# Mixed Models Part 1

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# In this workshop...

- We will take our first look at (generalised) linear mixed models - (G)LMMs.
- (G)LMMs allow for models with a combination of fixed and random effects (intercepts and slopes).
- We'll focus on designs with one factor of several levels, and 2 x 2 designs for continuous data.
- We'll also examine of measures of model fit, and using `emmeans()` to interpret interactions in factorial designs.

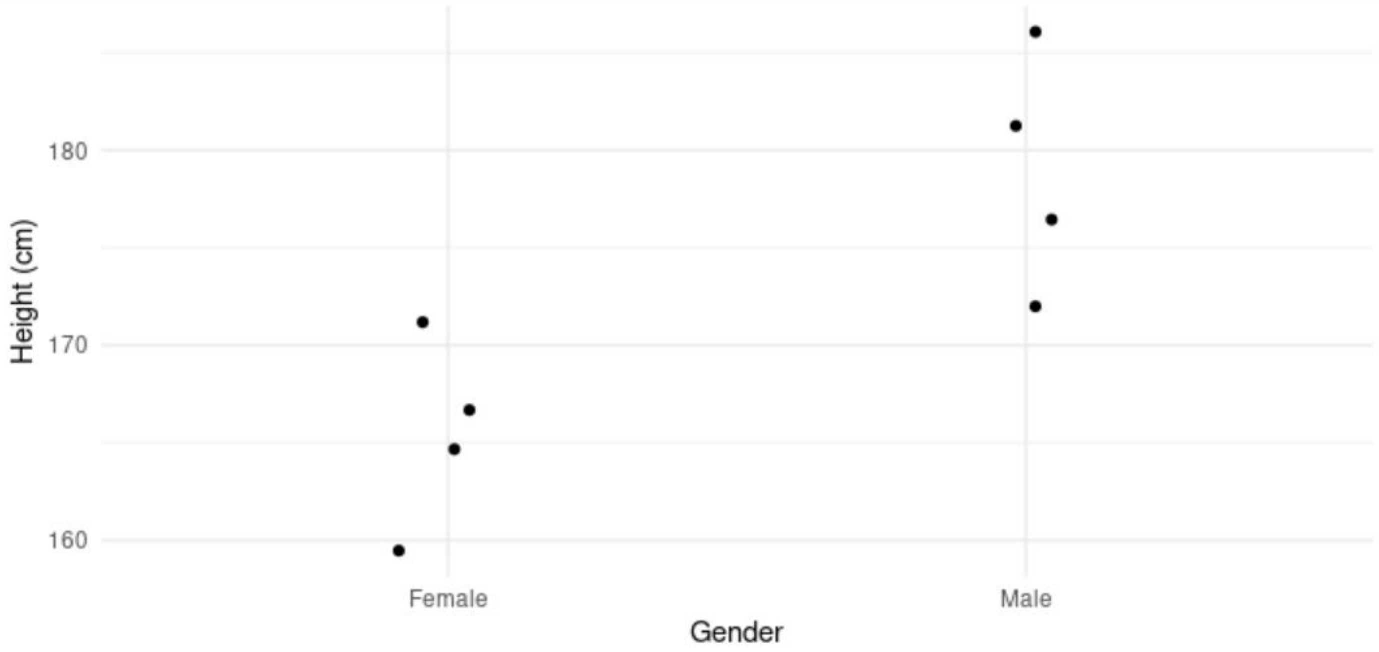
# Why linear mixed models?

(G)LMMs are more flexible than ANOVA, allow for multiple simultaneous random effects (e.g., subjects and items), subject and item covariates, nesting, unbalanced designs, cope with missing data, allow you to model both continuous and categorical IVs and DVs, operate over trial-level data, provide a good balance of Type I and Type II error, and allow you to determine the best statistical models to fit to your data that make the most theoretical sense...

# Recap – linear modelling

Here we have a measure of height for 4 males and 4 females. Can gender be used to predict height?

```
> gender_height_data
# A tibble: 8 x 3
  subject gender height
    <int> <fct>   <dbl>
1       1 male      170
2       2 male      180
3       3 male      175
4       4 male      185
5       5 female    160
6       6 female    170
7       7 female    165
8       8 female    165
```




It certainly looks like Males (on average) are taller than Females (on average).

