

Predictions and visualizations

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Week 3

Agenda

- Fitting some basic models
- Coefficient plots
- Using the coefficients to make predictions "by hand"
 - contrast with results from `predict()`
- Building predictions for new data
- Marginal effects

Learning objectives

- Understand how to pull different pieces out of the model
- Understand how multilevel models make their predictions for individual observations
 - And specifically how they differ from single-level regression models
- Be able to use the output from model objects to visualize different parts of the model.

Read in the data

Let's read in the popularity data so we can fit some really basic models.

You try first

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

```
## # A tibble: 2,000 x 7
##   pupil class extrav sex    texp popular popteach
##   <dbl> <dbl>   <dbl> <chr>  <dbl>   <dbl>   <dbl>
## 1      1      1      1      5 girl    24      6.3      6
## 2      2      1      1      7 boy     24      4.9      5
## 3      3      1      1      4 girl    24      5.3      6
## 4      4      1      1      3 girl    24      4.7      5
## 5      5      1      1      5 girl    24      6        6
## 6      6      1      1      4 boy     24      4.7      5
## 7      7      1      1      5 boy     24      5.9      5
## 8      8      1      1      4 boy     24      4.2      5
## 9      9      1      1      5 boy     24      5.2      5
## 10     10     1      1      5 boy     24      3.9      3
## # ... with 1,990 more rows
```

02:00

Fit a basic model

Fit each of the following models

- **popular** as the outcome, with a random intercept for **class**
- **popular** as the outcome, with **sex** included as a fixed effect and a random intercept for **class**
- **popular** as the outcome, with **sex** included as a fixed effect and a random intercept and slope for **class**

04:00

Models

```
library(lme4)  
m0 <- lmer(popular ~ 1 + (1|class), popular)  
m1 <- lmer(popular ~ sex + (1|class), popular)  
m2 <- lmer(popular ~ sex + (sex|class), popular)
```

Compare performance

Use whatever tests you'd like, and come up with the model you think fits the data best

```
library(performance)
compare_performance(m0, m1, m2) %>%
  print_md()
```

Table: Comparison of Model Performance Indices

Name	Model	AIC	BIC	R2 (cond.)	R2 (marg.)	ICC	RMSE	Sigma
m0	lmerMod	6336.51	6353.31	0.36	0.00	0.36	1.08	1.11
m1	lmerMod	5572.07	5594.48	0.53	0.26	0.37	0.89	0.91
m2	lmerMod	5571.05	5604.66	0.54	0.26			

04:00

Test of the Log-likelihood

```
test_likelihoodratio(m0, m1) %>%  
  print_md()
```

Name	Model	df	df_diff	Chi2	p
m0	lmerMod	3			
m1	lmerMod	4	1	766.44	1.07e-168

```
test_likelihoodratio(m1, m2) %>%  
  print_md()
```

Name	Model	df	df_diff	Chi2	p
m1	lmerMod	4			
m2	lmerMod	6	2	5.02	0.08

Pretty good evidence that **m1** displays the best fit

Coefficient plots

Package options

The **{parameters}** package (part of the **{easystats}** ecosystem) will get you where you want to be.

Alternatively, you could use the **{broom.mixed}** package (which is a spin-off of the **{broom}** package) which requires slightly less code.

I'll illustrate both

```
install.packages("broom.mixed")
```

{broom.mixed}

```
library(broom.mixed)
tidy(m0)
```

```
## # A tibble: 3 x 6
##   effect      group      term          estimate  std.error statistic
##   <chr>      <chr>      <chr>          <dbl>      <dbl>      <dbl>
## 1 fixed      <NA>      (Intercept)    5.077860    0.08739443  58.10278
## 2 ran_pars  class      sd__(Intercept) 0.8379169   NA          NA
## 3 ran_pars  Residual  sd__Observation 1.105348    NA          NA
```

Or get just the fixed effects

```
tidy(m0, effects = "fixed")
```

```
## # A tibble: 1 x 5
##   effect term          estimate  std.error statistic
##   <chr>  <chr>          <dbl>      <dbl>      <dbl>
## 1 fixed (Intercept)    5.077860  0.08739443  58.10278
```

Across models

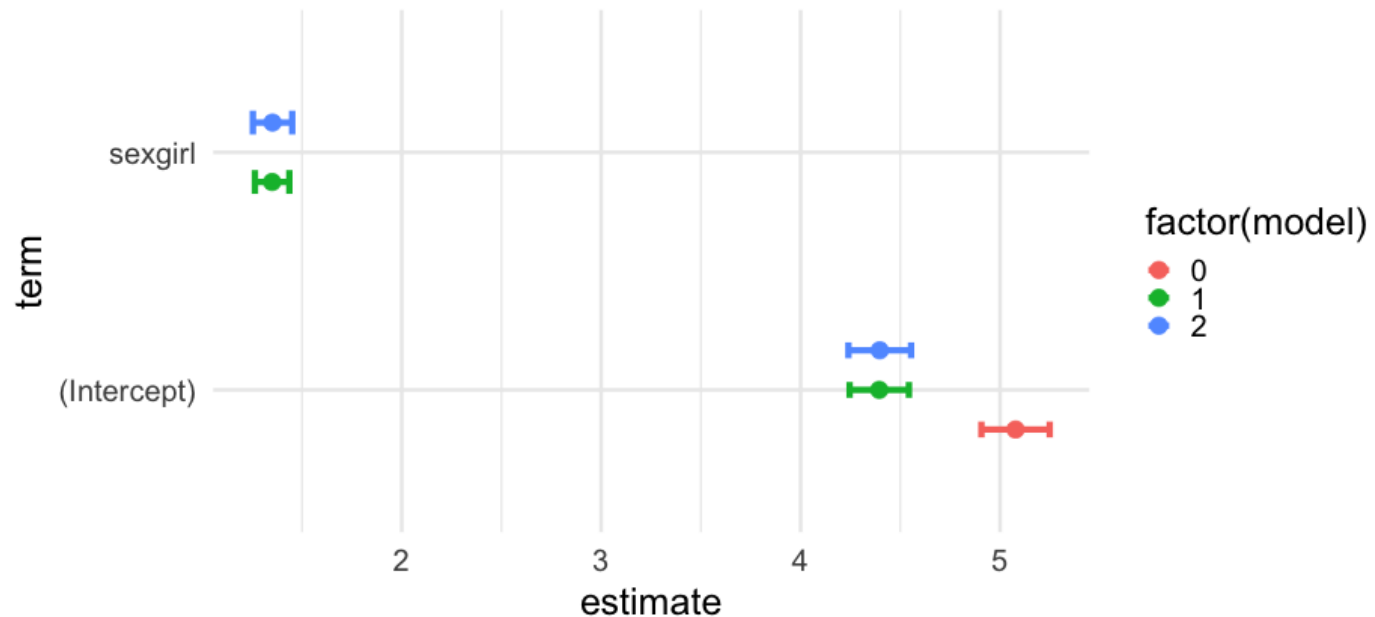
Let's tidy all three models, extracting just the fixed effects, and **adding in a 95% confidence interval**

```
models <- bind_rows(  
  tidy(m0, effects = "fixed", conf.int = TRUE),  
  tidy(m1, effects = "fixed", conf.int = TRUE),  
  tidy(m2, effects = "fixed", conf.int = TRUE),  
  .id = "model"  
) %>%  
  mutate(model = as.numeric(model) - 1)  
models
```

```
## # A tibble: 5 x 8  
##   model effect term          estimate std.error statistic conf.low  
##   <dbl> <chr>  <chr>          <dbl>      <dbl>      <dbl>    <dbl>  
## 1      0 fixed  (Intercept)  5.077860  0.08739443  58.10278  4.906570  
## 2      1 fixed  (Intercept)  4.394460  0.07586494  57.92478  4.245767  
## 3      1 fixed  sexgirl      1.350102  0.04403301  30.66113  1.263799  
## 4      2 fixed  (Intercept)  4.396820  0.08012978  54.87123  4.239768  
## 5      2 fixed  sexgirl      1.352175  0.05029920  26.88263  1.253590  
## # ... with 1 more variable: conf.high <dbl>
```

Plot

```
pd <- position_dodge(0.5)
ggplot(models, aes(estimate, term, color = factor(model))) +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high),
                position = pd,
                height = 0.2) +
  geom_point(position = pd)
```



Standardization

The nice thing about tidying the model output, is that the code on the previous slides *will always work* regardless of the model(s) you've fit.

Caveat

I don't actually think the prior plot is all that useful.

- Occasionally helpful to visualize differences between coefficients, but you'll usually want to omit the intercept
- Be careful about scales
- If you were to publish the prior plot, make it prettier and more accessible first

