

Workshop 4 - Mixed Models

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Workshop	Topic
1	Reproducibility and R
2	General Linear Model (Regression)
3	General Linear Model (ANOVA)
4	Mixed Models
5	Data Simulation and Advanced Data Visualisation
6	Reproducible Computational Environments and Presentations

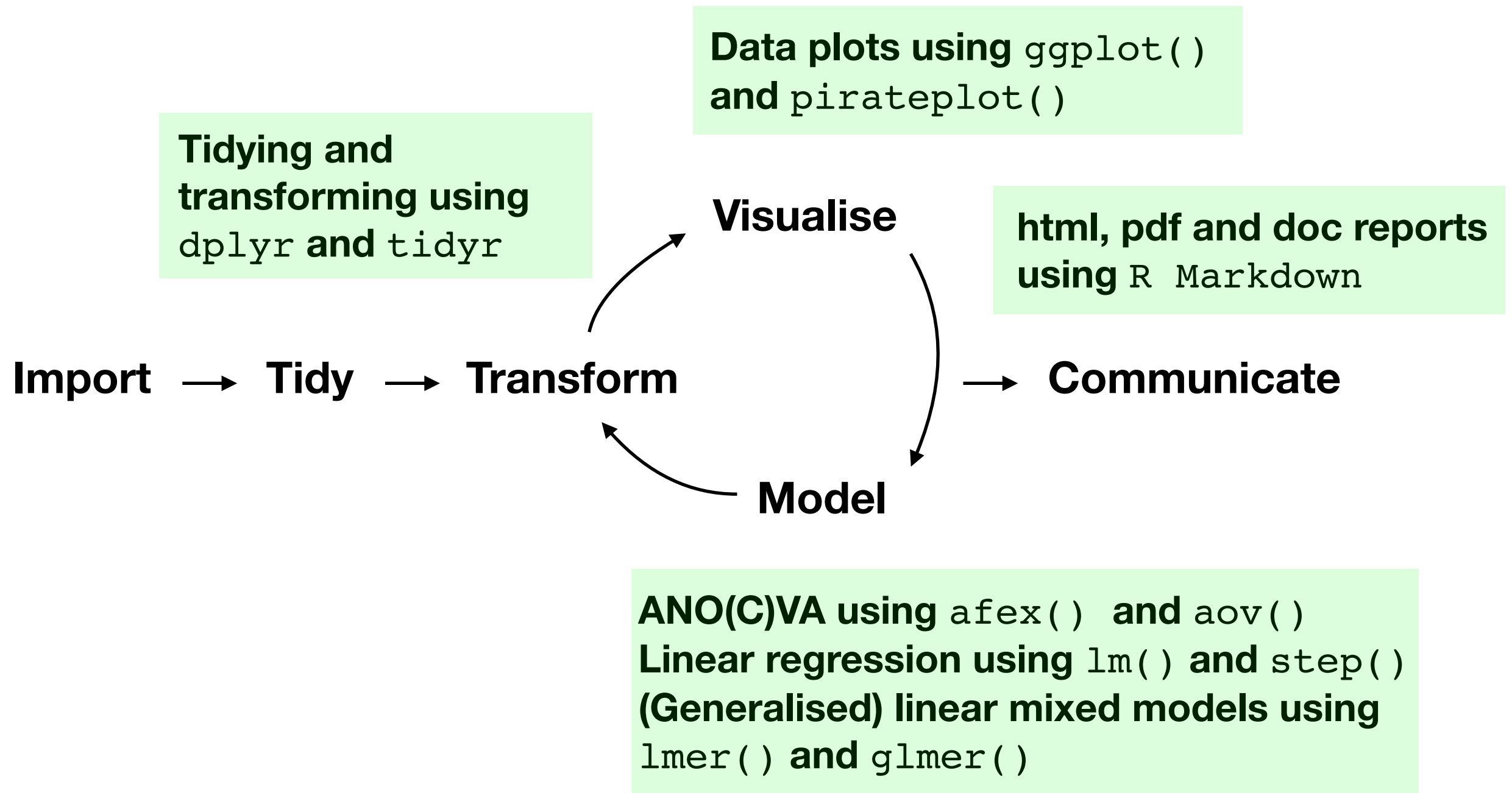
Assignment

Assignment to be completed by Semester 1 exam period.

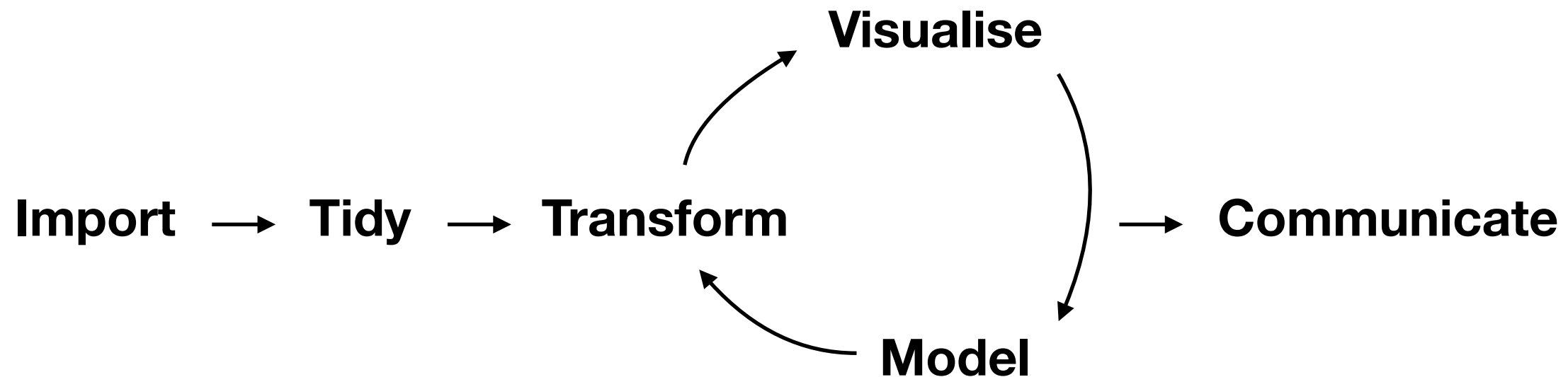
Plan for Today

- Tutorial this morning looking at linear models and (generalised) linear mixed models shortened to (G)LMMs.
- LMMs allow for models with a combination of fixed and random effects (intercepts and slopes).
- Focus on designs of one factor with several levels, and 2 x 2 designs for continuous and dichotomous data.
- Examination of measures of model fit, and using *emmeans* to interpret interactions.
- You doing all of the above in this afternoon's lab.

Workflow



Workflow



**(Generalised) linear mixed models using
`lmer()` and `glmer()`**

Why Linear Mixed Models?

We are going to look at linear modelling and then (generalized) linear mixed modelling. (G)LMMs have taken the biological and behavioural sciences by storm.

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

Recap - Linear modelling in R

Imagine we have data corresponding to males and females and their height.

```
> genderheightdata
# A tibble: 8 x 3
subject gender height
<chr>    <fct>    <chr>
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
```

We might be interested in whether height is predicted by gender.

So, we want to know whether Height is predicted by Gender.

Height ~ Gender

So, we fit a linear model like this:

```
ourmodel <- lm(height ~ gender, data = genderheightdata)
```

The model is stored in the variable `ourmodel`


```
> ourmodel <- lm(height ~ gender, data = genderheightdata)
> summary(ourmodel)
```

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

```
Residuals:
```

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

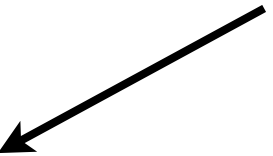
```
Coefficients:
```

	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
```

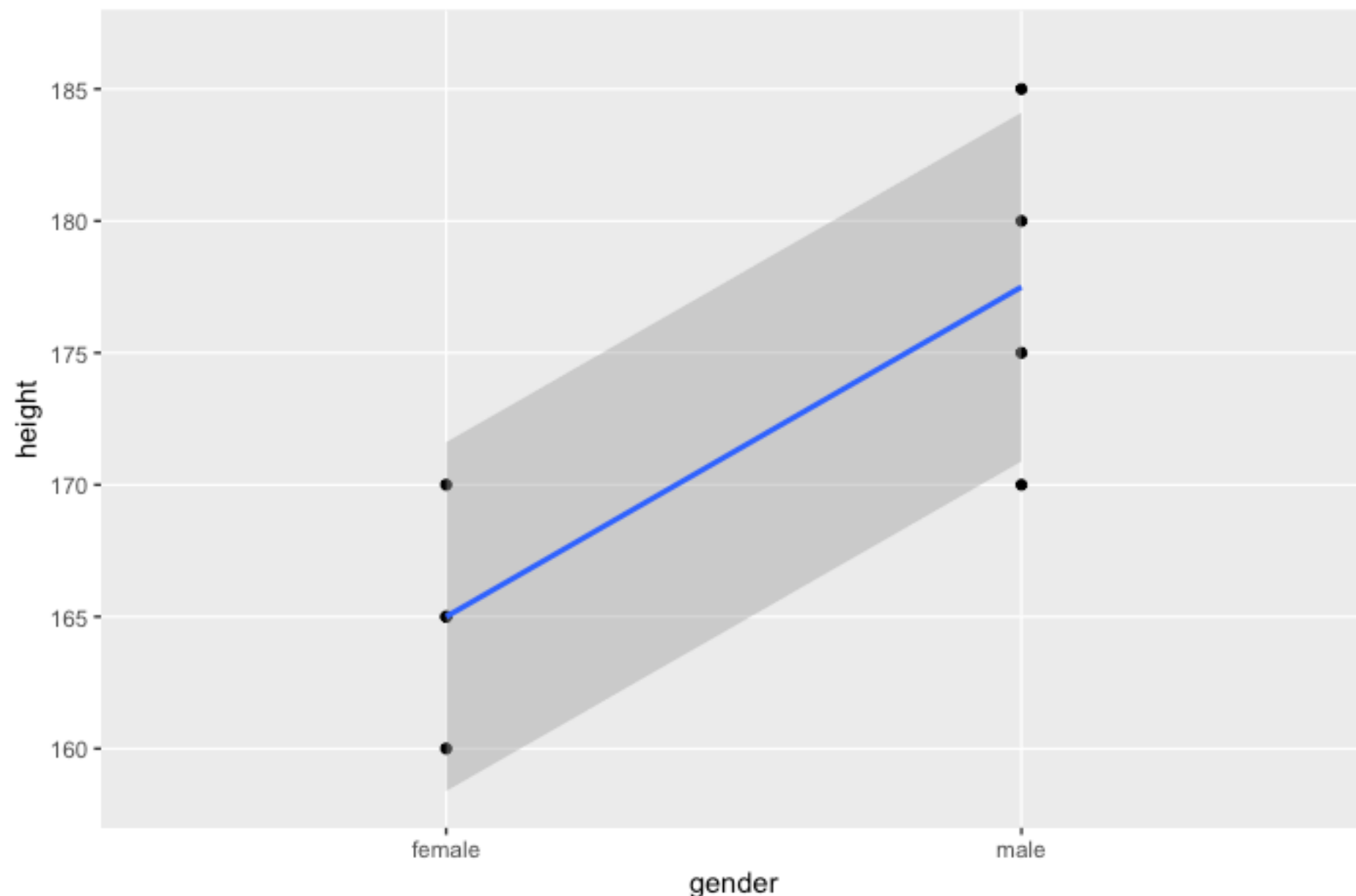
We have a significant predictor (Gender) and model (indicated by the F-ratio).



- For a model with one predictor, the p values associated with the model (i.e., the F value) and the predictor are the same. For models with more than one predictor, this won't be the case.
- The Intercept coefficient (165) corresponds to the mean Height of our reference category (Female). The estimate `gendermale` (12.5) is the *difference* between our reference category and our Males. Females were taken as the reference category (i.e., the intercept) simply because R chooses this on an alphabetical basis (and *Female* comes before *Male*).

We can use ggplot to graph our data. Using the “lm” method, we can generate the linear model (or regression) line.

```
ggplot(genderheightdata, aes(x = gender, y = height, group = 1)) +  
  geom_point() +  
  geom_smooth(method = "lm")
```



- Our predictor doesn't have to be categorical though. We're using the `ageheightdata` here.

```
> ageheightdata
# A tibble: 8 x 3
  subject    age height
  <dbl>   <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
```

Is Height predicted by Age?

```

> ourmodel <- lm(height ~ age, data = ageheightdata)
> summary(ourmodel)

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

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

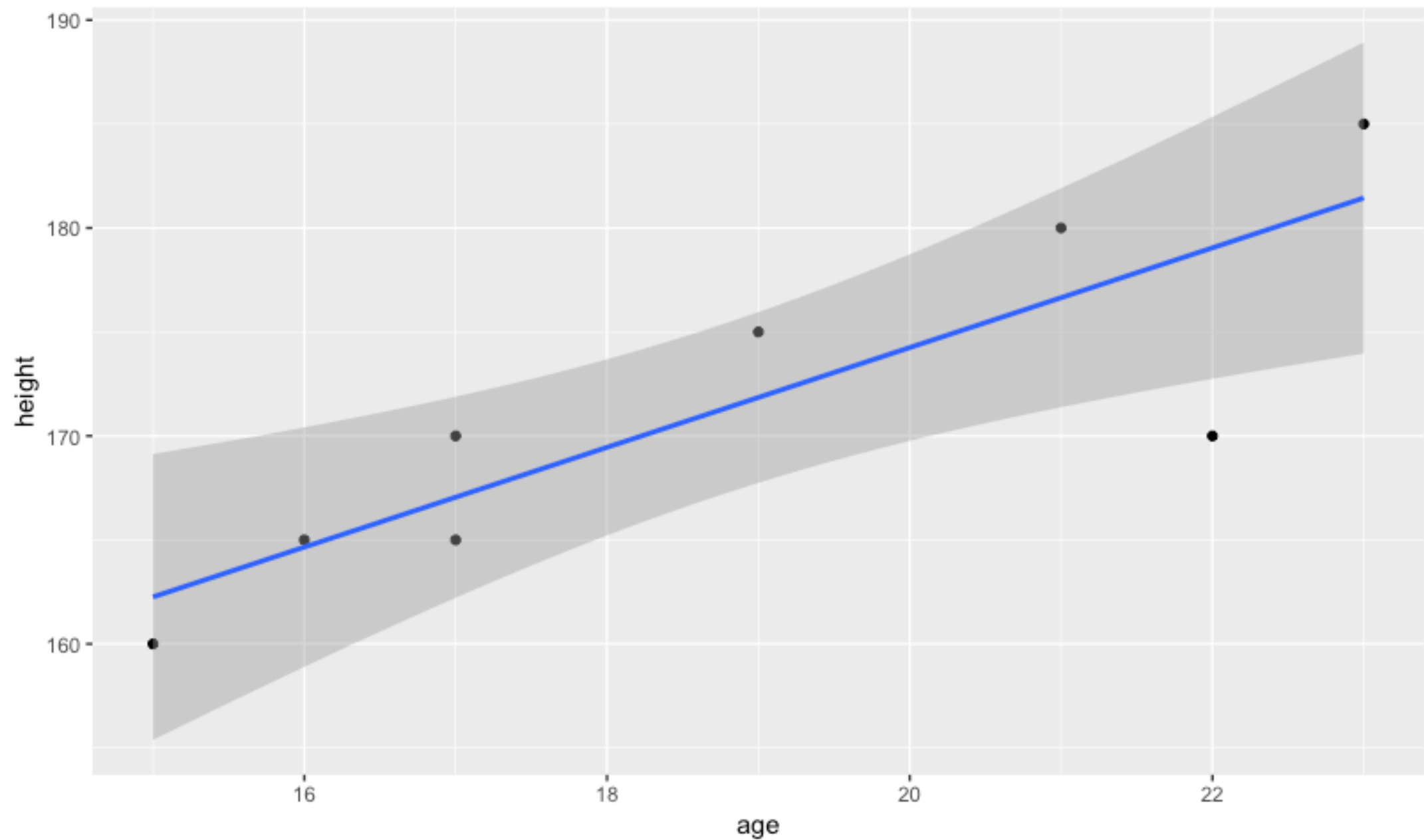
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)   126.281     11.411   11.067 3.24e-05 ***
age             2.398       0.602    3.984 0.00725 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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 breaks down at a certain age - but for the data we have, we can fit a linear function.

```
ggplot(ageheightdata, aes(x = age, y = height)) +  
  geom_point() +  
  geom_smooth(method = "lm")
```



Linear Mixed Models

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

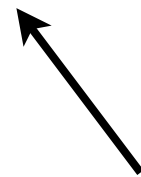
Imagine we are interested in how a person's reaction time varies whether they're responding to Large or Small target items.

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).

- 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*:

$rt \sim \text{condition} + (1 \mid \text{subject}) + \text{error}$



This is our random effect and assumes a different intercept for each participant.

- 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 easier to respond to quickly - in other words, the Target Items will also have different baselines.

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

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

	subject	condition	item	rt
1	1	small	1	1127.4384
2	1	large	1	968.2830
3	1	small	2	1133.4436
4	1	large	2	1051.7208
5	1	small	3	952.1512
6	1	large	3	1131.0116
7	1	small	4	1242.9841
8	1	large	4	999.4708
9	1	small	5	1085.0351
10	1	large	5	865.3554

Showing 1 to 10 of 100 entries

10 participants, and 10 items. Each item appeared in two versions - Small vs. Large.

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.

For mixed effects linear modelling in R, we need to install the package *lme4*. This is the mixed effects model equivalent of *lm* which we used previously. We also want the *lmerTest* package and the *emmeans* package.

```
> install.packages("lme4")
```

```
> install.packages("lmerTest")
```

```
> install.packages("emmeans")
```

← Gives us p-values for our model estimates.

