

Regression for Linguists

WiSe23/24

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Course overview

This course fast tracks through different types of regression most relevant to linguistic research. These materials are by no means exhaustive, and should be supplemented by reading textbook length treatments. The majority of my materials lean heavily on Winter (2019), which I highly recommend. I also took inspiration from Sonderegger (2023a), which came out this year and I haven't fully explored yet. So far, it looks like a very thorough textbook that I would also recommend you check out.

Before you begin the course, I would like to paraphrase something Prof. Shravan Vasishth said in the opening remarks for the annual summer school for Statistical Methods for Linguistics and Psychology back in 2020 which has stuck with me: *get comfortable with partial knowledge*. We are not trained statisticians, and likely never will be (Vasishth himself is a certified statistician, in addition to professor of psycholinguistics). So get comfortable with partial understanding of the math behind these models, and focus on their application and interpretation.

Materials

This website is a work-in-progress. Materials will be updated/brushed up throughout the semester, with the binding course materials available on the course Moodle for those enrolled in the winter semester 2023/24.

This website was created to be viewed in HTML format. The accompanying (PDF) book version can be accessed by clicking on the PDF icon at the top right, but is not optimally formatted. Tables formatted for HTML output are particularly oddly formatted in PDF, as is the order of printed elements in relation to their accompanying text. For this reason, I strongly encourage to follow the web book.

Part I

Overview

Syllabus

Meeting	Lecture	Topic	Vorbereitung
2023-10-10	1	Equation of a line	Winter (2019): Ch. 1-3
2023-10-11	2	Linear regression	Winter (2019): Ch. 4 Winter (2013)
2023-10-12	3	Continuous predictors	Winter (2019): Ch. 5 Winter (2013)
2023-10-10	4	Multiple linear regression	Winter (2019): Ch. 6 Winter (2013)
2023-10-11	5	Categorical predictors	Winter (2019): Ch. 7 Winter (2013)
2023-10-12	6	Model assumptions	
2023-10-10	7	Logistic regression	Winter (2019): Ch. 12
2023-10-11	8	Log odds, logits, and odds ratio	
2023-10-12	9	Foundational Ideas	Vasisht & Nicenboim (2016)
2024-01-12	10	Independence assumption	Winter (2019): Ch. 14 Winter & Grice (2021); un
2024-01-12	11	LMMs 1: random intercepts	Winter (2019): Ch. 14
2024-01-26	12	GLMMs	
2024-01-26	13	LMMs 2: random slopes	
2024-02-09	14	TBD	
2024-02-09	15	TBD	

Resources and Set-up

Resources

This course is mainly based on Winter (2019), which is an excellent introduction into regression for linguists. For even more introductory tutorials, I recommend going through Winter (2013) and Winter (2014). For a more intermediate textbook, I'd recommend Sonderegger (2023b).

If you're interested in the foundational writings on the topic of (frequentist) linear mixed models in (psycho)linguistic research, I'd recommend reading Baayen (2008); Baayen et al. (2008); Barr et al. (2013a); Bates et al. (2015); Jaeger (2008); Matuschek et al. (2017); Vasishth (2022); Vasishth & Nicenboim (2016).

Assumptions about you

For this course, I assume that you are familiar with more classical statistical tests, such as the t-test, Chi-square test, etc. I also assume you are familiar with measures of central tendency (mean, median, mode) measures dispersion/spread (standard deviation), and with the concept of a normal distribution. Lacking this knowledge will not impeded your progress in the course, but is an important foundation on which we'll be building. We can review these concepts in-class as needed.

Software

- R: a statistical programming language (the underlying language)
- RStudio: an program that facilitates working with R; our preferred IDE integrated development environment
- LaTeX: a typesetting system that generates documents in PDF format
- why R?
 - R and RStudio are open-source and free software
 - they are widely used in science and business

Install R

- we need the free and open source statistical software R to analyze our data
- download and install R: <https://www.r-project.org>

Install RStudio

- we need RStudio to work with R more easily
- Download and install RStudio: <https://rstudio.com>
- it can be helpful to keep English as language in RStudio
 - we will find more helpful information if we search error messages in English on the internet
- If you have problems installing R or RStudio, check out this help page (in German): <http://methods-berlin.com/wp-content/uploads/Installation.html>

Install LaTeX

- we will not work with LaTeX directly, but it is needed in the background
- Download and install LaTeX: <https://www.latex-project.org/get/>

resources

- many aspects of this course are inspired by ([nordmann_applied_2022?](#)) and ([wickham_r_nodate?](#))
 - both freely available online (in English)
- for German-language resources, visit the website of [Methodengruppe Berlin](#)

Troubleshooting (EN: Troubleshooting)

- Error messages are very common in programming, at all levels.
- How to find solutions for these error messages is an art in itself
- Google is your friend! If possible, google in English to get more information

Session Information

The current version of this Quarto book was developed using R version 4.3.0 (2023-04-21) (Already Tomorrow) in RStudio version 2023.3.0.386 (Cherry Blossom). At the bottom of each chapter is a list of the packages (and version info) used in that chapter (under Session Information). I highly recommend you do the same at the bottom of each script that you write. You can easily do this by writing the following at the bottom of any Rmarkdown (.Rmd) or Quarto (.qmd) script:

```
# Session Info  
  
```{r}  
sessionInfo()
```
```

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Part II

Day 1: Simple linear regression

1 Understanding straight lines

Regression for Linguists

```
# suppress scientific notation
options(scipen=999)

# load libraries
pacman::p_load(tidyverse,
  broom,
  patchwork,
  knitr,
  kableExtra,
  gt,
  googlesheets4)

# tell googlesheets4 we don't want private
gs4_deauth()
```

Learning Objectives

Today we will learn...

- the equation of a line
- about intercepts, slopes, and residuals

Resources

This lecture is based on the readings for today's session: Winter (2013) and Winter (2019) (Ch. 3), and to a lesser extent (**debruine_understanding_2021?**); Winter (2014).

1.1 When to model your data

By the time we get to the point of wanting to model our data, we should have a pretty good idea of how our data look. We achieve this through running an exploratory data analysis (EDA), which consists of visualising your data and determining outliers (a question for another day: what *is* an outlier?), generating summary (i.e., descriptive) statistics, and just overall getting to know your data, without making any claims beyond your data.

However, an understanding of the data design and collection procedure is incredibly important and is necessary in order to appropriately fit a model to our data. In fact, planning out your analyses when designing your experiment is highly recommended in order to ensure your data will have the appropriate structure and that the assumptions made by your chosen analyses are taken into consideration before data collection.

The next step after conducting an EDA is to *model* your data, i.e., run **inferential statistics**, this is where we try to generalise beyond our data.

1.1.1 Statistical tests versus models

Many statistical courses and textbooks still put undue emphasis on classical statistical tests. However, these **common statistical tests are simplified linear models**, without the added benefits of linear models. In essence, statistical tests tell us something about our data, whereas statistical *models* can be used to make predictions about hypothetical future observations.

1.2 (Linear) Regression

Data exploration gives us an idea about what our data look like, but if we want to be able to make predictions about hypothetical observations, i.e., to *predict* values of our DV based on one (or more) IV(s), we need to fit a model to our data. This model can then *predict* values of our DV based on one (or more) IV(s), i.e., *predicting* an outcome variable (dependent variable, DV) from one or more predictors (independent variable, IV). Because we're making predictions, we need to take into account the variability (i.e., *error*) in our data.

1.2.1 Types of regression

1.3 Straight lines

- *linear regression* summarises the data with a straight line
 - we *model* our data as/fit our data to a straight line

| regression type | predictor | outcome |
|---|-----------------------|------------------------|
| simple regression | Single predictor | continuous (numerical) |
| multiple regression | multiple predictor | continuous (numerical) |
| hierarchical/linear mixed models/linear mixed effect models | include random effect | continuous (numerical) |
| generalised linear (mixed) models: logistic regression | as above | binary/binomial data |
| generalised linear (mixed) models: poisson regression | as above | count data |

- *straight lines* can be defined by
 - Intercept (b_0)
 - * value of Y when $X = 0$
 - Slope (b_1)
 - * gradient (slope) of the regression line
 - * direction/strength of relationship between x and y
 - * regression coefficient for the predictor
- so we need to define an intercept and a slope

1.3.1 A line = intercept and slope

- a line is defined by its intercept and slope
 - in a regression model, these two are called **coefficients**

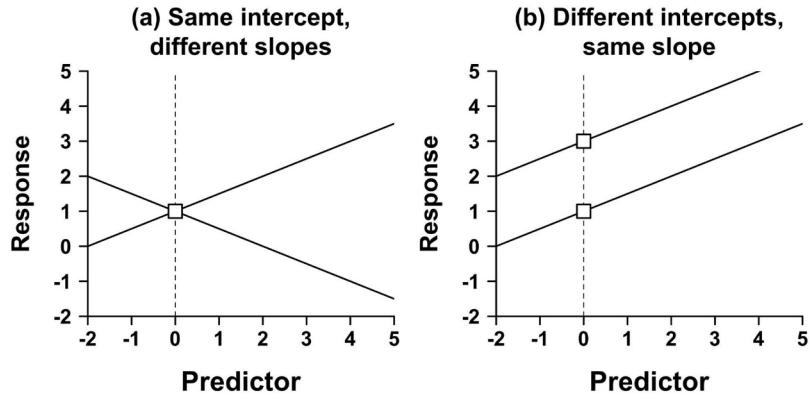


Figure 4.2. (a) Two lines with positive and negative slopes that go through the same intercept; (b) two lines with the same positive slope that have different intercepts

Figure 1.1: Image source: Winter (2019) (all rights reserved)

💡 Equation of a line

$$y = mx + c \quad (1.1)$$

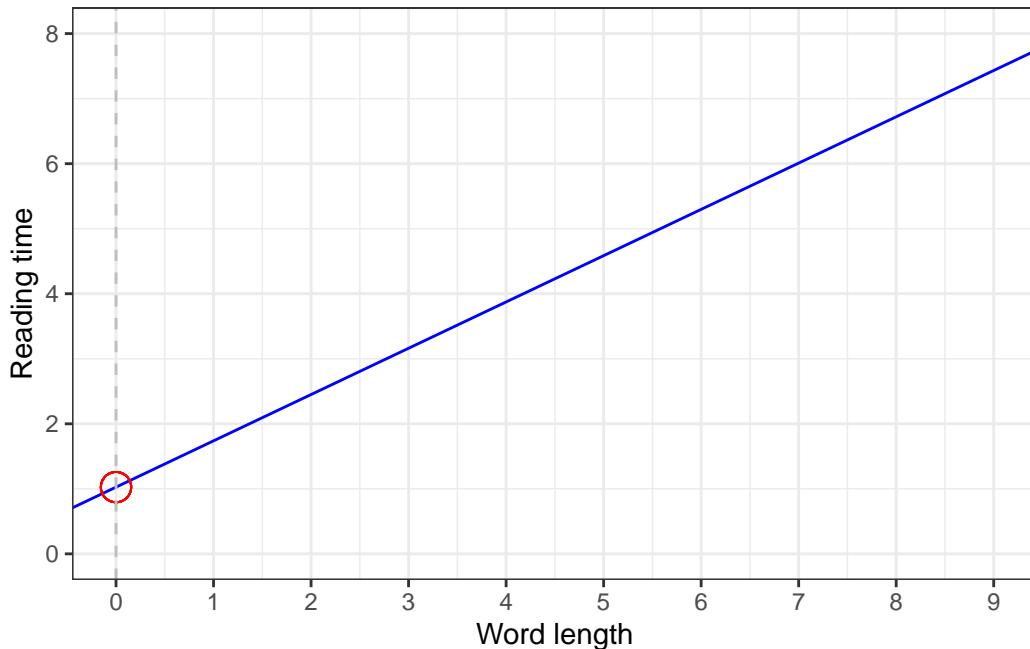
$$Y_i = (b_0 + b_1 X_i) \quad (1.2)$$

$$outcome_i = (model) \quad (1.3)$$

$$y_i = (intercept + slope * x_i) \quad (1.4)$$

1.3.2 Intercept (b_0)

- the value of y when $x = 0$



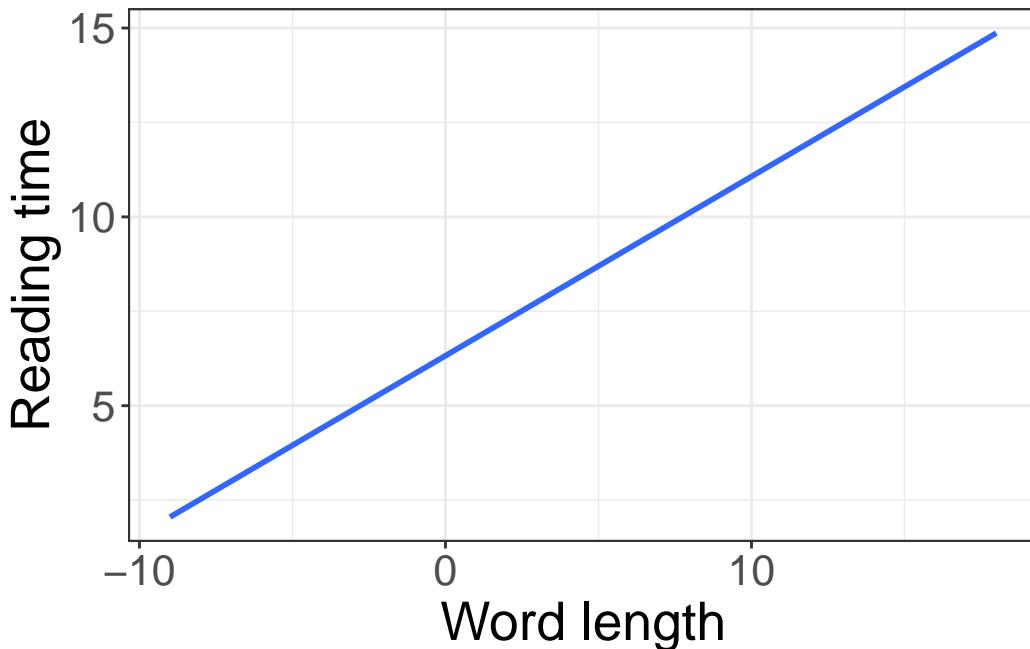
1.3.3 Slopes (b_1)

A slope describes a *change in y* (Δy) over a *change in x* (Δx), where Δ (the Greek letter *delta*) can be read as ‘difference’. So a slope’s value equals the difference in x for a difference of 1 unit in y . Positive slopes indicate that as x increases, y increases. A negative slope value indicates that as x increases, y decreases (or vice versa). A slope of 0 indicates there is no change in y as a function of x , or: there is no change in y when the value of x changes.

$$\text{slope} = \frac{\Delta y}{\Delta x} \quad (1.5)$$

This relationship between x and y is sometimes referred to as “rise over run”: how do you ‘rise’ in y for a given ‘run’ in x ? For example, if we were to measure children’s heights and ages, we would expect to find an increase in height for every increase in age. Or, for a linguistic example, we would expect to find longer whole-sentence *reading times* (a measure variable) for longer texts: if a sentence has 9 words (*I find straight lines to be really interesting and fun.*), we would expect longer reading times than a sentence with 3 words (*I love lines.*)).

- what is the intercept of this line?
- what is the slope of this line?



1.4 Error and residuals

- *fixed effects* (IV/predictors): things we can understand/measure
- *error* (random effects): things we cannot understand/measure
 - in biology, social sciences (and linguistic research), there will always sources of random error that we cannot account for
 - random error is less an issue in e.g., physics (e.g., measuring gravitational pull)

- *residuals*: the difference (vertical difference) between **observed data** and the **fitted values** (predicted values)