Let's fit a linear model using the `lm()` function.

```
height_model <- lm(height ~ gender, data = gender_height_data)
```

```
> summary(height_model)

Call:
lm(formula = height ~ gender, data =
gender_height_data)

Residuals:
   Min    1Q Median     3Q   Max
-7.500 -3.125  0.000  3.125  7.500

Coefficients:
        Estimate Std. Error t value Pr(>|t|)
(Intercept)  165.000     2.700  61.104 1.29e-09 ***
gendermale   12.500   3.819   3.273    0.017 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.'
0.1 ' ' 1

Residual standard error: 5.401 on 6 degrees of freedom
Multiple R-squared:  0.641,    Adjusted R-squared:
0.5812
F-statistic: 10.71 on 1 and 6 DF,  p-value: 0.01696
```

We can see here that Gender is a significant predictor ($p$ = 0.017)

```
> summary(height_model)

Call:
lm(formula = height ~ gender, data =
gender_height_data)

Residuals:
   Min     1Q Median     3Q    Max
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Multiple R-squared:  0.641,    Adjusted R-squared:
0.5812
F-statistic: 10.71 on 1 and 6 DF,  p-value: 0.01696
```
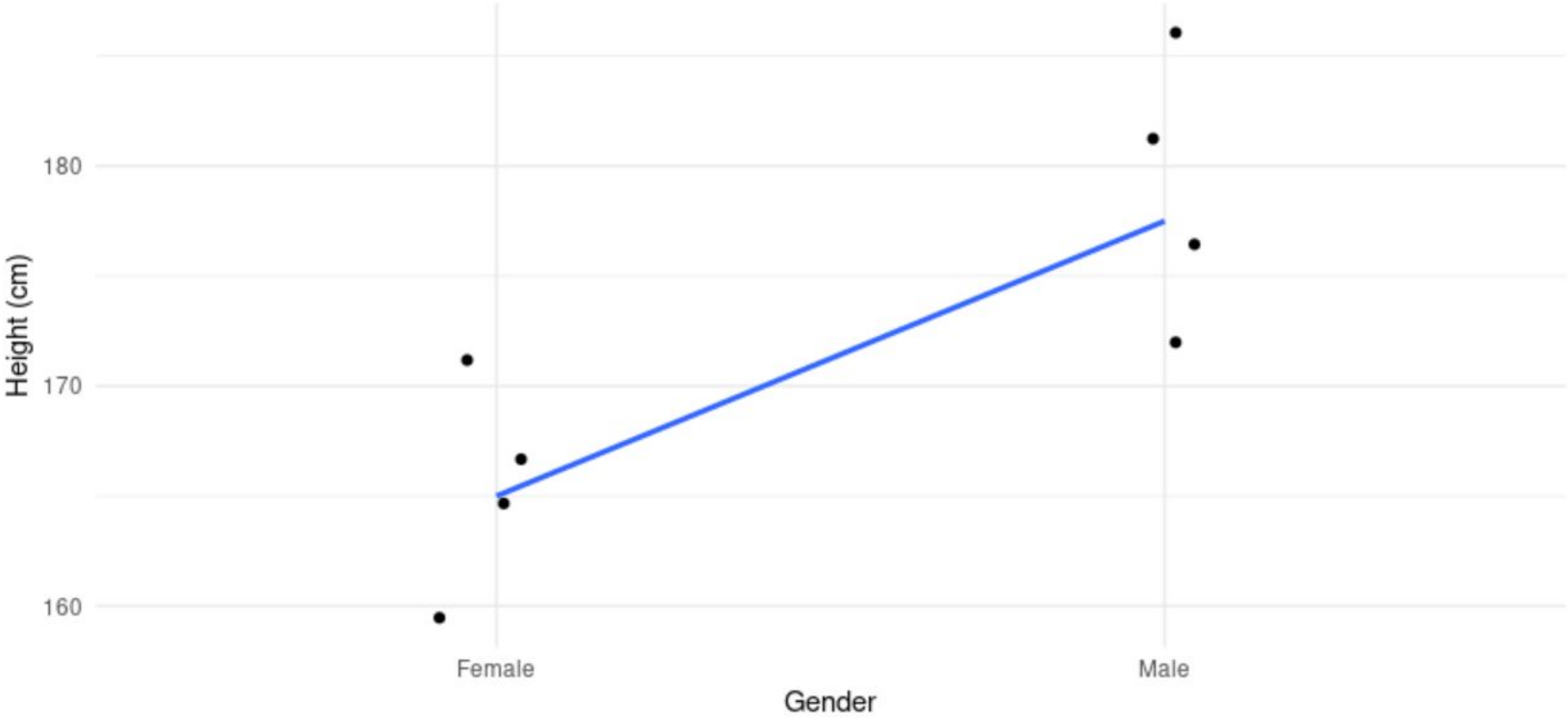

The Intercept (165) corresponds to the mean height of our reference category (Female).

The `gendermale` coefficient (12.5) is the difference between our reference category (Intercept) and our Males.