Remember then to load them:

```
> library(lme4)
```

```
> library(lmerTest)
```

```
> library(emmeans)
```

← Allows us to do pairwise comparisons.

```
> mixed_model <- lmer(rt ~ condition + (1 | subject) + (1 | item), data = fulldata)
> summary(mixed_model)
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: rt ~ condition + (1 | subject) + (1 | item)
Data: fulldata
```

REML criterion at convergence: 1276.5

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-2.59882	-0.62360	0.07231	0.57203	2.91523

Random effects:

Groups	Name	Variance	Std.Dev.
subject	(Intercept)	7952.1	89.17
item	(Intercept)	436.3	20.89
Residual		20938.7	144.70

Number of obs: 100, groups: subject, 10; item, 5

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1067.99	36.07	12.62	29.61	4.82e-13 ***
conditionsmall	187.83	28.94	85.00	6.49	5.46e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)
conditnsml1	-0.401

More
variability in
subjects than
in scenarios.

The intercept corresponds to the RT to the Large Condition - going from Large to Small contexts increases RT by around 188 ms.

- To determine whether our mixed effects model is significant, we need to know whether it differs from what we'd expect if Condition didn't influence Reaction Times.

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

- This model which we call `mixed_model_null` removes Condition as a predictor - in other words, it simply contains our random effects.

We can now compare the two models with each other using the anova function:

```
> anova(mixed_model, mixed_model_null)
```

This performs a likelihood ratio test on our 2 models and tells us whether they are significantly different from each other - this test only works with **nested** models - i.e., when one model is a subset of the other.

```

> anova(mixed_model, mixed_model_null)
refitting model(s) with ML (instead of REML)
Data: fulldata
Models:
mixed_model_null: rt ~ (1 | subject) + (1 | item)
mixed_model: rt ~ condition + (1 | subject) + (1 | item)

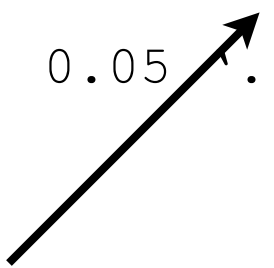
```

	Df	AIC	BIC	logLik	deviance	Chisq	Chi	Df	Pr(>Chisq)
mixed_model_null	4	1336.4	1346.8	-664.18	1328.4				
mixed_model	5	1303.8	1316.8	-646.91	1293.8	34.534		1	4.19e-09 ***

```

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```



This is the important bit as the chi-squared test tells us whether our models differ from each other. It does. Note the AIC, BIC, and deviance values are all lower for the model with our fixed effect.

Note, deviance equals the residual sum of squares in linear models.

- So far we have accounted for the possibility that our participants and items might have different reaction time baselines - that some people are faster at responding than others (which is why we introduced the separate random intercepts).
- But what if the *magnitude* of the effect of Condition is different for different participants, and also what if the effect of Condition is different for different items?


- All this means is that the slopes of our lines might vary as a function of participant (so the difference between the two levels of our Condition factor might be bigger for one person than for another) and as a function of item (so the difference between the two levels of our Condition factor might also be bigger for one item than for another).

```
> coef(mixed_model)
$subject
      (Intercept) conditionsmall
1      983.9157      187.825
10     1149.1395      187.825
2     1069.1966      187.825
3     1155.6409      187.825
4      975.1408      187.825
5      938.9609      187.825
6     1073.0511      187.825
7     1069.8418      187.825
8     1161.5529      187.825
9     1103.5083      187.825
```

```
$item
      (Intercept) conditionsmall
1     1078.522      187.825
2     1081.053      187.825
3     1059.536      187.825
4     1055.631      187.825
5     1065.233      187.825
```

The different intercepts for each item and for each participant take into account individual baseline differences. However, it doesn't take into account the fact our effect might be bigger for some participants than for others (and for some items than for others). In other words, the slopes are all currently the same (187.825).

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




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. These are our random effects.

```
> coef(mixed_model)
```

```
$subject
```

	(Intercept)	conditionsmall
1	1008.7029	118.34480
10	1181.1532	146.17094
2	1257.5895	-178.00567
3	1094.7593	328.35749
4	791.8356	520.54188
5	894.3442	241.83682
6	1007.5660	316.37449
7	1018.4388	288.19304
8	1244.7464	49.85042
9	1180.8127	46.58613

The slopes
between the
two levels of
our Condition
differ for each
participant...



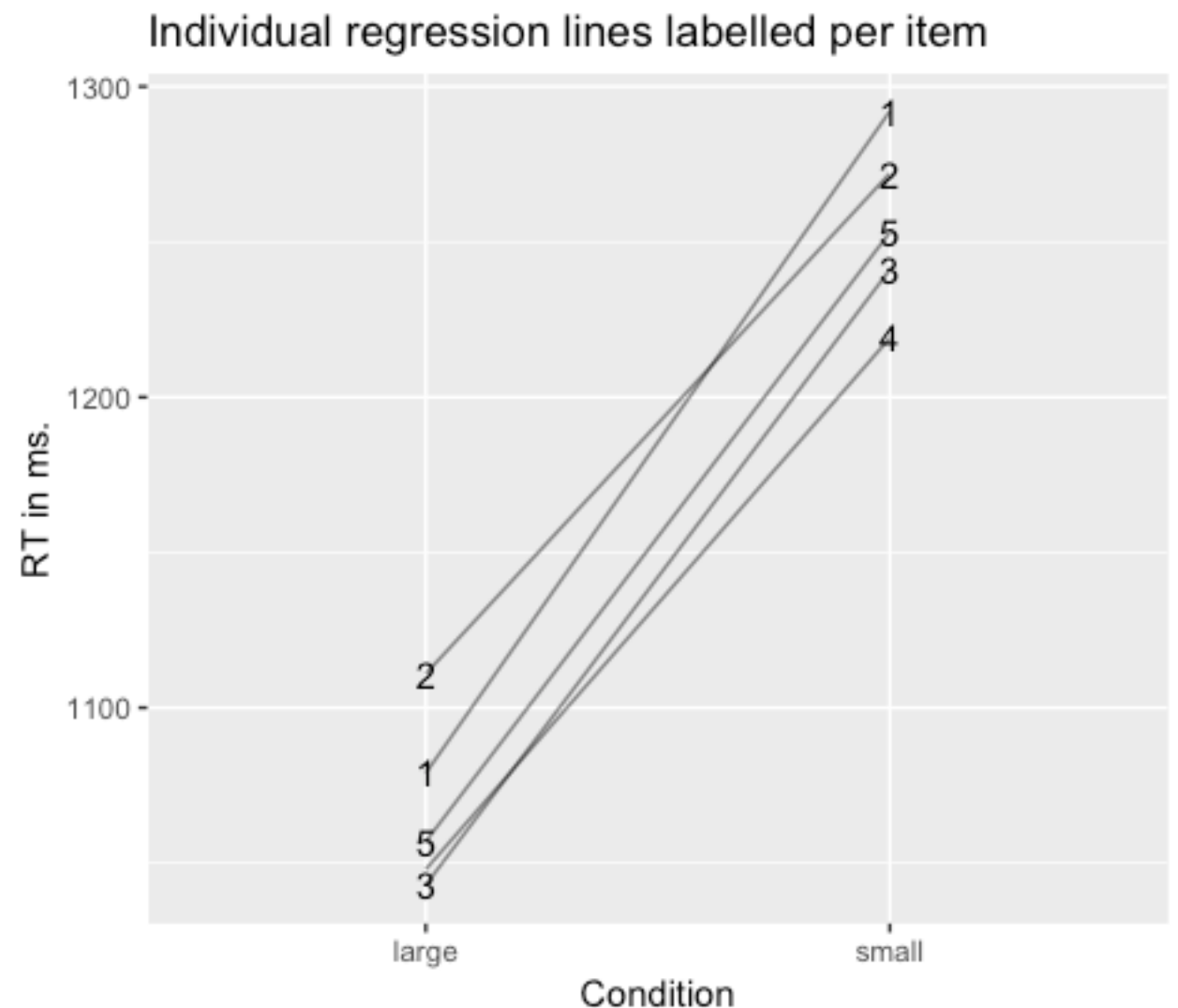
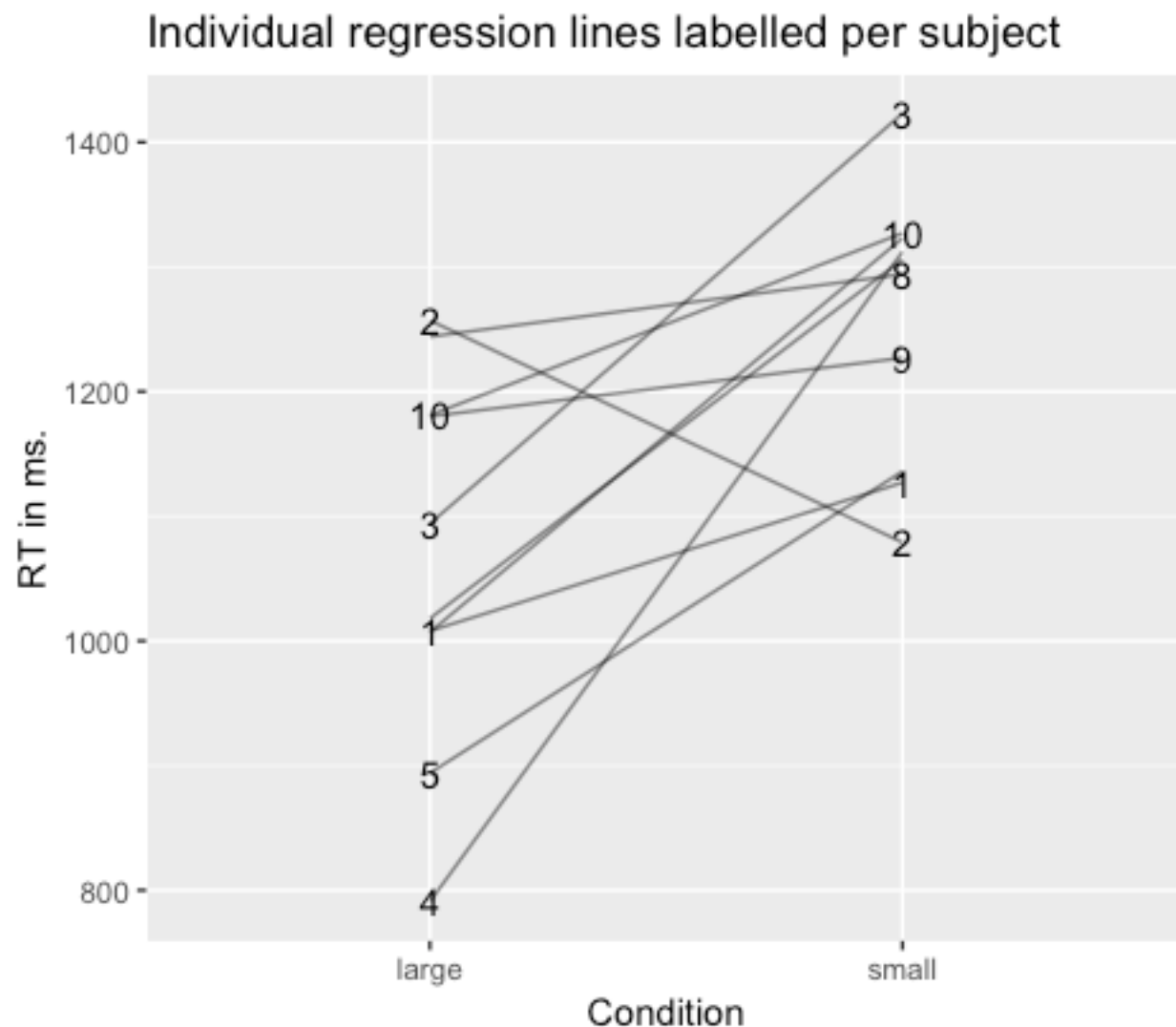
```
$item
```

	(Intercept)	conditionsmall
1	1079.387	213.2465
2	1111.258	160.7852
3	1043.521	198.1986
4	1048.069	171.1310
5	1057.739	195.7639

...and for each
item.



Plotting the slopes of our Condition factor



We see quite a lot of variability in our participants - incl. participant 2 who is going the other way (RT for Small targets is shorter than RT for Large targets)

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 following slides are adapted from Tristan Mahr's great blogpost: <https://www.tjmahr.com/plotting-partial-pooling-in-mixed-effects-models/>

The Dataset

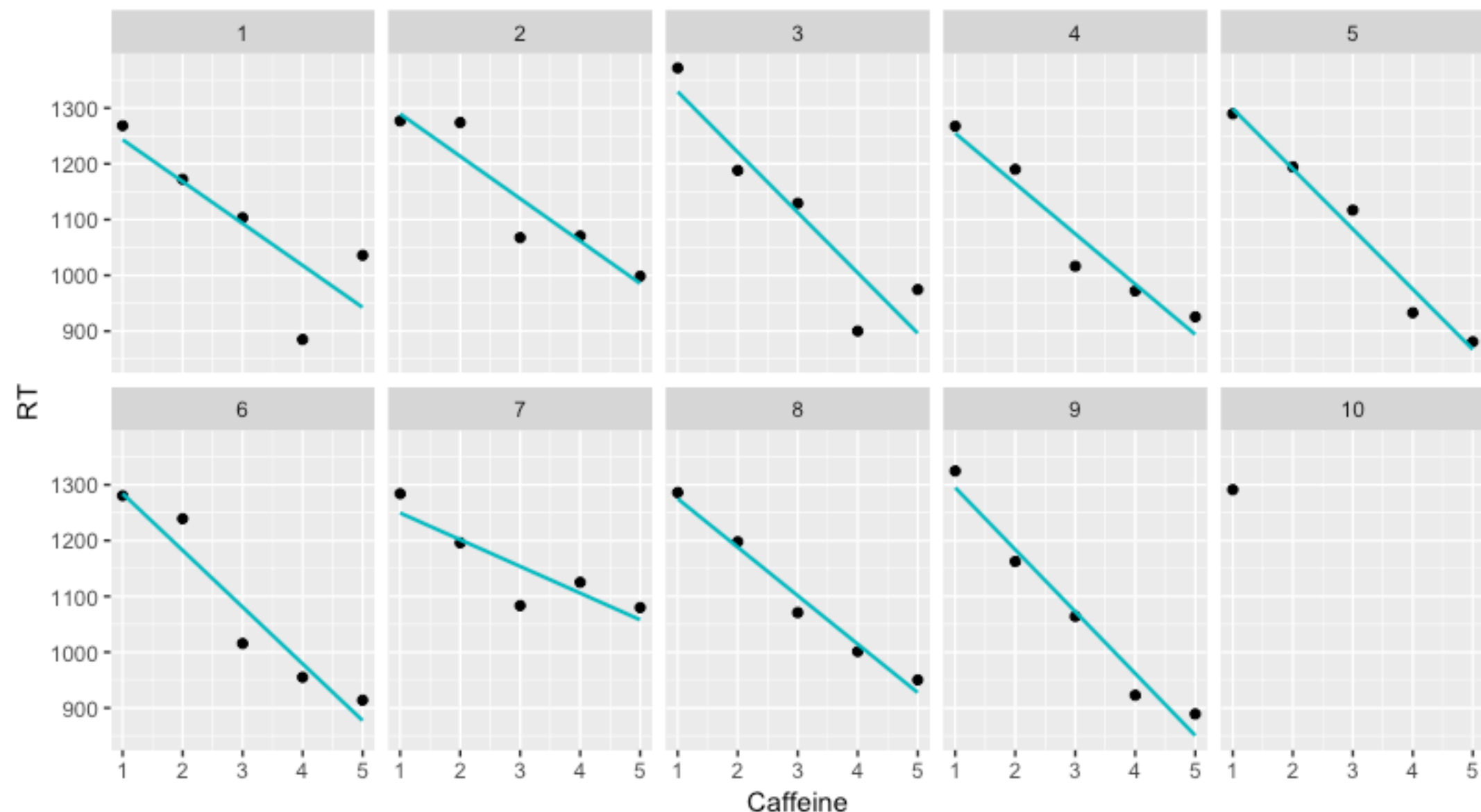
- We are going to use data from 10 participants with measures of reaction time and caffeine consumption.