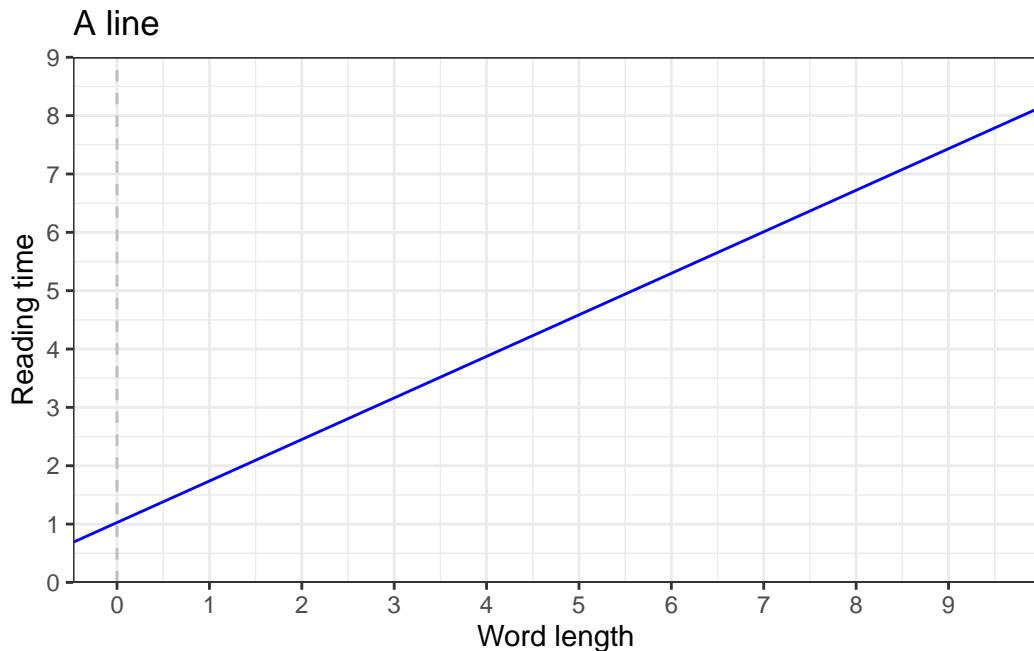
 Equation of a line

$$y = mx + c \quad (1.6)$$

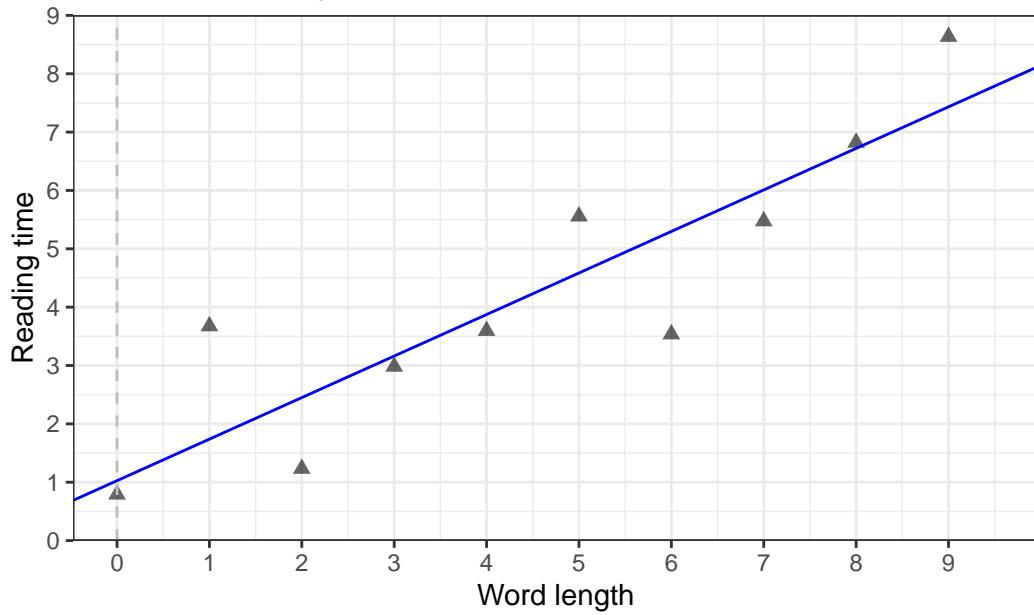
$$Y_i = (b_0 + b_1 X_i) + \epsilon_i \quad (1.7)$$

$$outcome_i = (model) + error_i \quad (1.8)$$

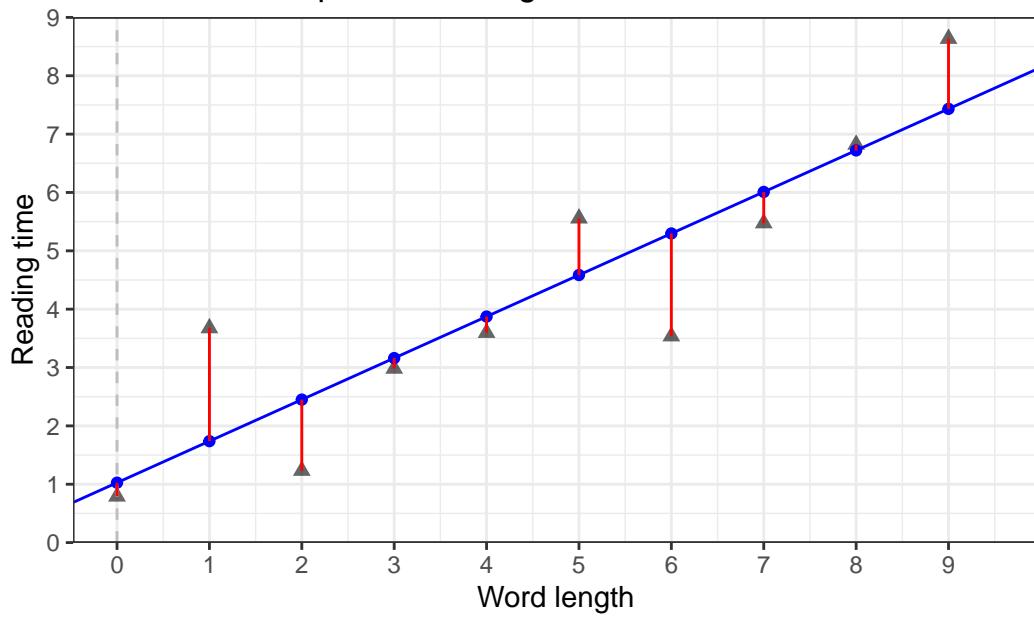
$$y_i = (intercept + slope * x_i) + error_i \quad (1.9)$$



A line with data points



A line with data points and regression line



1.4.1 Method of least squares

- so how is any given line chosen to fit any given data?
- the *method of least squares*
 - take a given line, and square all the residuals (i.e., *residual*²)
 - the line with the lowest *sum of squares* is the line with the best fit to the given data
 - why do we square the residuals before summing them up?
 - * so all values are positive (i.e., so that negative values don't cancel out positive values)
- this is how we find the *line of best fit*
 - R fits many lines to find the one with the best fit

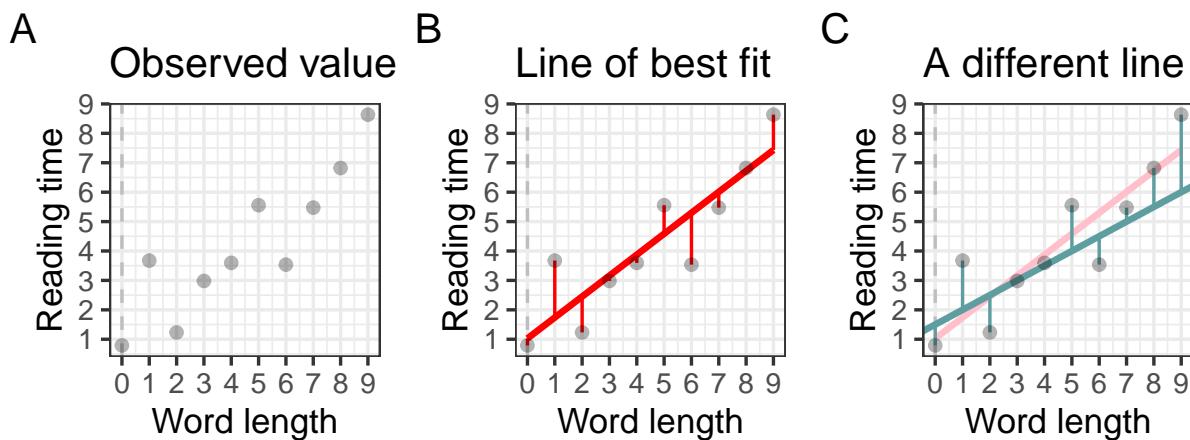


Figure 1.2: Observed values (A), Residuals for line of best fit (B), A line of worse fit with larger residuals (C)

Learning Objectives

Today we learned...

- the equation of a line
- about intercepts, slopes, and residuals

Important terms

| Term | Definition |
|------------------|---|
| Intercept | Value of y for $x=0$ |
| Slope | a change in x over a change in y ; regression coefficient for the predictor. Positive as x increases. |
| residuals/error | difference between observed data and the fitted values |
| interaction term | used to describe how effects of one predictor may be influenced by changes in another predictor |

1.5 Tasks

1.5.1 Task 1: pen-and-paper

You will receive a piece of paper with several grids on it. Follow the instructions, which include drawing some lines. If you aren't in-class, this is the paper we are using:

1.5.2 Task 2: simulating data

All of the figures we just saw (except Figure 1.1, which is from Winter (2019)) were generated in R. Simulating data and plotting is a great way to understand concepts, or even to map out our hypotheses. Let's use R for the first time to try to simulate some data in order to plot lines. Our goal will be to produce a line that has the following:

- intercept = 4.5
- slope = 3

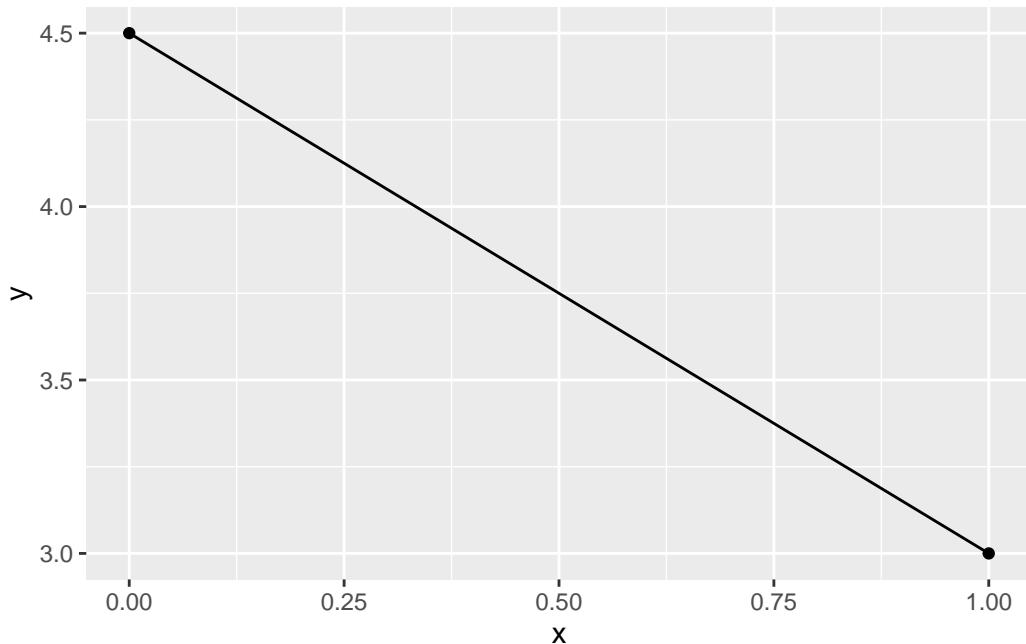
1.5.2.1 Planning

First, think about what steps will be required to create such plots. Can you come up with a workflow plan (without peaking at the next tasks)?

1.5.2.2 Producing our line

```
x <- c(0,1)
y <- c(4.5,3)
data <- cbind(x,y) |> as.data.frame()
ggplot(data = data) +
  aes(x = x, y = y) +
```

```
geom_line() +  
geom_point()
```



Session Info

Developed with Quarto using R version 4.3.0 (2023-04-21) (Already Tomorrow) and RStudio version 2023.9.0.463 (Desert Sunflower), and the following packages:

```
sessionInfo()
```

```
R version 4.3.0 (2023-04-21)  
Platform: aarch64-apple-darwin20 (64-bit)  
Running under: macOS Ventura 13.2.1
```

```
Matrix products: default  
BLAS: /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib  
LAPACK: /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib; /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib  
locale:  
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```

time zone: Europe/Berlin
tzcode source: internal

attached base packages:
[1] stats      graphics   grDevices utils      datasets   methods    base

other attached packages:
[1] googlesheets4_1.1.0 gt_0.9.0          kableExtra_1.3.4
[4] knitr_1.44        patchwork_1.1.3   broom_1.0.5
[7] lubridate_1.9.2  forcats_1.0.0       stringr_1.5.0
[10] dplyr_1.1.3      purrr_1.0.2        readr_2.1.4
[13] tidyverse_1.3.0   tibble_3.2.1       ggplot2_3.4.3
[16] tidyverse_2.0.0

loaded via a namespace (and not attached):
[1] gtable_0.3.4      xfun_0.39         lattice_0.21-8    gargle_1.4.0
[5] tzdb_0.4.0        vctrs_0.6.3        tools_4.3.0       generics_0.1.3
[9] curl_5.0.1        fansi_1.0.4        pacman_0.5.1     pkgconfig_2.0.3
[13] Matrix_1.5-4     webshot_0.5.4     lifecycle_1.0.3   farver_2.1.1
[17] compiler_4.3.0   munsell_0.5.0     htmltools_0.5.5  yaml_2.3.7
[21] pillar_1.9.0     magick_2.7.4      nlme_3.1-162     tidyselect_1.2.0
[25] rvest_1.0.3      digest_0.6.33    stringi_1.7.12   splines_4.3.0
[29] labeling_0.4.3   rprojroot_2.0.3   fastmap_1.1.1    grid_4.3.0
[33] here_1.0.1       colorspace_2.1-0   cli_3.6.1        magrittr_2.0.3
[37] utf8_1.2.3       withr_2.5.0       scales_1.2.1     backports_1.4.1
[41] googledrive_2.1.0 timechange_0.2.0   rmarkdown_2.22   httr_1.4.6
[45] cellranger_1.1.0 png_0.1-8        hms_1.1.3        evaluate_0.21
[49] viridisLite_0.4.2 mgcv_1.8-42     rlang_1.1.3     Rcpp_1.0.11
[53] glue_1.6.2        xml2_1.3.4       svglite_2.1.1    rstudioapi_0.14
[57] jsonlite_1.8.7    R6_2.5.1        systemfonts_1.0.4 fs_1.6.2

```

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2 Simple linear regression

Regression for Linguists

```
{#sec-simple-regression}
```

Learning Objectives

Today we will learn...

- how to fit a simple linear model with the `lm()` function
- how to interpret our model output

Set-up environment

Make sure you always start with a clean R Environment (`Session > Restart R`). This means you should have no objects stored in your Environment, and no packages loaded. To ensure this, you can go to the `Session` tab (up where you'll find `File`, `Help`, etc.), and select `Restart R`. You can also use the keyboard shortcut `Cmd/Ctrl+Shift+0` (that's a zero, not an 'oh').

In addition, I often prefer to run `options(scipen=999)` in order to suppress scientific notation, which writes very large or very small numbers in an unintuitive way. For example, `0.000005` is written `5e-06` in scientific notation.

```
# suppress scientific notation
options(scipen=999)
```

We'll also need to load in our required packages. Hopefully you've already install the required packages (if not, go to `?@sec-software`).

```
# load libraries
pacman::p_load(
```

```
tidyverse,  
here,  
broom,  
lme4,  
janitor,  
languageR)
```

2.1 Simple linear model: $RT \sim \text{frequency}$

Recall that $y \sim x$ can be read as “y as a function of x”, or “y predicted by x”. Following Winter (2019), we will first model some word frequency data. In this experiment, Our first model is given in equation 2.1:

$$RT \sim \text{frequency} \quad (2.1)$$

Let’s load our data using the `read_csv()` function from `readr`. I also use the `clean_names()` function from the `janitor` package, which tidies up variable names (e.g., no spaces, all lower case).

```
# load ELP_frequency.csv  
df_freq <- read_csv(here("data", "ELP_frequency.csv")) |>  
  clean_names()
```

2.1.1 Mini-EDA

Let’s explore the data a little bit, which is what we would normally do before fitting any models. First, let’s see how the data is structured.

```
# print head of df_freq  
head(df_freq)  
  
# A tibble: 6 x 3  
  word     freq     rt  
  <chr>   <dbl>   <dbl>  
1 thing    55522   622.  
2 life     40629   520.  
3 door     14895   507.  
4 angel    3992    637.
```

```
5 beer      3850  587.  
6 disgrace   409   705
```

Looks like there are only 3 columns: `word`, `freq`, and `rt`. We can assume that they correspond to the word, its frequency, and the reaction time, respectively. We can also see in our global environment that there are 12 observations, meaning 12 rows.

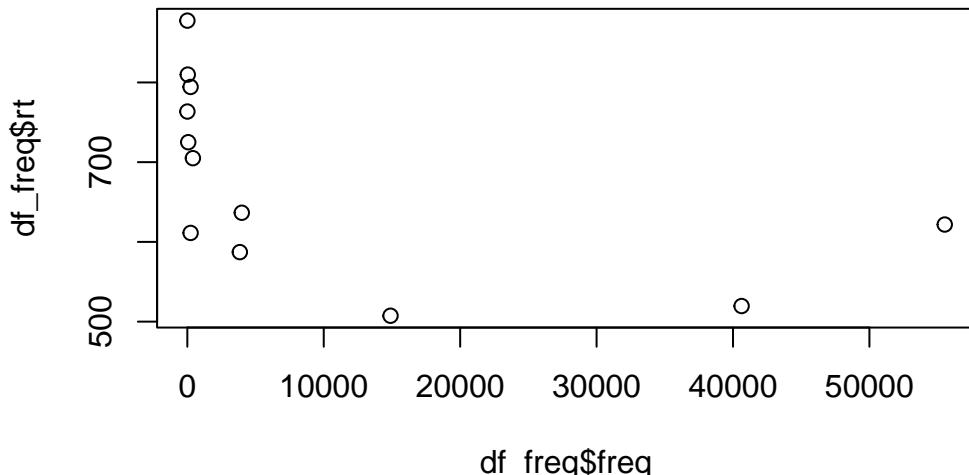
The `summary()` function provides summaries of each variable in a dataframe. For numeric variables, it will provide descriptive statistics for the centre and spread of the data (mean, median, quartiles). For categorical data, it will provide the count per category. For character variables, simply lists the number of observations.

```
summary(df_freq)
```

```
word                  freq                  rt  
Length:12           Min.    : 4.0    Min.    :507.4  
Class  :character   1st Qu.: 57.5   1st Qu.:605.2  
Mode   :character   Median  : 325.0  Median  :670.8  
                   Mean    :9990.2  Mean    :679.9  
                   3rd Qu.:6717.8  3rd Qu.:771.2  
                   Max.    :55522.0 Max.    :877.5
```

We see `freq` has a pretty big range, from 4 to 55522. `rt` has a range of 507.38 to 877.53, with an average reaction time of 679.9. Let's now get an overview of the relationship between `freq` and `rt`.

```
plot(df_freq$freq, df_freq$rt)
```



We see there are a lot of frequency values below roughly 400, and these seem to have higher reaction times than those with a higher frequency value. Let's fit these data to our first linear model to explore this effect of frequency on reaction times.

2.1.2 lm()

The the `lm()` function fits simple linear models. As arguments it takes a formula and a dataset, at minimum, as in equation 13.2.

$$lm(outcome \sim 1 + predictor, data = df_name) \quad (2.2)$$

The `lm()` function formula syntax can be read as: `outcome` predicted by the intercept (`1` is a placeholder for the intercept) and `predictor`. The intercept is included by default, so if you omit the `1` the intercept is still included in the formula. If you wanted to remove the intercept (which you often don't), you could replace `1` with `0`.