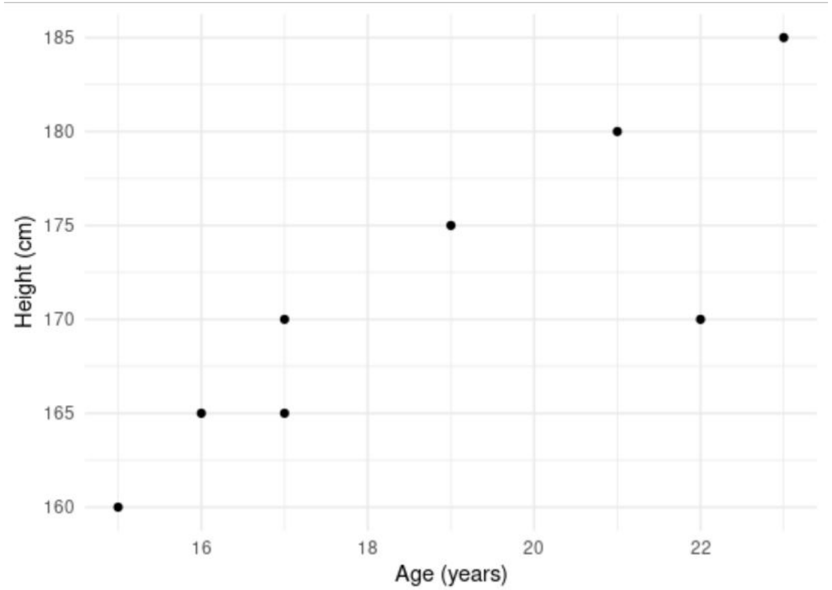
Females were taken as the reference category (i.e., the intercept) simply because R chooses this on an alphabetical basis.


Height (cm)
180
170
160
Female
Male
Gender

# How about with a non-categorical predictor?

Here we have age and height data - can age predict someone’s height in our dataset?

```
> age_height_data
# A tibble: 8 x 3
  subject   age height
    <int> <dbl>  <dbl>
1       1   22  170
2       2   21  180
3       3   19  175
4       4   23  185
5       5   15  160
6       6   17  170
7       7   16  165
8       8   17  165
```



# Let’s build a model...

```
> age_model <- lm(height ~ age, data = age_height_data)
> summary(age_model)

Call:
lm(formula = height ~ age, data = age_height_data)

Residuals:
   Min     1Q Median      3Q    Max 
-9.045 -2.104  1.646  3.201  3.557 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  126.281     11.411  11.067 3.24e-05 ***
age            2.398      0.602   3.984  0.00725 ** 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.721 on 6 degrees of freedom
Multiple R-squared:  0.7257,    Adjusted R-squared:  0.6799 
F-statistic: 15.87 on 1 and 6 DF,  p-value: 0.007252
```

For every increase in Age by 1, Height increases by 2.398. But of course, we know this relationship likely breaks down at a certain age - but for the data we have, we can fit a linear function.

# Linear Mixed Models in R

For mixed effects linear modelling in R, we need to install the package {lme4}. We also want the {lmerTest} package and the {emmeans} package.

```
> library(lme4)
> library(lmerTest)
> library(emmeans)
```

The `{lme4}` package is for model building, the `{lmerTest}` package is for p-value estimates of our model parameters, and the `{emmeans}` package will allow us to run follow-up tests on our models.

# Linear mixed models

- What happens when we have many observations per person that we want to model?

- Imagine we are interested in how a person’s reaction time varies whether they’re responding to Large or Small target items.

- We observe the same 10 people each responding to 5 Large and 5 Small target items.

- We have 10 observations per person. These observations are not independent of each other as (which is an assumption of a linear model).

# Linear mixed models

We can get around the lack of independence by treating participants as a *random effect* such that each participant has their own individual reaction time baseline.

This gives us a separate random intercept value for each participant - in other words, our model can account for individual variation.

This is a mixed effects model:

```
rt ~ condition + (1 | subject) + error
```

This is our random effect term and models each subject having a different random intercept.

# Linear mixed models

Imagine also that we have different Target Items (e.g., 10 different items that were presented in either in Large or Small format).

Each Target Item might have been a little different. One particular Target might just be responded to more quickly (regardless of what condition it was in) - in other words, the Target Items will also have different baselines.

# Linear mixed models

We can capture the random effect of Item in the same way that we did for participants:

```
rt ~ condition + (1 | subject) + (1 | item) + error
```

We now have two random effects and are modelling each Subject **and** each Item having their own individual intercept.

# Fixed vs. Random Effects

**Fixed Effect**
Data has been gathered from all the levels of the factor that are of interest. (Typically your experimental factors and maybe factors like age group - young vs. old for example).

**Random Effect**
The factor has many possible levels, interest is in all possible levels, but only a random sample of levels is included in the data. (Typically participants and items). Typically need > 5 levels in order to estimate effects.