{parameters}

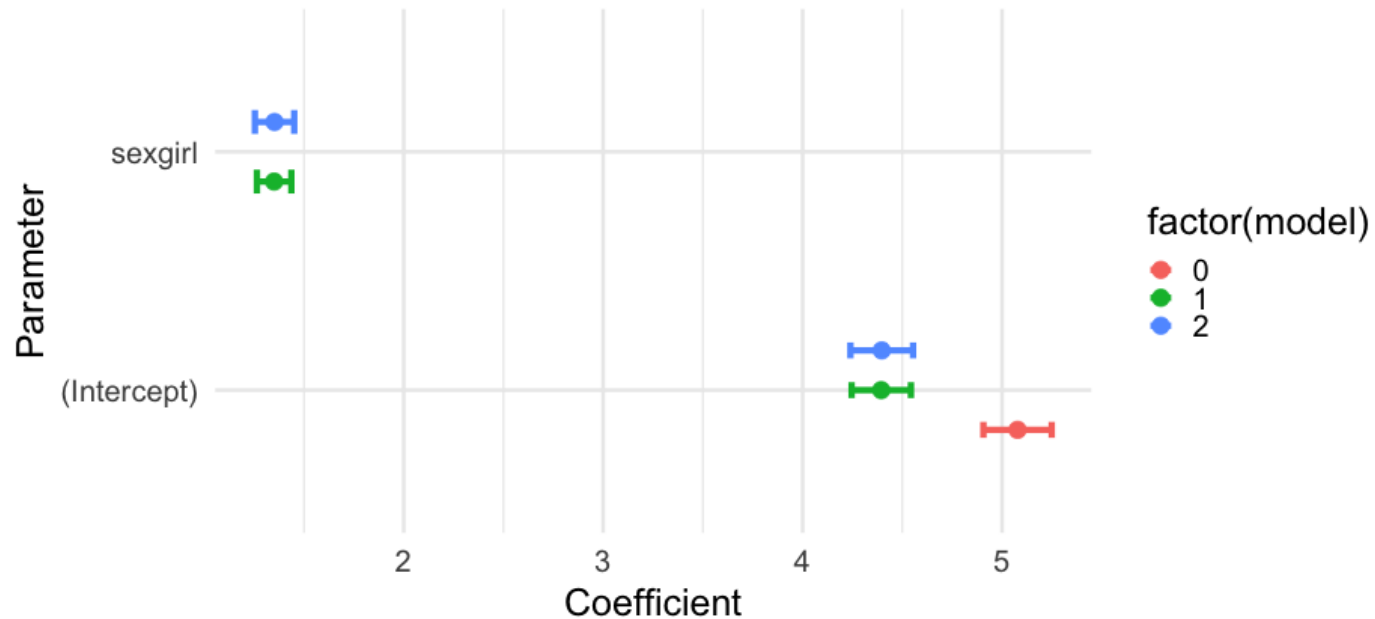
To get basically the same output from parameters:

```
library(parameters)
parameters(m0) %>%
  as_tibble()
```

```
## # A tibble: 1 x 10
##   Parameter      Coefficient      SE      CI    CI_low  CI_high
##   <chr>          <dbl>      <dbl> <dbl>    <dbl>    <dbl>
## 1 (Intercept)    5.077860 0.08739443 0.95 4.906570 5.249150
## # ... with 4 more variables: t <dbl>, df_error <int>, p <dbl>,
## #   Effects <chr>
```

```
models2 <- bind_rows(
  as_tibble(parameters(m0)),
  as_tibble(parameters(m1)),
  as_tibble(parameters(m2)),
  .id = "model"
) %>%
  mutate(model = as.numeric(model) - 1)
```

```
pd <- position_dodge(0.5)
ggplot(models2, aes(Coefficient, Parameter,
                    color = factor(model))) +
  geom_errorbarh(aes(xmin = CI_low, xmax = CI_high),
                position = pd,
                height = 0.2) +
  geom_point(position = pd)
```



Other parts of the model

From here on out, I'll just be using **{broom.mixed}** but either package should work, with minor tweaks.

Variance components

Notice that, by default, we don't have any uncertainty

```
tidy(m0)
```

```
## # A tibble: 3 x 6
##   effect    group    term          estimate std.error statistic
##   <chr>    <chr>    <chr>          <dbl>      <dbl>      <dbl>
## 1 fixed    <NA>    (Intercept)    5.077860  0.08739443  58.10278
## 2 ran_pars class    sd__(Intercept) 0.8379169 NA          NA
## 3 ran_pars Residual sd__Observation 1.105348  NA          NA
```

We can fix this by using bootstrap or profiled CIs

Bootstrap CIs

```
tidy(  
  m0,  
  effects = "ran_pars",  
  conf.int = TRUE,  
  conf.method = "boot"  
)
```

```
## Computing bootstrap confidence intervals ...
```

```
## # A tibble: 2 x 6
```

	effect	group	term	estimate	conf.low	conf.high
	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>
## 1	ran_pars	class	sd__(Intercept)	0.8379169	0.7223927	0.9570069
## 2	ran_pars	Residual	sd__Observation	1.105348	1.070679	1.137716

m2

Note this takes a bit of time, even though the model is pretty simple. Also these are standard deviations and a correlation, not variances/covariances

```
tidy(
  m2,
  effects = "ran_pars",
  conf.int = TRUE,
  conf.method = "boot"
)
```

```
## Computing bootstrap confidence intervals ...
```

```
##
```

```
## 37 message(s): boundary (singular) fit: see ?isSingular
```

```
## 10 warning(s): Model failed to converge with max|grad| = 0.00254628 (tol
```

```
## # A tibble: 4 x 6
```

	effect	group	term	estimate	conf.low
	<chr>	<chr>	<chr>	<dbl>	<dbl>
## 1	ran_pars	class	sd__(Intercept)	0.7389520	0.6309374
## 2	ran_pars	class	cor__(Intercept).sexgirl	-0.4442543	-1.0000000

Quick challenge

Can you make a dotplot with uncertainty for the variance components?

What about a plot showing both fixed effects and variance components?

06:00

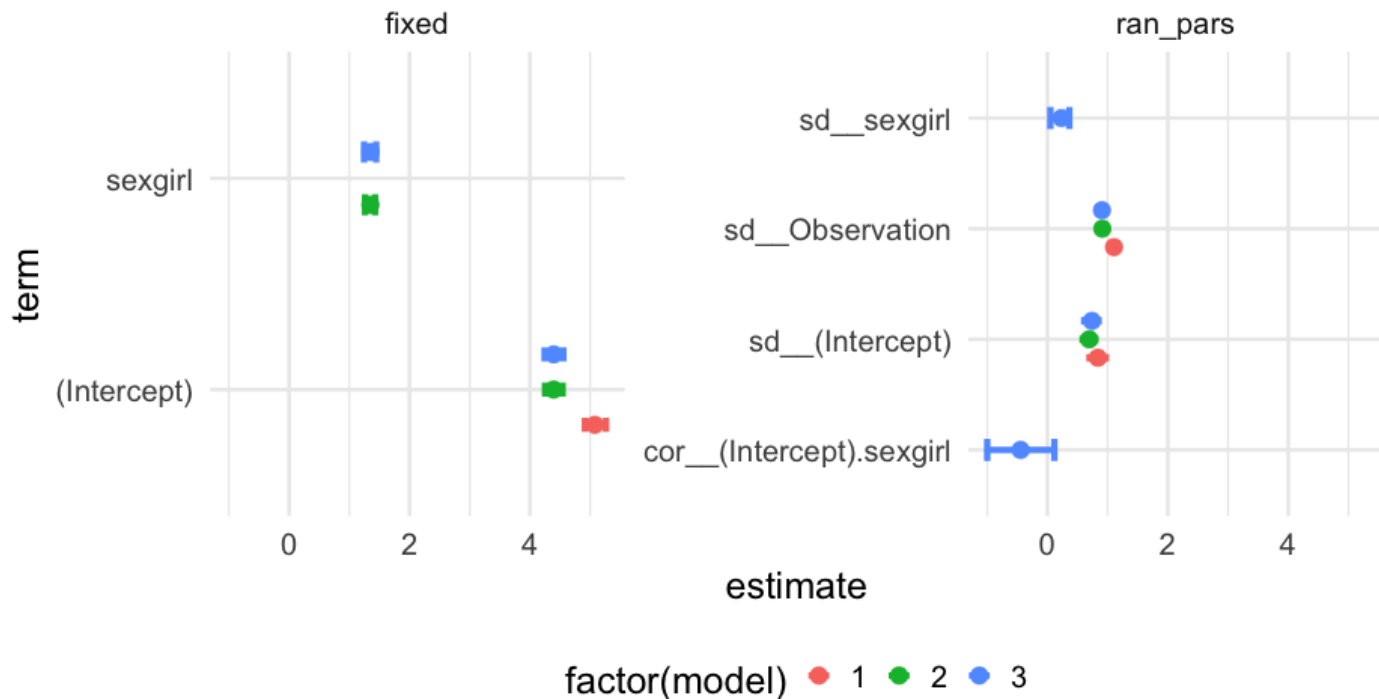
One approach

```
pull_model_results <- function(model) {  
  tidy(  
    model,  
    conf.int = TRUE,  
    conf.method = "boot"  
  )  
}  
full_models <- bind_rows(  
  pull_model_results(m0),  
  pull_model_results(m1),  
  pull_model_results(m2),  
  .id = "model"  
)
```

```
## Computing bootstrap confidence intervals ...  
##Computing bootstrap confidence intervals ...  
##Computing bootstrap confidence intervals ...  
##Computing bootstrap confidence intervals ...  
##Computing bootstrap confidence intervals ...
```

```
##  
## 30 message(s): boundary (singular) fit: see ?isSingular  
## 13 warning(s): Model failed to converge with max|grad| = 0.00215039 (tol
```

```
ggplot(full_models, aes(estimate, term, color = factor(model))) +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high),
    position = pd,
    height = 0.2) +
  geom_point(position = pd) +
  facet_wrap(~effect, scales = "free_y") +
  theme(legend.position = "bottom")
```



Random effects

Pop Quiz

What's the difference between the output from below and the output on the next slide?

```
tidy(m0, effects = "ran_vals")
```

```
## # A tibble: 100 x 6
##   effect    group level term          estimate std.error
##   <chr>    <chr> <chr> <chr>          <dbl>      <dbl>
## 1 ran_vals class 1      (Intercept) -0.002630828 0.2370649
## 2 ran_vals class 2      (Intercept) -0.8949875   0.2370649
## 3 ran_vals class 3      (Intercept) -0.3496155   0.2487845
## 4 ran_vals class 4      (Intercept)  0.3318175   0.2222273
## 5 ran_vals class 5      (Intercept)  0.1919485   0.2317938
## 6 ran_vals class 6      (Intercept) -0.6833977   0.2370649
## 7 ran_vals class 7      (Intercept) -0.8062842   0.2317938
## 8 ran_vals class 8      (Intercept) -1.019181    0.2370649
## 9 ran_vals class 9      (Intercept) -0.3844123   0.2370649
## 10 ran_vals class 10     (Intercept)  0.2226622   0.2178678
## # ... with 90 more rows
```

```
tidy(m0, effects = "ran_coefs")
```

```
## # A tibble: 100 x 5
##   effect      group level term      estimate
##   <chr>      <chr> <chr> <chr>      <dbl>
## 1 ran_coefs class 1      (Intercept) 5.075229
## 2 ran_coefs class 2      (Intercept) 4.182872
## 3 ran_coefs class 3      (Intercept) 4.728244
## 4 ran_coefs class 4      (Intercept) 5.409677
## 5 ran_coefs class 5      (Intercept) 5.269808
## 6 ran_coefs class 6      (Intercept) 4.394462
## 7 ran_coefs class 7      (Intercept) 4.271575
## 8 ran_coefs class 8      (Intercept) 4.058678
## 9 ran_coefs class 9      (Intercept) 4.693447
## 10 ran_coefs class 10     (Intercept) 5.300522
## # ... with 90 more rows
```


Answer

The output from `ran_vals` provides the estimate from $\alpha_j \sim N(0, \sigma)$.

The output from `ran_coefs` provides the class-level predictions, i.e., in this case, the intercept + the estimated `ran_vals`.