2.1.2.1 Running a model

Before we add our predictor `freq`, let's see what our model looks like without it. We can write it as:

```
lm(rt ~ 1, data = df_freq)
```

But it's useful to save the model as an object so that we can call on it later. It's often a good idea to have informative prefixes to your objects

```
fit_rt_1 <- lm(rt ~ 1, data = df_freq)
```

💡 Object naming

You may have wondered what the letters `df` are for when loading in our data set as `df_freq`. These letters stand for 'data frame', and serve as a reminder of what exactly that object in our environment is. We might also have wanted to plot the frequency data, in which case we could call save the plot as `fig_freq` or `plot_freq`. Here we are saving our model as `fit_rt_1`, using 'fit' to signal that this object is a model fit. You could also save it as `mod_freq_1`, `lm_freq_1`, or whatever you see fit. This simply helps keep our environment structured, which will become useful when you begin working with multiple datasets at a time.

2.1.2.2 Model output

Now that we've saved our model in our Environment, we can call it by name. Printing just the model gives us the formula and the coefficients.

```
# print model  
fit_rt_1
```

```
Call:  
lm(formula = rt ~ 1, data = df_freq)  
  
Coefficients:  
(Intercept)  
679.9
```

Recall that the `intercept` and `slope` are called `coefficients`. Why do we only see `Intercept`? Because we didn't include any predictors in our model. This output isn't very dense, however. We typically use the `summary()` function to print full model outputs.

```
summary(fit_rt_1)
```

```
Call:  
lm(formula = rt ~ 1, data = df_freq)  
  
Residuals:  
    Min      1Q      Median      3Q      Max  
-172.537 -74.677   -9.137   91.296  197.613  
  
Coefficients:  
            Estimate Std. Error t value     Pr(>|t|)  
(Intercept) 679.92     34.02   19.99 0.000000000538 ***  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
Residual standard error: 117.8 on 11 degrees of freedom
```

We see a lot more information here.

broom package

The `broom` package has some useful functions for printing model outputs

- `tidy()` produces a `tibble` (type of dataframe) of the `coefficients`
- `glance()` produces goodness of fit measures (which we won't discuss)

The outputs from `tidy()` and `glance()` can be fed into `kable` and/or `kable_styling()` to create formatted tables

```
tidy(fit_rt_1)
```

```
# A tibble: 1 x 5
  term      estimate std.error statistic p.value
  <chr>     <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept) 680.      34.0     20.0  5.38e-10
```

```
glance(fit_rt_1)
```

```
# A tibble: 1 x 12
  r.squared adj.r.squared sigma statistic p.value    df logLik    AIC    BIC
  <dbl>        <dbl>     <dbl>     <dbl>    <dbl> <dbl> <dbl> <dbl>
1 0            0         118.       NA       NA     -73.7 151. 152.
# i 3 more variables: deviance <dbl>, df.residual <int>, nobs <int>
```

`augment()` adds model values as columns to your dataframe (e.g., useful for plotting observed vs. fitted values).

```
augment(fit_rt_1, data = df_freq) %>% summary()
```

2.2 Interpreting model output

- let's take a closer look at our model summary

```
summary(fit_rt_1)
```

```
Call:
lm(formula = rt ~ 1, data = df_freq) #<1>
```

```

Residuals:
    Min      1Q   Median      3Q      Max
-172.537 -74.677 -9.137  91.296 197.613 #<2>

Coefficients:
            Estimate Std. Error t value     Pr(>|t|)    #<3>
(Intercept) 679.92     34.02   19.99 0.00000000538 *** #<4>
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1 #<5>

Residual standard error: 117.8 on 11 degrees of freedom #<6>

```

- ① formula repetition
- ② residuals: differences between observed values and those predicted by the model
- ③ names for columns `Estimates`, `standard error`, `t-value`, `p-value` (`Pr(>|t|)`)
- ④ Intercept (b_0)
- ⑤ Significance codes
- ⑥ R^2 , a measure of model fit (squared residuals); percentage of variance in the data shared with the predictor (higher numbers are better...this is pretty low)

2.2.0.1 Intercept

Our intercept is roughly 679.9 milliseconds; what does this number represent?

```
# print model intercept?
coef(fit_rt_1)[‘(Intercept)’]
```

```
(Intercept)
679.9167
```

```
# print data mean
mean(df_freq$rt)
```

```
[1] 679.9167
```

The intercept corresponds to the mean reaction time value. Let's explore this.

2.2.0.1.1 Intercept significance

In the model output, the intercept seems to be significant (indicated with a low p-value, and ***). What does this *mean*? Significance pretty much tells us if a number is equal to (or not statistically significantly different from) 0. So this tells us that the intercept (i.e., the mean reaction time) is different from 0. How do we interpret this? In most cases we don't. Whether or not the intercept is significantly different from 0 this isn't interesting or even theoretically relevant, as reaction times *shouldn't* be near 0, so neither should their mean. This is also true for formant frequencies, reading times, and other types of continuous linguistic data.

2.2.0.2 Standard Error

Standard error takes both the variability in our data and the sample size into account. The equation for standard error is:

$$SE = \frac{\hat{\sigma}}{\sqrt{n}} \quad (2.3)$$

where σ is the standard deviation, and n is the sample size. As a refresher, the equation for standard deviation (2.4) is the square root of the sum of all squared deviances from the mean ($\sum_{i=1}^n (x_i - \hat{\mu})^2$) divided by the sample size -1. Don't stress about the math for now, but it's helpful to try to understand where these values come from and what they represent.

$$\hat{\sigma} = \sqrt{\frac{\sum_{i=1}^n (x_i - \hat{\mu})^2}{n - 1}} \quad (2.4)$$

2.2.0.3 t-values

Simple linear regression is equivalent to a t-test. The one-sample *t*-test corresponds to an intercept-only.

```
df_freq %>%
  t.test(rt ~ 1, data = .)
```

One Sample t-test

```
data: rt
t = 19.988, df = 11, p-value = 0.000000000538
alternative hypothesis: true mean is not equal to 0
```

```

95 percent confidence interval:
 605.0461 754.7872
sample estimates:
mean of x
679.9167

df_freq %>%
  lm(rt ~ 1, data = .) %>%
  tidy() %>%
  mutate_if(is.numeric, round, 10)

# A tibble: 1 x 5
  term      estimate std.error statistic    p.value
  <chr>     <dbl>     <dbl>     <dbl>      <dbl>
1 (Intercept)   680.      34.0     20.0  0.000000005

```

The *real* power of linear regression is coming tomorrow and in January...multiple regression and mixed models. But for now, it's important to remember that the larger the t-value, the smaller the p-value. But more important is to not rely too heavily on p-values, as such black-and-white classifications have proven a poor substitute for understanding our data and our models.

2.2.0.4 p-values

 A word on t-values and p-values

t-values quantify the *difference* between population means.

p-values quantify the probability of obtaining a result equal to or greater than what was observed, given the assumption of no effect (the null hypothesis).

If the null hypothesis were true, we would expect no effect (a flat line). If we have a lot of evidence/are confident that there is an effect (the line (slope) is in fact *not* flat), then it would be unlikely that we would find such a result under the assumption that there is no effect (the line actually *is* flat) i.e., the null hypothesis. This is reflected in a small p-value.

2.2.0.5 Plotting rt ~ 1

- Figure 2.1 shows the intercept (red dot) amongst the observed data (black dots)
 - along the x-axis we have abstract numerical units (the values don't mean anything)

- what would the values of the intercept be?

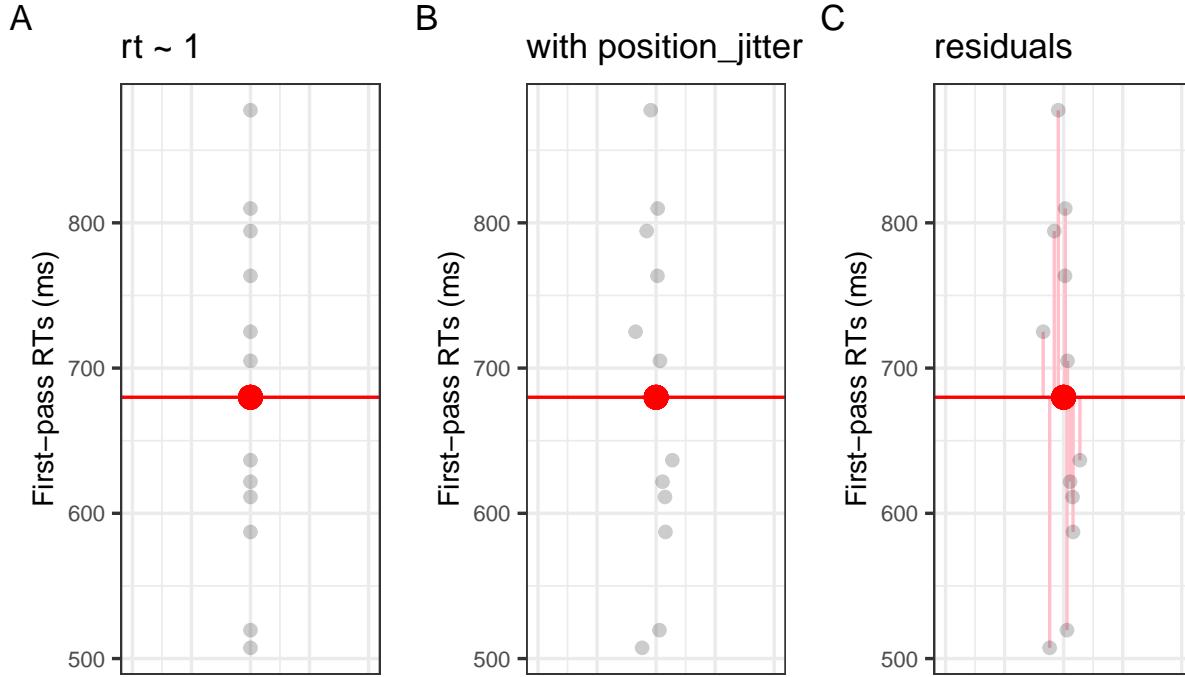
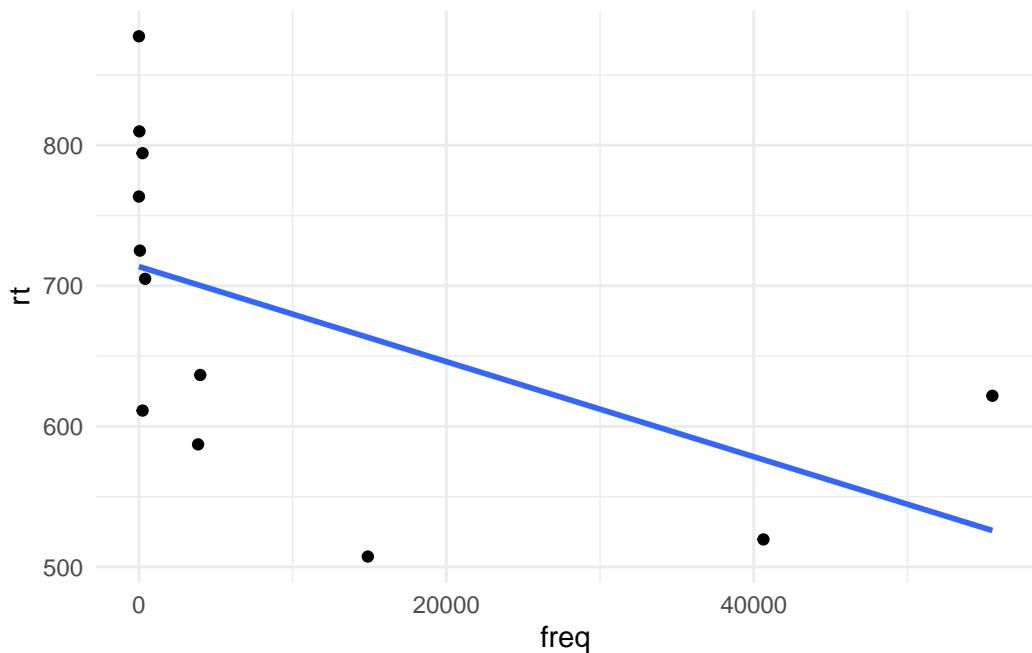


Figure 2.1: Visualisation of ‘ $rt \sim 1$ ’: observed values (black) and mean (intercept; red). Residuals would be the distance from each black dot to the y-value of the red dot

2.3 Adding a fixed effect (slope)

Now let's include a predictor, which will give us a *slope*. The slope represents the change in y (DV: `rt`) when we move 1-unit along y (IV: `freq`). In other words, it tells us the *effect* our IV has on the DV. Let's first plot the data:

```
df_freq |>
  ggplot() +
  aes(x = freq, y = rt) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



2.3.1 Fit model (treatment contrasts)

```
# fit simple linear model
fit_rt_freq <- lm(rt ~ freq, data = df_freq)
```

2.3.1.1 Model summary

```
summary(fit_rt_freq)
```

Call:

```
lm(formula = rt ~ freq, data = df_freq)
```

Residuals:

| Min | 1Q | Median | 3Q | Max |
|----------|---------|--------|--------|---------|
| -155.947 | -73.141 | 2.117 | 85.050 | 163.837 |

Coefficients:

| | Estimate | Std. Error | t value | Pr(> t) |
|-------------|------------|------------|---------|------------------|
| (Intercept) | 713.706298 | 34.639105 | 20.60 | 0.0000000016 *** |

```

freq      -0.003382   0.001699   -1.99      0.0746 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 104.6 on 10 degrees of freedom
Multiple R-squared:  0.2838,    Adjusted R-squared:  0.2121
F-statistic: 3.962 on 1 and 10 DF,  p-value: 0.07457

```

2.3.1.2 Intercept

The intercept in our last model was the mean reaction time. But now it's a different value.

```
# print model intercept
coef(fit_rt_freq)[‘(Intercept)’]
```

```
(Intercept)
713.7063
```

```
# print data mean
mean(df_freq$rt)
```

```
[1] 679.9167
```

Our intercept is no longer the grand mean of first-pass reading times...what is it?

2.3.1.3 Slope

Our slope was our slope -0.0033823. What does this correspond to?

```
# print slope
coef(fit_rt_freq)[‘freq’]
```

```
freq
-0.003382289
```

This is the change in y (our DV `rt`) for a 1-unit change in x (our IV: `freq`). So when we move up 1 unit in frequency, reaction times decrease by -0.0033823. Whether or not it makes sense to consider this number depends on the measurement unit your data is in, e.g., a unit change from one millimeter or one meter will have a drastically different slope value (say, for age), but the actual slope will be the exact same.

```
heights_m <- c(1.71, 1.56, .9, 2.06, 1.63)
heights_cm <- c(171, 156, 90, 206, 163)
heights_mm <- c(1710, 1560, 900, 2060, 1630)
year <- c(22,15,10,26,18)
months <- c(22,15,10,26,18)*12
days <- c(22,15,10,26,18)*365

df_heights_age <- cbind(year, months, days, heights_mm, heights_cm, heights_m) |> as.data...
pivot_longer(
  cols = c(heights_mm, heights_cm, heights_m),
  names_to = "unit",
  values_to = "height"
) |>
pivot_longer(
  cols = c(year, months, days),
  names_to = "unit_age",
  values_to = "age"
)

lm(heights_mm ~ year)
```

Call:

```
lm(formula = heights_mm ~ year)
```

Coefficients:

| (Intercept) | year |
|-------------|-------|
| 396.62 | 64.58 |

```
lm(heights_cm ~ days)
```

```
Call:  
lm(formula = heights_cm ~ days)
```

```
Coefficients:  
(Intercept)      days  
39.66230       0.01769
```

```
lm(heights_m ~ months)
```

```
Call:  
lm(formula = heights_m ~ months)
```

```
Coefficients:  
(Intercept)      months  
0.396623       0.005382
```

```
lm(heights_mm ~ year)
```

```
Call:  
lm(formula = heights_mm ~ year)
```

```
Coefficients:  
(Intercept)      year  
396.62         64.58
```

```
lm(heights_cm ~ year)
```

```
Call:  
lm(formula = heights_cm ~ year)
```

```
Coefficients:  
(Intercept)      year  
39.662         6.458
```

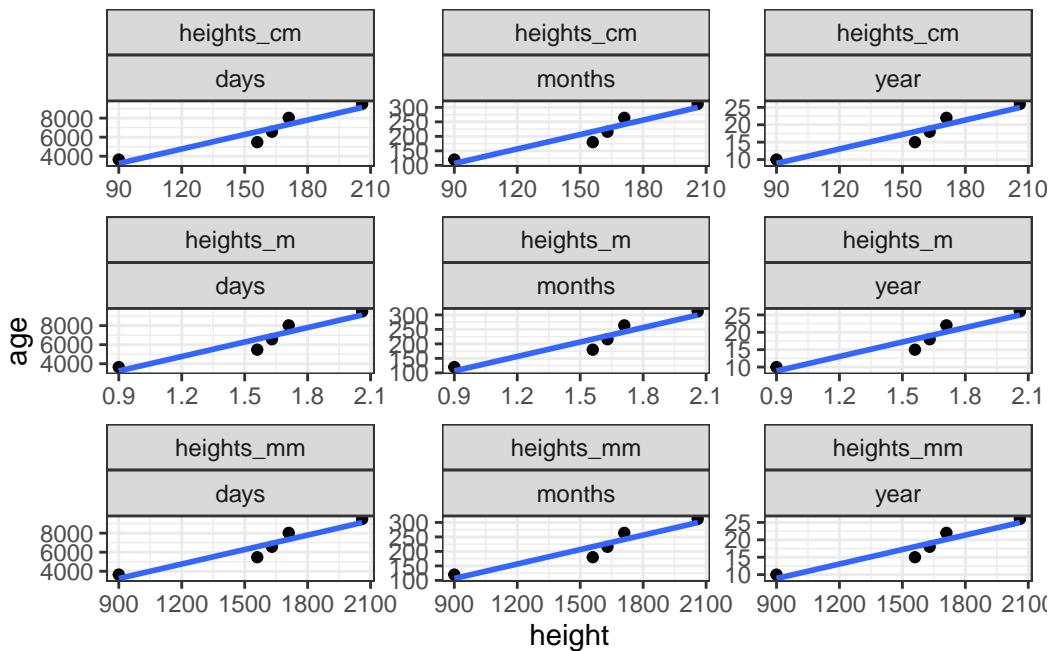
```
lm(heights_m ~ year)
```