# Linear mixed models

```
> mixed_model_data
# A tibble: 400 x 4
   subject item  condition  rt
   <fct>   <fct> <fct>    <int>
 1 1       1     small      908
 2 1       2     small      884
 3 1       3     small      849
 4 1       4     small      722
 5 1       5     small     1090
 6 2       1     small      890
 7 2       2     small      703
 8 2       3     small      781
 9 2       4     small      942
10 2       5     small      898
# … with 390 more rows
```

```
mixed_model_data %>%
  group_by(condition) %>%
  summarise(mean_rt = mean(rt), sd_rt
= sd(rt))

# A tibble: 2 x 3
  condition mean_rt sd_rt
  <fct>       <dbl> <dbl>
1 large        854.  87.8
2 small        804.  97.5
```

```
mixed_model <- lmer(rt ~ condition + (1 | subject) + (1 | item),
                  data = mixed_model_data)
summary(mixed_model)

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: rt ~ condition + (1 | subject) + (1 | item)
   Data: mixed_model_data

REML criterion at convergence: 4696.8

Scaled residuals:
      Min    1Q  Median   3Q     Max
-2.5385 -0.6366 -0.1475  0.6054  2.6043

Random effects:
 Groups    Name        Variance Std.Dev.
 subject    (Intercept) 1240.3   35.22
 item (Intercept)   442.8   21.04
 Residual           7126.7   84.42
Number of obs: 400, groups:  subject, 10; item, 5

Fixed effects:
            Estimate Std. Error     df t value Pr(>|t|)
(Intercept) 854.140     15.755  12.166  54.213 6.99e-16 ***
conditionsmall    -49.780      8.442  385.000  -5.897 8.12e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr)
conditnsmll -0.268
```

More variability in subjects than in items.

The intercept corresponds to the RT to the Large Condition (854 ms) - going from Large to Small contexts decreases RT by around 50 ms.

```
Fixed effects:
               Estimate Std. Error      df    t value Pr(>|t|)
(Intercept)     854.140     15.755  12.166  54.213 6.99e-16 ***
conditionsmall  -49.780      8.442 385.000  -5.897 8.12e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can see that the experimental condition is significant as we see the *p*-value associated with the t-test on the parameter is significant (*p* <.001).

We can also compare this model with our fixed effect of condition with a model which doesn't have this fixed effect. If the difference between the two models is significant, then we can conclude that the fixed effect is significant.

```
mixed_model_null <- lmer(rt ~ (1 | subject) + (1 | item),
                         data = mixed_model_data)
```

# Comparing Models Using LRT

We can use the Likelihood Ratio Test (LRT) to compare our model with the fixed effect of Condition to the model without.

```
anova(mixed_model, mixed_model_null)

Data: mixed_model_data
Models:
mixed_model_null: rt ~ (1 | subject) + (1 | item)
mixed_model: rt ~ condition + (1 | subject) + (1 | item)
                 npar AIC    BIC     logLik  deviance  Chisq Df  Pr(>Chisq)
mixed_model_null 4   4751.5 4767.5 -2371.8   4743.5
mixed_model      5   4720.1 4740.1 -2355.1   4710.1 33.368  1   7.626e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Data: mixed_model_data
Models:
mixed_model_null: rt ~ (1 | subject) + (1 | item)
mixed_model: rt ~ condition + (1 | subject) + (1 | item)
                 npar AIC    BIC     logLik deviance  Chisq Df Pr(>Chisq)
mixed_model_null 4  4751.5 4767.5 -2371.8   4743.5
mixed_model      5  4720.1 4740.1 -2355.1   4710.1 33.368  1  7.626e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We see the Likelihood Ratio Test is significant - note the AIC, BIC, and deviance values are all lower for the model with our fixed effect. Deviance is the same as the residual sum of squares in linear models.

LRTs should only be conducted with nested models - i.e., when one model is a subset of the other.

# Modelling differences in the magnitude of our effect

So far we have accounted for the possibility that our subjects and items might have different reaction time baselines - that some people are faster at responding that others (which is why we introduced the separate random intercepts).

But what if the *magnitude* of the effect of Condition is different for different subjects, and also what if the *magnitude* of the effect of Condition is different for different items?

# So far we are assuming constant magnitudes of the effect across subjects and items

```
coef(mixed_model)
$subject
   (Intercept) conditionsmall
1     896.2420         -49.78
2     872.6334         -49.78
3     858.2934         -49.78
4     901.0512         -49.78
5     874.9943         -49.78
6     839.7562         -49.78
7     842.9915         -49.78
8     801.1955         -49.78
9     841.2427         -49.78
10    812.9998         -49.78

$item
  (Intercept) conditionsmall
1     868.8340         -49.78
2     833.9098         -49.78
3     852.9328         -49.78
4     837.1982         -49.78
5     877.8252         -49.78
```

The different intercepts for each subjects and for each item take into account individual baseline differences.