Example

```
tidy(m0, effects = "ran_vals")$estimate[1:5] + fixef(m0)[1]
```

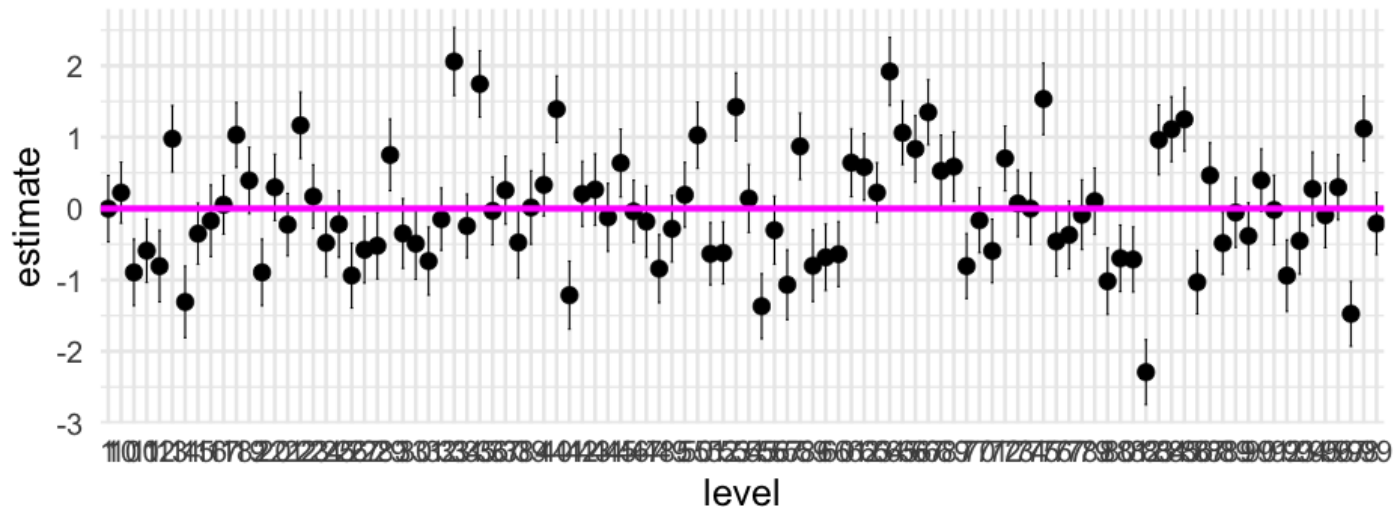
```
## [1] 5.075229 4.182872 4.728244 5.409677 5.269808
```

```
tidy(m0, effects = "ran_coefs")$estimate[1:5]
```

```
## [1] 5.075229 4.182872 4.728244 5.409677 5.269808
```

Let's plot the `ran_vals`

```
m0_ranvals <- tidy(m0, effects = "ran_vals", conf.int = TRUE)
ggplot(m0_ranvals, aes(level, estimate)) +
  geom_errorbar(aes(ymin = conf.low, ymax = conf.high),
               width = 0.2) +
  geom_point() +
  geom_hline(yintercept = 0, size = 2, color = "magenta")
```

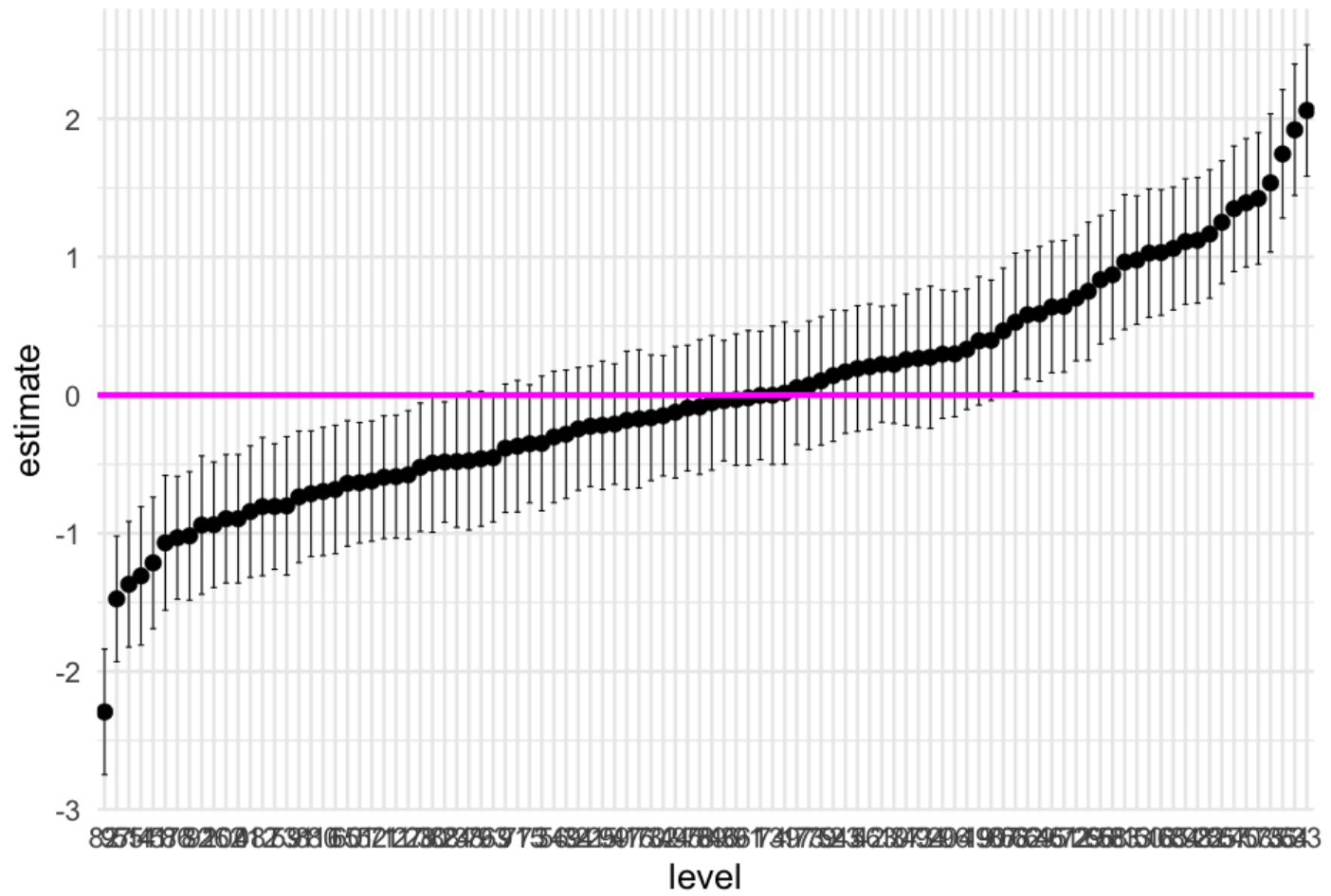


Not super helpful

Try again

Let's reorder the **level** according to the estimate

```
m0_ranvals %>%  
  mutate(level = reorder(factor(level), estimate)) %>%  
  ggplot(aes(level, estimate)) +  
  geom_errorbar(aes(ymin = conf.low, ymax = conf.high),  
                width = 0.5) +  
  geom_point() +  
  geom_hline(yintercept = 0, size = 2, color = "magenta")
```



Wrapping up coef plots

- Coefficient plots are generally fairly easy to produce, but often not the most informative
- Random effects plots are probs more informative than the fixed effects/variance components plots
- You can make either a lot more fancy, accessible, etc., and probably should if you're going to use it for publication.

Making
predictions
"by hand"

Reminder

Our raw data looks like this

popular

```
## # A tibble: 2,000 x 7
##   pupil class extrav sex    texp popular popteach
##   <dbl> <dbl>   <dbl> <chr> <dbl>   <dbl>   <dbl>
## 1     1     1     1     5 girl    24     6.3     6
## 2     2     2     1     7 boy     24     4.9     5
## 3     3     3     1     4 girl    24     5.3     6
## 4     4     4     1     3 girl    24     4.7     5
## 5     5     5     1     5 girl    24     6       6
## 6     6     6     1     4 boy     24     4.7     5
## 7     7     7     1     5 boy     24     5.9     5
## 8     8     8     1     4 boy     24     4.2     5
## 9     9     9     1     5 boy     24     5.2     5
## 10    10    10     1     5 boy     24     3.9     3
## # ... with 1,990 more rows
```

Thinking back

to standard regression

let's say we fit a model like this

```
m <- lm(popular ~ 1 + sex, data = popular)
```

Our estimated model is

$$\widehat{\text{popular}} = 4.28 + 1.57(\text{sex}_{\text{girl}})$$

Making a prediction

What would our model on the prior slide predict for the first student?

```
pupil1 <- popular[1, ]  
pupil1
```

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

```
coef(m)[1] + # intercept  
  coef(m)[2] * (pupil1$sex == "girl")
```

```
## (Intercept)  
##      5.853314
```

```
predict(m)[1]
```

```
##      1  
## 5.853314
```

What about this model?

If we use the predict function for `m2`, we get

```
predict(m2)[1]
```

```
##           1  
## 5.732849
```

How does the model come up with this prediction?

Use the next few minutes to see if you can write code to replicate it "by hand" as we did with the standard regression model

03:00

Thinking through the model

- We have classroom random effects for the intercept and slope
- This means the prediction for an individual is made up of:
 - Overall intercept +
 - Overall slope +
 - Classroom intercept offset (diff of classroom intercept from overall intercept) +
 - Classroom slope offset (diff of classroom slope from overall slope)

Do it!

