Data structuring and basic models

Agenda

- Restructuring data
- Fitting models:
  - Unconditional model
  - Random intercepts
  - Random slopes
- Homework 1

Today will be highly applied, and (I hope) mostly review

The only real difference is it will be in R

Restructuring data

First, load the data

```r
library(tidyverse)
theme_set(theme_minimal(25))
knitr::opts_chunk$set(fig.width = 9, fig.height = 6)
curran <- read_csv(here::here("data", "curran.csv"))
curran
```

```
## # A tibble: 405 x 15
##        id anti1 anti2 anti3 anti4    read1 read2       read3       read4 kidg
##     <dbl> <dbl> <dbl> <dbl> <dbl>    <dbl> <dbl>       <dbl>       <dbl>  <db
##  1     22     1     2    NA    NA 2.1        3.9 NA          NA
##  2     34     3     6     4     5 2.1        2.9  4.5         4.5
##  3     58     0     2     0     1 2.300000   4.5  4.2         4.600000
##  4    122     0     3     1     1 3.7        8   NA          NA
##  5    125     1     1     2     1 2.300000   3.8  4.3         6.2
##  6    133     3     4     3     5 1.8        2.6  4.100000    4
##  7    163     5     4     5     5 3.5        4.8  5.8         7.5
##  8    190     0    NA    NA     0 2.9        6.1 NA          NA
##  9    227     0     0     2     1 1.8        3.8  4          NA
## 10    248     1     2     2     0 3.5        5.7  7           6.9
## # … with 395 more rows, and 1 more variable: nmis <dbl>
```

About the data

> The data are a sample of 405 children who were within the first two years of entry to elementary school. The data consist of four repeated measures of both the child's antisocial behavior and the child's reading recognition skills. In addition, on the first measurement occasion, measures were collected of emotional support and cognitive stimulation provided by the mother. The data were collected using face-to-face interviews of both the child and the mother at two-year intervals between 1986 and 1992.

See here

Format

- Let's say we want to use reading scores as the outcome
- We have four columns of reading scores
- We can't specify multiple outcomes.

What do we do?

Make the data longer

Image from R for Data Science

Let's start it easy

First, let's select just the ID variable and the reading scores

```r
read <- curran %>%
  select(id, starts_with("read"))
read
```

```
## # A tibble: 405 x 5
##        id    read1 read2      read3      read4
##     <dbl>    <dbl> <dbl>      <dbl>      <dbl>
##  1     22 2.1        3.9 NA         NA
##  2     34 2.1        2.9  4.5        4.5
##  3     58 2.300000   4.5  4.2        4.600000
##  4    122 3.7        8   NA         NA
##  5    125 2.300000   3.8  4.3        6.2
##  6    133 1.8        2.6  4.100000   4
##  7    163 3.5        4.8  5.8        7.5
##  8    190 2.9        6.1 NA         NA
##  9    227 1.8        3.8  4         NA
## 10    248 3.5        5.7  7          6.9
## # … with 395 more rows
```

What should our data look like?

- Take two minutes to visualize what you think the data should look like
- Feel free to even sketch something out.
- We'll talk about it as a class after

id	read1	read2	read3	read4
22	2.1	3.9	NA	NA
34	2.1	2.9	4.5	4.5
58	2.3	4.5	4.2	4.6
122	3.7	8.0	NA	NA

02:00

Moving to longer

```
read %>%
  pivot_longer(cols = read1:read4,
               names_to = "timepoint",
               values_to = "score")
```

```
## # A tibble: 1,620 x 3
##       id timepoint    score
##    <dbl> <chr>        <dbl>
##  1    22 read1       2.1
##  2    22 read2       3.9
##  3    22 read3      NA
##  4    22 read4      NA
##  5    34 read1       2.1
##  6    34 read2       2.9
##  7    34 read3       4.5
##  8    34 read4       4.5
##  9    58 read1       2.300000
## 10    58 read2       4.5
## # … with 1,610 more rows
```

Alternative

You can also specify the columns that should *not* be pivoted

```
read %>%
  pivot_longer(-id,
               names_to = "timepoint",
               values_to = "score")
```

```
## # A tibble: 1,620 x 3
##       id timepoint     score
##    <dbl> <chr>         <dbl>
##  1    22 read1       2.1
##  2    22 read2       3.9
##  3    22 read3      NA
##  4    22 read4      NA
##  5    34 read1       2.1
##  6    34 read2       2.9
##  7    34 read3       4.5
##  8    34 read4       4.5
##  9    58 read1       2.300000
## 10    58 read2       4.5
## # … with 1,610 more rows
```

Are we done?

- In this case, we probably want to fit a growth model. That means `timepoint` needs to be numeric.
- There are numerous ways to do this – here are a few

Mutate

- Use `mutate()` to modify the column afterwords

Why did I subtract 1?

```
read %>%
  pivot_longer(-id,
               names_to = "timepoint",
               values_to = "score") %>%
  mutate(timepoint = parse_number(timepoint) - 1)
```

```
## # A tibble: 1,620 x 3
##        id timepoint    score
##     <dbl>     <dbl>    <dbl>
##  1     22         0  2.1
##  2     22         1  3.9
##  3     22         2 NA
##  4     22         3 NA
##  5     34         0  2.1
##  6     34         1  2.9
##  7     34         2  4.5
##  8     34         3  4.5
##  9     58         0  2.300000
## 10     58         1  4.5
```

Transform during the pivot

```
read %>%
  pivot_longer(-id,
               names_to = "timepoint",
               values_to = "score",
               names_transform = list(timepoint = parse_number))
```

```
## # A tibble: 1,620 x 3
##         id timepoint     score
##      <dbl>     <dbl>     <dbl>
##  1     22         1   2.1
##  2     22         2   3.9
##  3     22         3  NA
##  4     22         4  NA
##  5     34         1   2.1
##  6     34         2   2.9
##  7     34         3   4.5
##  8     34         4   4.5
##  9     58         1   2.300000
## 10     58         2   4.5
## # … with 1,610 more rows
```

Alternative transformation

This does the subtraction by 1 also

```
sub1 <- function(x) parse_number(x) - 1

read %>%
  pivot_longer(-id,
               names_to = "timepoint",
               values_to = "score",
               names_transform = list(timepoint = sub1))
```

```
## # A tibble: 1,620 x 3
##       id timepoint     score
##    <dbl>     <dbl>     <dbl>
##  1    22         0  2.1
##  2    22         1  3.9
##  3    22         2 NA
##  4    22         3 NA
##  5    34         0  2.1
##  6    34         1  2.9
##  7    34         2  4.5
##  8    34         3  4.5
##  9    58         0  2.300000
## 10    58         1  4.5
## # … with 1,610 more rows
```

Yet another approach

This one doesn't subtract 1, however

```
read %>%
  pivot_longer(-id,
               names_to = "timepoint",
               values_to = "score",
               names_prefix = "read",
               names_ptype = list(timepoint = "numeric"))
```

```
## # A tibble: 1,620 x 3
##       id timepoint     score
##    <dbl> <chr>         <dbl>
##  1    22 1              2.1
##  2    22 2              3.9
##  3    22 3             NA
##  4    22 4             NA
##  5    34 1              2.1
##  6    34 2              2.9
##  7    34 3              4.5
##  8    34 4              4.5
##  9    58 1              2.300000
## 10    58 2              4.5
## # … with 1,610 more rows
```

Moving back

Although moving longer is most often useful for multilevel modeling, occasionally we need to go wider – e.g., for a join.