However, this doesn’t take into account the fact our effect might be bigger for some subjects than for others (and for some items than for others). In other words, the slopes are all currently the same (-49.78).

# Let's model the variability in the magnitude of the effect

```
mixed_model_slopes <- lmer(rt ~ condition +
                               (1 + condition | subject) +
                               (1 + condition | item),
                               data = mixed_model_data)
```

These modified terms tell the model to expect different intercepts for condition (which we had before) as well as differing slopes as a function of the factor condition. Remember, these are our random effects.

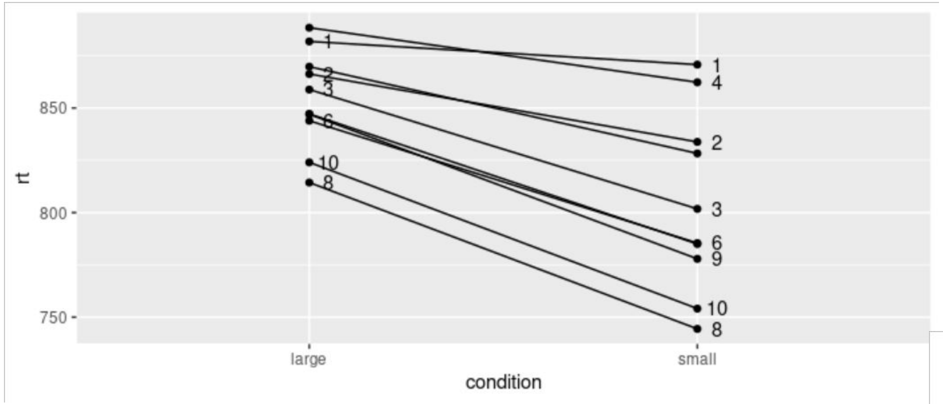
# Now let's look at the coefficients in our model

```
coef(mixed_model_slopes)
$subject
   (Intercept) conditionsmall
1     881.8123   -11.07787
2     866.2407   -32.46840
3     858.8051   -57.03899
4     888.3678   -26.08780
5     869.7440   -41.46898
6     843.8967   -58.48443
7     847.1946   -62.21594
8     814.3650   -69.96477
9     846.9626   -69.07433
10    824.0112   -69.91850

$item
  (Intercept) conditionsmall
1     868.9277   -51.97957
2     838.7420   -59.38390
3     844.5847   -28.36271
4     846.8623   -72.12582
5     871.5834   -37.04801
```

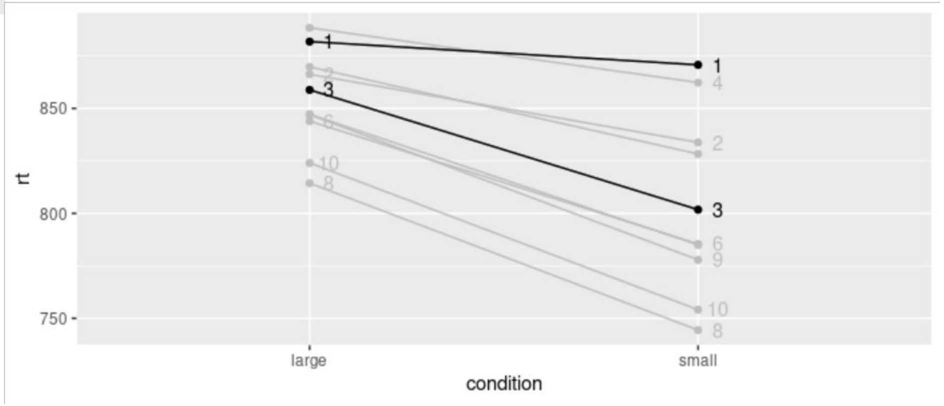
The slopes between the two levels of our condition differ for each subject...

...and also for each item.

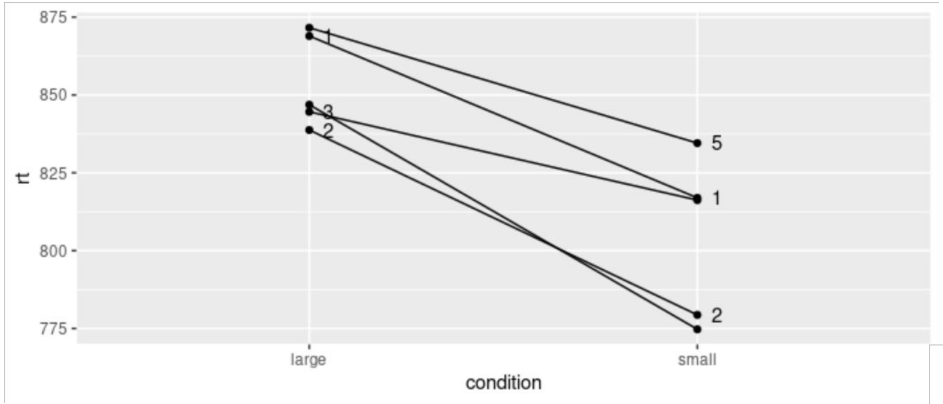
# Plotting the individual intercepts and slopes for subjects