First look back at the data

```
popular[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
```

Next extract the `ran_vals` for the corresponding class

```
m2_ranvals <- tidy(m2, effects = "ran_vals")
class1_ranvals <- m2_ranvals %>%
  filter(group == "class" & level == 1)
class1_ranvals
```

```
## # A tibble: 2 x 6
##   effect    group level term          estimate std.error
##   <chr>    <chr> <chr> <chr>          <dbl>      <dbl>
## 1 ran_vals class 1      (Intercept)  0.02657986 0.2240683
## 2 ran_vals class 1      sexgirl      -0.04272575 0.1956483
```

Make prediction

```
fixef(m2)
```

```
## (Intercept)      sexgirl  
##      4.396820      1.352175
```

```
fixef(m2)[1] + fixef(m2)[2]*(popular[1, ]$sex == "girl") +  
  class1_ranvals$estimate[1] + class1_ranvals$estimate[2]
```

```
## (Intercept)  
##      5.732849
```

Confirm

```
predict(m2)[1]
```

```
##      1  
## 5.732849
```

Challenge

- Without using the `predict()` function, calculate the predicted score for a boy in classroom **10** from **m2**

```
class10_ranvals <- m2_ranvals %>%  
  filter(group == "class" & level == 10)  
  
fixef(m2)[1] + class10_ranvals$estimate[1]
```

```
## (Intercept)  
##      4.675822
```

05:00

Confirm with `predict()`

```
test <- popular %>%  
  mutate(pred = predict(m2)) %>%  
  filter(class == 10 & sex == "boy")  
test
```

```
## # A tibble: 12 x 8  
##   pupil class extrav sex    texp popular popteach    pred  
##   <dbl> <dbl>   <dbl> <chr> <dbl>   <dbl>    <dbl>    <dbl>  
## 1     1     10         5 boy    21  5.4         5 4.675822  
## 2     3     10         5 boy    21  3.4         3 4.675822  
## 3     5     10         5 boy    21 5.100000    7 4.675822  
## 4     7     10         5 boy    21  5.4         4 4.675822  
## 5     8     10         5 boy    21  4.9         4 4.675822  
## 6    11     10         6 boy    21  4.4         6 4.675822  
## 7    12     10         6 boy    21  4.9         5 4.675822  
## 8    14     10         6 boy    21  4.8         3 4.675822  
## 9    15     10         3 boy    21  3.6         3 4.675822  
## 10   16     10         5 boy    21  5         6 4.675822  
## 11   17     10         3 boy    21  5.5         5 4.675822  
## 12   18     10         6 boy    21  5         4 4.675822
```


More on the predict function

- Once you have the model parameters, you can predict for any values of those parameters

Let's fit a slightly more complicated model, using a different longitudinal file than what you used (or are using) in the homework

```
library(equatiomatic)
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
```

Model

You try first

- Fit a model with **wave** and **treatment** as predictors of students' **score**. Allow the intercept and the relation between **wave** and **score** to vary by student.

```
m <- lmer(score ~ wave + treatment + (wave|sid),  
          data = sim_longitudinal)
```

02:00

Plot predictions

Let's first just limit our data to the first three students.

```
first_three <- sim_longitudinal %>%  
  ungroup() %>%  
  filter(sid %in% 1:3)
```

Now try creating a new column in the data with the model predictions for these students. Specify `newdata = first_three` to only make the predictions for those cases.

02:00

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

```
## # A tibble: 30 x 9  
##       sid school district group treatment prop_low wave score  
##   <int>  <int>    <int> <chr>   <fct>      <dbl> <dbl>  <dbl>  
## 1      1      1        1    1 medium 1      0.1428571 0 102.2686  
## 2      1      1        1    1 medium 1      0.1428571 1 102.0135  
## 3      1      1        1    1 medium 1      0.1428571 2 102.5216  
## 4      1      1        1    1 medium 1      0.1428571 3 102.2792  
## 5      1      1        1    1 medium 1      0.1428571 4 102.2834  
## 6      1      1        1    1 medium 1      0.1428571 5 102.7963  
## 7      1      1        1    1 medium 1      0.1428571 6 103.0441  
## 8      1      1        1    1 medium 1      0.1428571 7 102.8868  
## 9      1      1        1    1 medium 1      0.1428571 8 103.9101  
## 10     1      1        1    1 medium 1      0.1428571 9 103.2392  
## # ... with 20 more rows, and 1 more variable: model_pred <dbl>
```

Plot

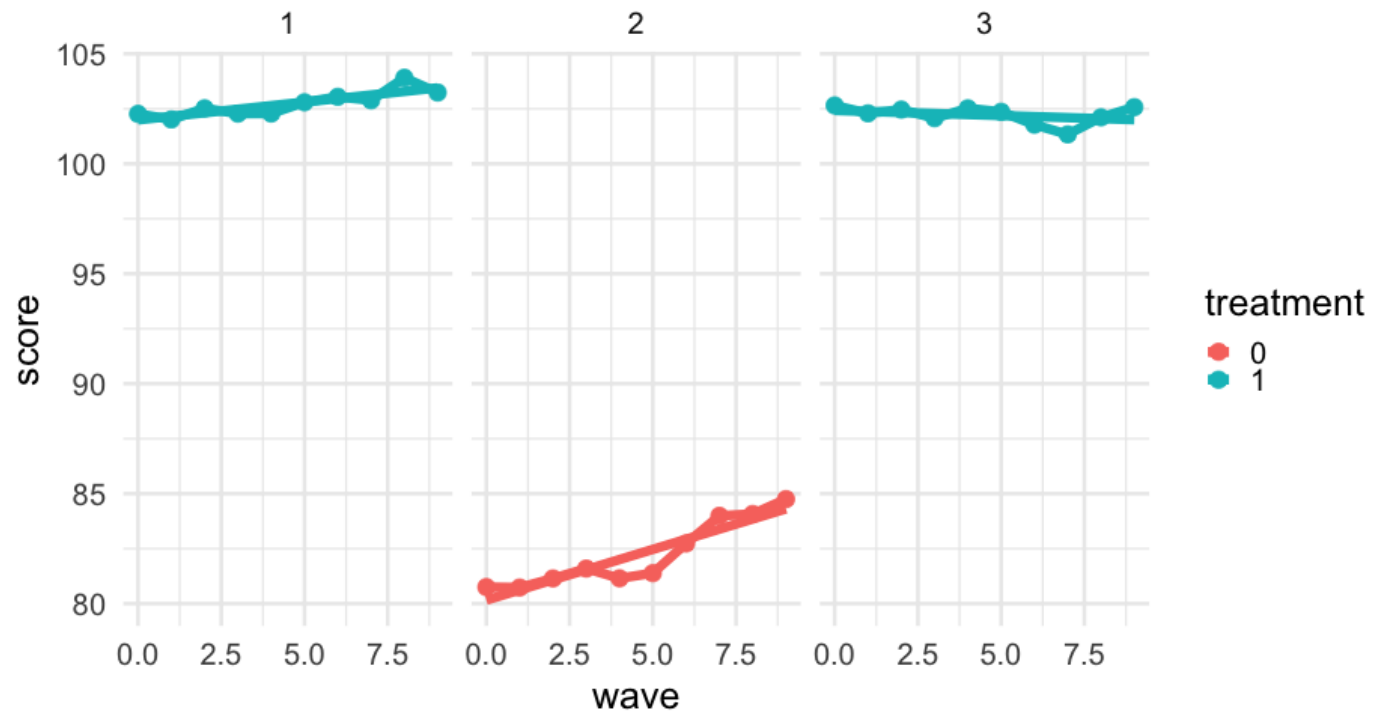
Try creating a plot with a different **facet** for each **sid** showing the observed trend (relation between **wave** and **score**) as compared to the model prediction. Color the line by whether or not the student was in the treatment group or not.

03:00

```

first_three %>%
  mutate(model_pred = predict(m, newdata = first_three)) %>%
  ggplot(aes(wave, score, color = treatment)) +
  geom_point() +
  geom_line() +
  geom_line(aes(y = model_pred)) +
  facet_wrap(~sid)

```



Predictions outside our data

Student 2 has a considerably lower intercept. What would we predict the trend would look like if they had been in the treatment group?

Try to make this prediction on your own for all time points

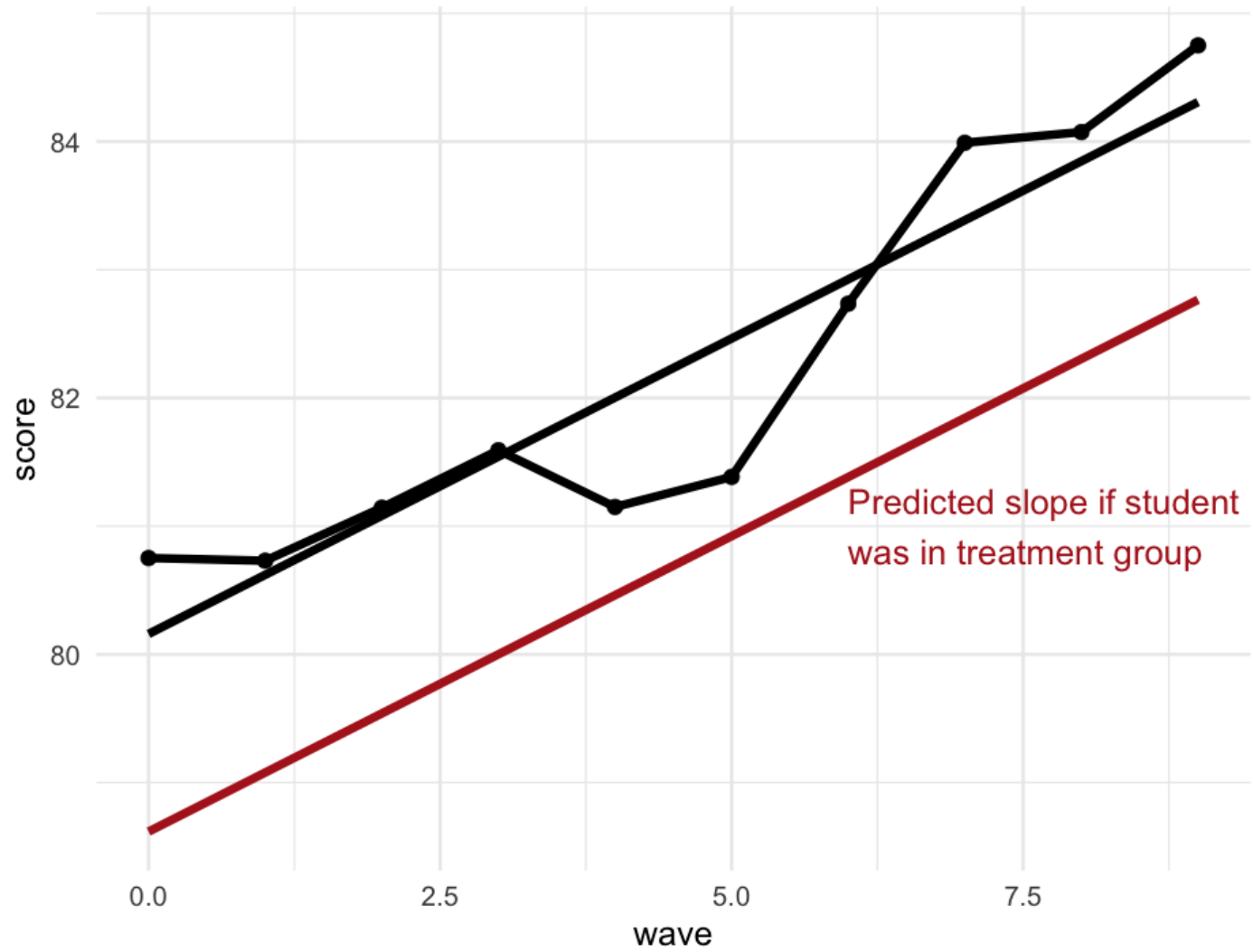
02:00

```
stu2_trt <- data.frame(  
  sid = 2,  
  wave = 0:9,  
  treatment = factor("1", levels = c(0, 1))  
)  
  
predict(m, newdata = stu2_trt)
```

```
##           1           2           3           4           5           6           7  
## 78.61702 79.07803 79.53903 80.00004 80.46104 80.92205 81.38305  
##           8           9          10  
## 81.84406 82.30506 82.76607
```