First, let's create a longer data object

```
l <- read %>%
  pivot_longer(-id,
               names_to = "timepoint",
               values_to = "score",
               names_transform = list(timepoint = sub1))
```

Now let's move it back

Use `pivot_wider()` instead

```
l %>%
  pivot_wider(names_from = timepoint,
              values_from = score)
```

```
## # A tibble: 405 x 5
##         id      `0`    `1`        `2`       `3`
##      <dbl>    <dbl> <dbl>      <dbl>     <dbl>
##  1     22 2.1          3.9 NA        NA
##  2     34 2.1          2.9  4.5       4.5
##  3     58 2.300000     4.5  4.2       4.600000
##  4    122 3.7          8   NA        NA
##  5    125 2.300000     3.8  4.3       6.2
##  6    133 1.8          2.6  4.100000  4
##  7    163 3.5          4.8  5.8       7.5
##  8    190 2.9          6.1 NA        NA
##  9    227 1.8          3.8  4        NA
## 10    248 3.5          5.7  7         6.9
## # … with 395 more rows
```

Challenge

Let's go back to the full `curran` data. See if you can get your data to look like the below.

There are, again, multiple ways to do this, including only through pivot_longer

```
## # A tibble: 3,240 x 10
##       id kidgen momage kidage homecog homeemo  nmis variable timepoint v
##    <dbl>  <dbl>  <dbl>  <dbl>   <dbl>   <dbl> <dbl> <chr>        <dbl> <
##  1    22      0     28   6.08      13      10     4 anti             0
##  2    22      0     28   6.08      13      10     4 anti             1
##  3    22      0     28   6.08      13      10     4 anti             2
##  4    22      0     28   6.08      13      10     4 anti             3
##  5    22      0     28   6.08      13      10     4 read             0
##  6    22      0     28   6.08      13      10     4 read             1
##  7    22      0     28   6.08      13      10     4 read             2
                        28   6.08      13      10     4 read             3
                        28   6.83       9       9     0 anti             0
                        28   6.83       9       9     0 anti             1
                 ore rows
```

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More transforming

Our data is probably still not in the format we want. Can you get it in the format like the below?

```
## # A tibble: 1,620 x 10
##       id kidgen momage kidage homecog homeemo  nmis timepoint  anti
##    <dbl>  <dbl>  <dbl>  <dbl>   <dbl>   <dbl> <dbl>     <dbl> <dbl>
##  1    22      0     28   6.08      13      10     4         0     1  2.1
##  2    22      0     28   6.08      13      10     4         1     2  3.9
##  3    22      0     28   6.08      13      10     4         2    NA NA
##  4    22      0     28   6.08      13      10     4         3    NA NA
##  5    34      1     28   6.83       9       9     0         0     3  2.1
##  6    34      1     28   6.83       9       9     0         1     6  2.9
##  7    34      1     28   6.83       9       9     0         2     4  4.5
##  8    34      1     28   6.83       9       9     0         3     5  4.5
##  9    58      0     28   6.5        9       6     0         0     0  2.3
## 10    58      0     28   6.5        9       6     0         1     2  4.5
## # … with 1,610 more rows
```

04:00

Another example

Read in the letter sounds data

```
ls <- read_csv(here::here("data", "ls19.csv"))
ls
```

```
## # A tibble: 962 x 13
##    county       distid dist_name              instid inst_name             inst
##    <chr>         <dbl> <chr>                   <dbl> <chr>                 <chr
##  1 All Counties   9999 Statewide                9999 Statewide             Stat
##  2 Baker          1894 Baker SD 5J              1894 Baker SD 5J           Dist
##  3 Baker          1895 Huntington SD 16J        1895 Huntington SD 16J     Dist
##  4 Baker          1896 Burnt River SD 30J       1896 Burnt River SD 30J    Dist
##  5 Baker          1897 Pine Eagle SD 61         1897 Pine Eagle SD 61      Dist
##  6 Benton         1898 Monroe SD 1J             1898 Monroe SD 1J          Dist
##  7 Benton         1899 Alsea SD 7J              1899 Alsea SD 7J           Dist
##  8 Benton         1900 Philomath SD 17J         1900 Philomath SD 17J      Dist
##  9 Benton         1901 Corvallis SD 509J        1901 Corvallis SD 509J     Dist
## 10 Clackamas      1902 Clackamas ESD            1902 Clackamas ESD         Dist
## # … with 952 more rows, and 5 more variables: hispanic_latino <dbl>, ame
## #   multi_racial <dbl>, native_hawaiian_pacific_islander <dbl>, white <c
```

LS Data

- Average scores on the letter sounds portion of the kindergarten entry assessment for every school in the state, by race.
- Data missing if *n* too small
- Remember – you (generally) don't need to dummy-code variables in R
- Try structuring this data so you could estimate between-district variability, while accounting for race/ethnicity

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Self-regulation data

- Same basic data with a different outcome and a different structure.
- Try restructuring this one

```
selfreg <- read_csv(here::here("data", "selfreg19.csv"))
selfreg
```

```
## # A tibble: 6,734 x 13
##    county       distid dist_name   instid inst_name   inst_type selfreg_
##    <chr>         <dbl> <chr>        <dbl> <chr>       <chr>
##  1 All Counties   9999 Statewide     9999 Statewide   State
##  2 All Counties   9999 Statewide     9999 Statewide   State
##  3 All Counties   9999 Statewide     9999 Statewide   State
##  4 All Counties   9999 Statewide     9999 Statewide   State
##  5 All Counties   9999 Statewide     9999 Statewide   State
                  9999 Statewide     9999 Statewide   State
                  9999 Statewide     9999 Statewide   State
                  1894 Baker SD 5J   1894 Baker SD 5J District
                  1894 Baker SD 5J   1894 Baker SD 5J District
                  1894 Baker SD 5J   1894 Baker SD 5J District
## # … with 6,724 more rows, and 4 more variables: Hispanic.Latino <dbl>, M
## #   Native.Hawaiian.Pacific.Islander <dbl>, White <dbl>
```

06:00

A bit of a caveat

- The preceding examples would lead to sort of fundamentally flawed analyses
- We'd be estimating each district mean as the mean of the school means
- There are ways to account for this, which we may or may not get into later in the term
- Could potentially try weighting each school mean by the school size