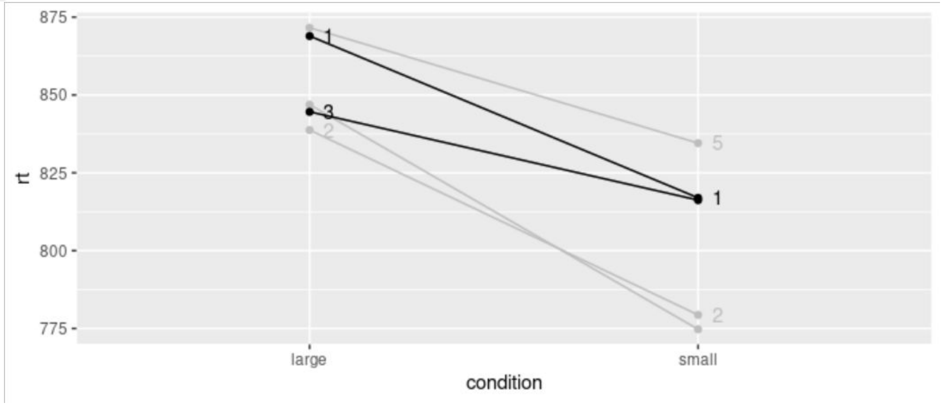

Let's just look at subjects 1 and 3 - for subject 1 we can see the difference between conditions looks pretty small compared to the difference for subject 3.



# Plotting the individual intercepts and slopes for items




Let's just look at items 1 and 3 - for these items, the reaction times for the `small` condition are pretty much the same - but for the `large` condition item 1 is about 25 ms. slower than for item 3.



# Partial Pooling in LMMs

LMMs use partial pooling to estimate the parameters of the model coefficients.

Partial pooling takes account of the individual slopes and intercepts for each level of the random effect structure, but also the slope and intercept of the overall model (which ignores how things vary from one participant to the next).

The use of partial pooling is one reason why LMMs are so powerful - they can cope with missing data (by being sensitive to properties of the overall dataset) and are not too affected by extreme data points (because they know these are quite unlikely in the context of the larger dataset - shrinkage reduces the influence of these extreme values on your parameter estimates).

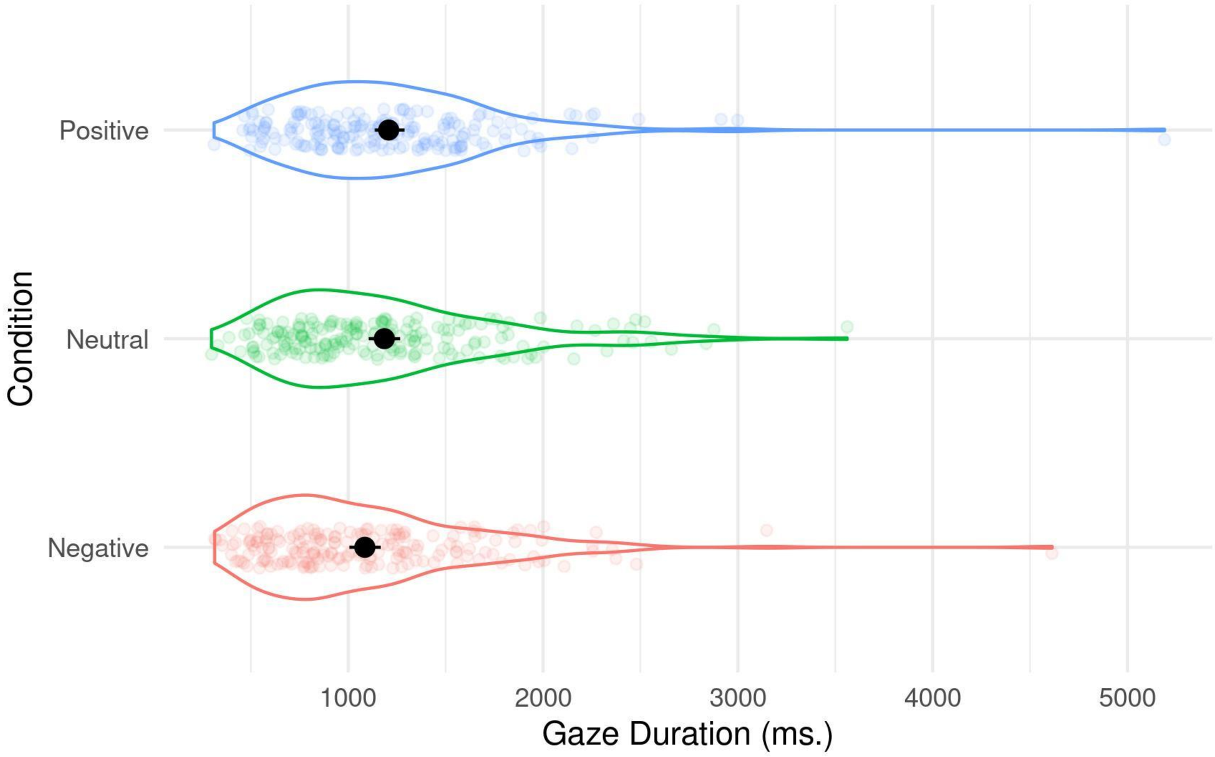
Have a look at this great blogpost by Tristan Mahr:
https://www.tjmahr.com/plotting-partial-pooling-in-mixed-effects-models/

