     1280.7065  904.8054  904.8054
## 6    .         .         .         .      904.8054 1280.7065  904.8054
## 7    .         .         .         .      904.8054  904.8054 1280.7065
## 8    .         .         .         .      904.8054  904.8054  904.8054
```

Next time

Modeling growth (part 1)

Also Homework 2 is assigned