```
Call:
lm(formula = heights_m ~ year)
```

Coefficients:

| (Intercept) | year |
|-------------|---------|
| 0.39662 | 0.06458 |

```
ggplot(data = df_heights_age) +
  aes(x = height, y = age) +
  facet_wrap(unit ~ unit_age, scales = "free") +
  geom_point() +
  geom_smooth(method = "lm", se = F) +
  theme_bw()
```



2.4 Model assumptions

Now that we've fit a model and understand the output, it's time to think about whether this model is a good fit for our data. We first have to understand some assumptions that need to be met in regression modelling. Importantly, these assumptions relate to the *residuals* of our model, not the raw data points themselves. The two assumptions we'll focus on for now are

the assumptions of *normality* of the residuals, and the constant *variance* of the residuals. Both assumptions are often diagnosed visually, so it takes some practice to learn what looks right.

2.4.1 Normality

When a model satisfies the normality assumption, its *residuals* (i.e., the difference between the *fitted* and *observed* values) will be approximately normally distributed. Normality is typically visualised using a histogram (Figure 2.2 A) and/or a quantile-quantile (Q-Q) plot (Figure 2.2 B).

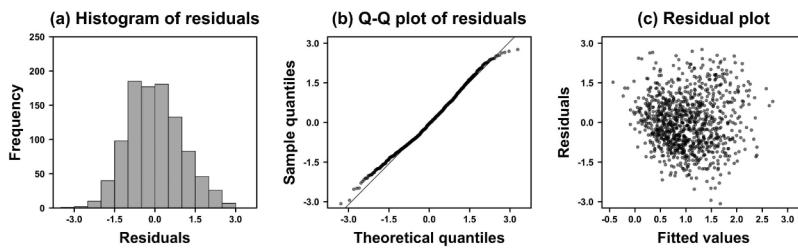


Figure 6.1. (a) Histogram, (b) Q-Q plot, and (c) residual plot of icon_mdl

Figure 2.2: Image source: Winter (2019) (all rights reserved)

Note

Winter (2019)'s description of how QQ plots are generated (p. 110):

To create this plot, every residual is transformed into a percentile (or quantile) [...] The question the Q-Q plot answers is: what is the corresponding numerical value of the 13.8th percentile on the normal distribution? If the values are the same, they will fit on a straight line, which indicates that the two distributions (the distribution of the residuals and the theoretical normal distribution) are very similar.

2.4.2 Constant variance

When a model satisfies the constant variance assumption (also called *homoscedasticity*, or the absence of *heteroscedasticity*), the spread of residuals will be equal across the regression line. This is typically visualised using a residual plot, which should look like a blob (Figure 2.2 C).

2.4.3 Visualising model assumptions

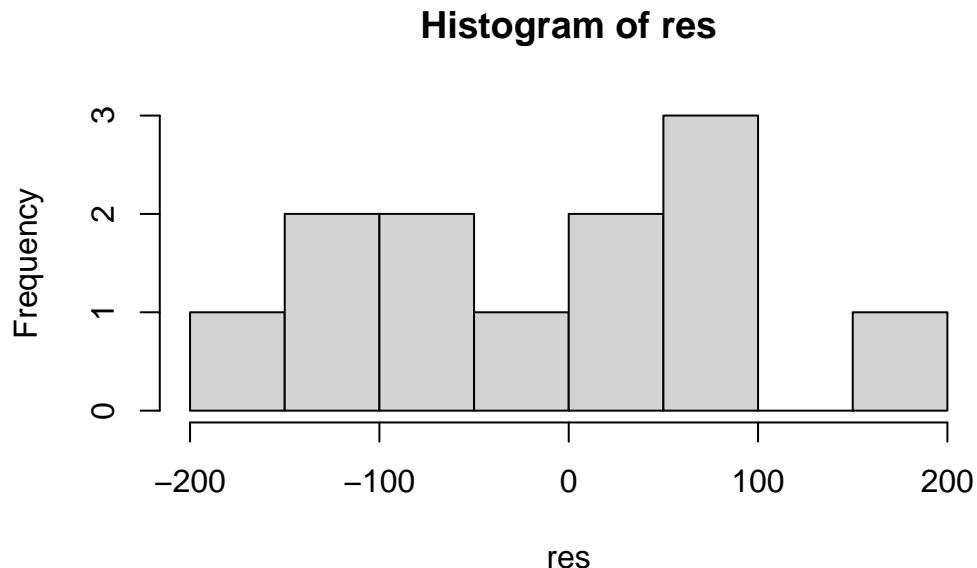
Let's plot our residuals to assess whether our model satisfies the assumptions of normality and constant variance.

2.4.3.1 Histogram

We can do this how it's done in Winter (2019) (in Ch. 6, p. 110-111), by first extracting the residuals from the model and then fitting them using the base R function `hist()`.

```
# extract residuals
res <- residuals(fit_rt_freq)

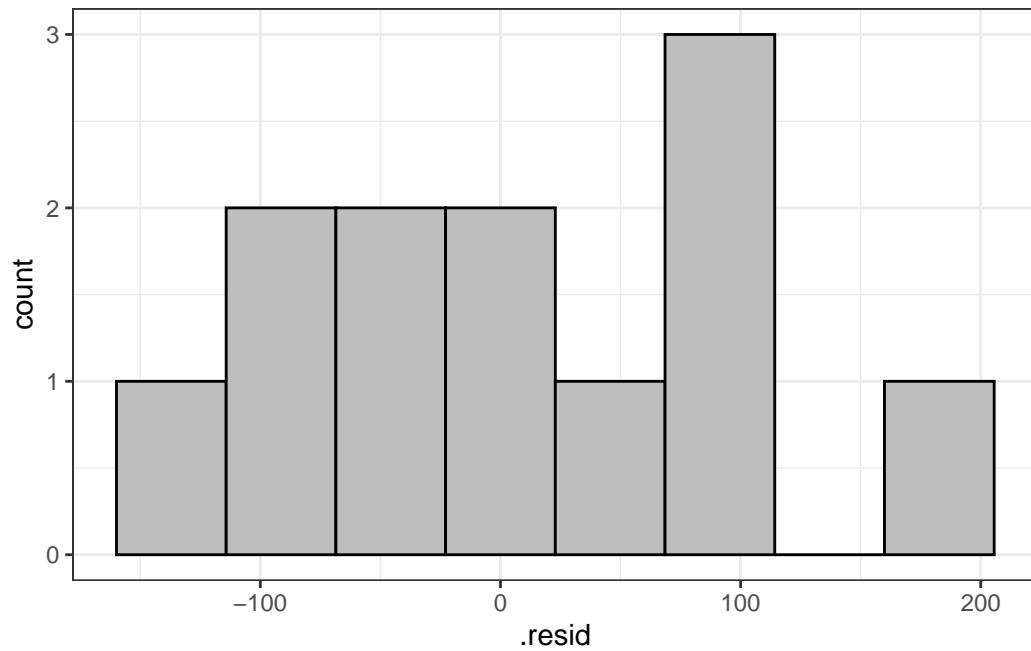
# plot histogram
hist(res)
```



Or, we can use the `augment()` function from `broom` to append model values to our original data frame, and then feed this into `ggplot()` from `ggplot2` (or even feed it into `hist()`).

```
# or, add to df
df_freq <- broom::augment(fit_rt_freq, df_freq)
```

```
# and create ggplot  
df_freq |>  
  ggplot() +  
  aes(x = .resid) +  
  geom_histogram(bins = 8, fill = "grey", colour = "black") +  
  theme_bw()
```

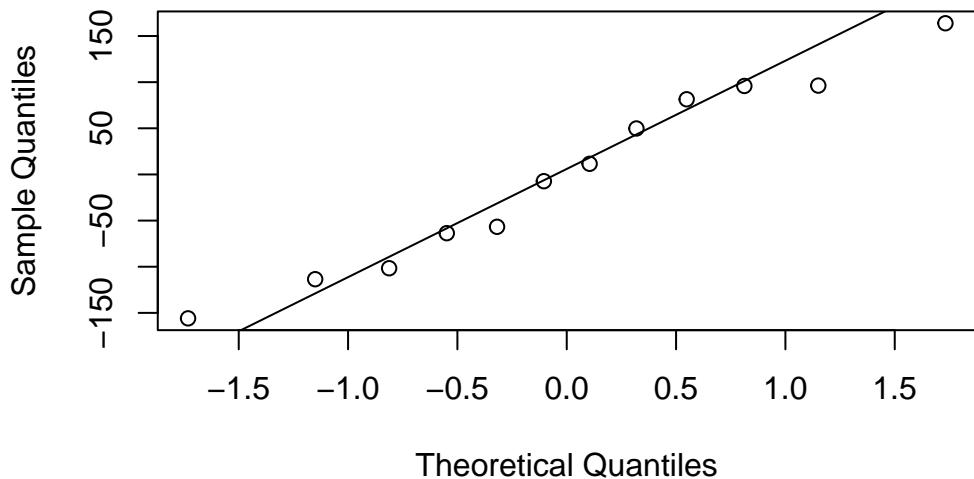


2.4.3.2 Q-Q plot

Again, we can do it Bodo's way:

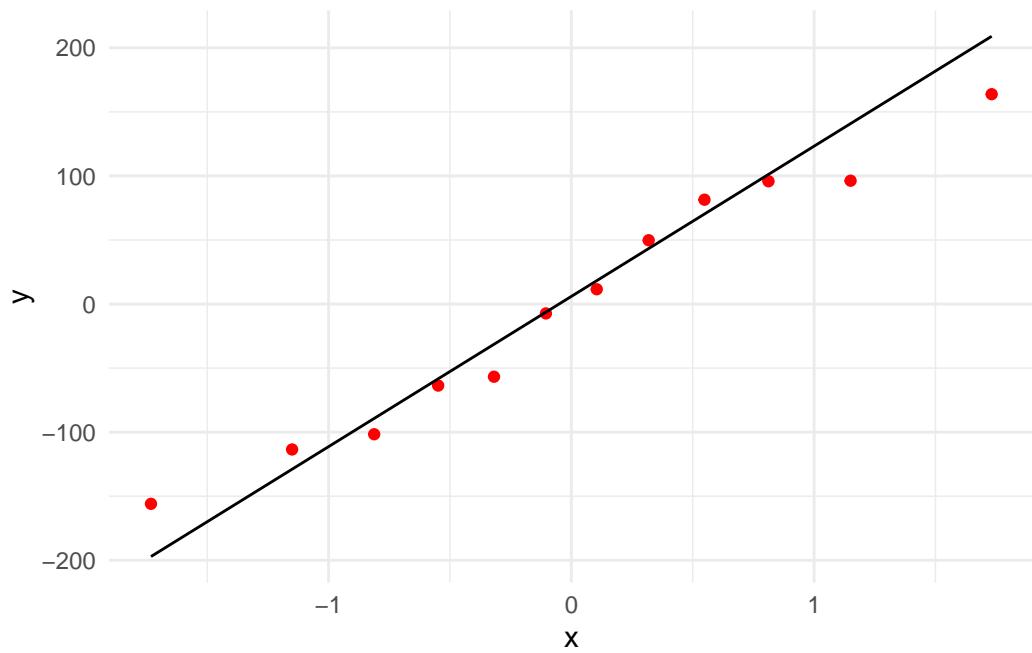
```
qqnorm(res)  
qqline(res)
```

Normal Q–Q Plot



Or using `augment()` and `ggplot()`.

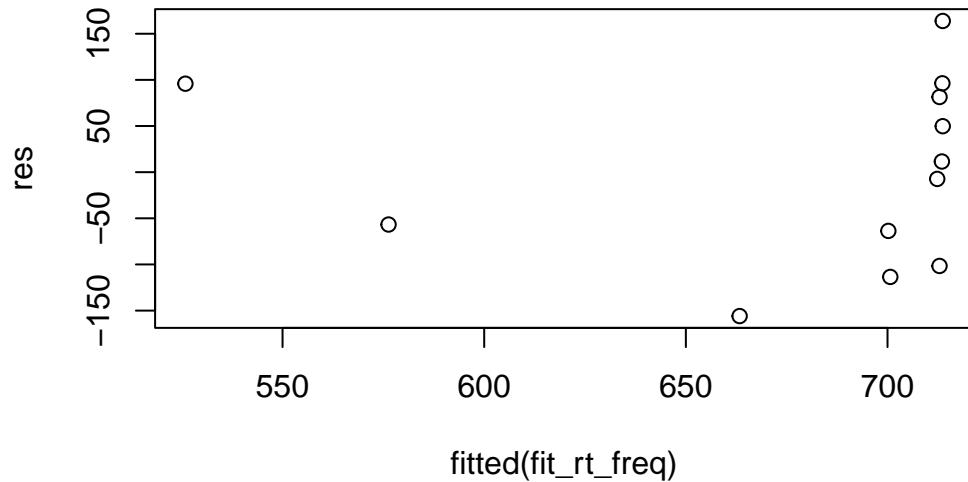
```
df_freq |>
  ggplot() +
  aes(sample = .resid) +
  geom_qq(colour = "red") +
  geom_qq_line()
```



2.4.3.3 Residual plot

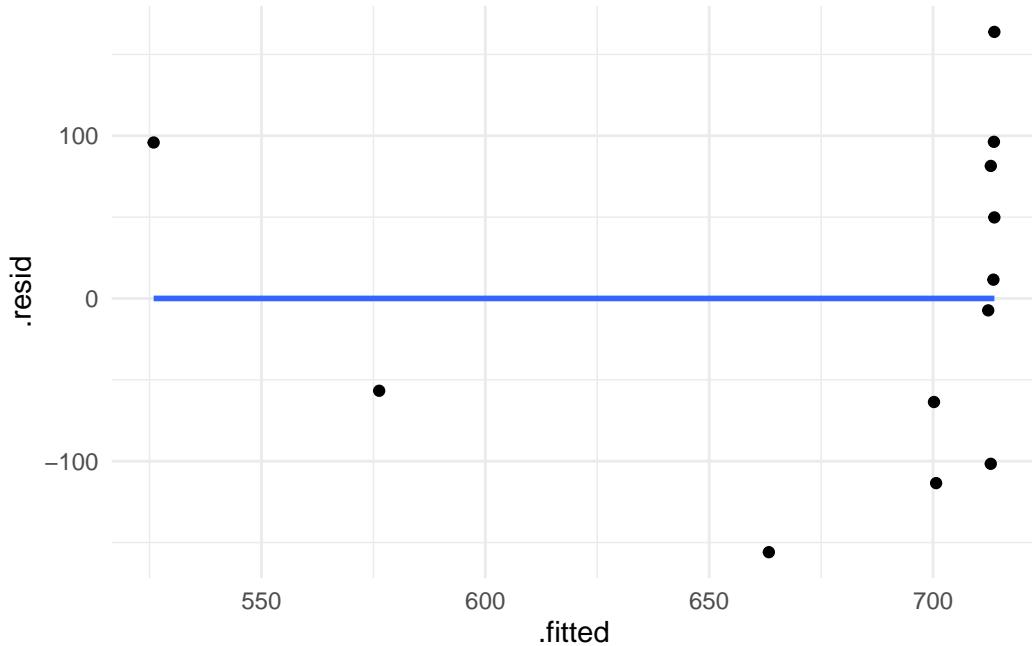
Bodo's way:

```
plot(fitted(fit_rt_freq), res)
```



Or with ggplot:

```
df_freq |>  
  ggplot() +  
  aes(x = .fitted, y = .resid) +  
  geom_point() +  
  geom_smooth(method = "lm", se = F)
```



2.4.4 performance package

I like to use the `performance` package to visualise model fit (Lüdecke et al., 2021).

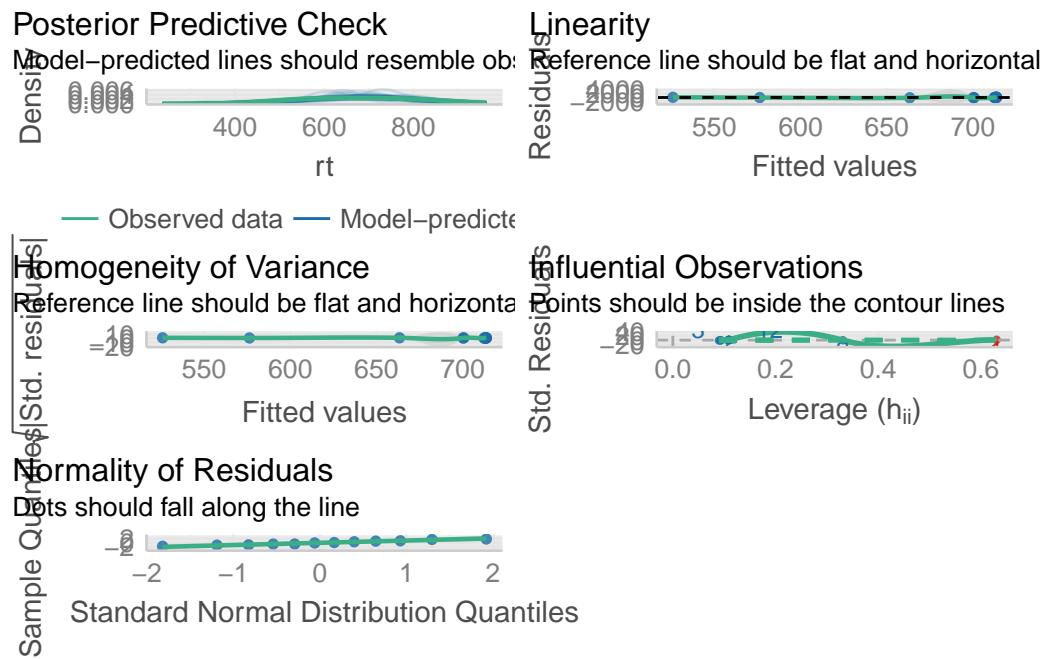
```
performance::check_normality(fit_rt_freq)
```

OK: residuals appear as normally distributed ($p = 0.702$).