Modeling

Back to curran data

- Let's fit a basic two-level growth model

- We'll compare a random intercepts model to a random slopes model and talk about some of the complexities involved

Unconditional growth model

Model fitting

- We could start with a fully unconditional model (not unconditional growth), but that's really a misspecification in this case – we know we have to account for time.
- Let's first fit a model with random intercepts
- A reminder of what the data look like

```
d
```

```
## # A tibble: 1,620 x 10
##        id kidgen momage kidage homecog homeemo  nmis timepoint  anti
##     <dbl>  <dbl>  <dbl>  <dbl>   <dbl>   <dbl> <dbl>     <dbl> <dbl>
##  1    22      0     28   6.08      13      10     4         0     1  2.1
##  2    22      0     28   6.08      13      10     4         1     2  3.9
##  3    22      0     28   6.08      13      10     4         2    NA NA
##  4    22      0     28   6.08      13      10     4         3    NA NA
##  5    34      1     28   6.83       9       9     0         0     3  2.1
##  6    34      1     28   6.83       9       9     0         1     6  2.9
##  7    34      1     28   6.83       9       9     0         2     4  4.5
##  8    34      1     28   6.83       9       9     0         3     5  4.5
```

Fit the model

Let's talk through what's going on here:

```
library(lme4)
m_intercepts <- lmer(read ~ 1 + timepoint + (1|id),
                     data = d)
```

Notation

Raudenbush and Bryk

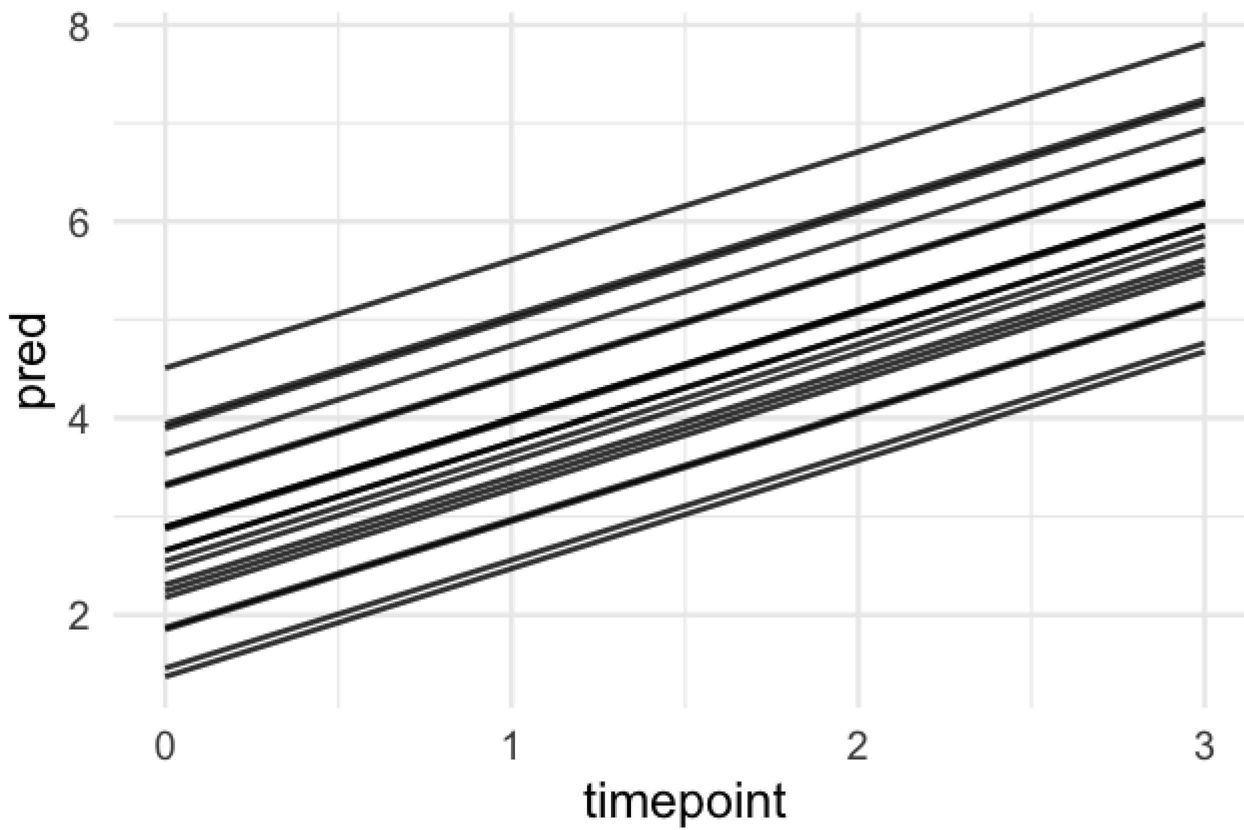
$$
\begin{aligned}
\mathbf{read}_{ij} &= \pi_{0jk} + \pi_{1jk}(\mathbf{timepoint}) + e_{ijk} \\
\pi_{0jk} &= \beta_{00k} + \beta_{01k}(\mathbf{FRL}) + r_{0jk} \\
\pi_{1jk} &= \beta_{10k}
\end{aligned}
$$

In Gelman & Hill

$$
\begin{aligned}
\mathbf{read}_i &\sim N\left(\alpha_{j[i]} + \beta_1(\mathbf{timepoint}), \sigma^2\right) \\
\alpha_j &\sim N\left(\mu_{\alpha_j}, \sigma^2_{\alpha_j}\right), \text{ for id j} = 1, \ldots, \text{J}
\end{aligned}
$$

What does this look like?