Compare

```
sim_longitudinal %>%
  filter(sid == 2) %>%
  mutate(model_pred = predict(m, newdata = .),
         trt_pred = predict(m, newdata = stu2_trt)) %>%
  ggplot(aes(wave, score)) +
  geom_point() +
  geom_line() +
  geom_line(aes(y = model_pred)) +
  geom_line(aes(y = trt_pred),
            color = "firebrick") +
  annotate(
    "text",
    x = 6,
    y = 81,
    hjust = 0,
    color = "firebrick",
    label = "Predicted slope if student\nwas in treatment group"
  )
```



Wait... negative?

Yes...

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

```
## lmer(formula = score ~ wave + treatment + (wave | sid), data = sim_longi
##           coef.est coef.se
## (Intercept) 97.95      1.38
## wave         0.17      0.03
## treatment1  -1.54      1.92
##
## Error terms:
##   Groups   Name                Std.Dev.  Corr
##   sid      (Intercept)  9.74
##           wave         0.29      -0.16
## Residual                    0.44
## ---
## number of obs: 1000, groups: sid, 100
## AIC = 2407.7, DIC = 2393.1
## deviance = 2393.4
```

Note – I'm just using an alternative function here to get it to fit on the slides easier

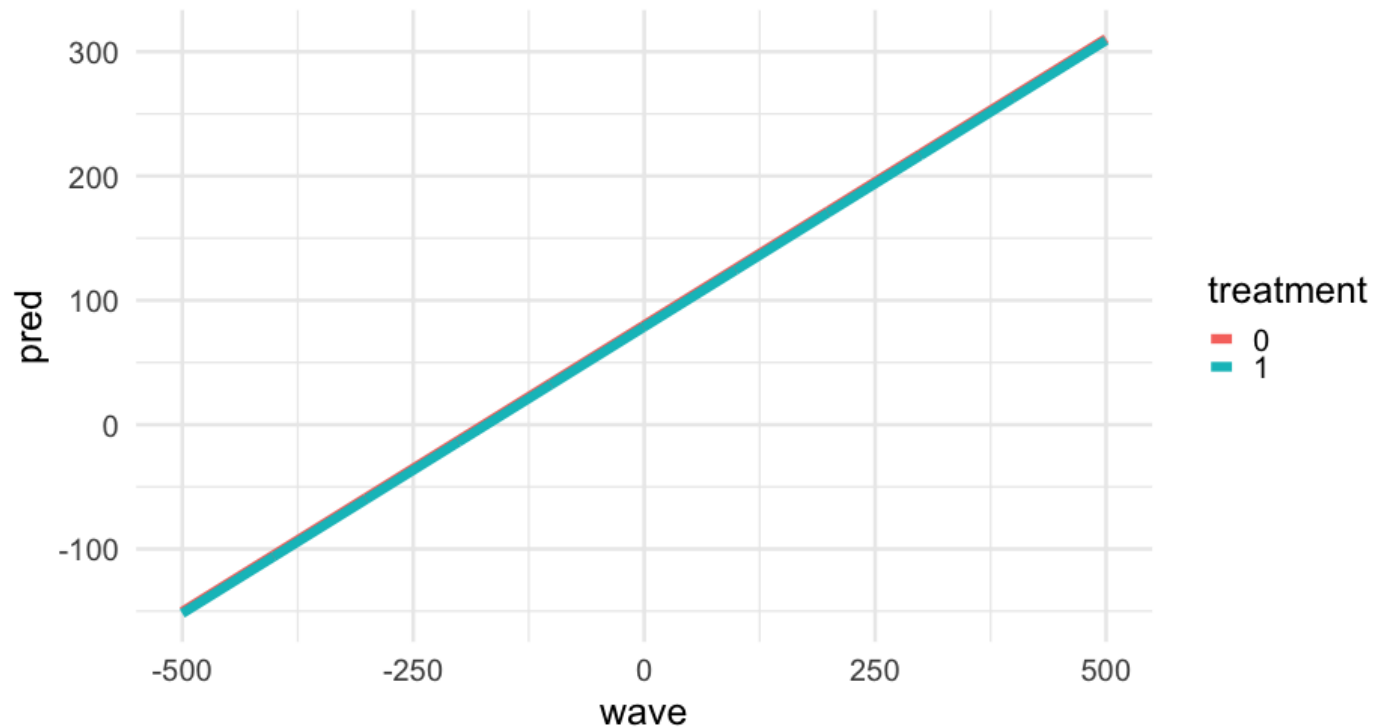
Other projections

We have a *linear* model. This means we can just extend the line to ∞ if we wanted to



```
newdata_stu2 <- data.frame(  
  sid = 2,  
  wave = rep(-500:500, 2),  
  treatment = factor(rep(c(0, 1), each = length(-500:500)))  
)
```

```
newdata_stu2 %>%  
  mutate(pred = predict(m, newdata = newdata_stu2)) %>%  
  ggplot(aes(wave, pred)) +  
  geom_line(aes(color = treatment))
```



Uncertainty

What to predict?

Let's say we want to predict what time points 10, 11, and 12 would look like for the first three students.

First, create the prediction data frame

```
pred_frame <- data.frame(  
  sid = rep(1:3, each = 13),  
  wave = rep(0:12),  
  treatment = factor(rep(c(1, 0, 1), each = 13))  
)  
  
head(pred_frame)
```

##	sid	wave	treatment
## 1	1	0	1
## 2	1	1	1
## 3	1	2	1
## 4	1	3	1
## 5	1	4	1
## 6	1	5	1

merTools

Next, load the **merTools** package

```
library(merTools)
```

Create a prediction interval with `predictInterval()`,
using simulation to obtain the prediction interval

```
m_pred_interval <- predictInterval(  
  m,  
  newdata = pred_frame,  
  level = 0.95  
)
```


m_pred_interval

##		fit	upr	lwr
## 1	101.95689	104.70036	99.03111	
## 2	102.17041	104.96307	99.29545	
## 3	102.31672	105.01382	99.59005	
## 4	102.42744	105.31661	99.72277	
## 5	102.61729	105.47049	99.72868	
## 6	102.64753	105.47524	100.06621	
## 7	102.90062	105.87357	100.09517	
## 8	103.03138	105.90216	100.36947	
## 9	103.17964	106.06368	100.51516	
## 10	103.39789	106.23082	100.64110	
## 11	103.52691	106.48261	100.79241	
## 12	103.72071	106.62076	101.01362	
## 13	103.87428	106.73002	101.04166	
## 14	80.12363	82.93524	77.33830	
## 15	80.54194	83.40248	77.85161	
## 16	81.03919	83.85368	78.29290	
## 17	81.51923	84.29643	78.68700	
## 18	81.96064	84.76050	79.31539	
## 19	82.39628	85.15011	79.78035	
## 20	82.87241	85.60984	80.14835	
## 21	83.35440	86.13067	80.62113	
## 22	83.84665	86.64580	81.07926	
## 23	84.26309	87.14835	81.40556	
## 24	84.77568	87.72724	81.84552	
## 25	85.19993	88.08393	82.47386	
## 26	85.62036	88.65231	82.75436	
## 27	102.35278	105.34362	99.55996	

Binding data together

Let's add these predictions back to our prediction data frame, then plot them

```
bind_cols(pred_frame, m_pred_interval)
```

##	sid	wave	treatment	fit	upr	lwr
## 1	1	0	1	101.95689	104.70036	99.03111
## 2	1	1	1	102.17041	104.96307	99.29545
## 3	1	2	1	102.31672	105.01382	99.59005
## 4	1	3	1	102.42744	105.31661	99.72277
## 5	1	4	1	102.61729	105.47049	99.72868
## 6	1	5	1	102.64753	105.47524	100.06621
## 7	1	6	1	102.90062	105.87357	100.09517
## 8	1	7	1	103.03138	105.90216	100.36947
## 9	1	8	1	103.17964	106.06368	100.51516
## 10	1	9	1	103.39789	106.23082	100.64110
## 11	1	10	1	103.52691	106.48261	100.79241
## 12	1	11	1	103.72071	106.62076	101.01362
## 13	1	12	1	103.87428	106.73002	101.04166
## 14	2	0	0	80.12363	82.93524	77.33830
## 15	2	1	0	80.54194	83.40248	77.85161
## 16	2	2	0	81.03919	83.85368	78.29290
## 17	2	3	0	81.51923	84.29643	78.68700
## 18	2	4	0	81.96064	84.76050	79.31539

Plot

```
bind_cols(pred_frame, m_pred_interval) %>%  
  ggplot(aes(wave, fit)) +  
  geom_ribbon(aes(ymin = lwr, ymax = upr),  
             alpha = 0.4) +  
  geom_line(color = "magenta") +  
  facet_wrap(~sid)
```

How?

What's really going on here?

See [here](#) for a full description, but basically:

1. Creates a simulated (with `n.sim` samples) distribution for each model parameter
2. Computes a distribution of predictions
3. Returns the specifics of the prediction distribution, as requested (e.g., `fit` is the mean or median, and `upr` and `lwr` are the corresponding quantiles for the uncertainty range)

Disclaimer

According to the **{lme4}** authors

There is no option for computing standard errors of predictions because it is difficult to define an efficient method that incorporates uncertainty in the variance parameters; we recommend `lme4::bootMer()` for this task.