```
performance::check_heteroscedasticity(fit_rt_freq)
```

OK: Error variance appears to be homoscedastic ($p = 0.980$).

```
performance::check_model(fit_rt_freq)
```



2.4.4.1 Coefficients table with `summary()`

```
> summary(fit_rt_freq)

Call:
lm(formula = rt ~ lifetime, data = df_freq, subset = rt > 0) #<1>

Residuals:                                         #<2>
    Min     1Q   Median     3Q    Max 
-228.99 -109.29 -26.99  58.86 777.71 

Coefficients:                                     #<3>
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 309.142     6.259  49.394 <0.0000000000000002 *** #<4>
lifetime1    31.701    12.517   2.533    0.0116 *      #<5>
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 57.46 on 541 degrees of freedom
Multiple R-squared:  0.01172,  Adjusted R-squared:  0.00989      #<6>
F-statistic: 6.414 on 1 and 541 DF,  p-value: 0.0116          #<7>
```

- ① formula
 - ② Residuals: differences between observed values and those predicted by the model
 - ③ Names for columns Estimates, SE, t-value, p-value
 - ④ Intercept (b_0), i.e., value of y (first-pass) with a move of one unit of x (lifetime)
 - ⑤ Slope (b_1), i.e., change in first fixation going from dead to living
 - ⑥ Output from an ANOVA
- what is the **intercept**?
 - is the **slope** positive or negative?
 - what is its value?
 - this is what the slope would look like:

Exploring the model

```
# how many observed values did we enter into the model?
df_freq |>
  nrow()

[1] 12

# how many observed values did we enter into the model?
length(fitted(fit_rt_freq))

[1] 12
```

Exploring the model: residuals

```
# what do our FITTED values look like?
head(fitted(fit_rt_freq))

  1       2       3       4       5       6
525.9148 576.2873 663.3271 700.2042 700.6845 712.3229

# what do our OBSERVED values look like?
head(df_freq$rt)

[1] 621.77 519.56 507.38 636.56 587.18 705.00
```

```
# what is the difference between the FITTED and OBSERVED values?  
head(df_freq$rt) - head(fitted(fit_rt_freq))
```

| 1 | 2 | 3 | 4 | 5 | 6 |
|-----------|------------|-------------|------------|-------------|-----------|
| 95.855154 | -56.727276 | -155.947103 | -63.644200 | -113.504485 | -7.322942 |

```
# what are our RESIDUALS?  
head(residuals(fit_rt_freq))
```

| 1 | 2 | 3 | 4 | 5 | 6 |
|-----------|------------|-------------|------------|-------------|-----------|
| 95.855154 | -56.727276 | -155.947103 | -63.644200 | -113.504485 | -7.322942 |

Exploring the model

- what were our coefficients?

```
coef(fit_rt_freq)
```

| (Intercept) | freq |
|---------------|--------------|
| 713.706297951 | -0.003382289 |

- what would be our predicted reaction time for a word with frequency of 0?

```
coef(fit_rt_freq)[‘(Intercept)’] + coef(fit_rt_freq)[‘freq’] * 0
```

```
(Intercept)  
713.7063
```

- ignore the (Intercept) label here, R just takes the first label when performing an operation on 2 vectors
- what is the mean of our predictor coded as +0.5?

```
coef(fit_rt_freq)[‘(Intercept)’] + coef(fit_rt_freq)[‘freq’] * 5000
```

```
(Intercept)  
696.7949
```

Table A1. Correspondences between some significance tests and linear models

| <i>Significance test</i> | <i>Linear model</i> | <i>Description</i> |
|---|--|--|
| <code>t.test(y ~ pred,
paired = FALSE)</code> | <code>lm(y ~ pred)</code> | An unpaired <i>t</i> -test corresponds to a linear model with a binary categorical predictor |
| <code>t.test(y, mu = 0)</code> | <code>lm(y ~ 1)</code> | One-sample <i>t</i> -test corresponds to an intercept-only model |
| <code>t.test(y ~ pred,
paired = TRUE)</code> | <code>lm(diffs ~ 1)</code> | A paired <i>t</i> -test corresponds to an intercept-only model fitted on differences |
| <code>chisq.test(xtab)</code> | <code>glm(y ~ x, family
= binomial)</code> | A chi-square test can be emulated with a logistic regression model |

Table A2. Correspondences between ANOVAs and linear models

| <i>ANOVA</i> | <i>Linear model</i> | <i>Description</i> |
|--------------------------------------|-------------------------------------|--|
| <code>aov(y ~ c3)</code> | <code>lm(y ~ c3)</code> | One-way ANOVA with three-level factor |
| <code>aov(y ~ c2 * c2)</code> | <code>lm(y ~ c2 * c2)</code> | 2 x 2 ANOVA (two-way ANOVA) |
| <code>aov(y ~ c2 * c3)</code> | <code>lm(y ~ c2 * c3)</code> | 2 x 3 ANOVA (and so on) |
| <code>aov(y ~ c2 * covariate)</code> | <code>lm(y ~ c2 * covariate)</code> | ANCOVA (analysis of covariance) with covariate (continuous predictor) and many other types of similar models |

Instead of repeated measures ANOVA, you can use mixed models. The linear model framework allows much more complex random effects structures, thus giving the user more flexibility in expressing their theories.

Figure 2.3: Image source: Winter (2019) (all rights reserved)

2.5 Reporting your model

Section

2.6 Summary

- we saw that the equation for a straight line boils down to its intercept and slope
- we fit our first linear model with a categorical predictor

Important terms

| Term | Definition |
|--------------------------|---|
| Coefficients | the slope and the intercept are coefficients |
| Simple linear regression | linear regression with a single predictor and a continuous outcome variable |
| fitted values | predicted values |
| continuous variable | a variable that can have an infinite number of values (an example would be reading what we measure; a.k.a. measure/outcome/response variable) |
| dependent variable | our predictor; a.k.a., predictor variable, fixed effects |
| independent variable | values of the intercept and slope of a lm() model |
| coefficients | equation of a line |
| | value of $y = \text{intercept} + (\text{slope} * \text{value of } x)$ |

Learning Objectives

Today we learned...

- how to fit a simple linear model with the `lm()` function
- how to interpret our model output

2.7 Task

Now it's your turn. Try to run the following `lm()` models:

1. total reading time at the *verb* region
2. total reading time at the *verb+1* region.

Session Info

Developed with Quarto using R version 4.3.0 (2023-04-21) (Already Tomorrow) and RStudio version 2023.9.0.463 (Desert Sunflower), and the following packages:

```
sessionInfo()
```

```
R version 4.3.0 (2023-04-21)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Ventura 13.2.1

Matrix products: default
BLAS:      /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
LAPACK:   /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib; 

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: Europe/Berlin
tzcode source: internal

attached base packages:
[1] stats      graphics    grDevices utils      datasets   methods    base

other attached packages:
[1] magick_2.7.4       googlesheets4_1.1.0  gt_0.9.0
[4] kableExtra_1.3.4   knitr_1.44        patchwork_1.1.3
[7] languageR_1.5.0    janitor_2.2.0    lme4_1.1-33
[10] Matrix_1.5-4      broom_1.0.5      here_1.0.1
[13] lubridate_1.9.2   forcats_1.0.0    stringr_1.5.0
[16] dplyr_1.1.3       purrr_1.0.2      readr_2.1.4
[19] tidyverse_1.3.0    tibble_3.2.1     ggplot2_3.4.3
[22] tidyverse_2.0.0

loaded via a namespace (and not attached):
[1] bitops_1.0-7        rlang_1.1.3       magrittr_2.0.3
[4] qqconf_1.3.2       snakecase_0.11.0 compiler_4.3.0
[7] mgcv_1.8-42         png_0.1-8        systemfonts_1.0.4
[10] vctrs_0.6.3        rvest_1.0.3      pkgconfig_2.0.3
[13] crayon_1.5.2       memuse_4.2-3    fastmap_1.1.1
[16] backports_1.4.1    labeling_0.4.3   caTools_1.18.2
[19] utf8_1.2.3         rmarkdown_2.22   tzdb_0.4.0
```

| | | |
|------------------------|--------------------|-------------------------|
| [22] pracma_2.4.2 | nloptr_2.0.3 | bit_4.0.5 |
| [25] xfun_0.39 | jsonlite_1.8.7 | parallel_4.3.0 |
| [28] R6_2.5.1 | stringi_1.7.12 | benchmarkme_1.0.8 |
| [31] boot_1.3-28.1 | cellranger_1.1.0 | Rcpp_1.0.11 |
| [34] iterators_1.0.14 | pacman_0.5.1 | splines_4.3.0 |
| [37] timechange_0.2.0 | tidyselect_1.2.0 | rstudioapi_0.14 |
| [40] yaml_2.3.7 | doParallel_1.0.17 | codetools_0.2-19 |
| [43] curl_5.0.1 | lattice_0.21-8 | opdisDownsampling_0.8.3 |
| [46] withr_2.5.0 | bayestestR_0.13.1 | benchmarkmeData_1.0.4 |
| [49] evaluate_0.21 | xml2_1.3.4 | pillar_1.9.0 |
| [52] foreach_1.5.2 | insight_0.19.3 | generics_0.1.3 |
| [55] vroom_1.6.3 | rprojroot_2.0.3 | hms_1.1.3 |
| [58] munsell_0.5.0 | scales_1.2.1 | minqa_1.2.5 |
| [61] glue_1.6.2 | tools_4.3.0 | see_0.8.0 |
| [64] robustbase_0.99-2 | webshot_0.5.4 | fs_1.6.2 |
| [67] grid_4.3.0 | datawizard_0.7.1 | colorspace_2.1-0 |
| [70] nlme_3.1-162 | performance_0.10.4 | googledrive_2.1.0 |
| [73] cli_3.6.1 | twosamples_2.0.1 | fansi_1.0.4 |
| [76] gargle_1.4.0 | viridisLite_0.4.2 | svglite_2.1.1 |
| [79] DEoptimR_1.1-3 | gtable_0.3.4 | digest_0.6.33 |
| [82] ggrepel_0.9.3 | qqplotr_0.0.6 | farver_2.1.1 |
| [85] htmltools_0.5.5 | lifecycle_1.0.3 | httr_1.4.6 |
| [88] bit64_4.0.5 | MASS_7.3-58.4 | |

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3 Continuous predictors

Regression for Linguists

This lecture is based on Ch. 5 (Correlation, Linear, and Nonlinear transformations) from Winter (2019).

Learning Objectives

Today we will learn...

- why and how to centre continuous predictors
- when and how to standardize continuous predictors
- why and how to log-transform continuous variables

Set-up environment

```
# suppress scientific notation
options(scipen=999)
```

We'll also need to load in our required packages. Hopefully you've already install the required packages (if not, go to `?@sec-software`).

```
# load libraries
pacman::p_load(
  tidyverse,
  here,
  broom,
  lme4,
  janitor,
  languageR)
```

Load data

```
df_freq <- read_csv(here("data", "ELP_frequency.csv")) |>  
  clean_names()
```

Reminder of our variables:

```
summary(df_freq)
```

| | word | freq | rt |
|------------------|-----------------|---------------|----|
| Length:12 | Min. : 4.0 | Min. :507.4 | |
| Class :character | 1st Qu.: 57.5 | 1st Qu.:605.2 | |
| Mode :character | Median : 325.0 | Median :670.8 | |
| | Mean : 9990.2 | Mean :679.9 | |
| | 3rd Qu.: 6717.8 | 3rd Qu.:771.2 | |
| | Max. :55522.0 | Max. :877.5 | |

Summary

In the last lectures we saw that the equation for a straight line boils down to its intercept and slope, and that linear regression fits a line to our data. This line results in predicted/fitted values, which fall along the line, and residuals, which are the difference between our observed values and the fitted values.

We also learned about two model assumptions: normality of residuals, and constant variance of residuals. We learned that we can plot these with histograms or Q-Q plots (normality), and residual plots (constant variance).

Now that we understand what a simple linear does, we can take a step back and focus on what we put into the model. So far we've looked at reaction times (milliseconds) as a function of word frequency. However, we don't typically feed raw continuous data into a model, because most continuous linguistic variables are not normally distributed, and so a straight line will not fit it very well (because there will be some large variance for higher values).

3.1 Linear transformations

Linear transformations refer to constant changes across values that do not alter the relationship between these values. For example, adding, subtracting, or multiplying by a constant value will not alter the difference between values. Think of the example in the last lecture on

the relationship between heights and ages as a function of the measurement unit: the relationship between all the values did not alter, because the difference between heights millimeters, centimeters, and meters is constant, as is the difference between ages in days, months, or years. We'll now look at some common ways of linearly transforming our data, and the reasons behind doing so.

3.1.1 Centering

Centering is typically applied to predictor variables. Centering refers to subtracting the mean of a variable from each value, resulting in each centered value representing the original value's deviance from the mean (i.e., a mean-deviation score). What would a centered value of 0 represent in terms of the original values?

Let's try centering our frequency values. To create a new variable (or alter an existing variable), we can use the `mutate()` function from `dplyr`.

```
# add centered variable
df_freq <-
  df_freq |>
  mutate(freq_c = freq - mean(freq))
```

This can also be done with base R, but it's a lot more verbose.

```
# add centered variable with base R
df_freq$freq_c <- df_freq$freq - mean(df_freq$freq)
```

Now let's fit our models.

```
# run our model with the original predictor
fit_rt_freq <-
  lm(rt ~ freq, data = df_freq)

# run our model with the centered predictor
fit_rt_freq_c <-
  lm(rt ~ freq_c, data = df_freq)
```

If we compare the coefficients from `fit_rt_freq` and `fit_rt_freq_c`, what do we see? The only difference is the intercept values: 713.706298 (uncentered) and 679.9166667 (centered).

```
mean(df_freq$rt)
```

```
[1] 679.9167
```

The intercept for a centered continuous predictor variable corresponds to the mean of a continuous response variable. This is crucial in interpreting interaction effects, which we will discuss tomorrow. For more detail on interpreting interactions, see Chapter 8 in Winter (2019) (we won't be discussing this chapter as a whole).

💡 Centering interval data

If you have interval data with a specific upper and lower bound, you could alternatively subtract the median value. In linguistic research, this is most typically rating scale data. For example, if you have a dataset consisting of ratings from 1-7, you can centre these ratings by subtracting 4 from all responses. A centred response of -3 would correspond to the lowest rating (1), and of +3 to the highest rating (7), which 0 would correspond to a medial rating (4). This can also be helpful in plotting, as there is no question as to whether 1 or 7 was high or low, because all ratings are now centred around 0 (and negative numbers correspond to our intuition of low-ratings).

3.1.2 Standardizing (z-scoring)

We can also standardize continuous predictors by dividing centered values by the standard deviation of the sample. Let's look at our frequency/reaction time data again.

First, what are our mean and standard deviation? This will help us understand the changes to our variables as we center and standardize them.

```
mean(df_freq$freq)
```

```
[1] 9990.167
```

```
sd(df_freq$freq)
```

```
[1] 18558.69
```

What are the first six values of `freq` in the original scale?

```
df_freq$freq[1:6]
```

```
[1] 55522 40629 14895 3992 3850 409
```

What are the first six values of `freq_c` in the centered scale? These should be the values of `freq` minus the mean of `freq` (which we saw above is 9990.1666667).

```
df_freq$freq_c[1:6]
```

```
[1] 45531.833 30638.833 4904.833 -5998.167 -6140.167 -9581.167
```

Now, let's create our standardised z-scores for frequency by dividing these centered values by the standard deviation of `freq` (which will be the same as the standard deviation of `freq_c`), and which we saw is 18558.6881679. Again, this can be done with `mutate()` from `dplyr`, or by using base R syntax.