Below is a random sample of the model predictions for 20 participants



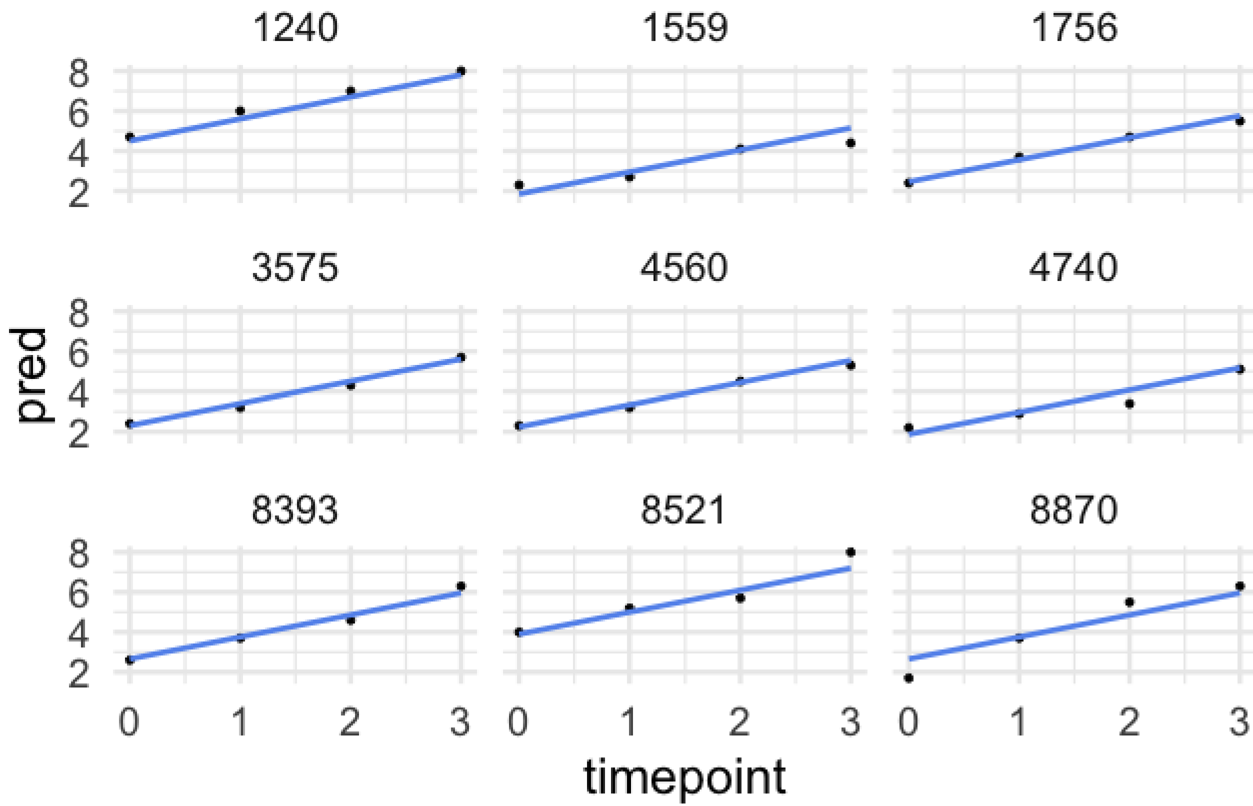
Parallel slopes

- Had we of fit a standard regression model we would have had one slope to represent the trend of all participants, which would (fairly clearly) be less than ideal

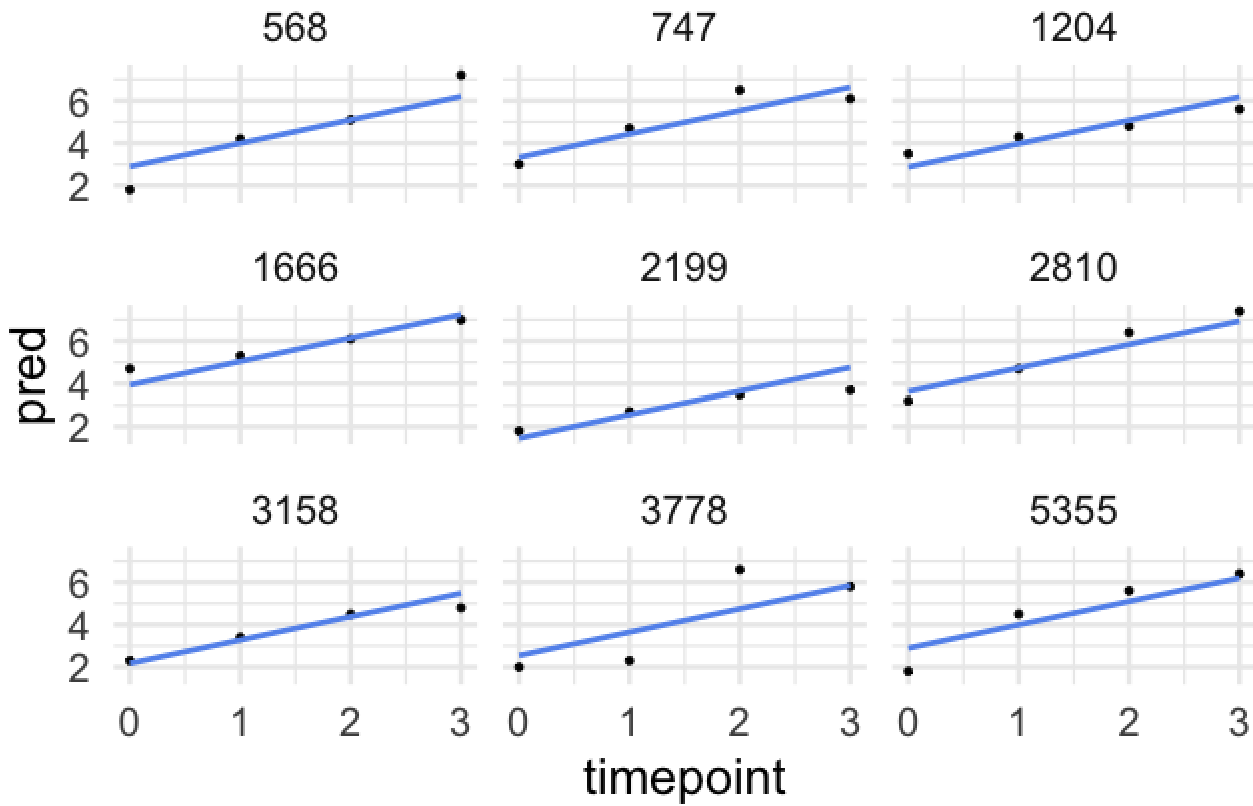
- Now, we've allowed each participant to have a different *starting* point, but constrained the rate of change to be constant.

- How reasonable is this assumption?

Random sample of 9 participants



And 9 different participants



I would argue this is looking pretty good

Plotting

- I realize I didn't echo the code for the prior plots
- You can look at the source code if you want
- We will talk about making these types of plots next week

Model summary

```
summary(m_intercepts)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lme
## Formula: read ~ 1 + timepoint + (1 | id)
##    Data: d
##
## REML criterion at convergence: 3487.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.6170 -0.5207  0.0383  0.5214  3.7428
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  id       (Intercept) 0.7797   0.8830
##  Residual             0.4609   0.6789
## Number of obs: 1325, groups:  id, 405
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)   2.70374    0.05257 569.45801   51.43   <2e-16 ***
## timepoint     1.10134    0.01759 965.48963   62.62   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
```

Random slopes

Modeling

- Let's fit a second model that allows each participant to have a different slope

```
m_slopes <- lmer(read ~ 1 + timepoint + (1 + timepoint|id),
                 data = d)
```

Quick note on syntax

I'm being very explicit in the above about what I'm estimating. However, intercepts are generally implied. So the above is equivalent to

```
m_slopes <- lmer(read ~ timepoint + (timepoint|id),
                 data = d)
```

which is actually how I generally write it

Important!

You are not only estimating an additional variance component (variance of the intercept and variance of the slope), but also the *covariance* among them.