```
> str(data_all)
'data.frame': 50 obs. of 3 variables:
 $ subject : int  1 1 1 1 1 2 2 2 2 2 ...
 $ caffeine: int  1 2 3 4 5 1 2 3 4 5 ...
 $ rt      : num 1268 1172 1103 885 1036 ...
```

- Contains 50 observations from 10 participants with measures of reaction time and caffeine consumed (measured in cups of coffee).

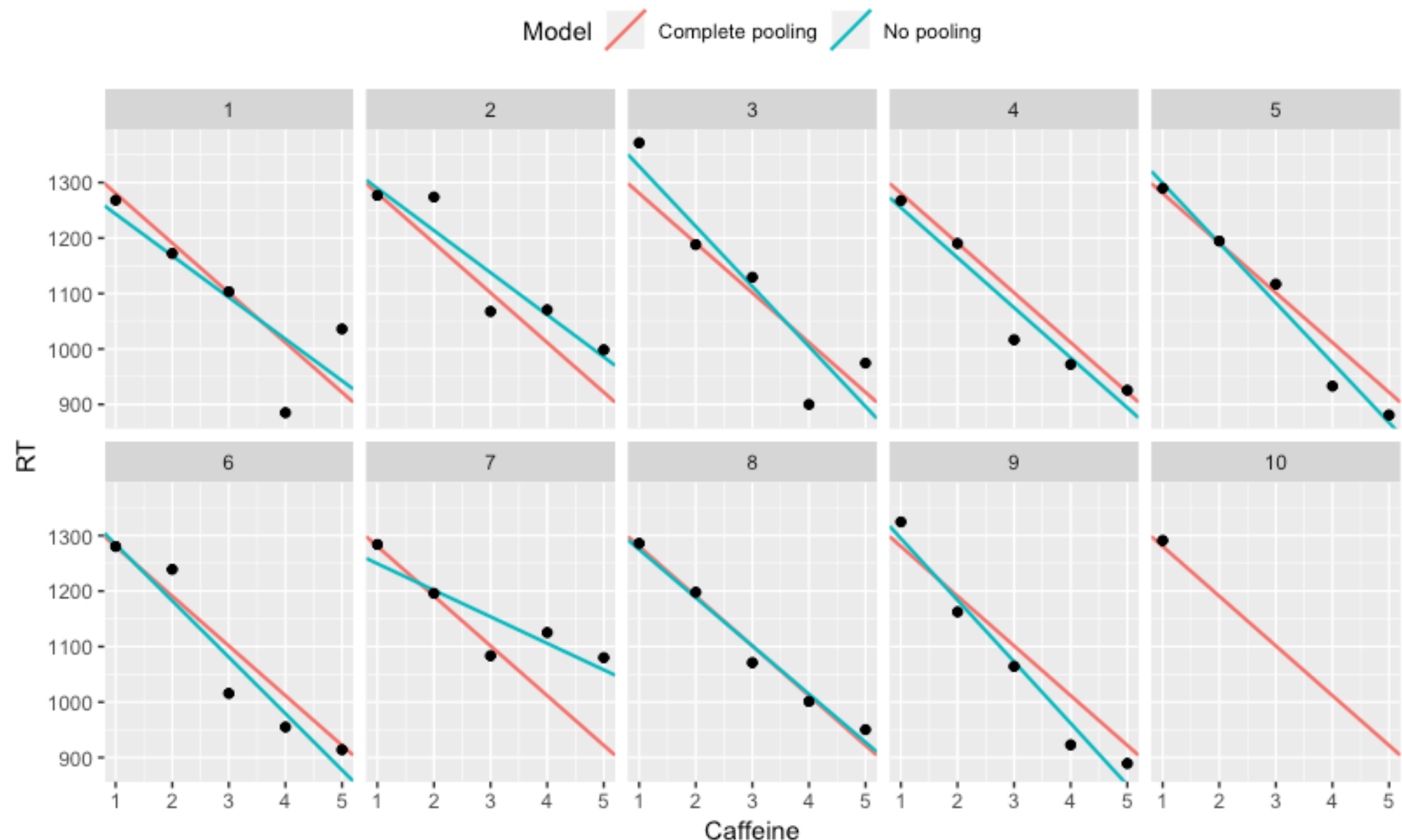
No Pooling

- We plot Reaction Time against Coffee Consumption separately for each Subject we are also adding a regression line by Subject. This is known as No Pooling.



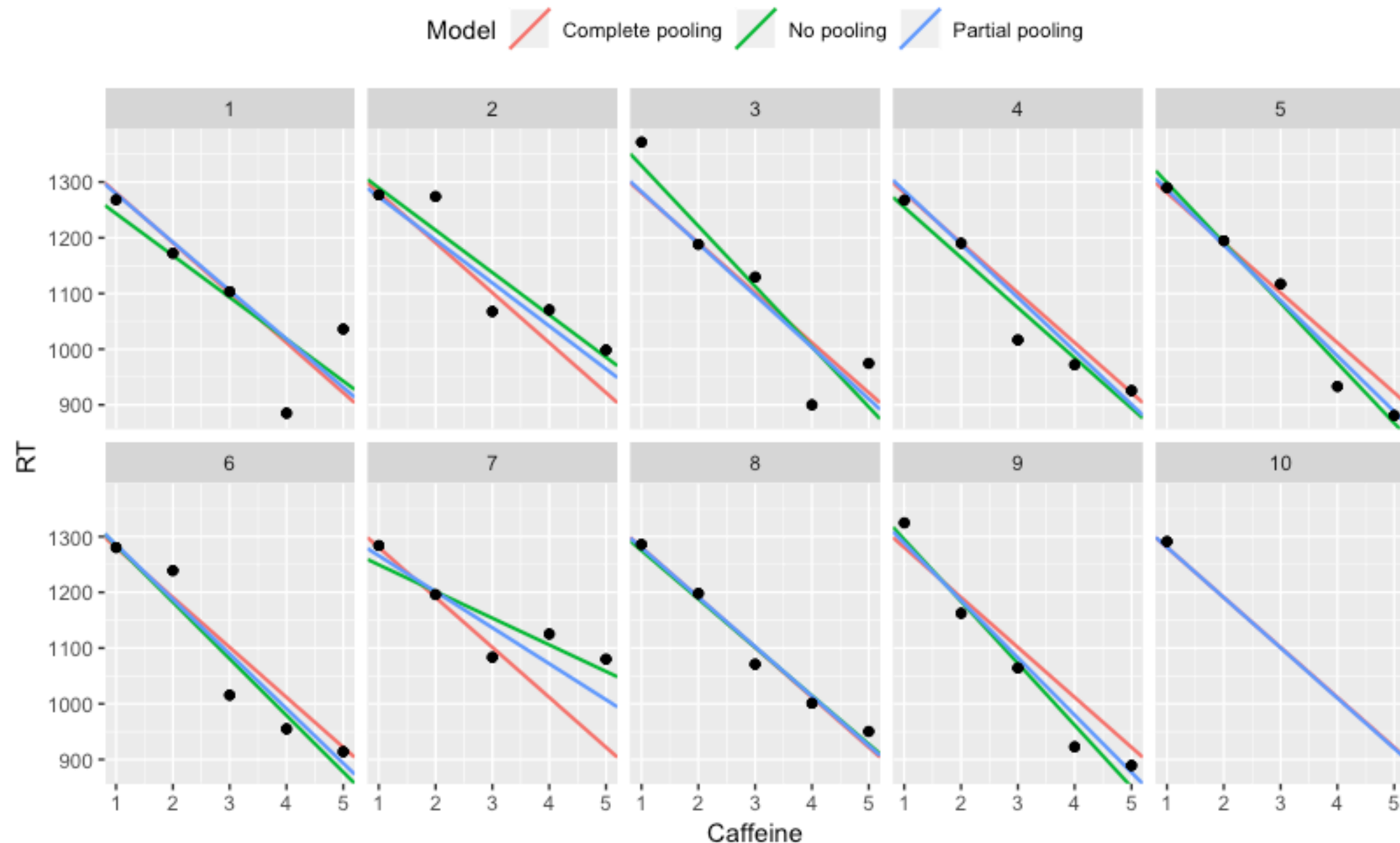
Complete Pooling

- In Complete Pooling, we fit an overall regression line to our entire dataset ignoring differences from one participant to the next.



Partial Pooling

- In Partial Pooling, we pool information from both sets of lines to improve our parameter estimates.



Partial Pooling

- Most of the time the partial pooling and no pooling lines are similar to each other - when they differ, it's because the partial pooling line is being drawn towards the complete pooling line. In other words, it's being affected by the dataset in its entirety.
- For participants with incomplete data, the partial pooling model is like the complete pooling model. The complete pooling and the partial pooling lines are basically parallel - i.e, they have the same slope. That's a reasonable guess given so little information.
- The process by which partial pooling pulls more extreme estimates towards an overall average (i.e., the complete pooling line) is known as *shrinkage*. Subject 7 is a good example of this happening.

Partial Pooling

- 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).

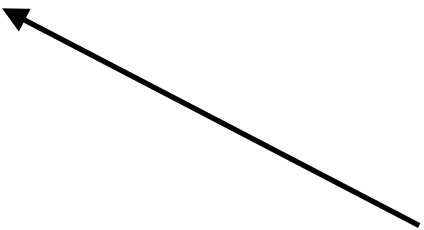
Examples of LMMs for Factorial Designs

- In the first case, we will look at a model where we have one factor with three levels. We have two sets of data we want to analyse - one is eye gaze duration data, the other is the number of times people re-read a section of text.
- In the second case, we will look at a model for a 2 x 2 repeated measures design - this time just with eye gaze duration data as people read a section of text.

One factor with Three levels

- We are going to analyse eye movement data associated with reading a segment of text in one of three conditions - Positive, Negative, or Neutral.

```
1 #install the lme4, lsmeans and lmerTest packages first
2 install.packages ("lme4")
3 install.packages ("lmerTest")
4 install.packages ("emmeans")
5 library (lme4)
6 library (lmerTest)
7 library(emmeans)
```



The *lmerTest* package gives us p -values for our fixed effects, while the *emmeans* allows us to conduct pairwise comparisons.

Read in the data file:

```
> DV <- read_csv("DV_1factor.csv")
```

You can use the function *as.factor* to turn your variable into a factor:

```
> DV$Condition <- as.factor(DV$Condition)
```

You can type the following to check the number of levels of the factor:

```
> levels(DV$Condition)
```

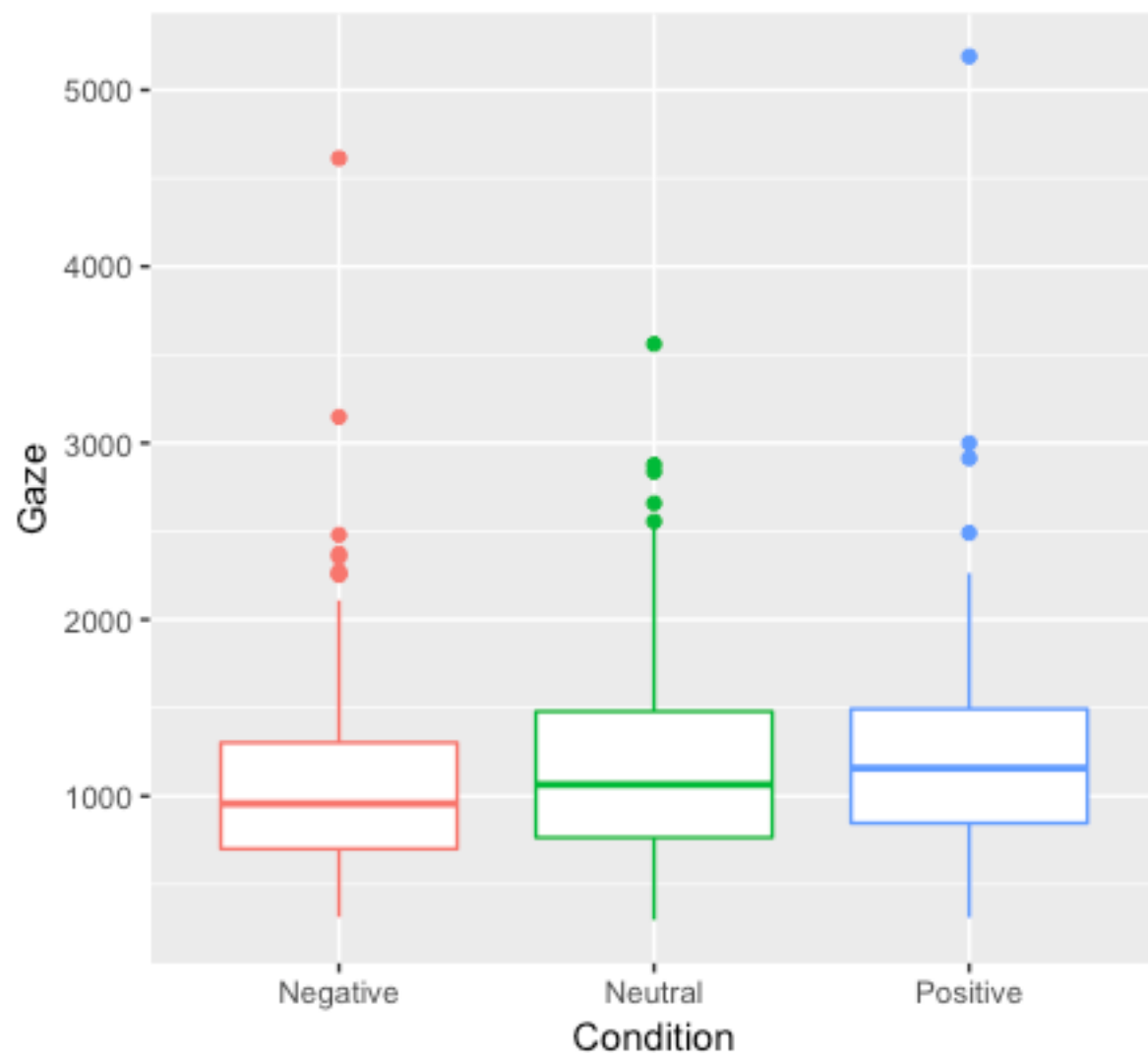
```
> str(DV)
```

```
Classes 'spec_tbl_df', 'tbl_df', 'tbl' and 'data.frame': 574 obs. of 5  
variables:
```

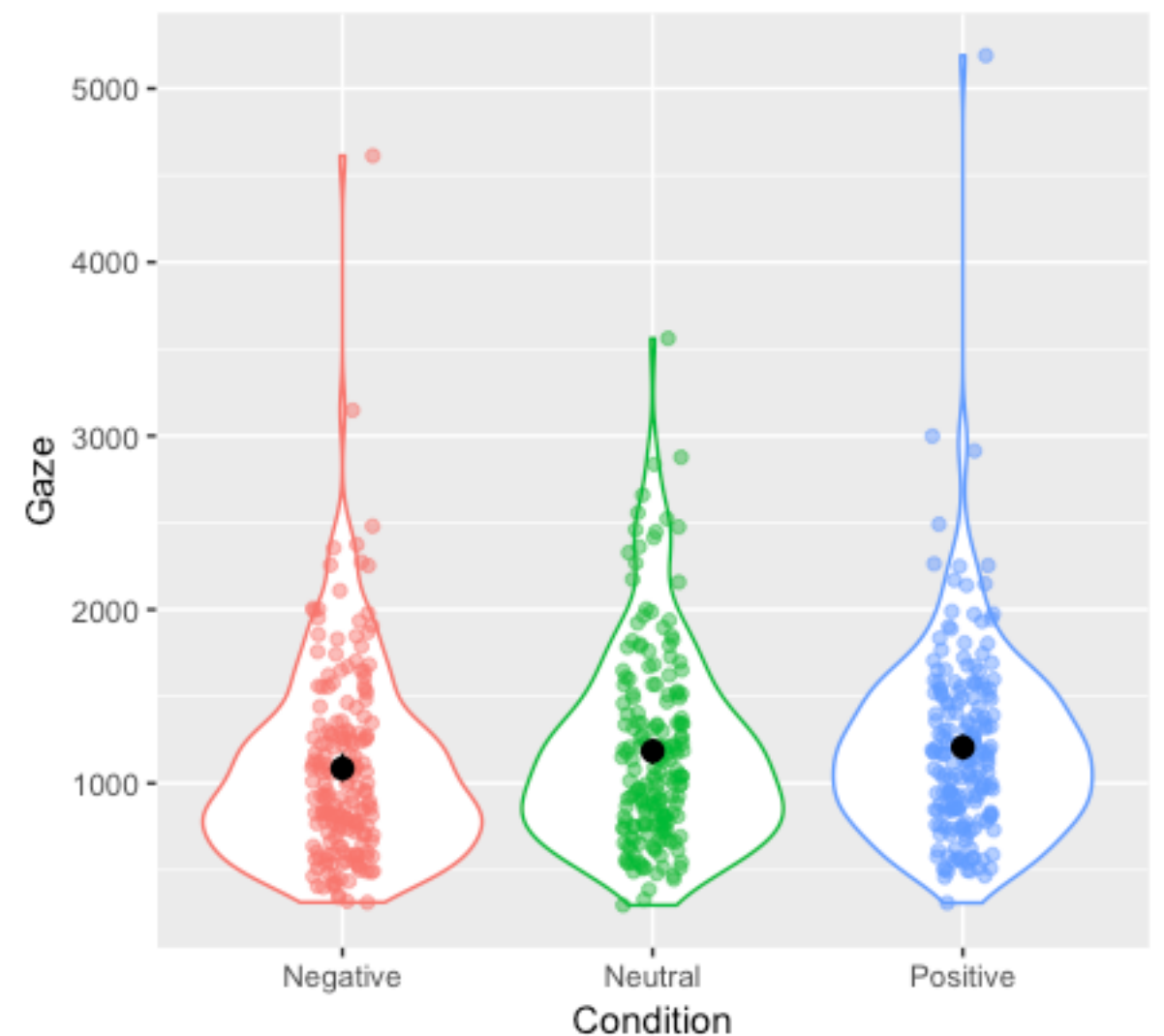
```
$ Subject : chr "S1" "S1" "S1" "S1" ...  
$ Item    : chr "I1" "I2" "I3" "I4" ...  
$ Condition: Factor w/ 3 levels "Negative","Neutral",...: 2 3 1 2 3 1 2 3  
1 2 ...  
$ Region  : chr "R3" "R3" "R3" "R3" ...  
$ Gaze    : num 867 1061 771 626 1283 ...
```


Visualising the Data

```
ggplot(DV, aes(x = Condition, y = Gaze, colour = Condition)) +  
  geom_boxplot() + guides(colour = FALSE)
```



```
ggplot(DV, aes(x = Condition, y = Gaze, colour = Condition)) + geom_violin() +  
  geom_jitter(width = .1, alpha = .5) +  
  stat_summary(fun.data = "mean_cl_boot", colour = "black") +  
  guides(colour = FALSE)
```




```
25 model.null <- lmer (Gaze ~ (1 + Condition| Subject) + (1 + Condition| Item), data=DV, REML=TRUE)
26 model.full <- lmer (Gaze ~ Condition + (1 + Condition| Subject) + (1 + Condition| Item), data=DV, REML=TRUE)
27 anova (model.null, model.full)
28 summary (model.full)
```

- Line 25 creates a variable called model.null associated with just random effects of Subjects and Items. Note there is no fixed effect.
- Line 26 create a variable called model.full which includes both the random and fixed effects.
- Line 27 tests where the model.full is a better fit to our data and model.null. If it is, it means adding the fixed effect means we are able to explain our data better than if we don't add it.
- Line 28 then asks for the model.full parameters to be displayed.

The Output

```
> anova(model.null, model.full)
refitting model(s) with ML (instead of REML)
Data: DV
Models:
object: Gaze ~ (1 + Condition | Subject) + (1 + Condition | Item)
..1: Gaze ~ Condition + (1 + Condition | Subject) + (1 + Condition |
..1: Item)
      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
object 14 8773.4 8834.4 -4372.7   8745.4
..1    16 8771.2 8840.8 -4369.6   8739.2 6.236    2   0.04425 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



For model comparisons, a different parameter estimator must be used (R will do this for you). REML should be used to estimate parameters when you report them.