# One Factor Design Example

Imagine we measured 24 subjects' gaze duration while reading a sentence that appeared in one of three conditions - Negative, Neutral, and Positive. We had 24 items. The study is repeated measures (so everyone saw every condition).

```
head(tidied_factor_1_data)
# A tibble: 6 x 4
  subject item  condition  gaze
  <fct>   <fct> <fct>     <dbl>
1 S1      I1   Neutral     867
2 S1      I2   Positive    1061
3 S1      I3   Negative    771
4 S1      I4   Neutral     626
5 S1      I5   Positive    1283
6 S1      I6   Negative    846
```

# One Factor Design Example



# Building our model - attempt 1

```
factor_1_model <- lmer(gaze ~ condition + (1 + condition | subject) +
                       (1 + condition | item), data = tidied_factor_1_data)

boundary (singular) fit: see ?isSingular
```

The warning we receive suggests we might be trying to estimate more parameters that can be estimated using the data set of the size we have. In other words, our model may be too complex. One solution would be to ignore the warning - especially if there is a strong theoretical reason to model all of the terms. Another solution would be to simplify the random effects structure until the warning goes away.

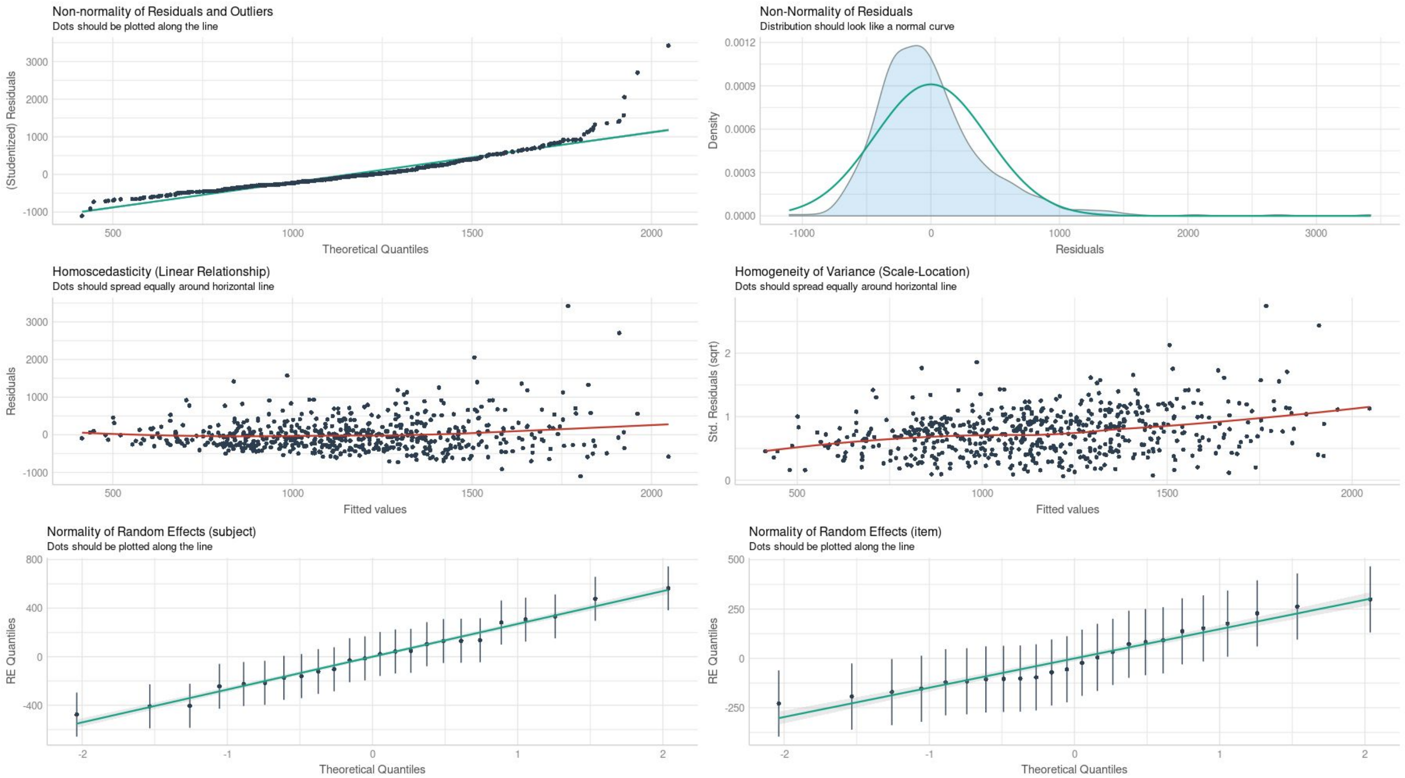
# Building our model - attempt 2

```
factor_1_model <- lmer(gaze ~ condition + (1 | subject) + (1 | item),
                    data = tidied_factor_1_data)
```