In Gelman & Hill Notation

$$
\begin{aligned}
\textbf{read}_i &\sim N\left(\alpha_{j[i]} + \beta_{1j[i]}(\textbf{timepoint}), \sigma^2\right) \\
\begin{pmatrix} \alpha_j \\ \beta_{1j} \end{pmatrix} &\sim MVN\left(\begin{pmatrix} \mu_{\alpha_j} \\ \mu_{\beta_{1j}} \end{pmatrix}, \begin{pmatrix} \sigma^2_{\alpha_j} & \rho_{\alpha_j\beta_{1j}} \\ \rho_{\beta_{1j}\alpha_j} & \sigma^2_{\beta_{1j}} \end{pmatrix}\right), \textbf{for id j} = 1, .
\end{aligned}
$$

Contrast this with R & B

Raudenbush and Bryk

$$
\begin{aligned}
\textbf{read}_{ij} &= \pi_{0jk} + \pi_{1jk}(\textbf{timepoint}) + e_{ijk} \\
\pi_{0jk} &= \beta_{00k} + \beta_{01k}(\textbf{FRL}) + r_{0jk} \\
\pi_{1jk} &= \beta_{10k} + r_{1jk}
\end{aligned}
$$

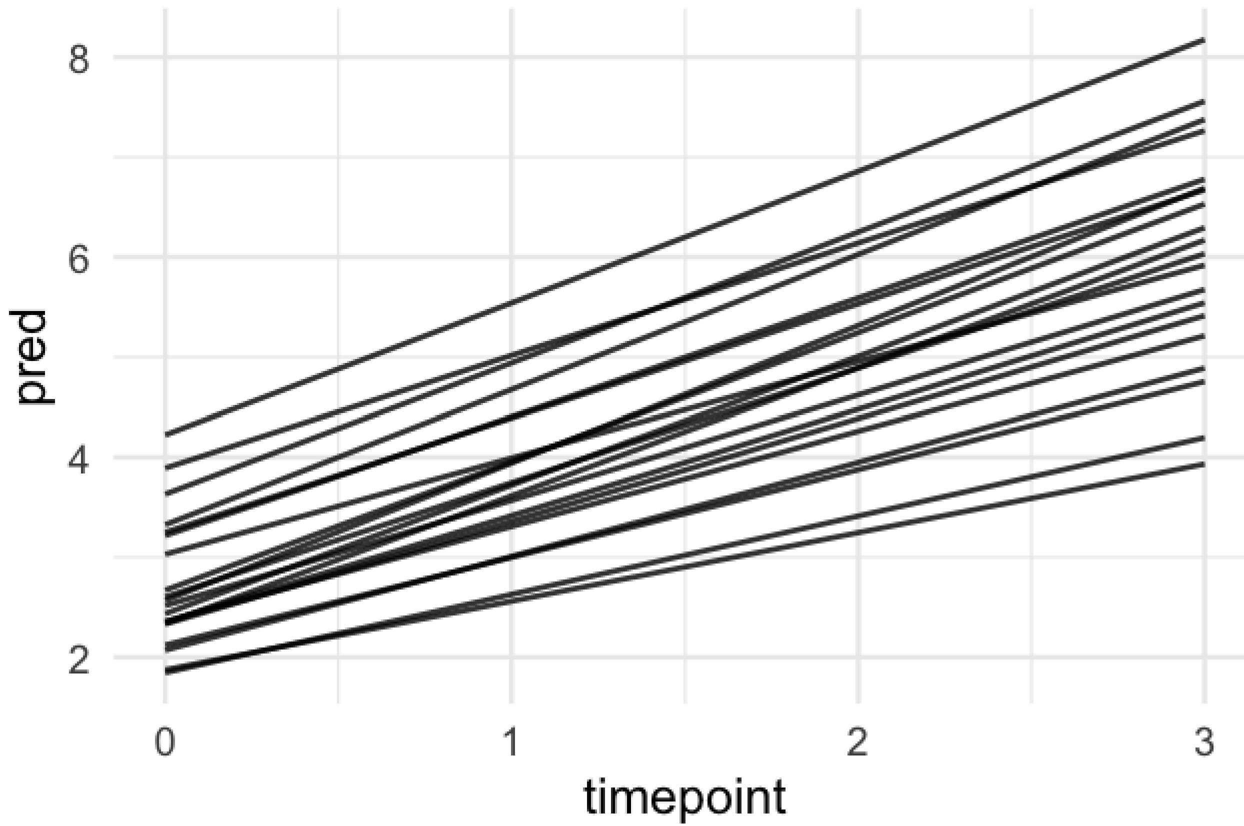
The covariance estimation is less clear, unless we add the additional distributional assumptions part

$$e_{ijk} \sim N\left(0, \sigma\right)$$

$$\begin{pmatrix} r_{0jk} \\ r_{1jk} \end{pmatrix} \sim MVN\left(\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \tau_{00} & \tau_{01} \\ \tau_{10} & \tau_{11} \end{pmatrix}\right), \textbf{for id j} = 1, \ldots, \textbf{J}$$