- Our two models differ significantly from each other. The one that fits our data the best has the lower AIC value. AIC is the Akaike Information Criterion and measures how much ‘information’ is not captured by our model (values that are relatively lower are better). NOTE - absolute AIC values cannot be interpreted - they have to be compared with the AIC value of another model.

```

Random effects:
Groups   Name                Variance Std.Dev. Corr
Subject (Intercept)         108205   328.95
        ConditionNeutral    2589     50.88  -1.00
        ConditionPositive    6425     80.16  -1.00  1.00
Item     (Intercept)         32985   181.62
        ConditionNeutral    1296     36.00   0.00
        ConditionPositive    3897     62.42  -0.54  0.84
Residual                    204916   452.68
Number of obs: 574, groups: Subject, 24; Item, 24

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   1083.76     83.40   30.15  12.994 6.88e-14 ***
ConditionNeutral  101.04     48.05   52.01   2.103  0.0403 *
ConditionPositive 123.54     50.70   22.73   2.437  0.0231 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```



- This is what we're mainly interested in. We know the model itself is significantly better than the null model. These comparisons tell us what differences are driving the effect.

- Think of these like the contrasts that are used to interpret significant ANOVAs. In this case, the Neutral and Positive conditions are each being compared to the Negative condition (or the intercept of the regression line). The estimates tell us that the intercept is 1084 (which is the Negative condition mean). The Neutral mean is $1084 + 101$, while the Positive mean is $1084 + 124$.

A few points to note so far...

- Models can only be compared to each other using the ANOVA function 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.
- If using treatment coding for Contrasts, sometimes the Intercept (or reference level condition) chosen by R isn't the one you might want. You can change it using: `DV$Condition <- relevel (DV$Condition, ref = 3)` where `ref` corresponds to the level of the factor `Condition` you want as the intercept, `DV` corresponds to the datafile, and `Condition` corresponds to the factor you want to relevel.

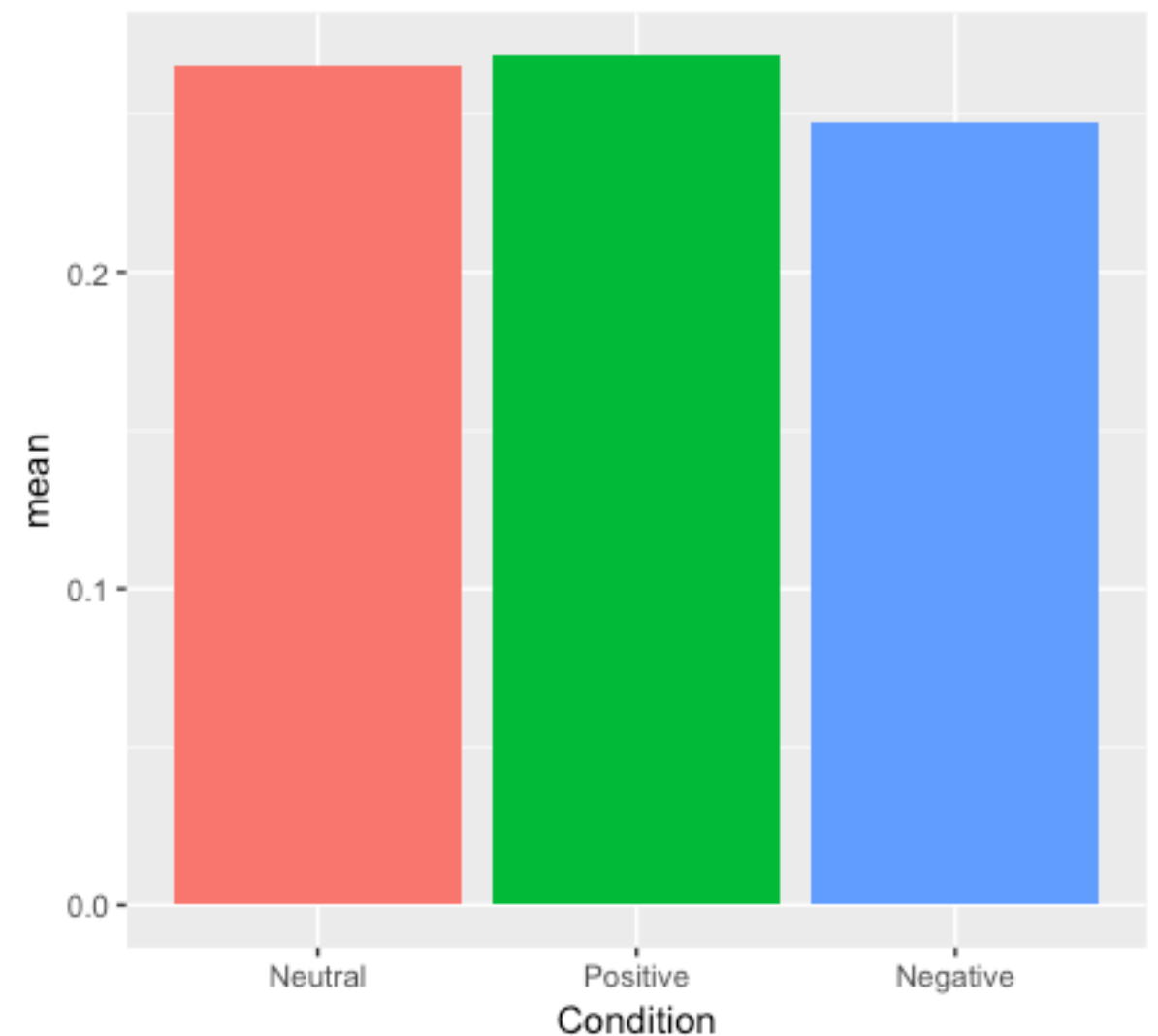
What if our DV isn't a continuous variable?

- In eye movement work, we measure both gaze time (ms.) and also the number of times people re-read a region of text. For any one person reading a region of text, they either re-read it, or they don't. Thus, the data are binary (not continuous). In our data set, 1 corresponds to a region being re-read, 0 to not being re-read.

for workshop.R* × RO × DV ×					
Filter					
	Subject	Item	Condition	Region	DV
1	S1	I2	Positive	R3	0
2	S1	I3	Negative	R3	0
3	S1	I4	Neutral	R3	0
4	S1	I5	Positive	R3	0
5	S1	I6	Negative	R3	0
6	S1	I7	Neutral	R3	1
7	S1	I8	Positive	R3	0
8	S1	I9	Negative	R3	0
9	S1	I10	Neutral	R3	0
10	S1	I11	Positive	R3	0
11	S1	I12	Negative	R3	0
12	S1	I13	Neutral	R3	0

Showing 1 to 12 of 553 entries

- Here is our data file - our DV is categorical - either 1 or 0.



- Looks like we might have *slightly* fewer regressions in the Negative condition.

- For binomial data, we have to use the generalised linear model (`glmer`) and the binomial distribution. This is the syntax for such a model with both fixed and random effects:

```
model.full <- glmer (DV ~ Condition + (1 + Condition|Subject) + (1 + Condition|Item), data=R0, family=binomial)
```

- When we run it, we get an error (that you will get used to seeing again and again!)

```
> model.full <- glmer (DV ~ Condition + (1 + Condition|Subject) + (1 + Condition|Item), data=R0, family=binomial)
Warning message:
In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv,  :
  Model failed to converge with max|gradl| = 0.0171702 (tol = 0.001, component 1)
```


- So what can we do? We need to simplify the random effects structures. We can do this by dropping terms one by one until we find a model that can be fitted to our data. For example, we could drop the random slope from our items random effect first.
- For this particular example, the most complex model that works involves only random intercepts.

```
> model.interceptonly <- glmer(DV ~ Condition + (1 | Subject) + (1 | Item), data = RO, family = binomial)
> model.null <- glmer(DV ~ (1 | Subject) + (1 | Item), data = RO, family = binomial)
> anova(model.interceptonly, model.null)
```

```

> anova(model.interceptonly, model.null)
Data: RO
Models:
model.null: DV ~ (1 | Subject) + (1 | Item)
model.interceptonly: DV ~ Condition + (1 | Subject) + (1 | Item)

```

	Df	AIC	BIC	logLik	deviance	Chisq	Chi	Df	Pr(>Chisq)
model.null	3	601.97	614.91	-297.98	595.97				
model.interceptonly	5	605.70	627.28	-297.85	595.70	0.2617		2	0.8773

- Our model with a fixed effect of Condition, and with random intercepts is no better than our model with just the random intercepts. In fact, it's worse - look at the AIC values. So we have no effect of Condition in our re-reading data.

What can we conclude from non-significant results?

- With NHST, a non-significant result means we cannot reject the null hypothesis. But it does not mean our data support the null hypothesis. There may be other hypotheses that our data fit.
- What we can do is estimate the Bayes factor associated with our data in support of the null and experimental model.

- Wagenmakers (2007) details a means to estimating the Bayes Factor (BF) of our data in support of one model or another using BIC. Essentially, it gives us a measure of the extent to which our data support a particular model.
- BFs are estimated using the BIC value for each model - BIC penalises additional parameters so the BF captures possible overfitting (i.e., too many parameters on our model).
- $BF = \exp ((BIC2 - BIC1)/2)$

```
> anova(model.interceptonly, model.null)
Data: RO
Models:
model.null: DV ~ (1 | Subject) + (1 | Item)
model.interceptonly: DV ~ Condition + (1 | Subject) + (1 | Item)
      Df      AIC      BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
model.null      3 601.97 614.91 -297.98   595.97
model.interceptonly  5 605.70 627.28 -297.85   595.70 0.2617      2    0.8773
```

**Interpretation of the Bayes Factor in Terms of Evidence
(cf. Raftery, 1995, Table 6)**

Bayes Factor BF_{01}	$\Pr(H_0 D)$	Evidence
1–3	.50–.75	weak
3–20	.75–.95	positive
20–150	.95–.99	strong
>150	>.99	very strong

```
> anova (model.interceptonly, model.null)
Data: RO
Models:
model.null: DV ~ (1 | Subject) + (1 | Item)
model.interceptonly: DV ~ Condition + (1 | Subject) + (1 | Item)
      Df      AIC      BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
model.null      3 601.97 614.91 -297.98   595.97
model.interceptonly 5 605.70 627.28 -297.85   595.70 0.2617      2    0.8773
```

$$BF = \exp ((BIC2 - BIC1)/2)$$

$$BF = \exp ((627.28-614.91)/2)$$

$$BF = 485$$

A BF of 485 is “Very Strong” evidence in support of the null hypothesis.

Writing up LMM Results

- The analyses were carried out using the *lme4* package (Bates, Maechler, Bolker, & Walker, 2017) to fit the linear mixed models for the reading time measure in R (R Development Core Team, 2017). The *glmer* function in the *lme4* package with Laplace approximation was used for the Re-reading measure. Below we report regression coefficients (b), standard errors, and *t*-values (for duration measures). Restricted maximum likelihood estimation was used for the reporting of linear mixed model parameters.
- Then you'll report the descriptive statistics and the parameter estimates...

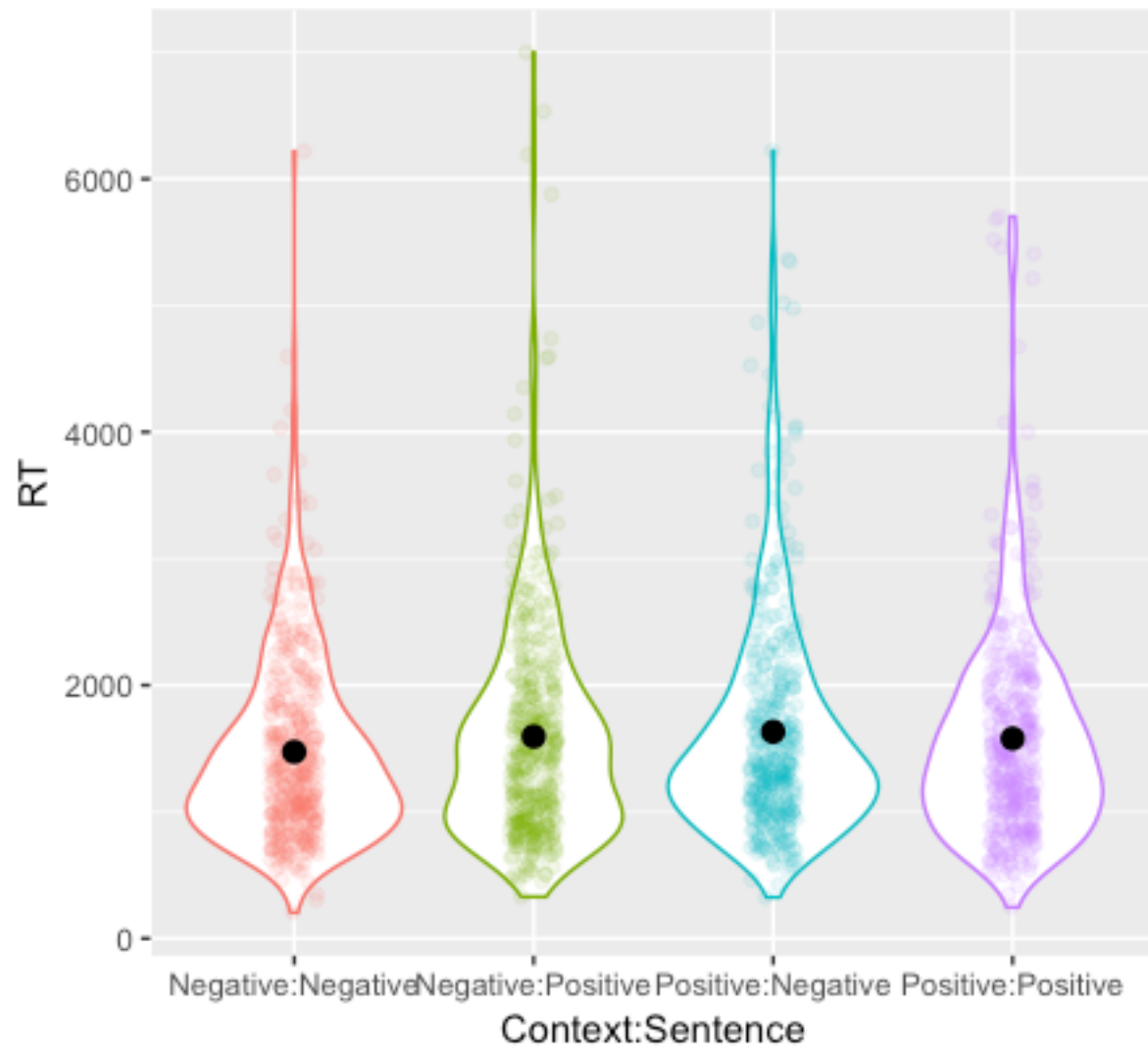
LMMs for a 2 x 2 Repeated Measures Design

- Now let's take a 2 x 2 repeated measures design. We measured people's eye movements as they read either positive or negative information. Prior context set up expectations that the story was likely to continue with positive vs. negative information.
- Factor 1 is Context (Positive vs. Negative)
- Factor 2 is Sentence Type (Positive vs. Negative)

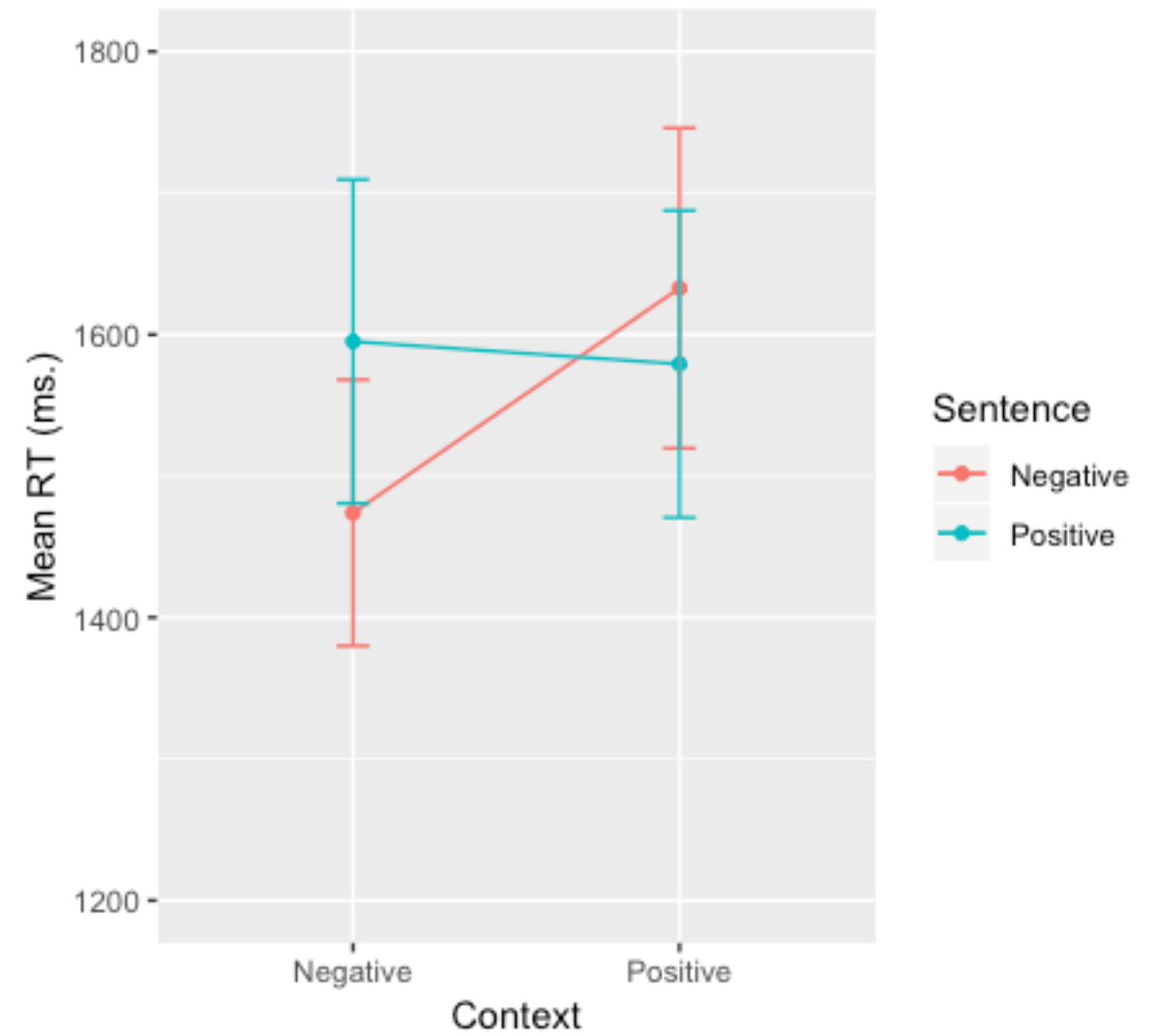
DV × Workshop script2.R* ×						
← → ↺ Filter						
	Subject ▾	Item ▾	RT ▾	Context ▾	Sentence ▾	
1	1	3	1270	Positive	Negative	
2	1	7	739	Positive	Negative	
3	1	11	982	Positive	Negative	
4	1	15	1291	Positive	Negative	
5	1	19	1734	Positive	Negative	
6	1	23	1757	Positive	Negative	
7	1	27	1052	Positive	Negative	
8	2	4	1706	Positive	Negative	
9	2	8	533	Positive	Negative	
10	2	12	1009	Positive	Negative	
11	2	16	939	Positive	Negative	
12	2	20	1848	Positive	Negative	
13	2	24	1435	Positive	Negative	
14	2	28	922	Positive	Negative	
Showing 1 to 15 of 1,680 entries						

- We have Subject number, Item number, RT (reading time), Context and Sentence.

Visualise



Raw data



Aggregated data

- The first thing we need to do is to apply contrast weightings to our two factors. By default, the contrasts are dummy or treatment coded. We need to change them to deviation coded. This helps make the coefficients in the LMM make more sense as the intercept of the LMM will correspond to the Grand Mean (i.e., the mean of all four conditions).