```
# standardise using the tidyverse
df_freq <-
  df_freq |>
  mutate(freq_z = freq_c/sd(freq))

# standardize with base R
df_freq$freq_z <- df_freq$freq_c/sd(df_freq$freq)

head(df_freq)

# A tibble: 6 x 5
  word      freq      rt freq_c freq_z
  <chr>    <dbl>    <dbl>  <dbl>   <dbl>
1 thing     55522    622.  45532.  2.45 
2 life      40629    520.  30639.  1.65 
3 door      14895    507.  4905.   0.264 
4 angel     3992     637. -5998.  -0.323 
5 beer      3850     587. -6140.  -0.331 
6 disgrace   409     705. -9581.  -0.516
```

💡 Correlation

3.2 Non-linear transformations

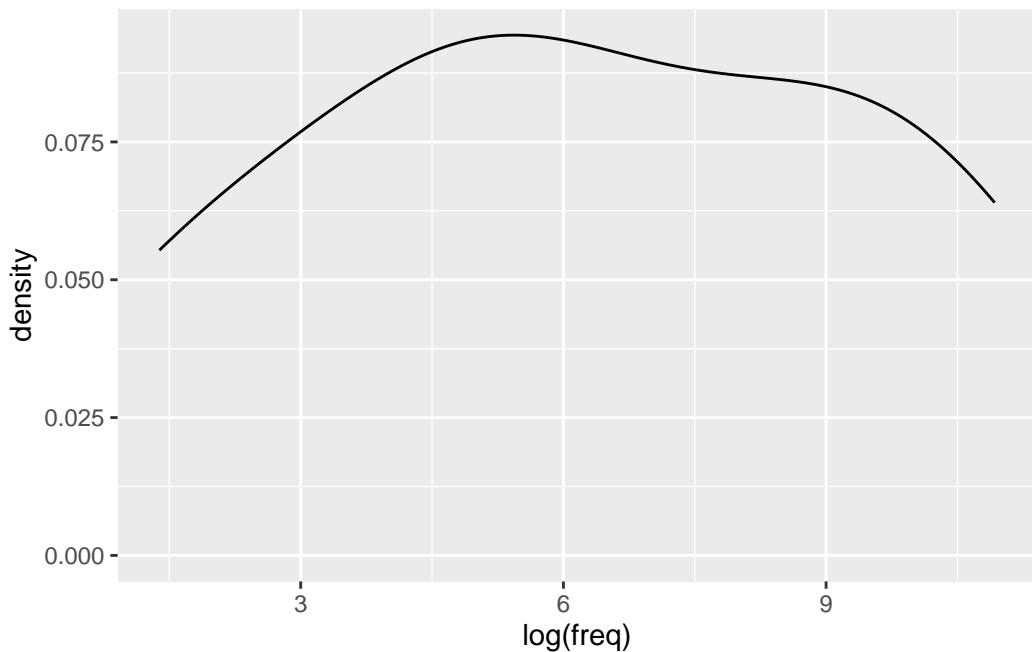
This is really the meat and potatoes of dealing with continuous variables (depending on your subfield). In linguistic research, and especially experimental research, we often deal with

continuous variables truncated/bound at 0. Reaction times, reading times and formant frequencies are all examples of such types of data: there is no such thing as a negative reading time or fundamental frequency. The problem with these types of data is that they are almost never normally distributed, which has implications for the normality of residuals for any line that tries to fit to these data. Very often, this type of data will have a ‘positive skew’, or a long tail off to the right (assuming larger values are plotting to the right). This shape is not symmetrical, meaning that the residuals tend to be much larger for larger values. It is also often the case that these very large, exceptional values will have a stronger influence on the line of best fit, leading to the coefficient estimates that are “suboptimal for the majority of data points” [@Baayen (2008); p. 92]. How do we deal with this nonnormality? We use non-linear transformations, the most common of which is the log-transformation.

3.2.1 Log-transformation

Let’s look at our reaction time data again. We’ll log-transform our reaction time data and frequency data. Note that in Winter (2019), frequency is transformed using log to the base 10 for interpretability, but we’ll stick to the natural logarithm.

```
df_freq |>
  ggplot() +
  aes(x = log(freq)) +
  geom_density()
```



```

df_freq <-
  df_freq |>
    mutate(rt_log = log(rt),
           freq_log = log(freq))

lm(rt_log ~ freq_log, data = df_freq) |> tidy()

# A tibble: 2 x 5
  term      estimate std.error statistic p.value
  <chr>      <dbl>     <dbl>     <dbl>     <dbl>
1 (Intercept)  6.79     0.0611    111.   8.56e-17
2 freq_log     -0.0453   0.00871   -5.20  4.03e- 4

# or, log-transform directly in the model syntax
lm(log(rt) ~ log(freq), data = df_freq) |> tidy()

# A tibble: 2 x 5
  term      estimate std.error statistic p.value
  <chr>      <dbl>     <dbl>     <dbl>     <dbl>
1 (Intercept)  6.79     0.0611    111.   8.56e-17
2 log(freq)    -0.0453   0.00871   -5.20  4.03e- 4

```

Learning Objectives

Today we learned...

- why and how to centre continuous predictors
- when and how to standardize continuous predictors
- why and how to log-transform continuous variables

Important terms

| Term | Definition | |
|--------------------|--|------|
| Centering | type of linear transformation | ‘c’ |
| standardizing | linear transformation (applied for multiple continuous predictors) | ‘d’ |
| log-transformation | non-linear transformation for positively skewed continuous variables | ‘lo’ |

Take-home messages

Continuous data are often transformed before fitting a model to this data. Linear transformations, like adding or multiplying all values by a single value, are often performed on continuous predictors by means of centring and standardizing (when there are multiple continuous predictors). Non-linear transformations are often performed on continuous data with a positive skew (a few values much larger than the majority) in order to satisfy the normality assumption. Although the normality assumption refers to the normality of *residuals*, the distribution of the data will have implications for the distribution of the residuals. The most common non-linear transformation is the log-transformation (the inverse of the exponential), which shrinks values, especially making big numbers smaller. This has the result of squeezing big numbers towards smaller numbers, reducing the spread in the distribution (e.g., the log of 3 is 1.0986123, the log of 30 is 3.4011974, and the log of 30 is 5.7037825).

What to do with this information? If you have continuous data truncated at 0 (with no upperbound, e.g., reaction time data or fundamental frequency), visualise the data (histogram and Q-Q plot) in order to check its distribution. If it is not normally distributed, you will likely want to log-transform it. Is this data your *response* variable? Then that is all you will likely want to do. Is this data a *predictor* variable? Then you will want to centre it (subtract the mean of this variable from all values). Do you have more than one continuous predictor variable? Then standardizing these variables will facilitate the interpretation of interaction effects (we'll talk about these soon).

3.3 Task

3.4 Assessing assumptions

1. Re-run the models `fit_rt_freq`, `fit_rt_freq_c`, and `fit_log`
2. Produce diagnostic plots for each of them (histograms, Q-Q plots, residual plots)
3. Interpret the plots

3.5 Model comparison

1. Use the `glance()` function to inspect the R^2 , AIC, and BIC of each model.
2. Which is the best fit? Why?

Session Info

Developed with Quarto using R version 4.3.0 (2023-04-21) (Already Tomorrow) and RStudio version 2023.9.0.463 (Desert Sunflower), and the following packages:

```
sessionInfo()
```

```
R version 4.3.0 (2023-04-21)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Ventura 13.2.1

Matrix products: default
BLAS:      /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
LAPACK:   /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib; 

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: Europe/Berlin
tzcode source: internal

attached base packages:
[1] stats      graphics    grDevices utils      datasets   methods    base

other attached packages:
[1] googlesheets4_1.1.0  gt_0.9.0          kableExtra_1.3.4
[4] knitr_1.44           patchwork_1.1.3   languageR_1.5.0
[7] janitor_2.2.0        lme4_1.1-33       Matrix_1.5-4
[10] broom_1.0.5         here_1.0.1        lubridate_1.9.2
[13]forcats_1.0.0        stringr_1.5.0     dplyr_1.1.3
[16] purrrr_1.0.2        readr_2.1.4       tidyr_1.3.0
[19] tibble_3.2.1         ggplot2_3.4.3     tidyverse_2.0.0

loaded via a namespace (and not attached):
[1] gtable_0.3.4      xfun_0.39        gargle_1.4.0      lattice_0.21-8
[5] tzdb_0.4.0        vctrs_0.6.3       tools_4.3.0       generics_0.1.3
[9] curl_5.0.1        parallel_4.3.0   fansi_1.0.4       pacman_0.5.1
[13] pkgconfig_2.0.3   webshot_0.5.4    lifecycle_1.0.3   farver_2.1.1
[17] compiler_4.3.0    munsell_0.5.0    snakecase_0.11.0  htmltools_0.5.5
[21] yaml_2.3.7        crayon_1.5.2     pillar_1.9.0      nloptr_2.0.3
[25] MASS_7.3-58.4    boot_1.3-28.1   nlme_3.1-162     tidyselect_1.2.0
[29] rvest_1.0.3       digest_0.6.33    stringi_1.7.12   labeling_0.4.3
```

```
[33] splines_4.3.0      rprojroot_2.0.3    fastmap_1.1.1      grid_4.3.0
[37] colorspace_2.1-0   cli_3.6.1        magrittr_2.0.3     utf8_1.2.3
[41] withr_2.5.0       scales_1.2.1     backports_1.4.1   bit64_4.0.5
[45] googledrive_2.1.0 timechange_0.2.0   rmarkdown_2.22    httr_1.4.6
[49] bit_4.0.5         cellranger_1.1.0  hms_1.1.3        evaluate_0.21
[53] viridisLite_0.4.2 rlang_1.1.3     Rcpp_1.0.11       glue_1.6.2
[57] xml2_1.3.4        vroom_1.6.3     svglite_2.1.1    rstudioapi_0.14
[61] minqa_1.2.5       jsonlite_1.8.7   R6_2.5.1         fs_1.6.2
[65] systemfonts_1.0.4
```

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Part III

Day 2: Multiple regression

4 Multiple Regression

Regression for Linguists

Summary

- we saw that the equation for a straight line boils down to its intercept and slope
- we fit our first linear model with a continuous predictor

Learning Objectives

Today we will learn...

- what multiple regression is
- how to include multiple predictor variables
- how to interpret slopes in multiple regression
- how to interpret interaction effects
- about the assumption of the absence of collinearity

Set-up environment

```
# suppress scientific notation
options(scipen=999)
```

We'll also need to load in our required packages. Hopefully you've already install the required packages (if not, go to [?@sec-software](#)).

```
# load libraries
pacman::p_load(
    tidyverse,
```

```
here,
broom,
janitor,
languageR)
```

Load data

We'll use the full dataset of the frequency data.

```
df_freq_full <-
  read_csv(here("data", "ELP_full_length_frequency.csv")) |>
  clean_names() |>
  mutate(freq = 10^(log10freq), # inverse log10
        freq_log = log(freq)) |> # use natural logarithm
  relocate(word, rt, length, freq, freq_log)
```

We have 4 variables:

- word
- length
- rt
- freq
- freq_log
- log10freq

4.1 Multiple regression

So far we've worked with simple linear models, which fit a model to a predictor and response variable. These models do not differ so greatly from a one- or two-sample t -test (for a categorical predictor) or Pearson's r (for a standardised continuous predictor). You might be wondering then we would bother with linear regression. One reason is that it allows us to include *multiple* predictors in our models, which still boils down to modeling the mean, but while conditioning the mean on multiple variables at once.

Recall the equation of a line (4.1), which states that any value of y equals the intercept (b_0) plus the corresponding value of x multiplied by the slope (b_1x), plus the error, which are our residuals (e). In multiple regression, we can include more than one slope (4.2).

$$y = b_0 + b_1 x + e \quad (4.1)$$

$$y = b_0 + b_1 x + b_2 x + \dots + e \quad (4.2)$$

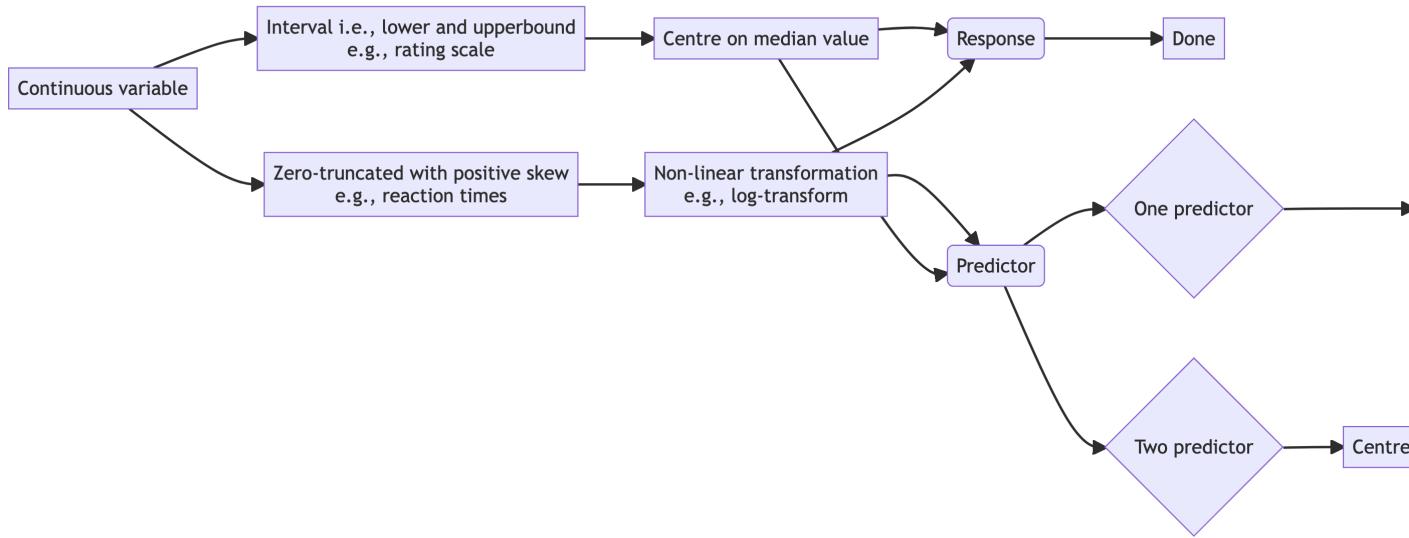


Figure 4.1: Flowchart of common steps for linear and non-linear transformations of continuous variables. Such decision trees are not a one-size-fits-all solution and cannot replace critical thinking and understanding of your data.

4.1.1 One predictor

Let's re-run our simple model with this dataset. Let's keep reaction times in the raw milliseconds for now for interpretability.

```

fit_freq_full <-
  lm(rt ~ log(freq), data = df_freq_full)

tidy(fit_freq_full)

# A tibble: 2 x 5
  term      estimate std.error statistic p.value
  <chr>     <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept) 907.      1.09      828.      0
2 log(freq)   -37.5     0.262     -143.     0

```

We see there is a decrease in reaction times (-37.5 milliseconds) for a 1-unit increase in log frequency. Let's look at the model fit using `glance()`.

```
glance(fit_freq_full)$r.squared
```

```
[1] 0.3834186
```

We see that the R -squared is 0.383, meaning our model describes 38% of the variance in response times. We can't be sure that this described variance is due solely to frequency, however. Our models only know what we tell them! Other effects that are correlated with frequency might be conflating the frequency effect, e.g., more frequent words tend to be shorter ([zipf_1949?](#)). Let's expand our model to include word length [4.3].

$$y = b_0 + b_1 * \logfrequency + b_2 * \text{wordlength} \quad (4.3)$$

4.1.2 Adding a predictor

Let's add `length` as a predictor to our model.

```

fit_freq_mult <-
  lm(rt ~ log(freq) + length, data = df_freq_full)

tidy(fit_freq_mult) |> select(term, estimate)

```

```
# A tibble: 3 x 2
  term      estimate
  <chr>    <dbl>
1 (Intercept) 748.
2 log(freq)   -29.5
3 length     19.5
```

We see that length is also a significant predictor of reaction times, with an increase in word length (+1 letter) corresponds to a 20ms increase in reaction times. Our intercept is also now 748ms, instead of 907ms. The 907ms intercept corresponds to the prediction for reaction times to a word with 0 log frequency and 0 word length, but this is not very interpretable. If we were to center both predictors, the intercept would be the reaction time for a wrd with average frequency and average length.

The slope for log frequency has also changed: from -37.5 to -29.5. This change tells us that some of the effect in our first model was confounded with length, as controlling for length weakens the effect of frequency.

```
glance(fit_freq_mult)$r.squared
```

```
[1] 0.4872977
```

We also see that including `length` increases the variance described by our model, reflected in the *R*-squared values (0.4872977 instead of 0.3834186).

4.2 Standardising our predictors

Recall that, when we have multiple continuous predictors, standardising them can help their interpretation, as their slopes are comparable. We could achieve this by centering each variable and then dividing by the standard deviation, or we could use the `scale()` function, which does just this.

```
# centre and then standardize
df_freq_full |>
  mutate(
    freq_z1 = (freq-mean(freq))/sd(freq),
    freq_z2 = scale(freq)) |>
  select(freq_z1, freq_z2) |>
  head()
```

```
# A tibble: 6 x 2
  freq_z1 freq_z2[,1]
  <dbl>      <dbl>
1 -0.0902    -0.0902
2 -0.0864    -0.0864
3 -0.0905    -0.0905
4 -0.0864    -0.0864
5 -0.0885    -0.0885
6 -0.0901    -0.0901
```

Let's use `scale()` for `freq` and `length`.

```
df_freq_full <-
  df_freq_full |>
  mutate(freq_z = scale(freq_log),
        length_z = scale(length))

fit_freq_z <-
  lm(rt ~ freq_z + length_z, data = df_freq_full)
```

First, let's check the R^2 :

```
glance(fit_freq_z)$r.squared
```

```
[1] 0.4872977
```

We see that our R^2 value is 0.4872977, just like above. This serves as a reminder that the predictors still represent the same variance in the underlying model, their units and scales have simply changed. What about our coefficients:

```
tidy(fit_freq_z) |> select(term, estimate)

# A tibble: 3 x 2
  term       estimate
  <chr>      <dbl>
1 (Intercept) 770.
2 freq_z      -60.6
3 length_z     43.3
```

Here, a 1-unit change always corresponds to a change of 1 standard deviation. Now we see that frequency has a larger magnitude than the effect of length. So, for each increase in frequency by 1 standard deviation (holding length constant), reaction times decrease by 29.5 ms.

4.2.1 Adding an interaction term

We won't spend much time talking about interactions, but please check out Ch. 8 (Interactions and nonlinear effects) in Winter (2019) for a more in-depth treatment. For now, what's important to know is that interactions describe how effects of one predictor may be influenced by changes in another predictor. We can add interaction terms of two predictors by connecting them with a colon (:).

```
lm(rt ~ freq_z + length_z + freq_z:length_z,  
  data = df_freq_full) |>  
  tidy() |> select(term, estimate)
```

```
# A tibble: 4 x 2  
  term            estimate  
  <chr>          <dbl>  
1 (Intercept)    766.  
2 freq_z        -63.9  
3 length_z       41.8  
4 freq_z:length_z -11.4
```

Or, we can simply connect the two predictors with an asterisk (*) to indicate that we want to look at both predictors and their interaction.