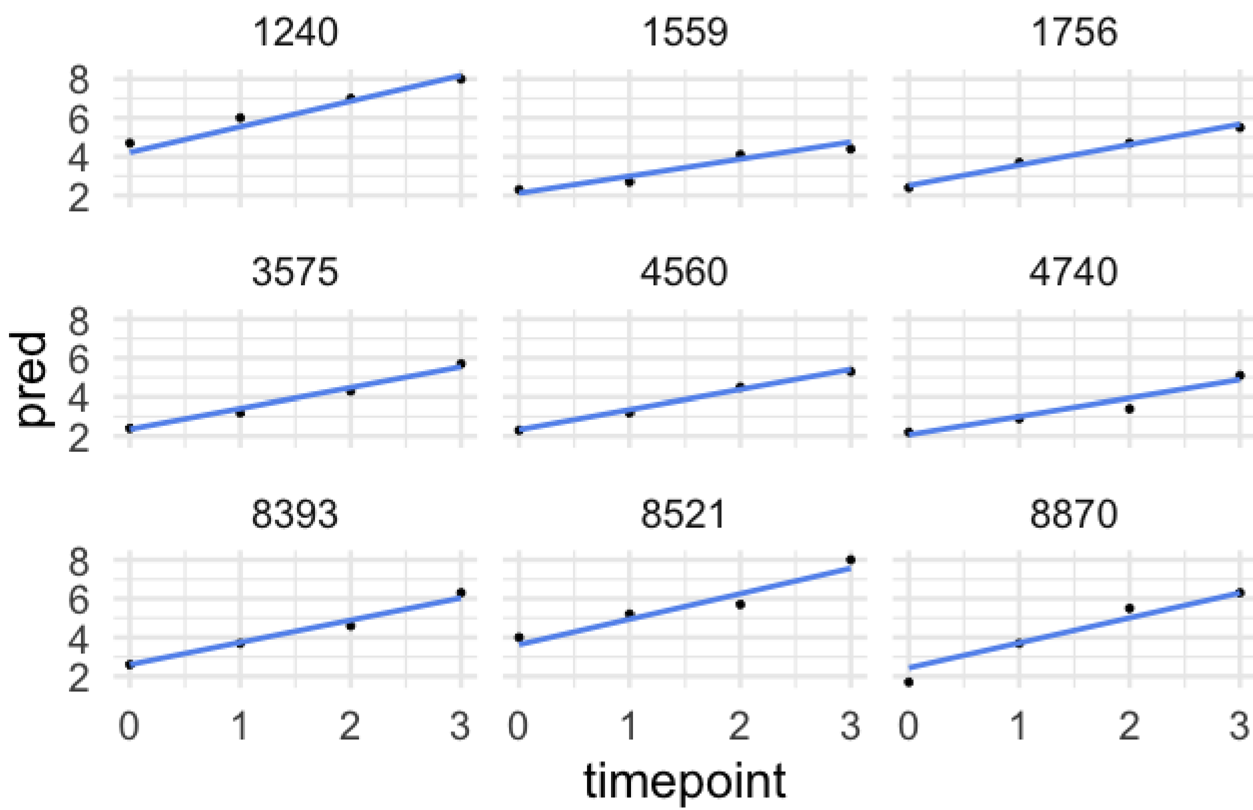
Random slopes

Same 20 participants from before. Do they look like they differ?

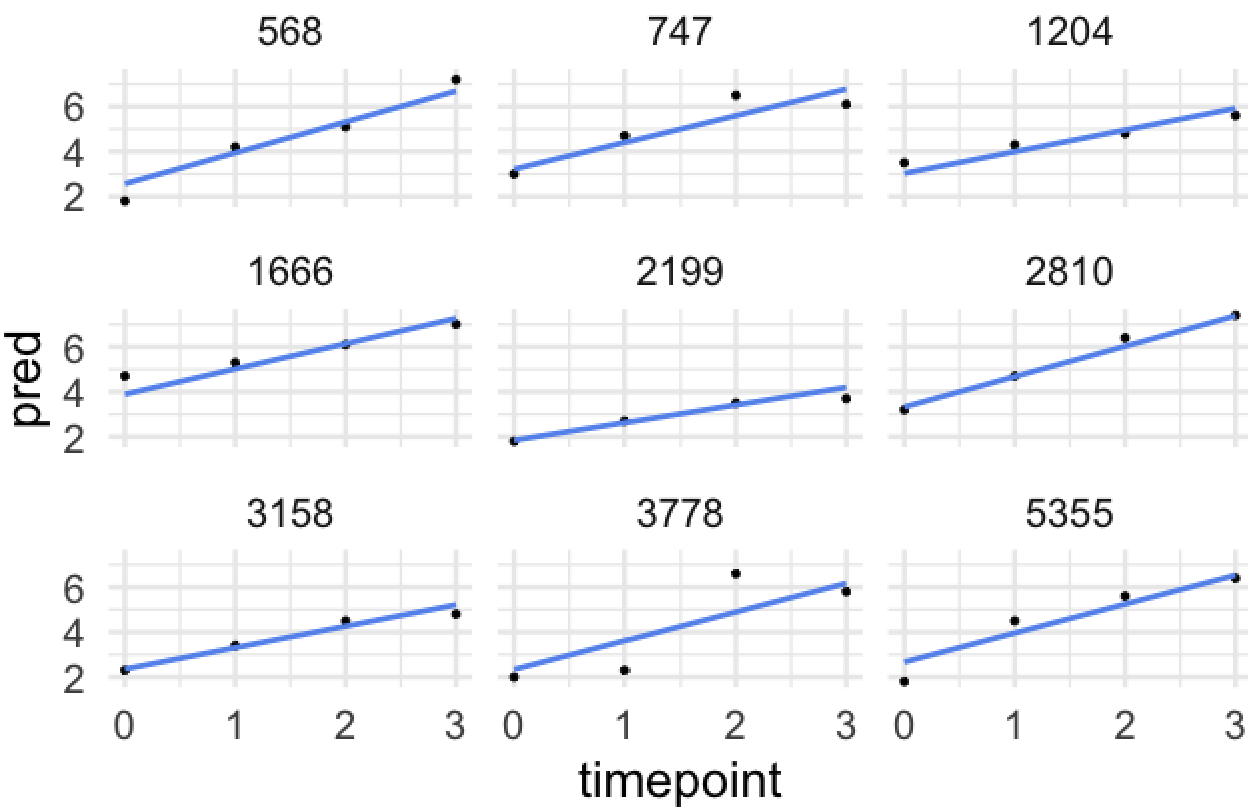


Look by participant

Same random sample of 9 participants



And an additional 9 different participants



What's the output look like

```r
summary(m_slopes)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lme
## Formula: read ~ 1 + timepoint + (1 + timepoint | id)
##    Data: d
##
## REML criterion at convergence: 3382
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.7161 -0.5201 -0.0220  0.4793  4.1847
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  id       (Intercept) 0.57309  0.7570
##           timepoint   0.07459  0.2731   0.29
##  Residual             0.34584  0.5881
## Number of obs: 1325, groups:  id, 405
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)   2.69609    0.04530 400.87693   59.52   <2e-16 ***
## timepoint     1.11915    0.02169 308.40833   51.60   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

Let's interpret each of the following

- $\alpha_{j[i]}$
- $\beta_{1j[i]}$
- $\sigma^2_{\alpha_j}$
- $\rho_{\alpha_j \beta_{1j}}$
- $\sigma^2_{\beta_{1j}}$

In equation form

$$\widehat{\textbf{read}}_i \sim N\left(\mathbf{2.7}_{\alpha_{j[i]}} + \mathbf{1.12}_{\beta_{1j[i]}}(\textbf{timepoint}), \mathbf{0.59}\right)$$

$$\left(\begin{array}{c} \alpha_j \\ \beta_{1j} \end{array}\right) \sim MVN\left(\left(\begin{array}{c} 0 \\ 0 \end{array}\right), \left(\begin{array}{cc} 0.76 & 0.29 \\ 0.29 & 0.27 \end{array}\right)\right)\text{, for id j} = 1, \ldots, \text{J}$$

P values

The **{lme4}** package does not report p–values. This is because its author, Douglas Bates, believes they are fundamentally flawed for multilevel models.

The link above is worth reading through, but basically it is not straightforward to calculate the denominator degrees of freedom for an F test. The methods that are used are approximations and, although generally accepted, are not guaranteed to be correct.

Alternatives

There are two primary work-arounds here:

- Don't use p–values, and instead just interpret the confidence intervals, or
- Use the same approximation that others use via **{lmerTest}** package.

Confidence intervals

Multiple options, but profiled or bootstrap confidence intervals are generally preferred, though computationally intensive. Note that these provide CIs for the variance components as well.