```
contrasts(DV$Sentence) <- matrix(c(.5, -.5))  
contrasts(DV$Context) <- matrix(c(.5, -.5))
```

- We are going to do is define our full model with our fixed effects and fully crossed Subject and Item random effects.
- Then we are going to define the null model with only the random effects.

```
model.full <- lmer(RT~Context*Sentence + (1+Context*Sentence|Subject) + (1+Context*Sentence|Item), data=DV, REML=TRUE)
```

```
model.null <- lmer(RT~(1+Context*Sentence|Subject) + (1+Context*Sentence|Item), data=DV, REML=TRUE)
```

- Note that we define our fixed effect using the notation `Context*Sentence`
- This is equivalent to `(Context + Sentence + Context:Sentence)` which corresponds to a main effect of Context, a main effect of Sentence and the interaction between the two (as represented by the colon symbol).

```

> anova(model.full, model.null)
refitting model(s) with ML (instead of REML)
Data: DV
Models:
model.null: RT ~ (1 + Context * Sentence | Subject) + (1 + Context * Sentence |
model.null:      Item)
model.full: RT ~ Context * Sentence + (1 + Context * Sentence | Subject) +
model.full:      (1 + Context * Sentence | Item)
      Df    AIC    BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
model.null 22 26720 26840 -13338    26676
model.full 25 26718 26853 -13334    26668 8.6625   3 0.03413 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

- Our model with the fixed effects (as well as the random effects) is a better fit for our data than is the model just with the random effects. Now we need to look at the model parameters using the `summary()` function...

```

> summary(model_full)

```

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)	
(Intercept)	1568.75	76.24	50.07	20.577	<2e-16	***
Context1	-69.01	39.87	25.94	-1.731	0.0954	.
Sentence1	-36.20	86.01	29.77	-0.421	0.6768	
Context1:Sentence1	-168.73	80.36	25.51	-2.100	0.0458	*

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

- We can see that the interaction is significant. But how do we know what difference(s) is/are driving this effect?
- Think back to ANOVA days - we need to now do something else...

- We can run pairwise comparisons. We can ask for a correction to be applied if we want to, but in this case we're doing to work out that correction by hand. There are only 2 theoretically meaningful pairwise comparisons, so we multiply the reported p value by 2 to manually apply Bonferroni correction.
- We use the `emmeans` function in the `emmeans` package.

```
> emmeans(model.full, pairwise~Context*Sentence, adjust="none")
$emmeans
```

Context	Sentence	emmean	SE	df	lower.CL	upper.CL
Negative	Negative	1473.962	81.92645	39.71	1308.344	1639.580
Positive	Negative	1627.340	97.87423	41.97	1429.818	1824.862
Negative	Positive	1594.530	96.56707	36.99	1398.865	1790.194
Positive	Positive	1579.181	90.79179	48.12	1396.644	1761.718

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

```
$contrasts
```

contrast	estimate	SE	df	t.ratio	p.value
Negative,Negative - Positive,Negative	-153.37807	50.68254	20.94	-3.026	0.0064
Negative,Negative - Negative,Positive	-120.56791	92.61292	30.57	-1.302	0.2027
Negative,Negative - Positive,Positive	-105.21905	92.22803	29.04	-1.141	0.2633
Positive,Negative - Negative,Positive	32.81016	97.35194	31.48	0.337	0.7383
Positive,Negative - Positive,Positive	48.15902	97.23988	26.58	0.495	0.6245
Negative,Positive - Positive,Positive	15.34886	62.02003	27.31	0.247	0.8064

Here we have the descriptive statistics associated with each of our 4 conditions.

Above are all the possible pairwise comparisons - only 2 are of theoretical interest to us:

1. A Negative meaning sentence following a Negative Context vs. the same Negative meaning following a Positive Context.
2. A Positive meaning sentence following a Negative Context vs. the same Positive meaning following a Positive Context.

\$contrasts

contrast		estimate	SE	df	t.ratio	p.value
Negative, Negative - Positive, Negative		-153.37807	50.68254	20.94	-3.026	0.0064
Negative, Negative - Negative, Positive		-120.56791	92.61292	30.57	-1.302	0.2027
Negative, Negative - Positive, Positive		-105.21905	92.22803	29.04	-1.141	0.2633
Positive, Negative - Negative, Positive		32.81016	97.35194	31.48	0.337	0.7383
Positive, Negative - Positive, Positive		48.15902	97.23988	26.58	0.495	0.6245
Negative, Positive - Positive, Positive		15.34886	62.02003	27.31	0.247	0.8064

- The two key comparisons reveal that Positive sentences are read no more quickly after Positive than after Negative context (1579 vs. 1595 ms.) while Negative Sentences are read more quickly after Negative than after Positive contexts (1474 vs. 1627 ms.)
- Note, the estimates in each contrast pairing corresponds to the difference between the comparison conditions for that pair.

- If we had re-reading (i.e., regression) data, we would also have to run an analysis using the *glmer* function on those data. The code would look like:

```
model.full <- glmer(Regressions ~ Context * Sentence + (1 + Context * Sentence |  
Subject) + (1 + Context * Sentence | Item), data = RO, family = binomial)
```

- To generate the pairwise comparisons (and to report the descriptives using the original measurement scale), we would use:

```
emmeans(model.full, pairwise ~ Context * Sentence, adjust = "none", type =  
"response")
```

- If we did not set the `type` parameter, then the descriptives would be on a log odds ratio scale (and harder to interpret).

Citing Packages

Remember to cite the packages you use, plus the version of R itself (with year info.) To find out how to cite a particular package, type:

```
> citation ("lme4")
```

To cite lme4 in publications use:

```
Douglas Bates, Martin Maechler, Ben Bolker, Steve Walker (2015). Fitting Linear Mixed-Effects Models  
Using lme4. Journal of Statistical Software, 67(1), 1-48. doi:10.18637/jss.v067.i01.
```

And to find out which version of R you are using:

```
> version
```

platform	x86_64-apple-darwin15.6.0
arch	x86_64
os	darwin15.6.0
system	x86_64, darwin15.6.0
status	
major	3
minor	4.3
year	2017
month	11
day	30
svn rev	73796
language	R
version.string	R version 3.4.3 (2017-11-30)
nickname	Kite-Eating Tree

Writing up These Results

The analyses were carried out using the *lme4* package (Bates, Maechler, Bolker, & Walker, 2015) to fit the linear mixed models for the reading time measure in *R* (R Development Core Team, 2017). Pairwise comparisons conducted with the *emmeans* package (Lenth, 2018) were used to investigate the significant interaction for the reading time measure. Below we report regression coefficients (*b*), standard errors, and *t*-values. Restricted maximum likelihood estimation was used for the reporting of linear mixed model parameters. Deviation coding was used for each of the two experimental factors (Barr et al., 2013). Absolute values of the *t*-value greater than or equal to 1.96 indicate an effect that is significant at approximately the .05 alpha level. For pairwise comparisons we report the *t*-values and *p*-values. Degrees of freedom are approximated using the Satterthwaite method.

	<i>b</i>	SE	<i>t</i>
Intercept	1569	76.24	20.577
Context	-36.20	86.01	-0.421
Sentence	-69.01	39.87	-1.731
Context x Sentence	-168.73	80.36	-2.100

You then report the two pairwise comparisons we conducted in the same way as you would do for ANOVA.

- When reporting the results of LMMs, it is important to provide all the information that someone would need to reproduce your analysis exactly. It's important to provide dates for the R packages you're using so that *exactly* the same version of R and associated packages can be used by someone else.
- We're moving toward a world where many of the top journals now ask for your analysis code to be uploaded as supplementary material. This could be your R script, or could be the R Markdown document. Either way, it should help with the need for reproducibility.

Addressing lack of convergence

Warning message:

```
In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv,  :  
  Model failed to converge with max|gradl| = 0.0171702 (tol = 0.001, component 1)
```

If you see this message (which you will - again and again and again and again and again), it means you have to simplify your random effects structure so that a model can be identified.

Addressing lack of convergence

Simplify your random effects structure step by step. For an experiment with two factors (Factor 1 and Factor 2) we could simplify the participant and item random effects like this:

`(1 + Factor 1*Factor 2 | Participant) + (1 + Factor 1*Factor 2 | Item)`

`(1 + Factor 1*Factor 2 | Participant) + (1 + Factor 1+Factor 2 | Item)`

`(1 + Factor 1+Factor 2 | Participant) + (1 + Factor 1+Factor 2 | Item)`

`(1 + Factor 1+Factor 2 | Participant) + (1 + Factor 1 | Item)`

...

If you think your random effects looks too sparse when settling on a model that converges, you could try dropping one effect term entirely and then simplifying the other:

$(1 + \text{Factor 1} * \text{Factor 2} | \text{Participant}) + (1 + \text{Factor 1} * \text{Factor 2} | \text{Item})$

$(1 + \text{Factor 1} + \text{Factor 2} | \text{Participant})$

$(1 + \text{Factor 1} | \text{Participant})$

$(1 + \text{Factor 2} | \text{Participant})$

...

You want to avoid random effects with just random intercepts (i.e., no slopes) as that can inflate the Type I error rate (Barr et al., 2013).

A few other LMM things...

- You can add participant and item covariates as fixed effects, and you can have a variety of continuous and categorical variables in your LMM. LMMs are *very* flexible.
- You'll find that sometimes several models fit your data - always run likelihood comparison tests to determine which is the best fit. If you have a selection where not one is statistically better than the others, choose the model that makes most *theoretical* sense.

The danger of over-fitting

- Sometimes you'll find yourself trying to fit an over-parameterised model - this is one whether you are trying to estimate more components of the model than your data/design supports.
- In the latest version of lme4, you'll receive a "singular fit" error if your model appears over-parameterised - one solution is simplify the random effects structure (usually by removing random slopes) in a way that makes theoretical sense until you arrive at a model that fits (but doesn't overfit) your data.
- Having said that, if the random effects structure makes complete theoretical sense then you might not want to simplify it. Often it's a judgement call...
- Read more in "Parsimonious mixed models" by Bates et al. here: <https://arxiv.org/abs/1506.04967>

Important Point

- Add as many random slopes (not just random intercepts) as your experimental design allows and is theoretically sensible - for most cases, we expect variation between participants in terms of how they'll respond to different levels of an experimental condition (which is why we add participants as a random slope) and also variation between our experimental items to different levels of an experimental condition (which is why we also add items as a random slope).
- If the full model with random slopes and intercepts does not converge, then gradually simplify your random effects structures (e.g., drop an interaction term first, then drop a main effect etc.) until you find a model that does converge.

LMMs for Ordinal DVs

- Often we might collect data using a Likert scale. These data are ordinal and so we should use the cumulative-link mixed model function (CLMM) in the package called `ordinal`. Works similarly to LMMs in `lme4` but with one or two minor syntax changes...
- An example: we had 42 participants rate images of sports on a scale of 0-10 corresponding to how much they liked each one. Before each rating measure, they saw a video of a sport that matched or mismatched the one they then had to rate (with a neutral video as baseline).

- We want to know whether people's ratings were influenced by whether or not the sport they rated matched the one they had just seen.
- We have Subject, Image, and SportType as our random effects.
- VideoCondition corresponds to our condition - 2 is match, 3 is mismatch, and 4 is neutral.
- Our DV is the column 'ratings'.

	Subject	order	Image	SportType	VideoCondition	RTs	Questionnaire	SportExperienceTest1	SportExperienceTest2	ratings
1	1	1	5	5	2	2644	21	0	0	7
2	1	2	2	2	2	1606	21	0	0	4
3	1	3	10	10	2	1512	21	0	0	6
4	1	4	1	1	2	2217	21	0	0	8
5	1	5	3	3	2	1988	21	0	0	2
6	1	6	9	9	2	2876	21	0	0	9

- Plotting our data suggests the Congruent condition is producing higher scores than our other two conditions.



- Before we build our null and experimental models, we need to ensure our DV is coded as an ordinal variable.

```
> Main$ratings <- as.ordered(Main$ratings)
```

```
> model.clm.null <- clmm(ratings ~ 1 + (1 + VideoCondition | Subject) + (1 +  
VideoCondition | SportType) + (1 + VideoCondition | Image), data = Main)
```

```
> model.clm4 <- clmm(ratings ~ VideoCondition + (1 + VideoCondition | Subject) +  
(1 + VideoCondition | SportType) + (1 + VideoCondition | Image), data = Main)
```

- The syntax for our null model requires we have an explicit intercept (represented by a 1 in the fixed effects structure) similar to when we built regression models (this is different to how we specify a null model in `lme4` syntax).

- First, let's test whether our experimental model and null models differ:

```
> anova(model.clm.null, model.clm4)
```

```
## Likelihood ratio tests of cumulative link models:
##
##          formula:
## model.clm.null ratings ~ 1 + (1 + VideoCondition | Subject) + (1 + VideoCondition | SportType) + (1 +
VideoCondition | Image)
## model.clm4      ratings ~ VideoCondition + (1 + VideoCondition | Subject) + (1 + VideoCondition |
SportType) + (1 + VideoCondition | Image)
##          link: threshold:
## model.clm.null logit flexible
## model.clm4     logit flexible
##
##          no.par    AIC  logLik LR.stat df Pr(>Chisq)
## model.clm.null      28 10841 -5392.6
## model.clm4          30 10837 -5388.4  8.5295  2    0.01406 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- We can see that they do - and our experimental model has the lower AIC value.

- Let's explore the effect of our Condition factor using *emmeans*:

```
> emmeans(model.clm4, pairwise ~ VideoCondition, adjust = "none")
```

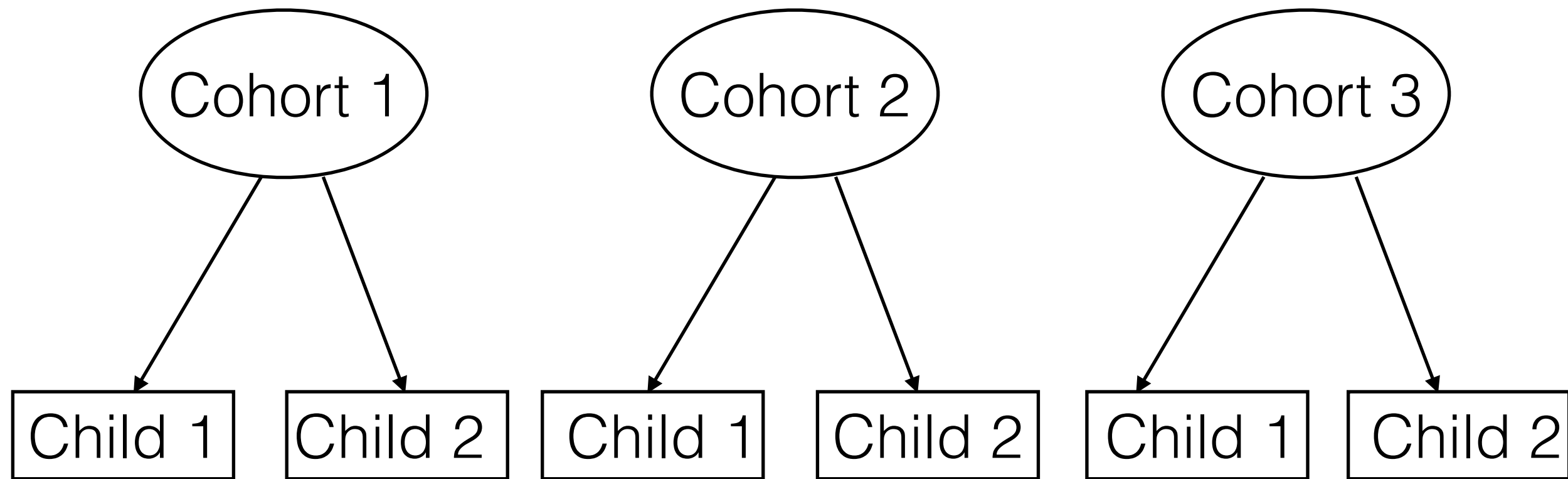
```
## $emmeans
## VideoCondition      emmean        SE    df  asymp.LCL asymp.UCL
## Congruent          0.6084163 0.2597503 Inf   0.0993151 1.1175176
## Incongruent         0.2917028 0.2449736 Inf  -0.1884367 0.7718422
## Neutral             0.3153088 0.2436285 Inf  -0.1621942 0.7928119
##
## Confidence level used: 0.95
##
## $contrasts
## contrast              estimate        SE    df  z.ratio p.value
## Congruent - Incongruent  0.31671360 0.09146945 Inf    3.463  0.0005
## Congruent - Neutral      0.29310751 0.09391144 Inf    3.121  0.0018
## Incongruent - Neutral    -0.02360608 0.08587502 Inf   -0.275  0.7834
```

- The pairwise comparisons tell us that the Congruent condition differs from the Incongruent and Neutral conditions, but that the Incongruent and Neutral conditions do not differ.
- We can conclude that people's ratings for how much they liked particular sports were influenced by whether they had just seen a video depicting the sport. When the video and sport matched, they give the sport a higher rating when when the video and sport mismatched.

Crossed vs. Nested Random Effects

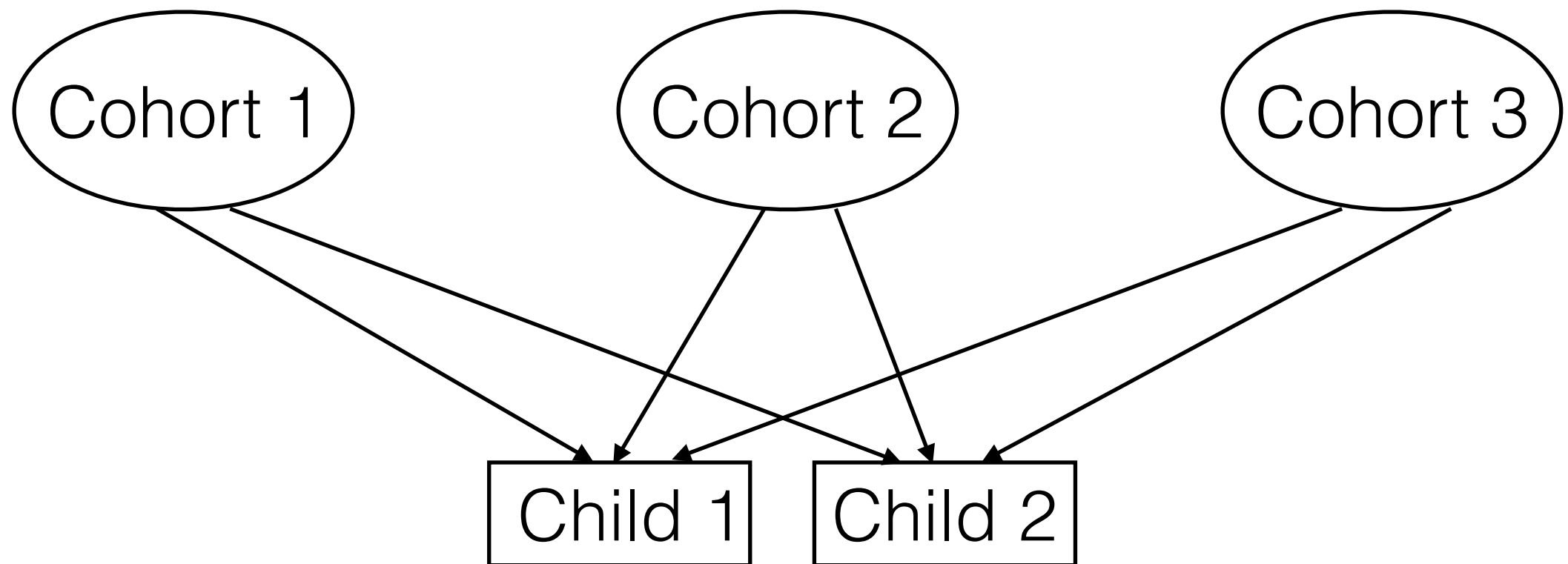
- In most experimental designs, your participant and item random factors are likely to be crossed - so random effects notation for a one factor experiment is $(1 + \text{Factor} | \text{Subjects}) + (1 + \text{Factor} | \text{Items})$
- In some cases though, your factors might be **nested**. Nesting is a property of your data.
- To illustrate:

Nested



Child has an identifier that refers to a different child in each Cohort. Each child appears only in one Cohort. Child is nested within Cohort so random effects structure would be
(1+Factor | Cohort/Child)

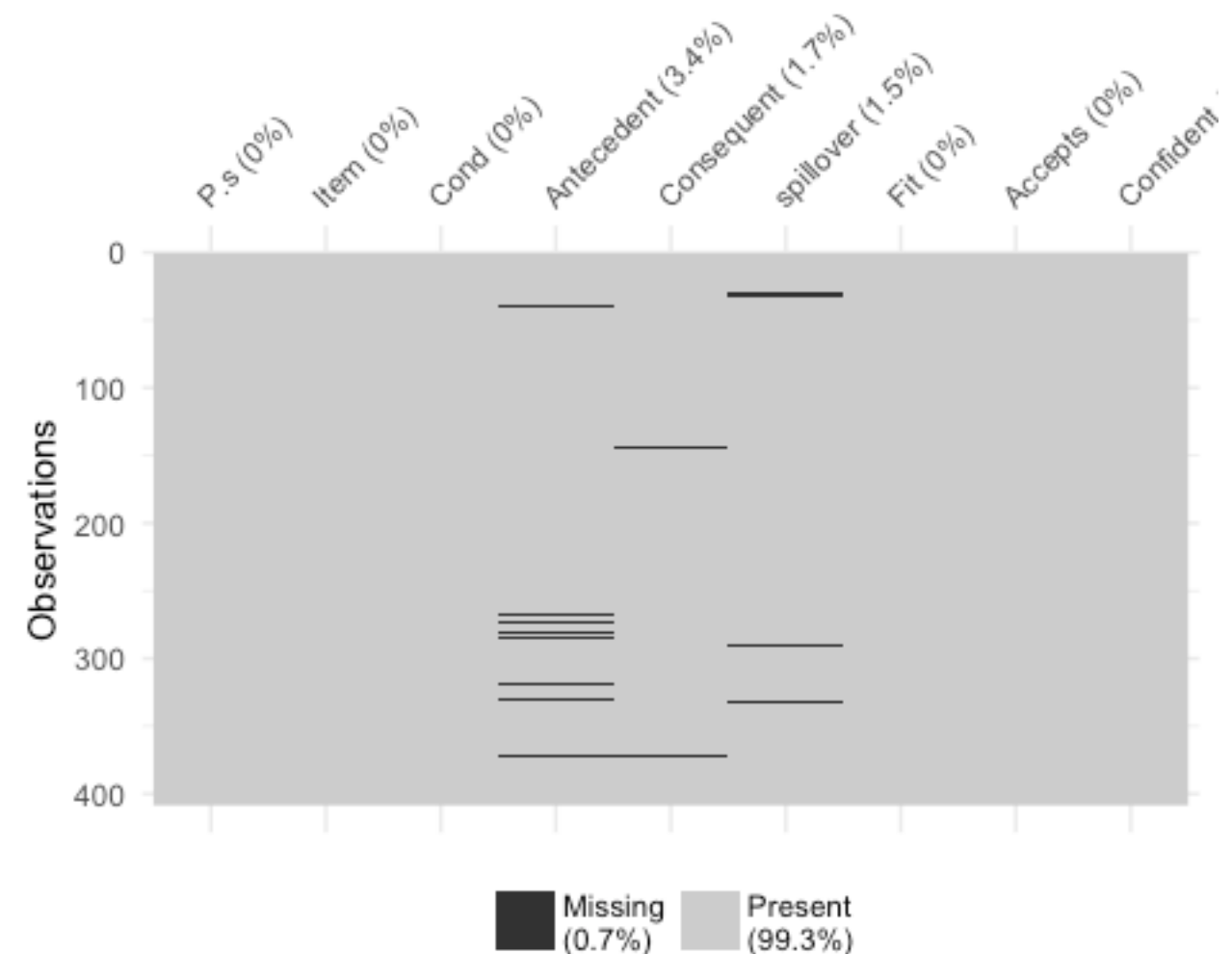
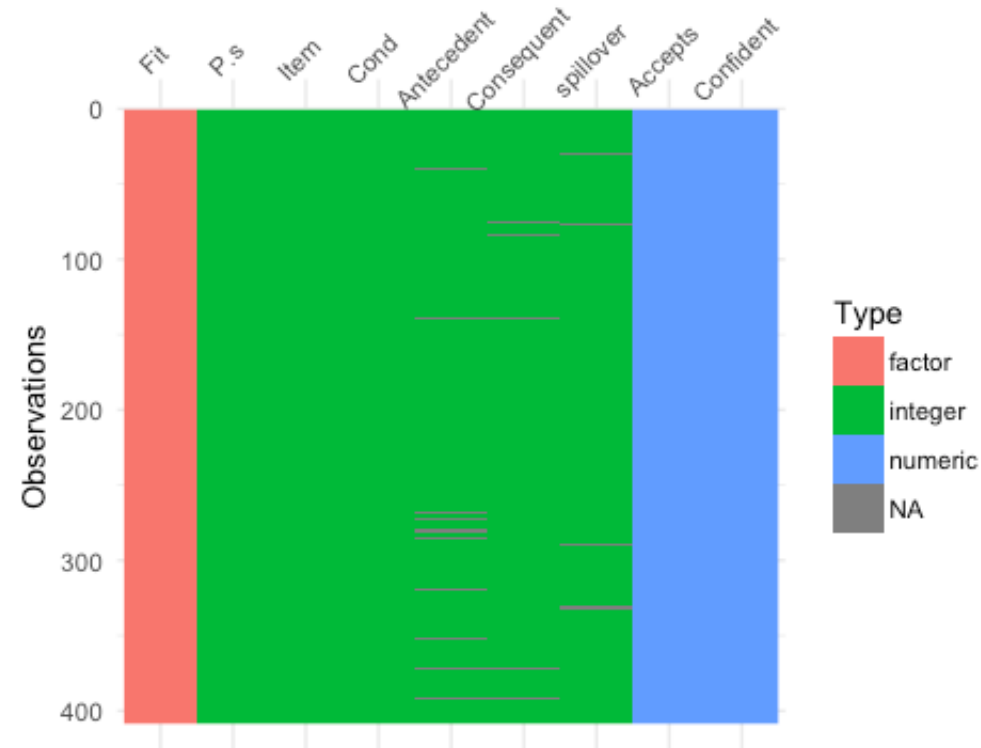
Crossed



Each child appears in each Cohort. The levels are crossed so random effects structure would be $(1 + \text{Factor} \mid \text{Cohort}) + (1 + \text{Factor} \mid \text{Child})$

Visualising our whole dataset using “visdat”

```
1 install.packages ("visdat")
2 library (visdat)
3
4 #read in data file
5 RPs_plus_ratings <- read_csv("~/Desktop/Air Work/R analyses/Igor study/RPs_plus_ratings.csv")
6
7 #make Fit a factor
8 RPs_plus_ratings$Fit <- factor (RPs_plus_ratings$Fit)
9
10 #create an index so we can remove item 9
11 index <- RPs_plus_ratings$Item != "9"|
12
13 #visualise the data
14 vis_dat(RPs_plus_ratings[index,])
15
16 #visualise missing data
17 vis_miss(RPs_plus_ratings[index,])
18
```

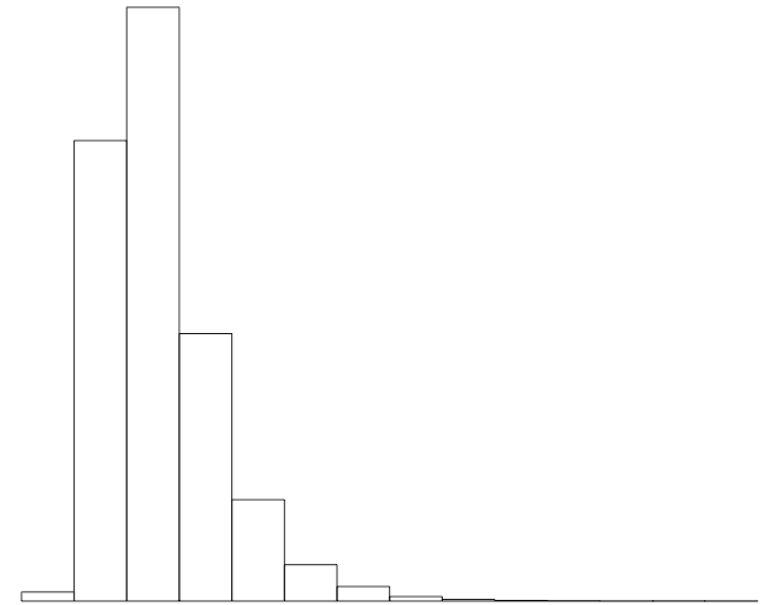


What about normality?

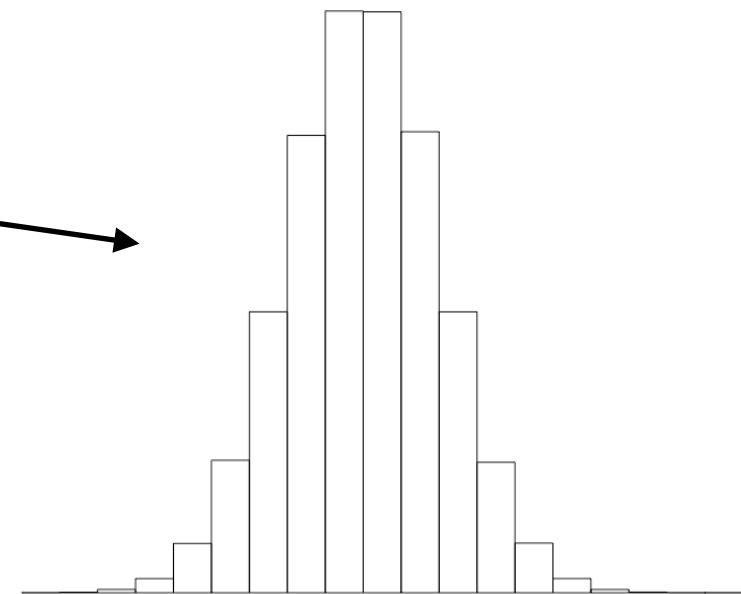
- In LMMs (as with the GLM) we need to worry about the normality of the residuals...
- You can check normality in a number of ways.
- Graphically, you can use the *qqnorm* function (which produces a Q-Q plot), and *hist* (which produces a histogram) applied to the model residuals.
- Statistically, you could use the *shapiro.test* function applied to a distribution of data. Be aware that for large datasets, even small deviations from normality will result in a significant Shapiro test. So best not to use this...

Log transform (**not** recommended)

Typically, RT data are non-normal and more often the DV looks like this.



We can log transform our DV to approximate something that looks a bit more like the normal distribution (could also look at inverse RT). But there are risks around transforming data and it's generally not recommended (Lo & Andrews, 2015)

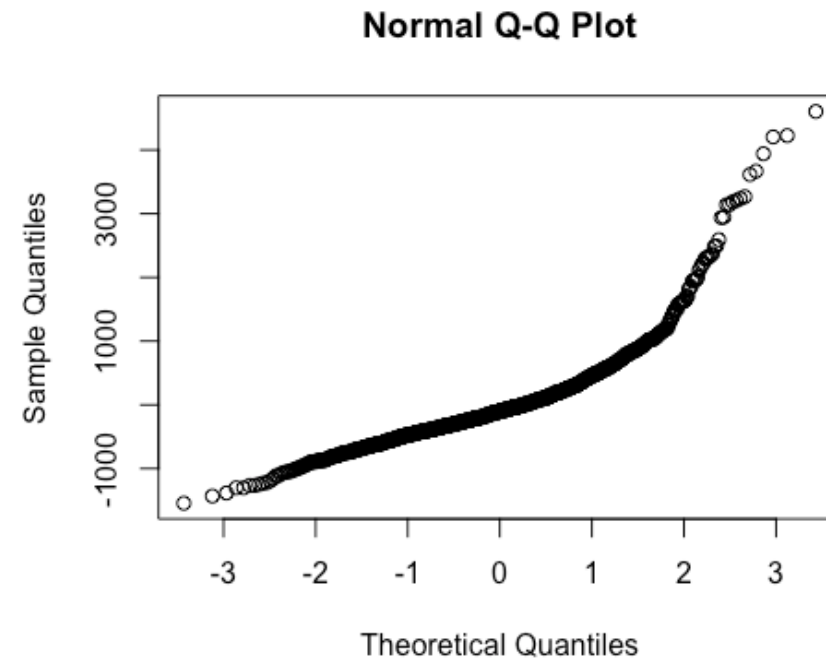


- Normality test on the model residuals from the untransformed data:

```
> qqnorm(residuals(model.full))
> shapiro.test(residuals(model.full))
```

Shapiro-Wilk normality test