```
lm(rt ~ freq_z*length_z,  
  data = df_freq_full) |>  
  tidy() |> select(term, estimate)
```

```
# A tibble: 4 x 2  
  term            estimate  
  <chr>          <dbl>  
1 (Intercept)    766.  
2 freq_z        -63.9  
3 length_z       41.8  
4 freq_z:length_z -11.4
```

The model estimates are the same for both models. The intercept is the predicted reaction time for a word with the mean length and mean frequency. Notice that the interaction slope is negative, meaning when both `freq` and `length` increase, reaction times will decrease.

4.3 Model assumptions

We've already discussed the assumptions of normality and homoscedasticity (constant variance), which both refer to the residuals of a model. We typically assess these assumptions visually, with histogram and Q-Q plots.

4.3.1 Normality and Homoscedasticity

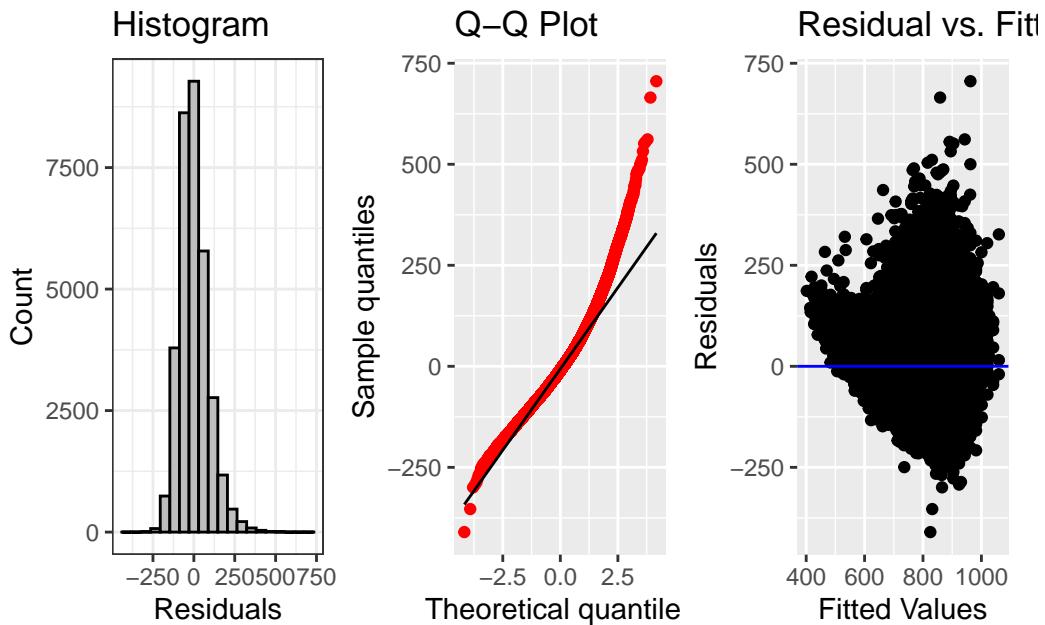
For our model

```
fig_hist <-
  fit_freq_z |>
  ggplot() +
  aes(x = .resid) +
  geom_histogram(bins = 20, fill = "grey", colour = "black") +
  theme_bw() +
  labs(title='Histogram', x='Residuals', y='Count')

fig_qq <-
  fit_freq_z |>
  ggplot() +
  aes(sample = .resid) +
  geom_qq(colour = "red") +
  geom_qq_line() +
  labs(title='Q-Q Plot', x='Theoretical quantiles', y='Sample quantiles')

fig_res <-
  fit_freq_z |>
  ggplot() +
  aes(x = .fitted, y = .resid) +
  geom_point() +
  geom_hline(yintercept = 0, colour = "blue") +
  labs(title='Residual vs. Fitted Values Plot', x='Fitted Values', y='Residuals')

fig_hist + fig_qq + fig_res
```



The histogram looks approximately normally distributed, with a bit of a positive skew. The Q-Q plot suggests a less-normal distribution, with the model estimates fitting larger reaction times more poorly. The residual plot also shows that the variance of the residuals is not constant, with much larger residual variance for larger fitted values. This tells us we should probably log reaction times. Let's try it all again, with log-transformed reaction times.

4.3.2 Log-transformed response variable

```
fit_freq_log_z <-  
  lm(log(rt) ~ freq_z*length_z,  
    data = df_freq_full)  
  
glance(fit_freq_log_z)$r.squared  
  
[1] 0.5176913  
  
tidy(fit_freq_log_z) |> select(term, estimate)  
  
# A tibble: 4 x 2  
  term        estimate  
  <fct>     <dbl>  
1 (Intercept)  1.00  
2 freq_z      0.000  
3 length_z    0.000  
4 freq_z:length_z -0.000
```

```

<chr>           <dbl>
1 (Intercept)    6.63
2 freq_z        -0.0826
3 length_z      0.0524
4 freq_z:length_z -0.00779

```

We see now that our values are much smaller, because they're on the log-scale.

```
exp(6.63 + -0.0826*5 + 0.0524*2)
```

```
[1] 556.5739
```

```
exp(6.63 + -0.0826*4 + 0.0524*2)
```

```
[1] 604.499
```

```
exp(6.63 + -0.0826*1 + 0.0524*6)
```

```
[1] 955.0847
```

```
tidy(fit_freq_log_z)
```

```

# A tibble: 4 x 5
  term            estimate std.error statistic p.value
  <chr>          <dbl>     <dbl>      <dbl>     <dbl>
1 (Intercept)    6.63     0.000636   10428.    0
2 freq_z        -0.0826   0.000666   -124.     0
3 length_z       0.0524   0.000649    80.7     0
4 freq_z:length_z -0.00779 0.000581   -13.4    8.51e-41

```

```

fig_hist <-
fit_freq_log_z |>
  ggplot() +
  aes(x = .resid) +
  geom_histogram(bins = 20, fill = "grey", colour = "black") +
  theme_bw()

```

```

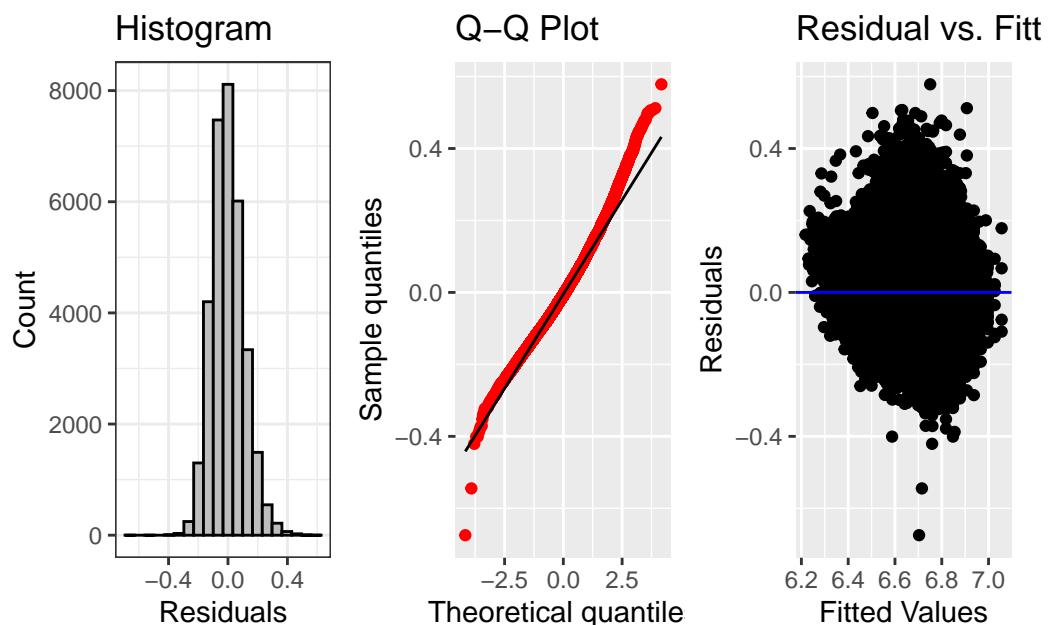
  labs(title='Histogram', x='Residuals', y='Count')

fig_qq <-
fit_freq_log_z |>
  ggplot() +
  aes(sample = .resid) +
  geom_qq(colour = "red") +
  geom_qq_line() +
  labs(title='Q-Q Plot', x='Theoretical quantiles', y='Sample quantiles')

fig_res <-
  fit_freq_log_z |>
  ggplot() +
  aes(x = .fitted, y = .resid) +
  geom_point() +
  geom_hline(yintercept = 0, colour = "blue") +
  labs(title='Residual vs. Fitted Values Plot', x='Fitted Values', y='Residuals')

fig_hist + fig_qq + fig_res

```



Looks much better.

4.3.3 Collinearity

Collinearity refers to when continuous predictor variables are correlated, which can make the interpretation of their coefficients difficult, and the results spurious. Regression assumes there is an *absence* of collinearity, i.e., our predictor variables are not correlated.

To assess collinearity, you can use the `vif()` function from the `car` package to compare *variance inflation factors*. VIF values close to 1 indicates there is not a high degree of collinearity between your variables.

```
car::vif(fit_freq_log_z)

freq_z          length_z freq_z:length_z
1.246509       1.184641      1.068283
```

Collinearity is a conceptual problem, and is something that you need to consider in the planning stage. Typically, we want to include predictors that we have specific predictions or research questions about. Shoving a bunch of predictors in a model to see what comes out significant is bad practice. Rather, we should have a principled approach to model building and variable selection. This is not to say that exploratory analyses should be avoided, but that this comes with caveats.

4.3.4 Adjusted R^2

Although we should avoid throwing any old predictor into our model, adjusted R^2 is a more conservative version of R^2 that takes into account the number of predictors in a model. For each additional predictor, adjusted R^2 includes the number of predictors (k) in its denominator (bottom half of a division), which means that the more predictors there are, the smaller R^2 will be, unless each additional predictor explains sufficient variance to counteract this penalisation.

```
glance(fit_freq_log_z)$adj.r.squared
```

```
[1] 0.5176475
```

If we were to look at the (adjusted) R^2 of our simple linear regression model, where log reaction times are predicted by standardised log frequency, we see that there is a large increase in our model which includes length and its interaction. This suggests that our model is not overfit, and that length contributes to the variance explained by the model.

```
glance(lm(log(rt) ~ freq_z, data = df_freq_full))$adj.r.squared
```

```
[1] 0.4148675
```

If we likewise compare to the same model without an interaction term ($\log(\text{reaction times}) \sim \text{frequency} * \text{length}$), we see that the adjusted R^2 is not very different. If the adjusted R^2 were much lower, this would indicate that including the interaction term leads to overfitting.

```
glance(lm(log(rt) ~ freq_z + length_z, data = df_freq_full))$adj.r.squared
```

```
[1] 0.5150461
```

Important terms

| Term | Definition | Equation/Code |
|--------------|--|-----------------|
| Collinearity | Correlation between two predictors (linear model assumes non-collinearity) | car::vif(model) |

Learning Objectives

Today we learned...

- what multiple regression is
- how to include multiple predictor variables
- how to interpret slopes in multiple regression
- how to interpret interaction effects
- about the assumption of the absence of collinearity

4.4 Task

Load in the `english` dataset from the `languageR` package (Baayen & Shafaei-Bajestan, 2019) (code below). You don't need to load in any CSV file, because this dataset is available if you have the package loaded. From the manual:

This data set gives mean visual lexical decision latencies and word naming latencies to 2284 monomorphemic English nouns and verbs, averaged for old and young subjects, with various predictor variables.

(languageR manual, p. 29)

```
# load in 'english' dataset from languageR
df_freq_eng <- 
  as.data.frame(english) |>
  dplyr::select(RTlexdec, RTnaming, Word, LengthInLetters, AgeSubject, WrittenFrequency) |>
  rename(rt_lexdec = RTlexdec,
         rt_naming = RTnaming,
         freq_written = WrittenFrequency) |>
  clean_names() |>
  relocate(word)
```

We're keeping five variables:

- `word`: a factor with 2284 words
- `rt_lexdec`: numeric vector of log RT in visual lexical decision
- `rt_naming`: numeric vector of log RT in word naming
- `length_in_letters`: numeric vector with length of the word in letters
- `AgeSubject`: a factor with as levels the age group of the subject: young versus old.
- `freq_written`: numeric vector with log frequency in the CELEX lexical database

Take the following steps:

1. Perform an exploratory data analysis to understand the data (produce plots, tables, whatever you think necessary and can do).
2. Model the data, with *back-transformed* (raw) reaction times as a response variable and written frequency and length in letters as predictors. Perform any tranformations you think necessary. Run model diagnostic checks and assess model fit.
3. Re-run the model with log reaction times as a response variable and written frequency and length in letters as predictors. Perform any tranformations you think necessary. Run model diagnostic checks and assess model fit.
4. Remove length in letters as a predictor. How is model fit affected? What can you conclude?

Session Info

Developed with Quarto using R version 4.3.0 (2023-04-21) (Already Tomorrow) and RStudio version 2023.9.0.463 (Desert Sunflower), and the following packages:

```
sessionInfo()
```

```

R version 4.3.0 (2023-04-21)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Ventura 13.2.1

Matrix products: default
BLAS:      /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
LAPACK:    /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: Europe/Berlin
tzcode source: internal

attached base packages:
[1] stats      graphics   grDevices utils      datasets   methods    base

other attached packages:
[1] googlesheets4_1.1.0 gt_0.9.0          kableExtra_1.3.4
[4] knitr_1.44        patchwork_1.1.3   languageR_1.5.0
[7] janitor_2.2.0    broom_1.0.5         here_1.0.1
[10] lubridate_1.9.2  forcats_1.0.0       stringr_1.5.0
[13] dplyr_1.1.3      purrr_1.0.2        readr_2.1.4
[16] tidyverse_1.3.0   tibble_3.2.1       ggplot2_3.4.3
[19] tidyverse_2.0.0

loaded via a namespace (and not attached):
[1] gtable_0.3.4      xfun_0.39        gargle_1.4.0     tzdb_0.4.0
[5] vctrs_0.6.3       tools_4.3.0       generics_0.1.3   curl_5.0.1
[9] parallel_4.3.0    fansi_1.0.4      pacman_0.5.1    pkgconfig_2.0.3
[13] webshot_0.5.4    lifecycle_1.0.3   farver_2.1.1    compiler_4.3.0
[17] munsell_0.5.0    carData_3.0-5   snakecase_0.11.0 htmltools_0.5.5
[21] yaml_2.3.7       car_3.1-2       crayon_1.5.2    pillar_1.9.0
[25] abind_1.4-5      tidyselect_1.2.0  rvest_1.0.3     digest_0.6.33
[29] stringi_1.7.12   labeling_0.4.3   rprojroot_2.0.3  fastmap_1.1.1
[33] grid_4.3.0        colorspace_2.1-0  cli_3.6.1      magrittr_2.0.3
[37] utf8_1.2.3       withr_2.5.0      scales_1.2.1    backports_1.4.1
[41] bit64_4.0.5      googledrive_2.1.0 timechange_0.2.0 rmarkdown_2.22
[45] httr_1.4.6       bit_4.0.5       cellranger_1.1.0 hms_1.1.3
[49] evaluate_0.21    viridisLite_0.4.2 rlang_1.1.3    glue_1.6.2
[53] xml2_1.3.4       svglite_2.1.1   rstudioapi_0.14 vroom_1.6.3
[57] jsonlite_1.8.7   R6_2.5.1       systemfonts_1.0.4 fs_1.6.2

```

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5 Categorical predictors

Regression for Linguists

Learning Objectives

Today we will learn...

- about categorical predictors
- how to interpret different contrast coding

Set-up environment

```
# suppress scientific notation
options(scipen=999)
```

We'll also need to load in our required packages.

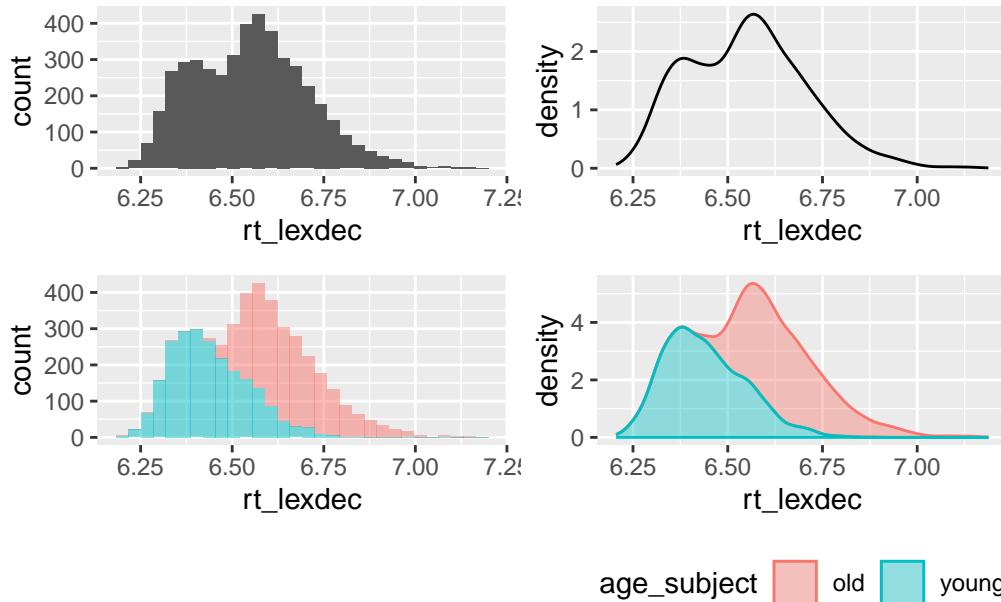
```
# load libraries
pacman::p_load(
  tidyverse,
  here,
  broom,
  lme4,
  janitor,
  languageR)
```

Load data

Let's continue working with the `english` dataset from the `languageR` package. Let's just call it `df_freq_eng`.