The `predictInterval()` function is an approximation, while `bootMer()` is the "gold standard" (it just takes a long time)

Bootstrapping

Write a function to compute the predictions for each bootstrap resample

```
pred_fun <- function(fit) {  
  predict(fit, newdata = pred_frame)  
}
```

Notice we're using the same prediction data frame

Now create BS Estimates

Note this takes a few seconds, and for bigger models may take a *long* time

```
b <- bootMer(  
  m,  
  nsim = 1000,  
  FUN = pred_fun,  
  use.u = TRUE,  
  seed = 42  
)
```

The predictions are stored in a matrix **t**

```
dim(b$t)
```

```
## [1] 1000 39
```

Each row of the matrix is the prediction for the given bootstrap estimate

Lots of options

There are lots of things you could do with this now. I'll move it to a data frame first

```
bd <- as.data.frame(t(b$t)) %>%  
  mutate(sid = rep(1:3, each = 13),  
         wave = rep(0:12, 3)) %>%  
  pivot_longer(  
    starts_with("V"),  
    names_to = "bootstrap_sample",  
    names_prefix = "V",  
    names_transform = list(bootstrap_sample = as.numeric),  
    values_to = "score"  
  ) %>%  
  arrange(sid, bootstrap_sample, wave)
```


bd

```
## # A tibble: 39,000 x 4
##       sid  wave bootstrap_sample    score
##   <int> <int>          <dbl>    <dbl>
## 1     1     1         0          1 102.1749
## 2     2     1         1          1 102.3497
## 3     3     1         2          1 102.5245
## 4     4     1         3          1 102.6992
## 5     5     1         4          1 102.8740
## 6     6     1         5          1 103.0488
## 7     7     1         6          1 103.2235
## 8     8     1         7          1 103.3983
## 9     9     1         8          1 103.5731
## 10    10     1         9          1 103.7478
## # ... with 38,990 more rows
```

Plot

```
ggplot(bd, aes(wave, score)) +  
  geom_line(aes(group = bootstrap_sample),  
            size = 0.1,  
            alpha = 0.5,  
            color = "cornflowerblue") +  
  facet_wrap(~sid)
```

Prefer ribbons?

```
bd_ribbons <- bd %>%  
  group_by(sid, wave) %>%  
  summarize(quantile = quantile(score, c(0.025, 0.975)),  
            group = c("lower", "upper")) %>%  
  pivot_wider(names_from = "group", values_from = "quantile")  
bd_ribbons
```

```
## # A tibble: 39 x 4  
## # Groups:   sid, wave [39]  
##       sid wave lower upper  
##   <int> <int> <dbl> <dbl>  
## 1     1     0 101.4553 102.4854  
## 2     1     1 101.7114 102.5782  
## 3     1     2 101.9408 102.6748  
## 4     1     3 102.1633 102.7898  
## 5     1     4 102.3576 102.9110  
## 6     1     5 102.5236 103.0809  
## 7     1     6 102.6428 103.2611  
## 8     1     7 102.7468 103.4728  
## 9     1     8 102.8555 103.6996  
## 10    1     9 102.9428 103.9153  
## # ... with 29 more rows
```

Join with real data

```
bd_ribbons <- left_join(first_three, bd_ribbons) %>%  
  mutate(pred = predict(m, newdata = first_three))
```

```
## Joining, by = c("sid", "wave")
```

Plot again

```
ggplot(bd_ribbons, aes(wave, score)) +  
  geom_ribbon(aes(ymin = lower, ymax = upper),  
             alpha = 0.5) +  
  geom_line(aes(y = pred), size = 1, color = "magenta") +  
  geom_point() +  
  facet_wrap(~sid)
```

Important

There are different types of bootstrap resampling you can choose from

- Do you want to randomly sample from the random effects also? `use.u = FALSE`
- Do you want to assume the random effect estimates are true, and just sample the rest? `use.u = TRUE`

Honestly – this is a bit confusing to me, and the results from `use.u = FALSE` didn't make much sense to me. But see [here](#) and [here](#) for more information

More
complications

Interactions

Let's create an interaction between **treatment** and **wave**

Conceptually: what would this mean?

Let's also add in a school-level random effect for the intercept

Interactions

Specified just like with `lm()`. Each of the below are equivalent

```
wave + treatment + wave:treatment
```

```
wave * treatment
```

where the latter just expands out to the former.

Adding additional levels

There are a few ways to do this:

- Assume your IDs are all unique
 - implicit nesting
- Don't worry and the IDs, and specify the nesting through the formula
 - Will result in equivalent estimates if the IDs are unique

See [here](#) for more examples

Implicit nesting

```
m1a <- lmer(score ~ wave*treatment +  
            (wave|sid) + (1|school),  
            data = sim_longitudinal)  
arm::display(m1a)
```

```
## lmer(formula = score ~ wave * treatment + (wave | sid) + (1 |  
##       school), data = sim_longitudinal)  
##               coef.est coef.se  
## (Intercept)      96.80      1.57  
## wave           0.40      0.03  
## treatment1      0.61      1.88  
## wave:treatment1 -0.45      0.04  
##  
## Error terms:  
##   Groups   Name          Std.Dev. Corr  
##   sid      (Intercept)  9.16  
##           wave         0.19      -0.13  
##   school   (Intercept)  3.27  
## Residual              0.44  
## ---  
## number of obs: 1000, groups: sid, 100; school, 15  
## AIC = 2330, DIC = 2301.2  
## deviance = 2306.6
```

Explicit nesting

```
m1b <- lmer(score ~ wave*treatment +  
            (wave|sid:school) + (1|school) ,  
            data = sim_longitudinal)  
arm::display(m1b)
```

```
## lmer(formula = score ~ wave * treatment + (wave | sid:school) +  
##       (1 | school), data = sim_longitudinal)  
##               coef.est coef.se  
## (Intercept)      96.80      1.57  
## wave              0.40      0.03  
## treatment1       0.61      1.88  
## wave:treatment1 -0.45      0.04  
##  
## Error terms:  
##   Groups      Name      Std.Dev.  Corr  
##   sid:school (Intercept)  9.16  
##              wave        0.19    -0.13  
##   school     (Intercept)  3.27  
## Residual                0.44  
## ---  
## number of obs: 1000, groups: sid:school, 100; school, 15  
## AIC = 2330, DIC = 2301.2  
## deviance = 2306.6
```

Predictions "by hand"

This is now a three-level model. How does it differ from two-level models in terms of model predictions?

Let's make a prediction for the first student at the fourth time point:

```
sim_longitudinal[4, ]
```

```
## # A tibble: 1 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      1 medium 1      0.1428571 3 102.2792
```

The pieces

```
fixed <- fixef(m1a)
ranefs <- ranef(m1a)
fixed
```

```
##      (Intercept)          wave      treatment1 wave:treatment1
##      96.7973387      0.4010222      0.6080336      -0.4459053
```

```
# Pull just the ranefs for sid 1 and school 1
sid_ranefs <- ranefs$sid[1, ]
sid_ranefs
```

```
##      (Intercept)          wave
## 1      1.85279 0.1936603
```

```
sch_ranefs <- ranefs$school[1, ]
sch_ranefs
```

```
## [1] 2.795928
```

Putting it together

```
(fixed[1] + sid_ranefs[1] + sch_ranefs) + # intercept  
((fixed[2] + sid_ranefs[2]) * 3) + # fourth timepoint  
(fixed[3] * 1) + # treatment effect  
(fixed[4] * 3) # treatment by wave effect
```

```
##      (Intercept)  
## 1      102.5004
```

Confirm

```
predict(m1a, newdata = sim_longitudinal[4, ])
```

```
##           1  
## 102.5004
```


Predictions

Let's randomly sample 5 students in the first four school and display the model predictions for those students.

There are many ways to create the sample, here's one:

```
samp <- sim_longitudinal %>%  
  filter(school %in% 1:4) %>%  
  group_by(school, sid) %>%  
  nest()  
samp
```

```
## # A tibble: 28 x 3  
## # Groups:   sid, school [28]  
##       sid school data  
##   <int>  <int> <list>  
## 1      1      1 1 <tibble[,6] [10 x 6]>  
## 2     33     3 3 <tibble[,6] [10 x 6]>  
## 3     34     4 4 <tibble[,6] [10 x 6]>  
## 4     46     1 1 <tibble[,6] [10 x 6]>  
## 5     61     1 1 <tibble[,6] [10 x 6]>  
## 6     77     2 2 <tibble[,6] [10 x 6]>  
## 7     78     3 3 <tibble[,6] [10 x 6]>
```

Select 5 rows for each school

```
set.seed(42)
samp %>%
  group_by(school) %>%
  sample_n(5)
```

```
## # A tibble: 20 x 3
## # Groups:   school [4]
##       sid school data
##   <int>   <int> <list>
## 1      1      1 1 <tibble[,6] [10 x 6]>
## 2     76      1 1 <tibble[,6] [10 x 6]>
## 3     31      1 1 <tibble[,6] [10 x 6]>
## 4     16      1 1 <tibble[,6] [10 x 6]>
## 5     46      1 1 <tibble[,6] [10 x 6]>
## 6     62      2 2 <tibble[,6] [10 x 6]>
## 7      2      2 2 <tibble[,6] [10 x 6]>
## 8     92      2 2 <tibble[,6] [10 x 6]>
## 9     77      2 2 <tibble[,6] [10 x 6]>
## 10    47      2 2 <tibble[,6] [10 x 6]>
## 11    63      3 3 <tibble[,6] [10 x 6]>
## 12    18      3 3 <tibble[,6] [10 x 6]>
## 13    33      3 3 <tibble[,6] [10 x 6]>
```

unnest()

```
set.seed(42)
samp <- samp %>%
  group_by(school) %>%
  sample_n(5) %>%
  unnest(data) %>%
  ungroup()
samp
```

```
## # A tibble: 200 x 8
##   sid school district group treatment prop_low wave score
##   <int>  <int>    <int> <chr>   <fct>    <dbl> <dbl>  <dbl>
## 1      1      1      1     1 medium 1      0.1428571 0 102.2686
## 2      1      1      1     1 medium 1      0.1428571 1 102.0135
## 3      1      1      1     1 medium 1      0.1428571 2 102.5216
## 4      1      1      1     1 medium 1      0.1428571 3 102.2792
## 5      1      1      1     1 medium 1      0.1428571 4 102.2834
## 6      1      1      1     1 medium 1      0.1428571 5 102.7963
## 7      1      1      1     1 medium 1      0.1428571 6 103.0441
## 8      1      1      1     1 medium 1      0.1428571 7 102.8868
## 9      1      1      1     1 medium 1      0.1428571 8 103.9101
## 10     1      1      1     1 medium 1      0.1428571 9 103.2392
## # ... with 190 more rows
```