```
confint(m_slopes)
```

```
## Computing profile confidence intervals ...

##                   2.5 %    97.5 %
## .sig01       0.67961051 0.8365439
## .sig02       0.06898955 0.5434982
## .sig03       0.22282787 0.3213734
## .sigma       0.55548063 0.6238545
## (Intercept) 2.60721096 2.7850364
## timepoint   1.07653165 1.1622218
```

lmerTest

```r
library(lmerTest)

# refit model
m_slopes2 <- lmer(read ~ timepoint + (timepoint|id),
                  data = d)
```

New summary

```r
summary(m_slopes2)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lme
## Formula: read ~ timepoint + (timepoint | id)
##    Data: d
##
## REML criterion at convergence: 3382
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.7161 -0.5201 -0.0220  0.4793  4.1847
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  id       (Intercept) 0.57309  0.7570
##           timepoint   0.07459  0.2731   0.29
##  Residual             0.34584  0.5881
## Number of obs: 1325, groups:  id, 405
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)   2.69609    0.04530 400.87693   59.52   <2e-16 ***
## timepoint     1.11915    0.02169 308.40833   51.60   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

Comparing models

- How do we know which model is preferred?

- We don't want to overfit, but we also don't want to underfit

  - What do these terms mean again?

- Numerous approaches

  - χ^2 significance test of the change in the model deviance
  - Information criteria (AIC/BIC)
  - Cross validation procedures

Using built–in approaches

```
anova(m_intercepts, m_slopes)
```

```
## refitting model(s) with ML (instead of REML)

## Data: d
## Models:
## m_intercepts: read ~ 1 + timepoint + (1 | id)
## m_slopes: read ~ 1 + timepoint + (1 + timepoint | id)
##              npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## m_intercepts    4 3485.1 3505.8 -1738.5   3477.1
## m_slopes        6 3383.8 3414.9 -1685.9   3371.8 105.29  2  < 2.2e-16 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

What does this mean?

The {performance} package

Similar information, little bit nicer output

```r
library(performance)
compare_performance(m_intercepts, m_slopes) %>%
  print_md()
```

Table: Comparison of Model Performance Indices

Name	Model	AIC	BIC	R2 (cond.)	R2 (marg.)	ICC	RMSE	Sigma
m_intercepts	lmerModLmerTest	3495.56	3516.32	0.83	0.55	0.63	0.59	0.68
m_slopes	lmerModLmerTest	3394.00	3425.14	0.88	0.54	0.73	0.47	0.59

Likelihood ratio test

```
test_likelihoodratio(m_intercepts, m_slopes) %>%
  print_md()
```

Name	Model	df	df_diff	Chi2	p
m_intercepts	lmerModLmerTest	4			
m_slopes	lmerModLmerTest	6	2	105.56	1.20e-23

Or use Bayes factors

This is the default if the models are nested, as ours are