```
data: residuals(model.full)
W = 0.84583, p-value < 2.2e-16
```

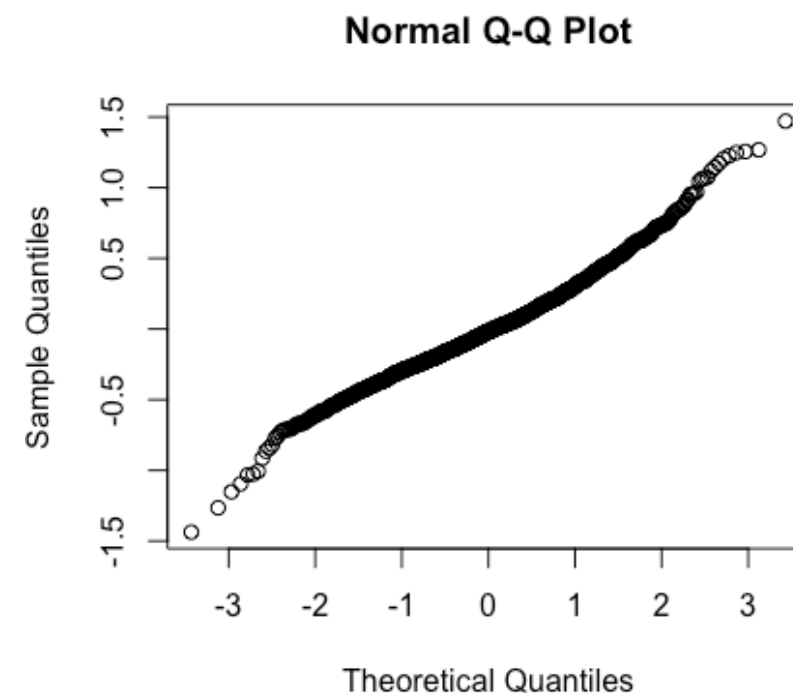


- Normality test on the model residuals from the log transformed data:

```
> model.full <- lmer (log(RT) ~ Sentence*Context + (1+Sentenc
e*Context|Subject) + (1+Sentence*Context |Item), data=DV, REM
L=TRUE)
> qqnorm(residuals(model.full))
> shapiro.test(residuals(model.full))
```

Shapiro-Wilk normality test

```
data: residuals(model.full)
W = 0.98321, p-value = 4.626e-13
```



- **Also need to check the residuals at the random effects level using the `ranef()` function to extract the random effects parameters.**

```
model.full <- lmer(RT ~ Context * Sentence + (1 + Context + Sentence | Subject) +  
                  (1 + Context + Sentence | Item), data = DV, REML = TRUE)
```

```
qqnorm(residuals(model.full))  
summary(model.full)
```

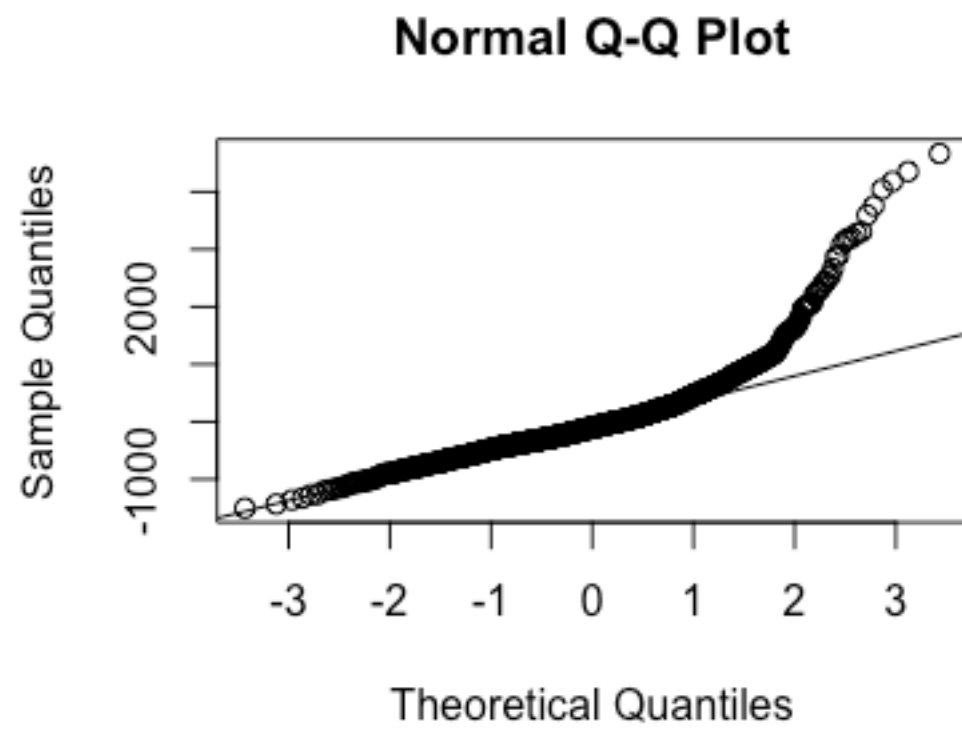
```
# checking residuals  
r_int <- lme4::ranef(model.full)$Subject$(Intercept) `  
qqnorm(r_int)  
qqline(r_int)
```

```
r_slope <- lme4::ranef(model.full)$Subject$Context1  
qqnorm(r_slope)  
qqline(r_slope)
```

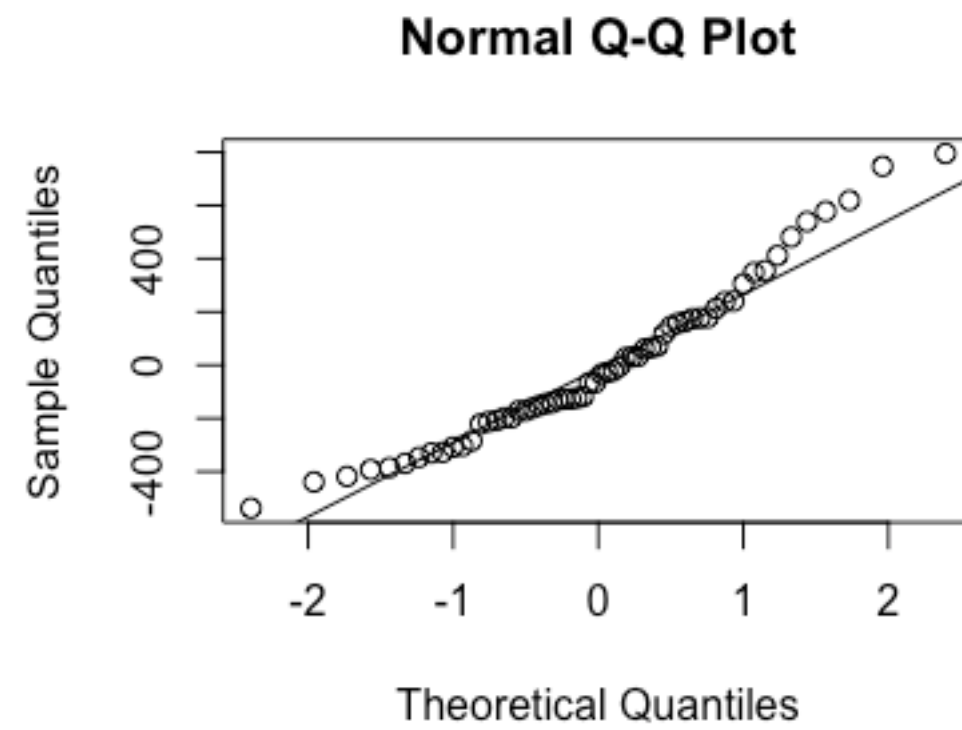
```
r_slope <- lme4::ranef(model.full)$Subject$Sentence1  
qqnorm(r_slope)  
qqline(r_slope)
```

- **This is for a crossed design - for nested random effects the above code will need a little modification...**

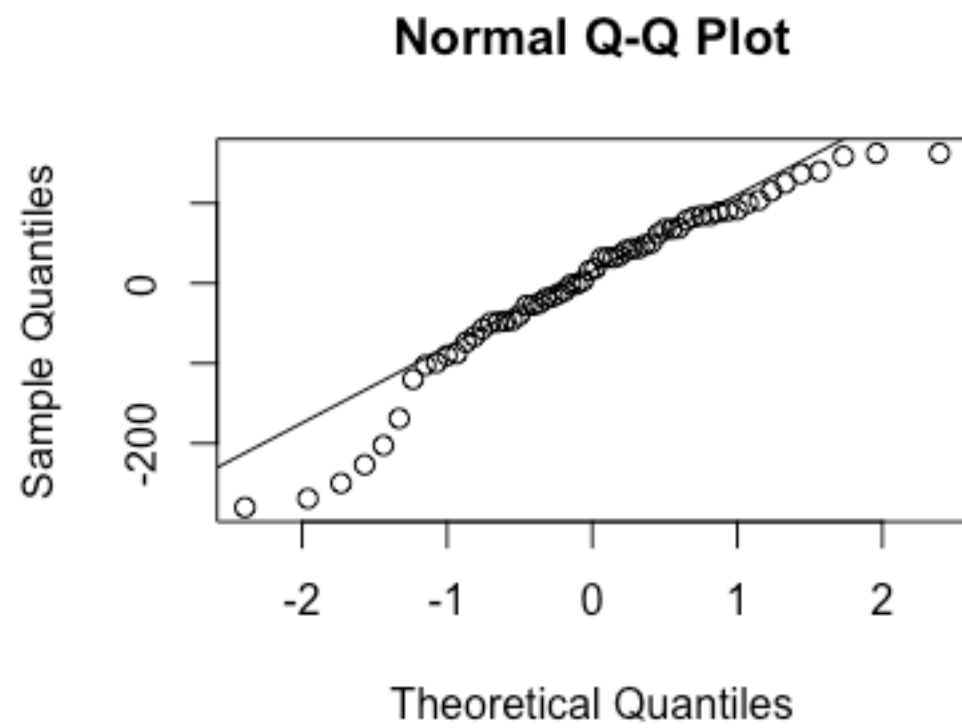
Overall residuals



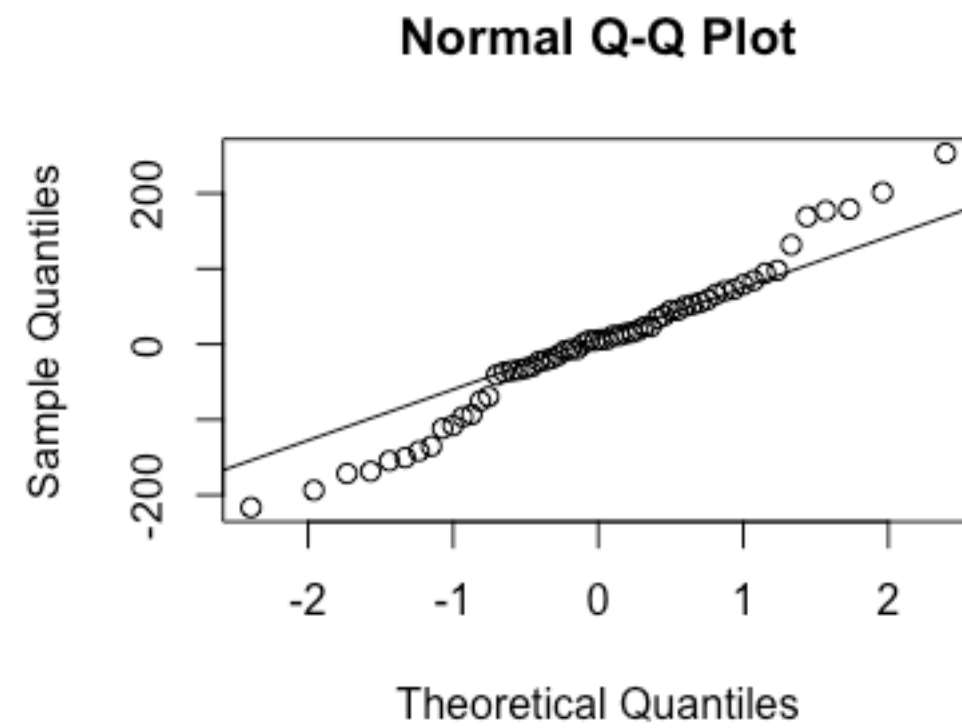
Intercept residuals



Factor 1 residuals



Factor 2 residuals



- The original analysis on the untransformed data:

```
Fixed effects:
              Estimate Std. Error      df t value Pr(>|t|)
(Intercept)    1568.75      76.24   50.07  20.577  <2e-16 ***
Context1       -36.20     86.01   29.77  -0.421   0.6768
Sentence1      -69.01     39.87   25.93  -1.731   0.0954 .
Context1:Sentence1 -168.73    80.36   25.51  -2.100   0.0458 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- The new analysis on the log transformed data:

```
Fixed effects:
              Estimate Std. Error      df t value
(Intercept)    7.23975    0.04967 49.13000 145.761
Sentence1       0.01392    0.05278 29.03000   0.264
Context1        0.04316    0.02258 28.62000   1.911
Sentence1:Context1 -0.09333    0.04618 25.55000  -2.021
```

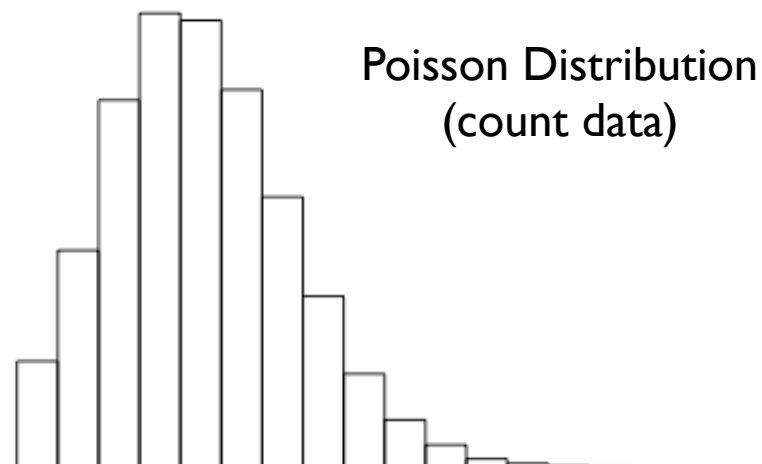
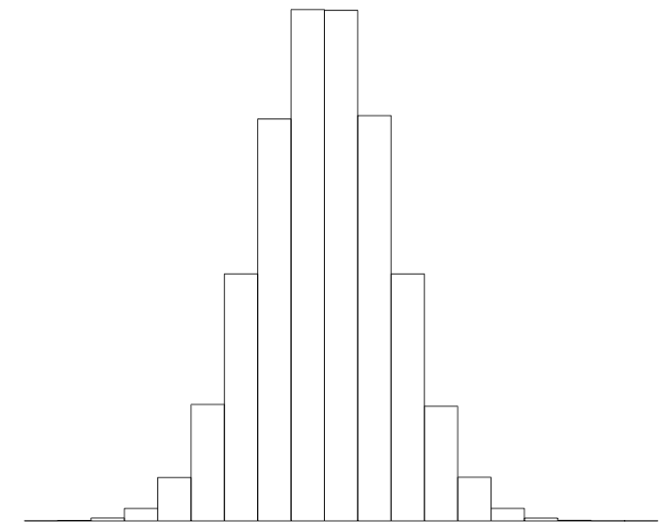
t-value of the interaction smaller than in analysis over untransformed data. With similar dfs, p will be bigger.

Other distributions under the GLMM via the function `glmer` are available...

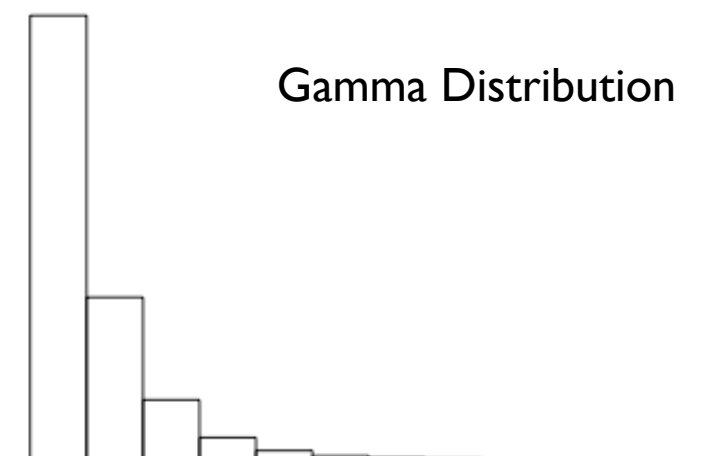
Usage

```
family(object, ...)  
  
binomial(link = "logit")  
gaussian(link = "identity")  
Gamma(link = "inverse")  
inverse.gaussian(link = "1/mu^2")  
poisson(link = "log")  
quasi(link = "identity", variance = "constant")  
quasibinomial(link = "logit")  
quasipoisson(link = "log")
```

Normal (Gaussian) Distribution



Poisson Distribution
(count data)



Gamma Distribution

- Standard linear model assumes a normal distribution of residuals. In the *generalised* linear mixed model, we can assume a distribution in our model that doesn't involve a normal distribution. We have already looked at the binomial.
- Gamma distribution is another possibility (see Kliegl et al. 2010, Lo & Andrews, 2015, for discussion).

```
model1 <- glmer(RT ~ Sentence*Context + (1+Sentence*Context|Subject) + (1+Sentence*Context|Item), data=DV, family=Gamma)
summary(model1)
```

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	7.28232	0.06731	108.20
Sentence1	0.02284	0.07679	0.30
Context1	0.04276	0.01701	2.51
Sentence1:Context1	-0.10806	0.03403	-3.18

t-value of the
interaction larger than
in previous analysis.