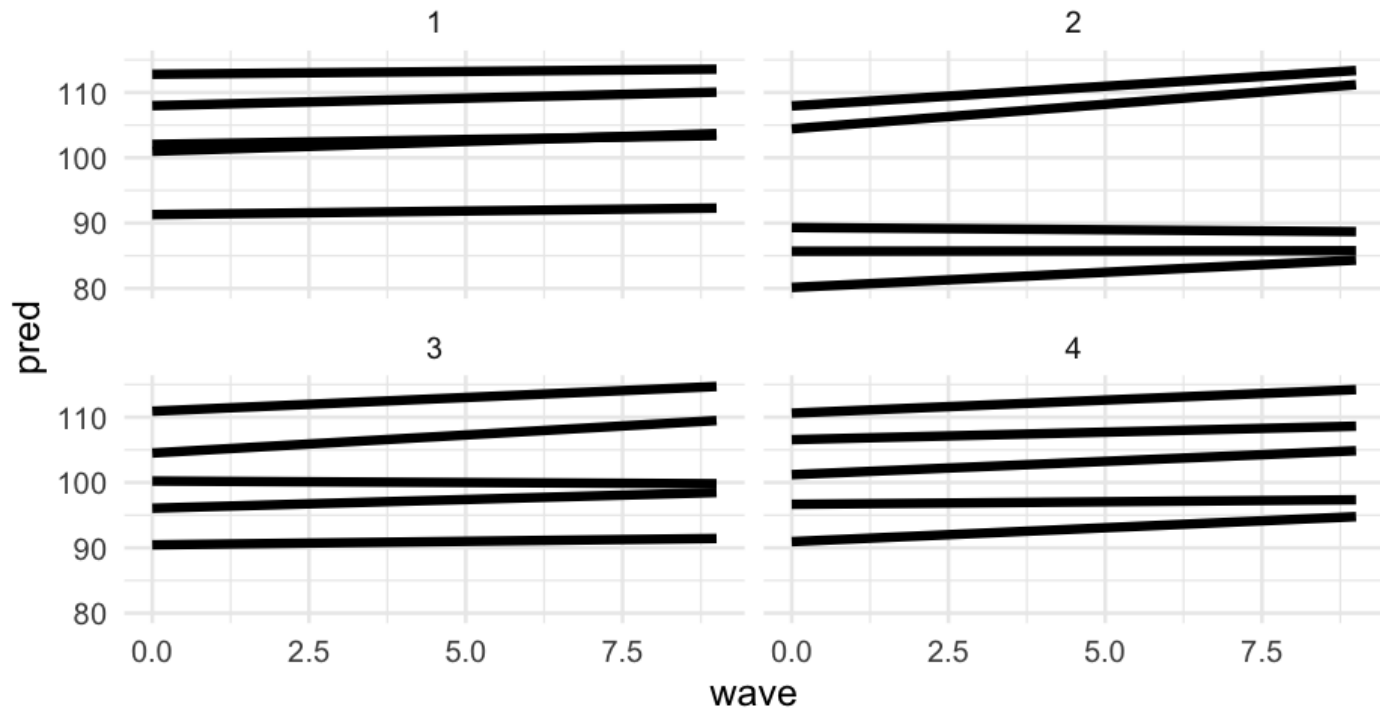
Make prediction

```
samp %>%  
  mutate(pred = predict(m1a, newdata = samp))
```

```
## # A tibble: 200 x 9  
##       sid school district group treatment prop_low wave score  
##   <int>  <int>    <int> <chr>   <fct>      <dbl> <dbl>  <dbl>  
## 1      1      1        1    1 medium    1      0.1428571 0 102.2686  
## 2      1      1        1    1 medium    1      0.1428571 1 102.0135  
## 3      1      1        1    1 medium    1      0.1428571 2 102.5216  
## 4      1      1        1    1 medium    1      0.1428571 3 102.2792  
## 5      1      1        1    1 medium    1      0.1428571 4 102.2834  
## 6      1      1        1    1 medium    1      0.1428571 5 102.7963  
## 7      1      1        1    1 medium    1      0.1428571 6 103.0441  
## 8      1      1        1    1 medium    1      0.1428571 7 102.8868  
## 9      1      1        1    1 medium    1      0.1428571 8 103.9101  
## 10     1      1        1    1 medium    1      0.1428571 9 103.2392  
## # ... with 190 more rows, and 1 more variable: pred <dbl>
```

Plot

```
samp %>%  
  mutate(pred = predict(m1a, newdata = samp)) %>%  
  ggplot(aes(wave, pred, group = sid)) +  
  geom_line() +  
  facet_wrap(~school)
```



Marginal effects

Marginal effect

A marginal effect shows the relation between one variable in the model and the outcome, while averaging over the other predictors in the model

Let's start by making the models slightly more complicated

```
m2 <- lmer(score ~ wave*treatment + group + prop_low +  
            (wave|sid) + (1|school) ,  
            data = sim_longitudinal)
```

```
arm::display(m2, detail = TRUE)
```

```
## lmer(formula = score ~ wave * treatment + group + prop_low +  
##       (wave | sid) + (1 | school), data = sim_longitudinal)  
##               coef.est coef.se t value  
## (Intercept)      97.62      4.70  20.78  
## wave              0.40      0.03  14.38  
## treatment1        0.82      1.91   0.43  
## grouplow         -4.83      4.00  -1.21  
## groupmedium      -3.61      3.75  -0.96  
## prop_low          9.34     10.21   0.91  
## wave:treatment1 -0.45      0.04 -11.42  
##  
## Error terms:  
##   Groups   Name          Std.Dev. Corr  
##   sid      (Intercept)  9.18  
##           wave         0.19    -0.13  
##   school   (Intercept)  3.41  
## Residual              0.44  
## ---  
## number of obs: 1000, groups: sid, 100; school, 15  
## AIC = 2319.8, DIC = 2313.2  
## deviance = 2304.5
```


Marginal effect

Let's look at the relation between **wave** and **score** by **treatment**, holding the other values constant.

First, build a prediction data frame. We'll make population-level prediction – i.e., ignoring the random effects.

```
marginal_frame1 <- data.frame(  
  wave = rep(0:9, 2),  
  treatment = as.factor(rep(c(0, 1), each = 10)),  
  group = factor("high", levels = c("low", "medium", "high")),  
  prop_low = mean(sim_longitudinal$prop_low, na.rm = TRUE),  
  sid = -999,  
  school = -999  
)
```

The length of each of these variables can sometimes get a little tricky

marginal_frame1

##	wave	treatment	group	prop_low	sid	school
## 1	0	0	high	0.3	-999	-999
## 2	1	0	high	0.3	-999	-999
## 3	2	0	high	0.3	-999	-999
## 4	3	0	high	0.3	-999	-999
## 5	4	0	high	0.3	-999	-999
## 6	5	0	high	0.3	-999	-999
## 7	6	0	high	0.3	-999	-999
## 8	7	0	high	0.3	-999	-999
## 9	8	0	high	0.3	-999	-999
## 10	9	0	high	0.3	-999	-999
## 11	0	1	high	0.3	-999	-999
## 12	1	1	high	0.3	-999	-999
## 13	2	1	high	0.3	-999	-999
## 14	3	1	high	0.3	-999	-999
## 15	4	1	high	0.3	-999	-999
## 16	5	1	high	0.3	-999	-999
## 17	6	1	high	0.3	-999	-999
## 18	7	1	high	0.3	-999	-999
## 19	8	1	high	0.3	-999	-999
## 20	9	1	high	0.3	-999	-999

Make predictions!

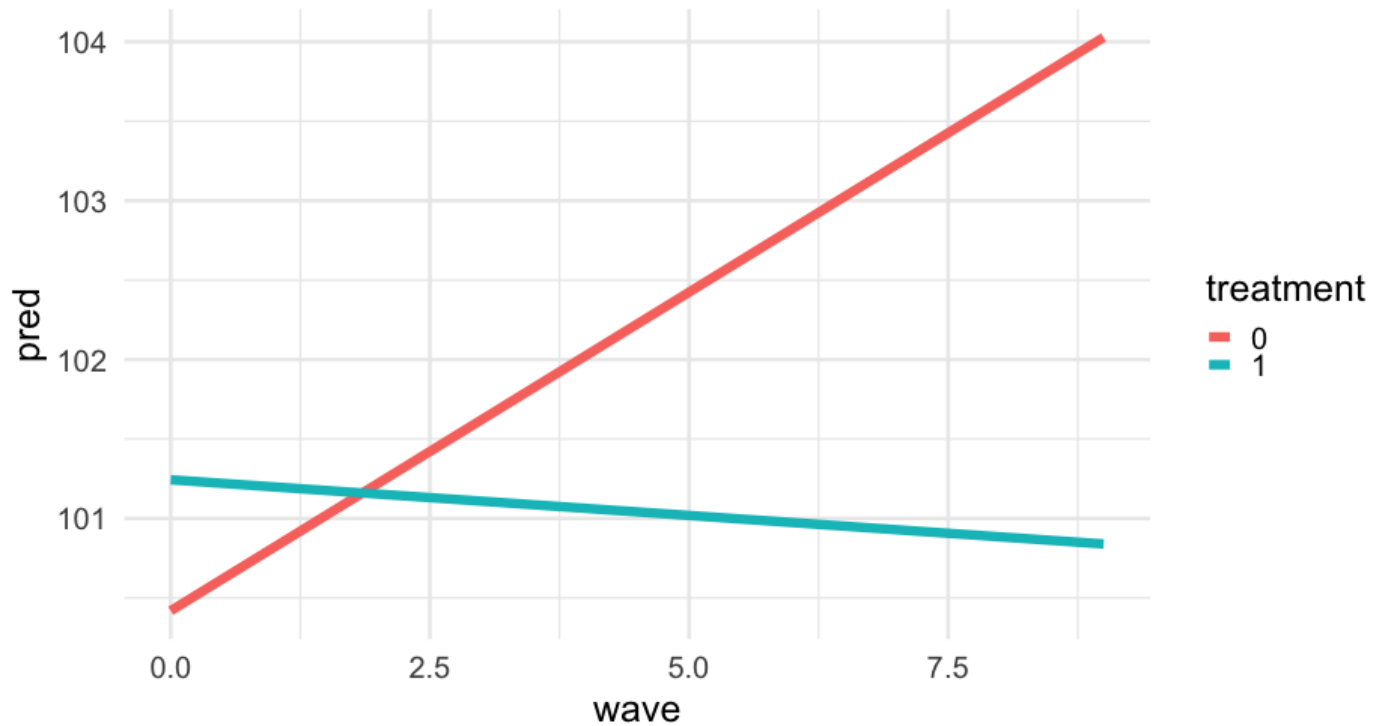
Note that we have to specify to allow new levels

```
marginal_frame1 <- marginal_frame1 %>%  
  mutate(pred = predict(m2,  
                        newdata = marginal_frame1,  
                        allow.new.levels = TRUE))  
marginal_frame1
```