```
test_performance(m_intercepts, m_slopes) %>%
  print_md()
```

Name	Model	BF
m_intercepts	lmerModLmerTest	
m_slopes	lmerModLmerTest	> 1000

Models were detected as nested and are compared in sequential order.

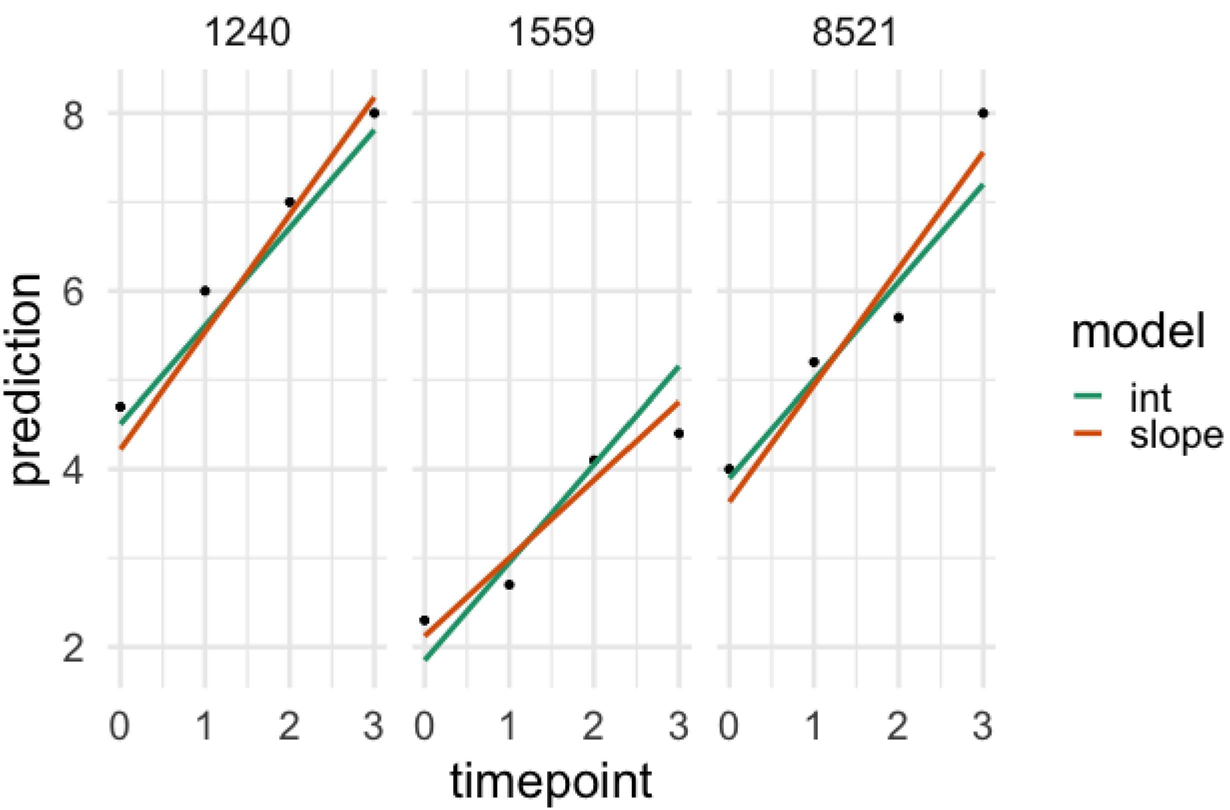
Quick note on Bayes factors

- Pure Bayesians typically hate them – they are sometimes called a Bayesain p–value
- Tests under which model the observed data are more likely
- Larger values indicate less support for the comparison model
- I would advise you only use it in combination with other sources of evidence

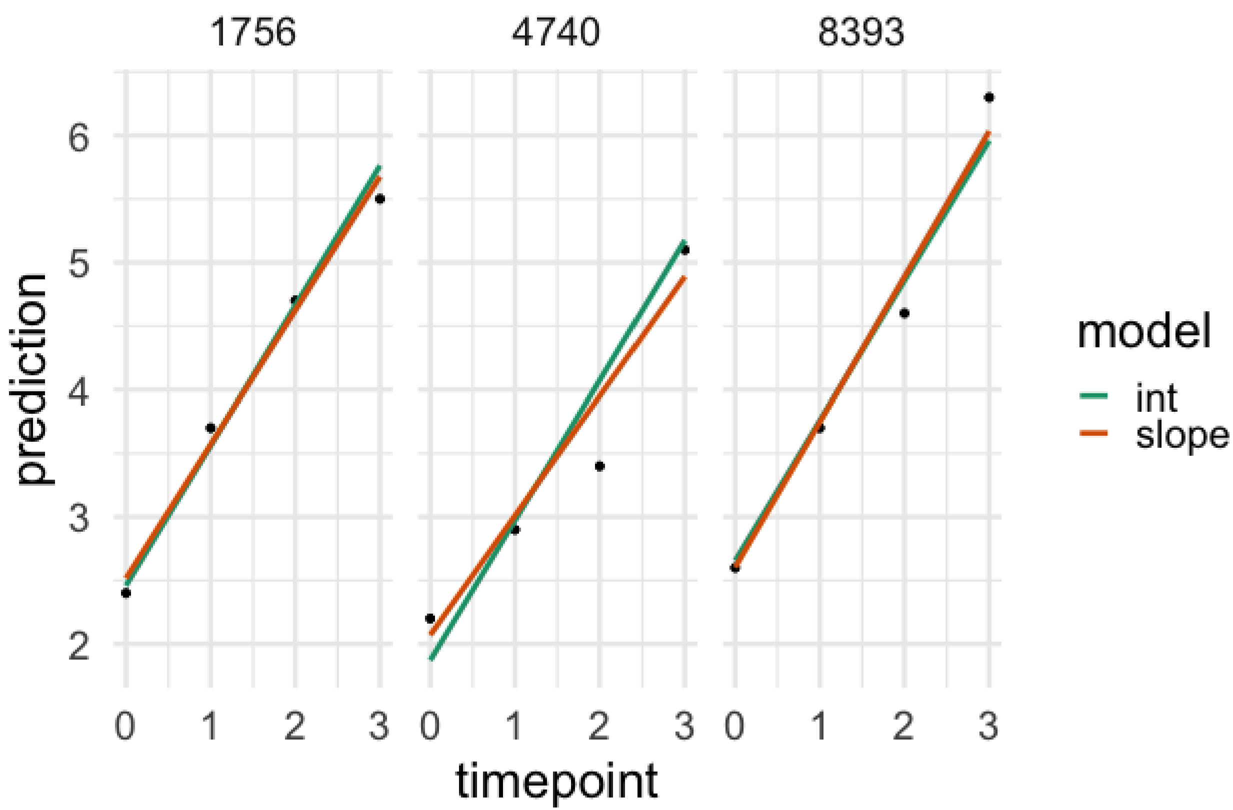
See here for more information

Final comparison

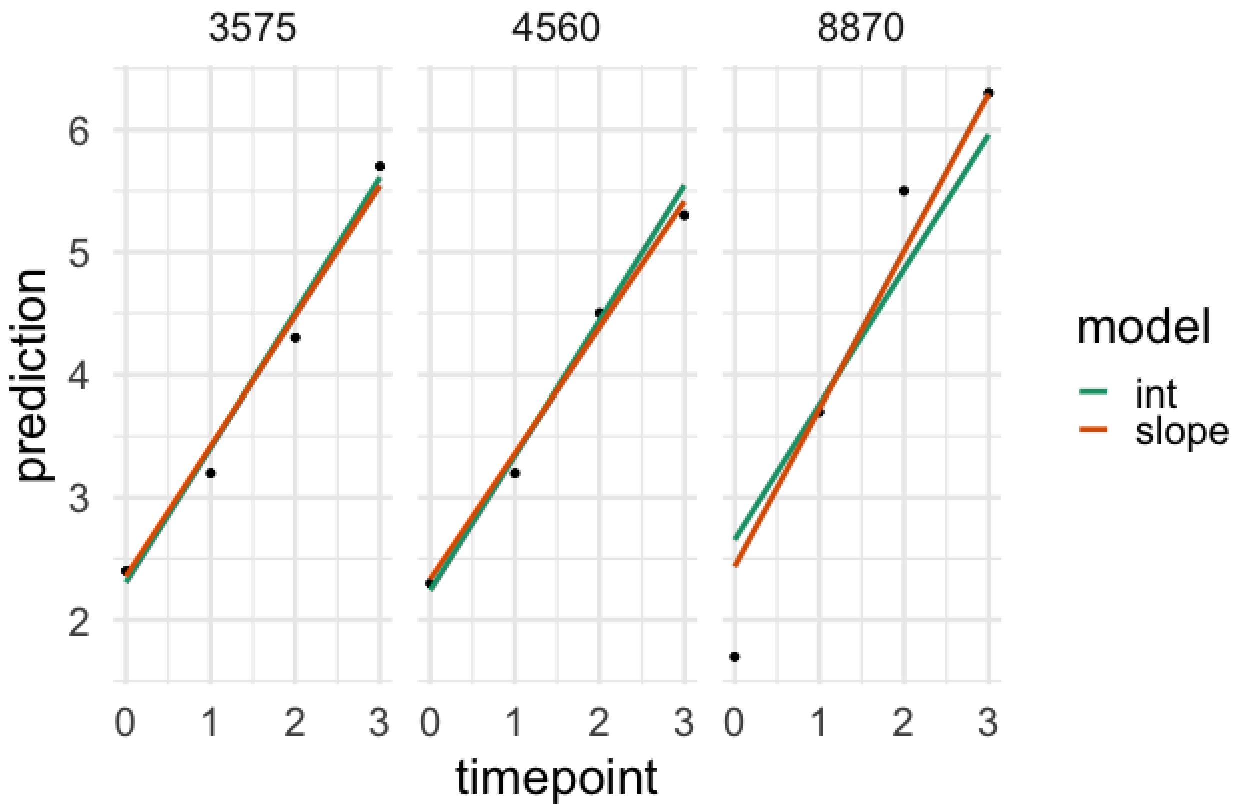
Let's look at the predictions for a few individual participants



Another 3 participants



One more set



3575
4560
8870
prediction
timepoint
6
5
4
3
2
0
1
2
3
model
int
slope

Conclusions

Given the evidence we've looked at I would conclude:

- Both models are a considerable improvement over a linear regression model
- The random intercepts and slopes model is a better fit to the data than the random intercepts only model
- There is more variability in initial starting point than rate of change (which is typical)

- There was a modest correlation between the intercept and the slope, suggesting those who start higher also have steeper rates of change (but this was minor)

Questions

Homework 1

Next time

- Model predictions and visualizations