If we drop both random slopes, we end up with a model that doesn't generate the warning. We can then use the `check_model()` function from the {performance} package to check our model assumptions.

```
check_model(factor_1_model)
```

# Checking our assumptions



# Interpreting our model

```
summary(factor_1_model)
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: gaze ~ condition + (1 | subject) + (1 | item)
   Data: tidied_factor_1_data

REML criterion at convergence: 8713.1

Scaled residuals:
       Min      1Q  Median      3Q      Max
-2.4240 -0.6246 -0.1505  0.4069  7.5250

Random effects:
 Groups   Name        Variance Std.Dev.
 subject  (Intercept)  81340   285.2
 item   (Intercept)  29586   172.0
 Residual              206838   454.8
Number of obs: 574, groups:  subject, 24; item, 24

Fixed effects:
                      Estimate       Std. Error      df       t value Pr(>|t|)
(Intercept)           1083.90        75.53           45.12    14.350  < 2e-16 ***
conditionNeutral      100.84         46.55           525.13   2.166   0.03073 *
conditionPositive     123.40         46.48           525.09   2.655   0.00818 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
               (Intr) cndtnN
conditnNtrl -0.308
conditnPstv -0.309  0.501
```

These tests compare the Intercept to first the Neural condition, then to the Positive.

# LRT

So the summary on the previous slide tells us only part of the story. Let's compare the model with the fixed effect of condition to a model without.

```
factor_1_model_null <- lmer(gaze ~ (1 | subject) + (1 | item),
                            data = tidied_factor_1_data)

anova(factor_1_model, factor_1_model_null)

Data: tidied_factor_1_data
Models:
factor_1_model_null: gaze ~ (1 | subject) + (1 | item)
factor_1_model: gaze ~ condition + (1 | subject) + (1 | item)
                    npar AIC    BIC    logLik   deviance  Chisq Df Pr(>Chisq)
factor_1_model_null 4 8758.1 8775.6 -4375.1    8750.1
factor_1_model      6 8754.2 8780.3 -4371.1    8742.2   7.9515  2   0.01877 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The models differ - factor_1_model has lower deviance (lower residual sum of squares).

# Which level(s) of our factor differ(s) from which other level(s)?

We're going to use the `emmeans()` function from the {emmeans} package.

```
emmeans(factor_1_model, pairwise ~ condition)
$emmeans
 condition emmean   SE   df lower.CL upper.CL
 Negative  1084 75.5 45.1        932   1236
 Neutral   1185 75.5 45.1   1033  1337
 Positive  1207 75.5 45.0   1055  1359

Degrees-of-freedom method: kenward-roger
Confidence level used: 0.95

$contrasts
 contrast              estimate   SE  df    t.ratio p.value
 Negative - Neutral   -100.8     46.5 525  -2.166  0.0780
 Negative - Positive   -123.4    46.5 525  -2.655  0.0222
 Neutral - Positive   -22.6      46.5 525  -0.485  0.8783

Degrees-of-freedom method: kenward-roger
P value adjustment: tukey method for comparing a family of 3 estimates
```

Note, with Tukey corrected multiple comparisons only the Negative vs. Positive comparison is significant.

# A few points to note...

Models can only be compared to each other using the LRT if they are nested - in other words, if one model is a subset of the other. Models with different fixed and random effects structures cannot be compared in this way - use AIC or BIC comparisons.

AIC is the Akaike Information Criterion and measures how much ‘information’ is not captured by our model (values that are lower are better).

Absolute AIC values cannot be interpreted - they have to be compared with the AIC value of another model. AIC penalises the addition of new parameters in a model - but not as much as BIC.