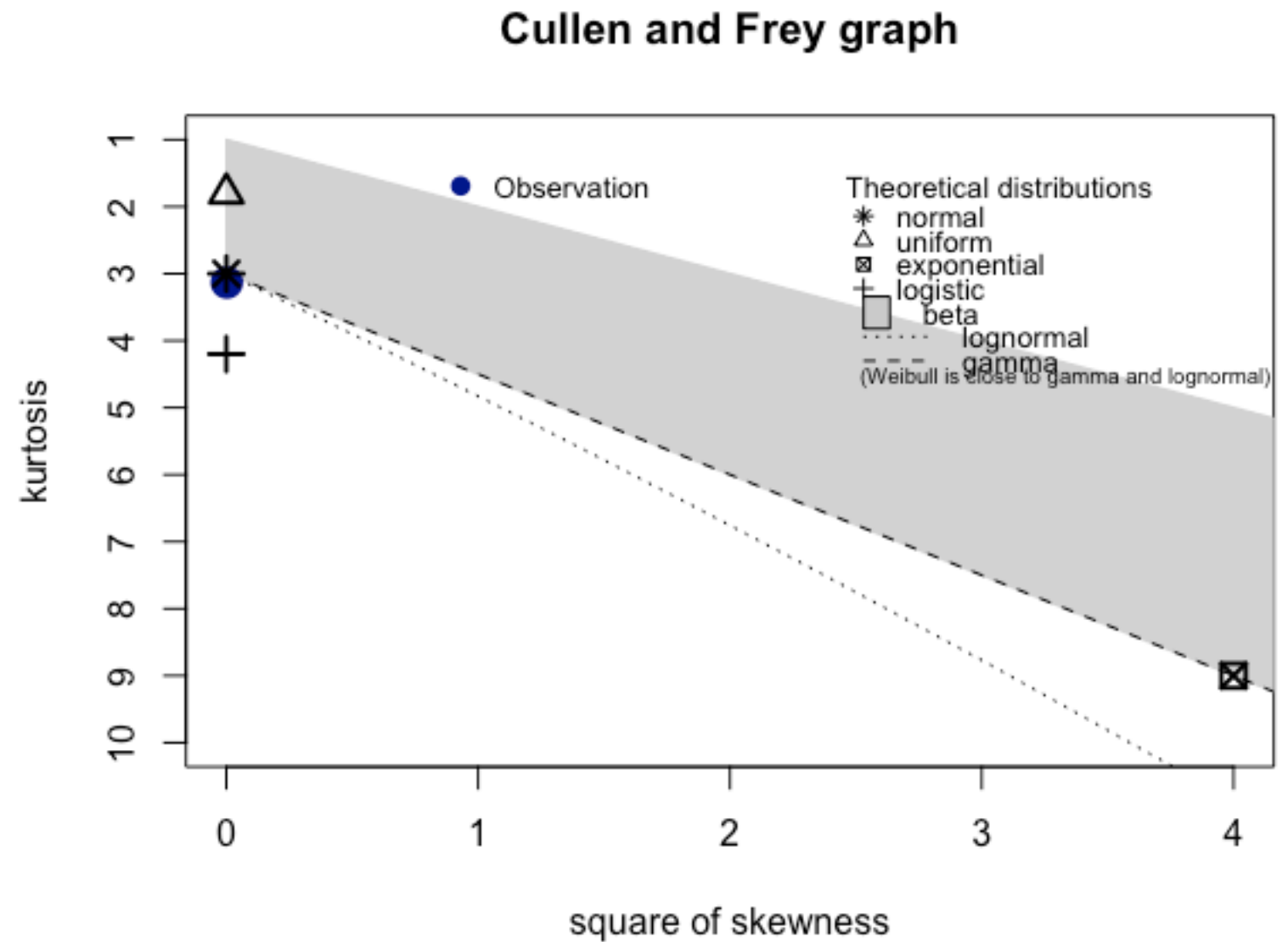
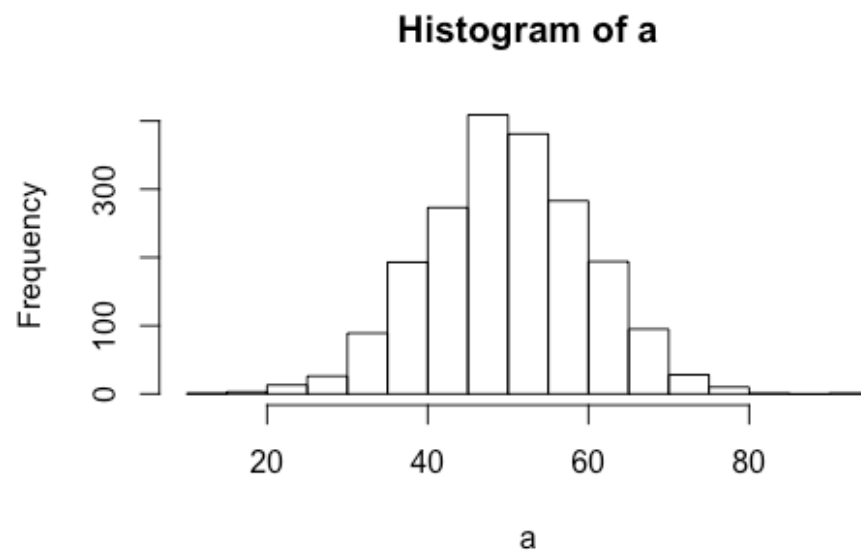
So what to do?

- In this example, all three analyses told basically the same story - there is an effect in our interaction term. They differ in terms of the value of the t-statistic associated with testing this.
- It's an issue - but if each possible way of analysing the data (incl. log transform and GLMM under the Gamma distribution) produces the same story, probably don't need to worry too much.
- Key is to be transparent in the write-up (did you transform the data? If so, how? What distribution do you assume your data come from?). **Most importantly, publicly archive your data and analysis code so it can be examined by others.**

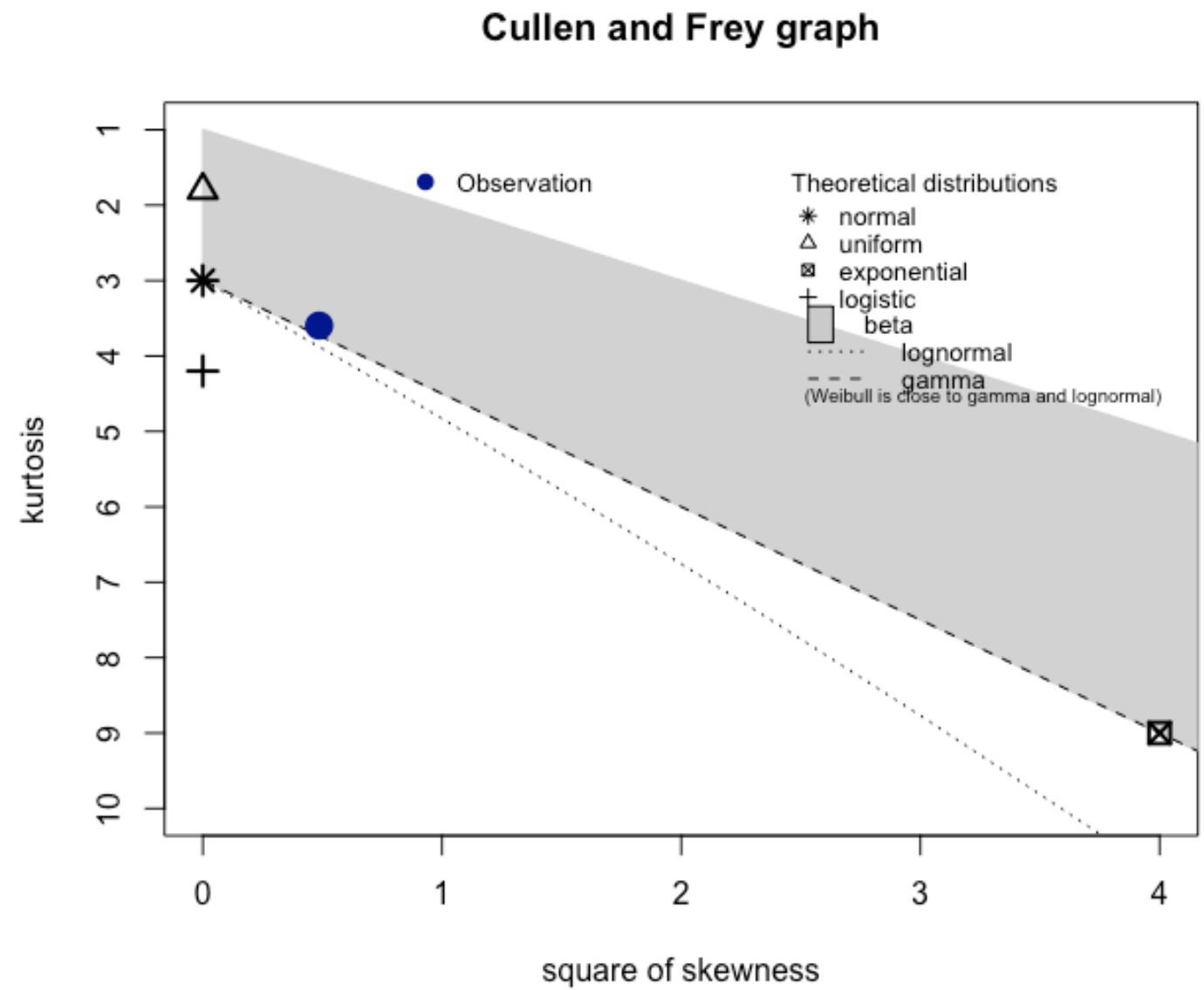
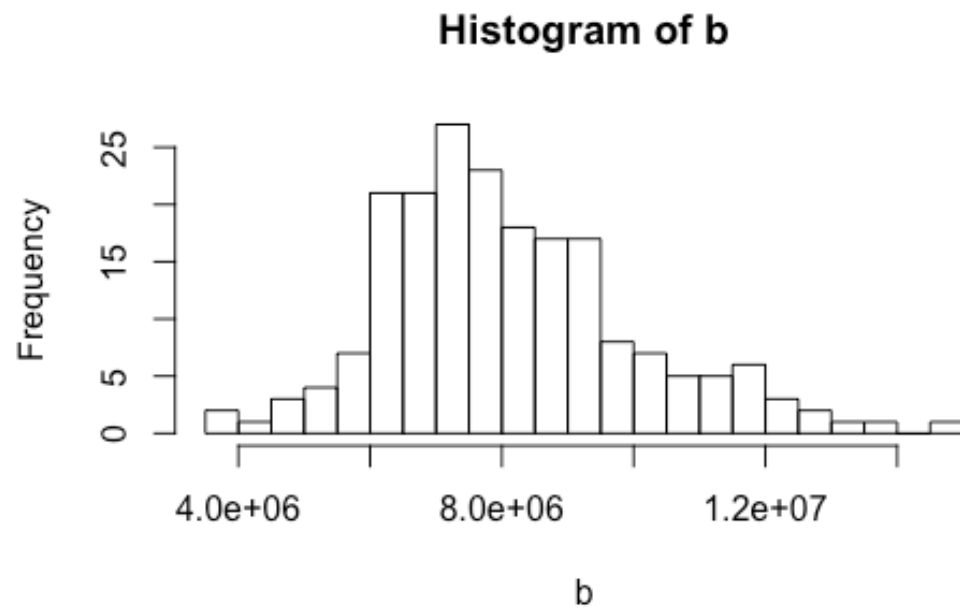
Determining the likely distribution of our data

- We can use the function `descdist` from the package `fitdistrplus` to plot any set of data on a Cullen and Frey graph - this will help us determine what known distribution of data our data match.
- First, I'm going to create some data drawn from the normal distribution and plot that sample...

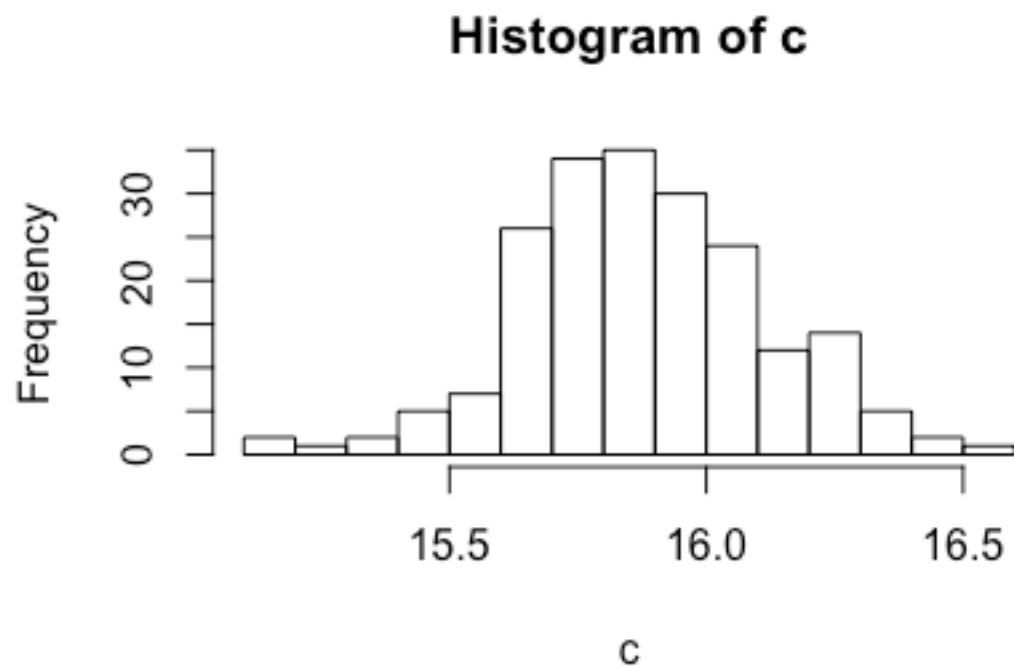
```
> library(fitdistrplus)
> a <- rnorm(2000, mean=50, sd=10)
> descdist(a)
```



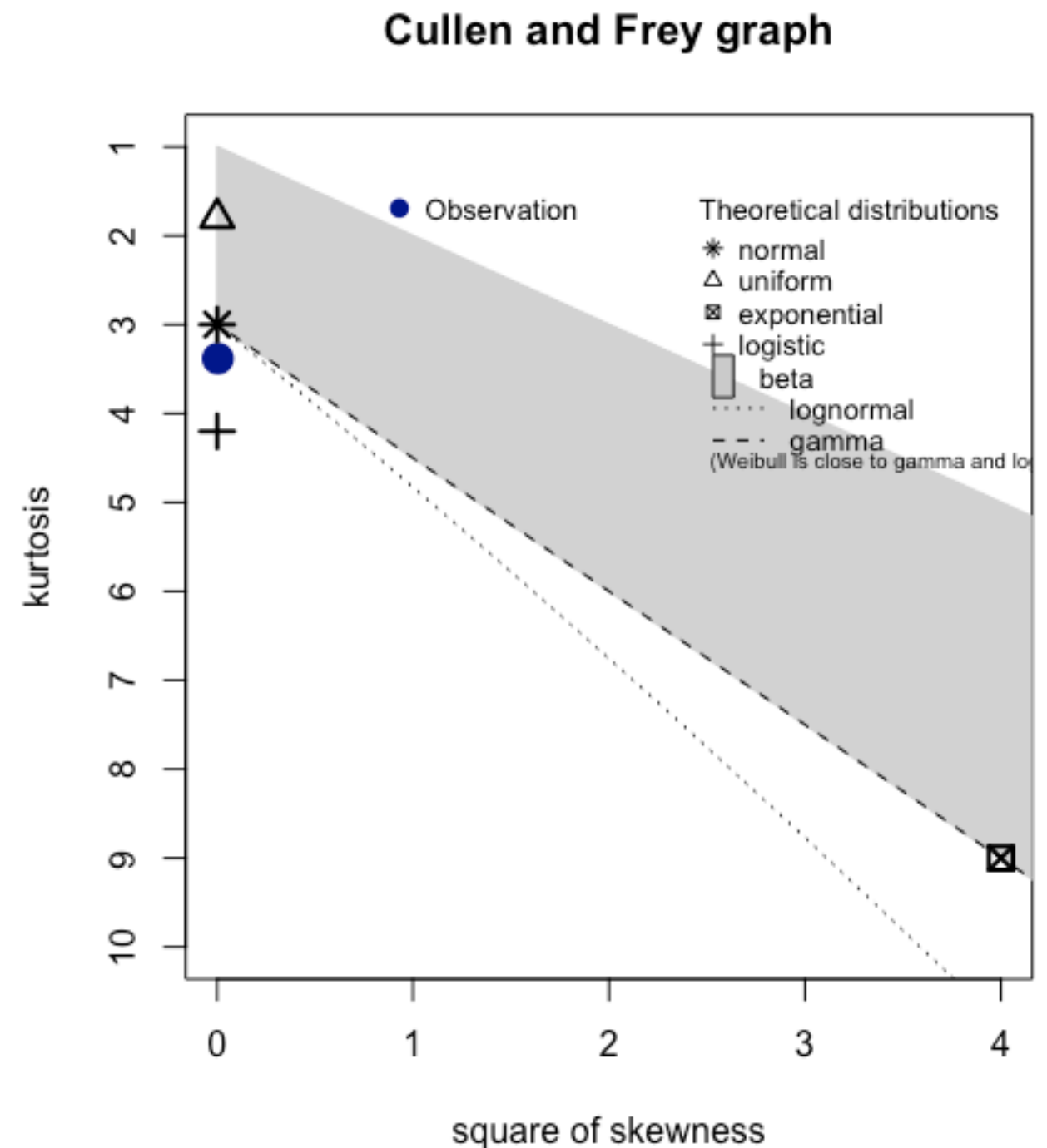
- Now some positively skewed data:



- We can log transform the data and then view on a Cullen and Frey graph...



Understanding the distribution our data is likely sampled from will help us avoid analysis pitfalls.



Further Reading

Baayen, R.H., Davidson, D.J., Bates, D.M. (2008). Mixed-effects modeling with crossed random effects for subjects and items. *Journal of Memory and Language*, 59, 390-412.

Barr, D.J., Levy, R., Scheepers, C., & Tilly, H. J. (2013). Random effects structure for confirmatory hypothesis testing: Keep it maximal. *Journal of Memory and Language*, 68, 255–278.

Kliegl, R., Masson, M. E. J., and Richter, E. M. (2010). A linear mixed model analysis of masked repetition priming. *Visual Cognition*, 18, 655–681.

Lo, S., and Andrews, S. (2015). To transform or not to transform: using generalized linear mixed models to analyse reaction time data. *Frontiers in Psychology*, 6:1171.

Mirman, D. (2014). *Growth curve analysis and visualization using R*. New York, NY: CRC Press.

Winter, B. (2013). Linear models and linear mixed effects models in R with linguistic applications. arXiv:1308.5499. [<http://arxiv.org/pdf/1308.5499.pdf>]