##	wave	treatment	group	prop_low	sid	school	pred
## 1	0	0	high	0.3	-999	-999	100.4186
## 2	1	0	high	0.3	-999	-999	100.8196
## 3	2	0	high	0.3	-999	-999	101.2207
## 4	3	0	high	0.3	-999	-999	101.6217
## 5	4	0	high	0.3	-999	-999	102.0227
## 6	5	0	high	0.3	-999	-999	102.4237
## 7	6	0	high	0.3	-999	-999	102.8248
## 8	7	0	high	0.3	-999	-999	103.2258
## 9	8	0	high	0.3	-999	-999	103.6268
## 10	9	0	high	0.3	-999	-999	104.0278
## 11	0	1	high	0.3	-999	-999	101.2433
## 12	1	1	high	0.3	-999	-999	101.1984
## 13	2	1	high	0.3	-999	-999	101.1536
## 14	3	1	high	0.3	-999	-999	101.1087
## 15	4	1	high	0.3	-999	-999	101.0638

Plot it

```
ggplot(marginal_frame1, aes(wave, pred, color = treatment)) +  
  geom_line()
```



Why do this?

As the model gets more complicated, it can be increasingly difficult to understand the fixed effects.

Plotting the marginal effects regularly helps (e.g., for interactions and non-linear terms)

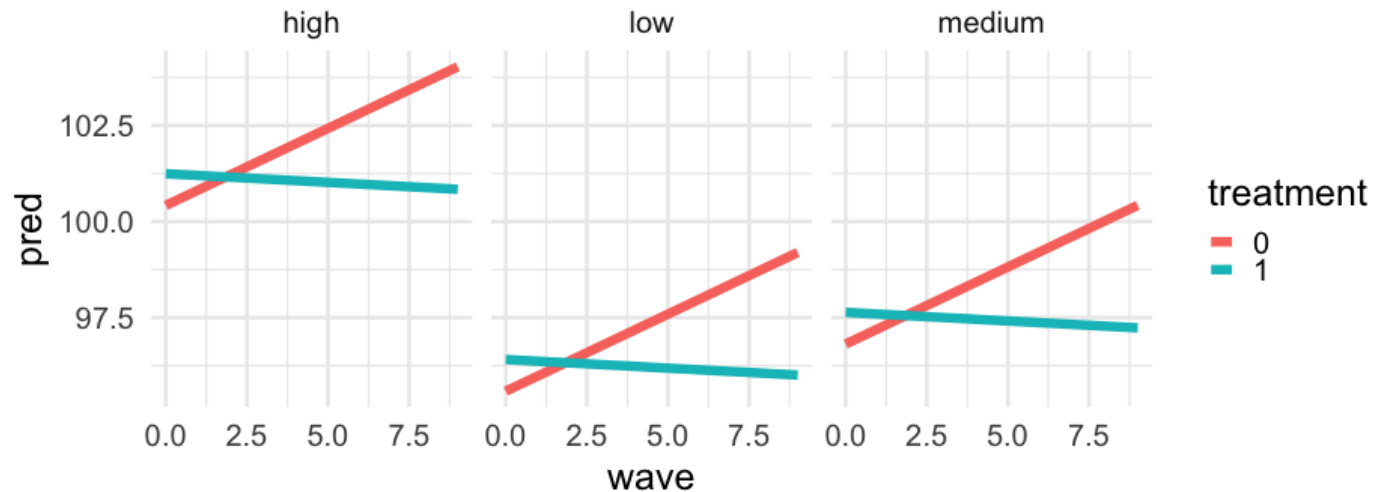
Try again

This time, let's look at the same thing, but for all groups, still holding `prop_low` constant.

```
marginal_frame2 <- data.frame(
  wave = rep(0:9, 2*3),
  treatment = as.factor(rep(c(0, 1), each = 10*3)),
  group = factor(
    rep(
      rep(c("low", "medium", "high"), each = 10),
      2
    )
  ),
  prop_low = mean(sim_longitudinal$prop_low, na.rm = TRUE),
  sid = -999,
  school = -999
)
```

Predict & plot

```
marginal_frame2 %>%  
  mutate(  
    pred = predict(m2,  
                  newdata = marginal_frame2,  
                  allow.new.levels = TRUE)  
  ) %>%  
  ggplot(aes(wave, pred, color = treatment)) +  
  geom_line() +  
  facet_wrap(~group)
```



Automated method

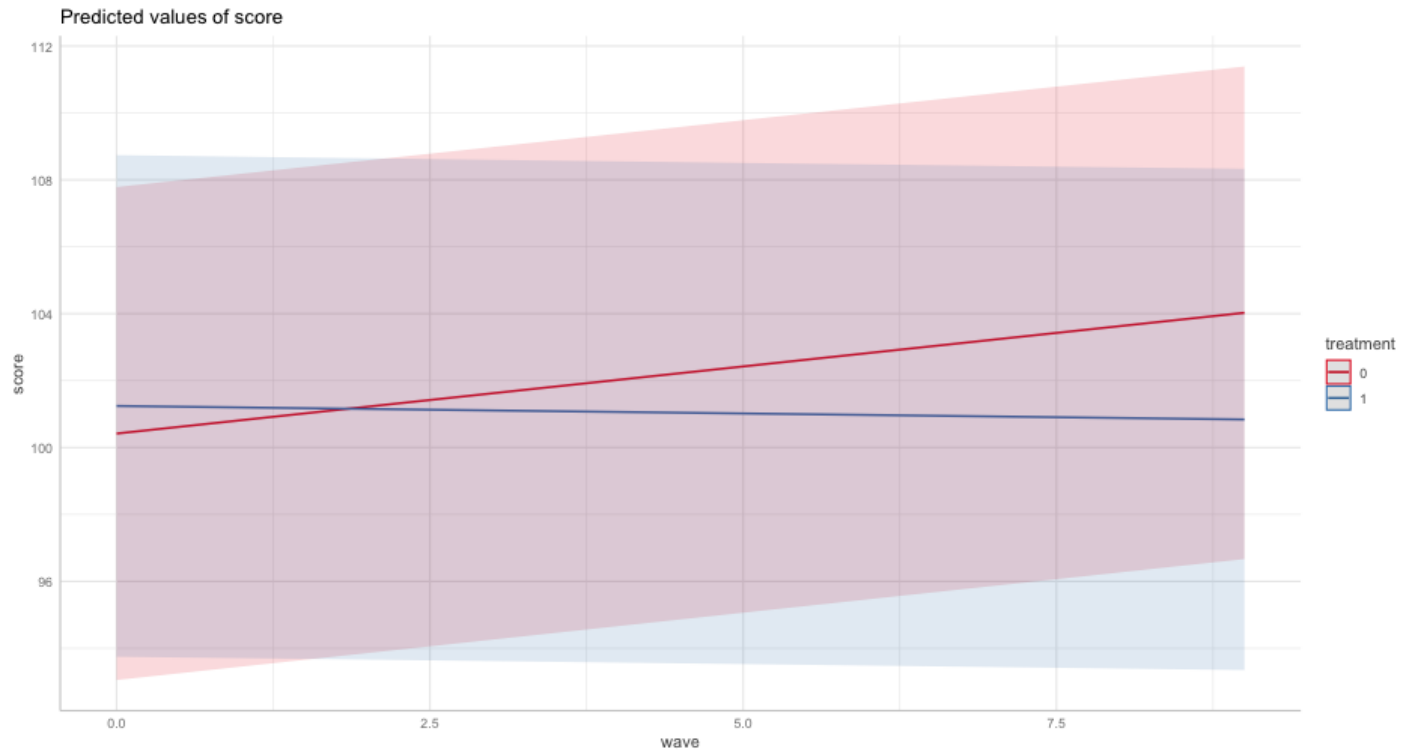
We can build this up on our own with new data frames

```
library(ggeffects)
ggpredict(m2, "wave")
```

```
## # Predicted values of score
## # x = wave
##
## x | Predicted |          95% CI
## -----
## 0 |    100.42 | [93.05, 107.78]
## 1 |    100.82 | [93.46, 108.18]
## 2 |    101.22 | [93.86, 108.58]
## 3 |    101.62 | [94.26, 108.98]
## 5 |    102.42 | [95.07, 109.78]
## 6 |    102.82 | [95.47, 110.18]
## 7 |    103.23 | [95.87, 110.58]
## 9 |    104.03 | [96.67, 111.39]
##
## Adjusted for:
## * treatment =      0
## *      group = high
## * prop_low = 0.30
## *      sid = 0 (population-level)
## *      school = 0 (population-level)
```


Even automated plotting!

```
ggpredict(m2, c("wave", "treatment")) %>%  
  plot()
```



Individual observation

We can get these prediction intervals for specific levels also

```
ggpredict(m2, "wave", condition = c(sid = 1, school = 1))
```

```
## # Predicted values of score
## # x = wave
##
## x | Predicted |          95% CI
## -----
## 0 |      100.42 | [93.05, 107.78]
## 1 |      100.82 | [93.46, 108.18]
## 2 |      101.22 | [93.86, 108.58]
## 3 |      101.62 | [94.26, 108.98]
## 5 |      102.42 | [95.07, 109.78]
## 6 |      102.82 | [95.47, 110.18]
## 7 |      103.23 | [95.87, 110.58]
## 9 |      104.03 | [96.67, 111.39]
##
## Adjusted for:
## * treatment =      0
## *      group = high
## *  prop_low = 0.30
```

All categorical groups

Note – things aren't perfect here, but it's still helpful.

```
ggpredict(m2, c("wave", "treatment", "group"),  
          condition = c(sid = 1, school = 1)) %>%  
  plot()
```

Next time

- Digging into the variance–covariance matrix of the random effects
- Finally discussing Gelman & Hill notation in more depth
- Homework 1 is due, Homework 2 assigned