```
df_freq_eng <-  
  as.data.frame(english) |>  
  dplyr::select(RTlexdec, RTnaming, Word, LengthInLetters, AgeSubject, WrittenFrequency) |>  
  rename(rt_lexdec = RTlexdec,  
         rt_naming = RTnaming,  
         freq_written = WrittenFrequency) |>  
  clean_names() |>  
  # standardize continuous predictors  
  mutate(  
    freq_z = scale(freq_written),  
    length_z = scale(length_in_letters)  
  ) |>  
  relocate(word) |>  
  arrange(word)
```

In your exploratory data analysis, you might've noticed a *bimodal* distribution.



This looks like a *bimodal* distribution, i.e., there are two *modes* (most frequent value, i.e., peak in a histogram). What might be driving this? We know that there were two subject groups: old and young. How does the distribution of these two groups look?

Running our model of the log reaction times as predicted by frequency and length, we see:

```
fit_freq_length <-  
  lm(rt_lexdec ~ freq_z*length_z,  
      data = df_freq_eng)  
  
glance(fit_freq_length)$r.squared  
  
[1] 0.1896649  
  
glance(fit_freq_length)$adj.r.squared  
  
[1] 0.1891323
```

Seems like we don't have any overfitting in our model (R^2 and adjusted R^2 are comparable). Let's look at our coefficients.

```
tidy(fit_freq_length) |> select(term, estimate)  
  
# A tibble: 4 x 2  
  term            estimate  
  <chr>          <dbl>  
1 (Intercept)    6.55  
2 freq_z        -0.0682  
3 length_z      0.00328  
4 freq_z:length_z -0.00196
```

There is a negative slope for frequency, indicating shorter reaction times for words with higher frequency (when holding length constant). There is a positive slope for length, indicating longer reaction times for longer words (holding frequency constant). There is also a negative interaction estimate, indicating that when both length and frequency increase, reaction times decrease. This seems similar to the dataset we explored in the previous sections. But, this bimodal distribution is suggesting we should include age group as a predictor, since the two groups seem to pattern differently in their reading times. Could it be that the effect of frequency and length also differ as a function of age group?

5.1 Categorical predictors

In linguistic research we often want to compare the effect of *groups* or categories, such as native or non-native speakers, or grammatical or ungrammatical stimuli. We might expect longer reading times for non-native (compared to native) speakers of a language, or for ungrammatical (versus grammatical) sentences. With our current dataset, we'd predict longer reading times for older participants than younger participants (although we should hypothesise *before* collecting and visualising our data!). How might these age effects interact with effects of word frequency and length?

5.1.1 Including a categorical predictor

What would happen if we just include `age_subject` in our model?

```
fit_age <-
  lm(rt_lexdec ~ freq_z*length_z + age_subject,
  data = df_freq_eng)
```

First, we see that adding age to our model results in a large increase in variance explained, and that the R^2 and adjusted R^2 values are comparable. In addition, the VIF values for all coefficients are near 1. This indicates that our predictors all contribute to the variance explained by the model and are not correlated.

```
glance(fit_age)$r.squared
```

```
[1] 0.6888949
```

```
glance(fit_age)$adj.r.squared
```

```
[1] 0.6886222
```

```
car::vif(fit_age)
```

| | freq_z | length_z | age_subject | freq_z:length_z |
|--|----------|----------|-------------|-----------------|
| | 1.012553 | 1.004461 | 1.000000 | 1.008108 |

Now that we see that our model is not overfit and that our predictors are not correlated, let's take a look at our model estimates.

```

tidy(fit_age) |> select(term, estimate)

# A tibble: 5 x 2
  term            estimate
  <chr>          <dbl>
1 (Intercept)    6.66
2 freq_z        -0.0682
3 length_z      0.00328
4 age_subjectyoung -0.222
5 freq_z:length_z -0.00196

```

In addition to the effects we observed in our earlier model, we see that there is a negative slope for `age_subjectyoung`, indicating that reaction times decrease when...what? How do we interpret a slope for a categorical variable? Regression works with numerical values, so how does a categorical variable get fit to a line? If we feed a categorical variable into the `lm()` function, the factor levels (i.e., the categories in a categorical variable) are given numerical values. We need to know what these values are in order to know how to interpret our model estimates. We call these numerical values mapped onto factor levels contrast coding, and we can check the contrasts of a given factor using the function `contrasts()`.

```
contrasts(df_freq_eng$age_subject)
```

| | |
|-------|-------|
| | young |
| old | 0 |
| young | 1 |

We see that `old` was coded at 0 and `young` as 1. This means that our slope for `age_subjectyoung` represents the change in reaction times when we move from `old` to `young`, which corresponds to a 1-unit change in our predictor (because the difference between 0 and 1 is 1). This is called treatment coding, or dummy coding, where one factor level is coded as 0 and the other as 1. Let's remove the continuous variable for now and focus on `age_subject`. Let's also look at raw reaction times, to more easily interpret the results.

```

fit_age <-
  lm(exp(rt_lexdec) ~ age_subject,
     data = df_freq_eng)

glance(fit_age)$r.squared

```

```
[1] 0.4682224
```

Our R^2 value is lower than when we included frequency and length, but higher still than our model with frequency and length but no age.

```
tidy(fit_age) |> select(term, estimate)

# A tibble: 2 x 2
  term            estimate
  <chr>          <dbl>
1 (Intercept)    787.
2 age_subjectyoung -157.
```

We see that there is an estimated decrease in reaction times of 157ms for the young group compared to the old group. But what does the intercept represent here? Let's look at our data again.

```
df_freq_eng |>
  select(rt_lexdec, age_subject) |>
  mutate(rt_lexdec = exp(rt_lexdec)) |>
  summary()

  rt_lexdec      age_subject
  Min.   : 495.4   old   :2284
  1st Qu.: 617.4   young:2284
  Median  : 699.6
  Mean   : 708.1
  3rd Qu.: 775.3
  Max.   :1323.2
```

And how does `rt_lexdec` differ between the groups?

```
df_freq_eng |>
  select(rt_lexdec, age_subject) |>
  mutate(rt_lexdec = exp(rt_lexdec)) |>
  summarise(mean = mean(rt_lexdec),
            min = min(rt_lexdec),
            max = max(rt_lexdec),
            .by = "age_subject"
  )
```

```

age_subject      mean     min     max
1       young 629.5473 495.38  971.8
2       old   786.7200 603.77 1323.2

```

We see here that the intercept for our model actually corresponds to the mean reaction time for the old group. Why is this? Recall that the intercept corresponds to the y value (reaction time) when x is 0. In treatment/dummy coding, one factor level is coded as 0. In our case this was `old`, and so the intercept corresponds to the mean reaction time for participants in the old group. How does R choose which variable to code as 0? It simply takes the first level name alphabetically: `old` comes before `young`, so `old` was automatically taken as the ‘baseline’ to which `young` was compared.

And if we were to add the slope to the intercept, we would get the mean for the *young* group. Why is this?

```
coef(fit_age)['(Intercept)'] + coef(fit_age)[‘age_subjectyoung’]
```

```
(Intercept)
629.5473
```

Why are the means for the two groups used? The mean is the value closest to all values in a univariate dataset, and regression aims to minimise residuals (recall the line of best fit). So, a line is fit between the means of these two factor levels to achieve minimal residuals. This actually is the same thing as a *t*-test:

```
t.test(exp(rt_lexdec) ~ age_subject, data = df_freq_eng)
```

```

Welch Two Sample t-test

data: exp(rt_lexdec) by age_subject
t = 63.406, df = 4144.6, p-value < 0.0000000000000022
alternative hypothesis: true difference in means between group old and group young is not eq
95 percent confidence interval:
152.3128 162.0325
sample estimates:
mean in group old mean in group young
786.7200          629.5473

```

If we compare this to our model, we see that the *t*- and *p*-values are identical (more on these later).

```

tidy(fit_age)

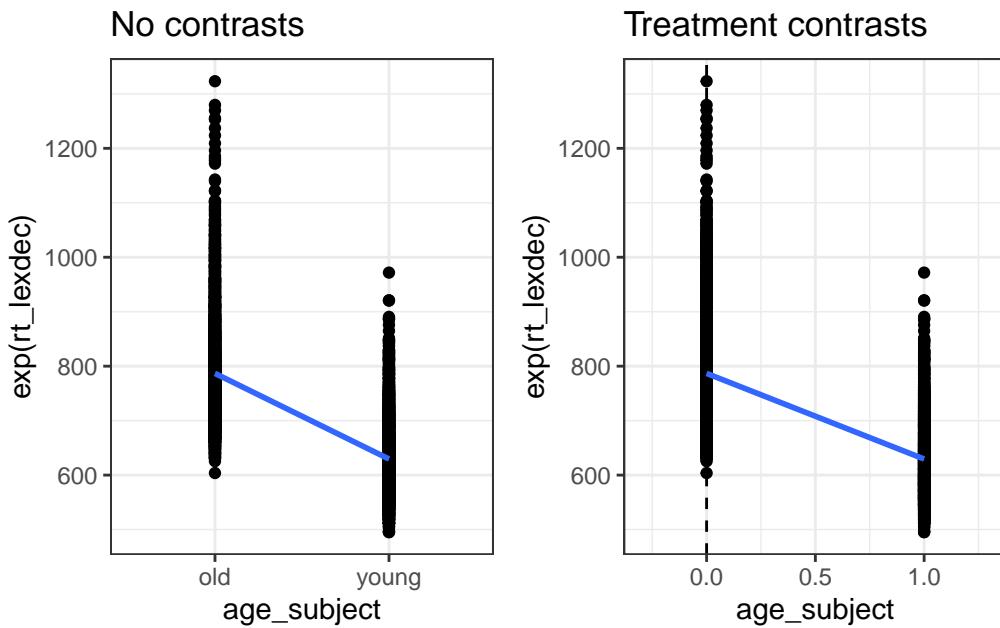
# A tibble: 2 x 5
  term            estimate std.error statistic p.value
  <chr>          <dbl>     <dbl>      <dbl>    <dbl>
1 (Intercept)    787.      1.75      449.     0
2 age_subjectyoung -157.     2.48      -63.4    0

fig_nocontrasts <-
df_freq_eng |>
  ggplot() +
  aes(x = age_subject, y = exp(rt_lexdec)) +
  labs(title = "No contrasts") +
  # geom_vline(xintercept = 0, linetype="dashed", size = .5) +
  geom_point(position = position_dodge(.6)) +
  geom_smooth(method = 'lm', aes(group=1)) + theme_minimal() +
  theme_bw()

fig_treatment <-
df_freq_eng |>
  mutate(age_subject = if_else(age_subject=="young", 1, 0)) |>
  ggplot() +
  aes(x = age_subject, y = exp(rt_lexdec)) +
  labs(title = "Treatment contrasts") +
  geom_vline(xintercept = 0, linetype="dashed", size = .5) +
  geom_point(position = position_dodge(.6)) +
  geom_smooth(method = 'lm', aes(group=1)) + theme_minimal() +
  theme_bw()

fig_nocontrasts + fig_treatment

```



5.2 Sum contrasts

Treatment/dummy coding is the default contrast coding scheme. Sum coding is another frequently used coding scheme, which is essentially centring categorical variables. Just as with continuous variables, the motivation for sum contrast coding mainly lies in the interpretation of interaction effects. How can we tell R we want to use sum contrast coding, and not dummy coding? There are different ways to do this:

```
# first, make sure your variable is a factor
df_freq_eng$age_subject <- as.factor(df_freq_eng$age_subject)
# check
class(df_freq_eng$age_subject)

[1] "factor"

# next, you could use the contr.sum() function
contrasts(df_freq_eng$age_subject) <- contr.sum(2) # where 2 means we have 2 levels
contrasts(df_freq_eng$age_subject)

[,1]
old      1
young   -1
```

Here we see that `old` is coded as -1 and `young` as $+1$. I prefer to use $+/-.5$ for reasons we don't need to go into here. I would also prefer to have `young` coded in the negative value, and `old` in the positive value. This aids in the way I interpret the slope: a change in reaction times for the older group compared to the younger group.

```
#or, you could manually control the sum contrasts
## check the order of the levels
levels(df_freq_eng$age_subject)

[1] "old"    "young"

## code 'old' as +.5 and 'young' as -.5
contrasts(df_freq_eng$age_subject) <- c(+0.5, -0.5)
contrasts(df_freq_eng$age_subject)

[,1]
old      0.5
young   -0.5
```

You could also choose to store the contrast values in their own variable.

```
df_freq_eng <-
  df_freq_eng |>
  mutate(age_numeric = ifelse(age_subject == "young", -0.5, +0.5))

df_freq_eng |>
  select(age_subject, age_numeric) |>
  head()

  age_subject age_numeric
338       young      -0.5
1790      old       0.5
3125      young      -0.5
3957      old       0.5
3313      young      -0.5
4145      old       0.5
```

Now, we can run our model using either `age_subject` or `age_numeric`.

```
fit_age_sum <-
  lm(exp(rt_lexdec) ~ age_subject,
     data = df_freq_eng)
```

```
glance(fit_age_sum)$r.squared
```

```
[1] 0.4682224
```

```
glance(fit_age)$r.squared
```

```
[1] 0.4682224
```

No difference in variance account for by our model.

```
tidy(fit_age_sum) |> select(term, estimate)
```

```
# A tibble: 2 x 2
  term      estimate
  <chr>      <dbl>
1 (Intercept)    708.
2 age_subject1   157.
```

But there is a difference in the intercept, and a change in sign in our slope. Why is this?

```
fig_sum1 <-
df_freq_eng |>
  mutate(age_subject = if_else(age_subject=="young",-1,1)) |>
  ggplot() +
  aes(x = age_subject, y = exp(rt_lexdec)) +
  labs(title = "Sum contrasts") +
  geom_vline(xintercept = 0, linetype="dashed", size = .5) +
  geom_point(position = position_dodge(.6)) +
  geom_smooth(method = 'lm', aes(group=1)) + theme_minimal() +
  theme_bw()

fig_sum5 <-
df_freq_eng |>
  mutate(age_subject = if_else(age_subject=="young",-0.5,.5)) |>
```

```

ggplot() +
  aes(x = age_subject, y = exp(rt_lexdec)) +
  labs(title = "Sum contrasts") +
  geom_vline(xintercept = 0, linetype="dashed", size = .5) +
  geom_point(position = position_dodge(.6)) +
  geom_smooth(method = 'lm', aes(group=1)) + theme_minimal() +
  theme_bw()

fig_treatment + fig_sum5 + plot_annotation(tag_levels = "A")

```

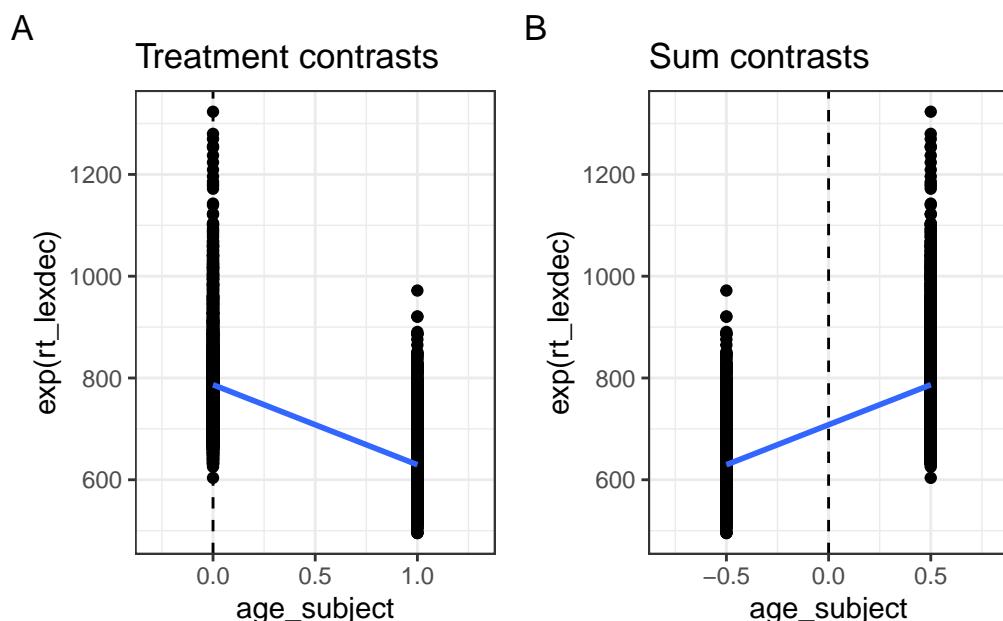


Figure 5.1: The difference in slope corresponds to which level is coded as 0 (dummy coding) or $-5/-1$ (sum coding)

As we see in Figure 5.1, the sign of the slope depends on how we've contrast coded our factor levels. In Figure 5.1 A, the `old` group is coded as 0 and `young` as 1. In Figure 5.1 B, the `young` group is coded as -0.5 and the `old` group as $+0.5$.

The intercept value is also now the overall mean of all observed reaction times, because now the y value when x equals zero lies in the middle of the two groups. The slope magnitude (i.e., size of the value) hasn't changed, because the difference between the two group means has not changed.

```
mean(exp(df_freq_eng$rt_lexdec))
```

```
[1] 708.1336
```

5.2.1 Exploring predicted values

Let's also explore the predicted values of our model with a categorical variable.

```
head(fitted(fit_age), n = 10)
```

```
338      1790      3125      3957      3313      4145      337      1789  
629.5473 786.7200 629.5473 786.7200 629.5473 786.7200 629.5473 786.7200  
3513      4345  
629.5473 786.7200
```

We see that there are only 2 values, 630 and 787. These correspond to the means for each group that we saw above. They also seem to be in a pattern: young-mean, old-mean, young-mean, old-mean, etc. How does this correspond to the age group of the participant for the first ten observations?

```
head(df_freq_eng$age_subject, n = 10)
```

```
[1] young old    young old    young old    young old    young old  
attr(,"contrasts")  
[1]  
old    0.5  
young -0.5  
Levels: old young
```

The first ten observations in our data are in young-old pairs. What are the first values in the raw data?

```
head(exp(df_freq_eng$rt_lexdec), n = 10)
```

```
[1] 623.61 775.67 617.10 715.52 575.70 742.19 592.42 748.37 541.67 824.76
```

And what is the difference between these reaction times and the fitted values?

```
head(exp(df_freq_eng$rt_lexdec), n = 10) - head(fitted(fit_age), n = 10)
```

| term | description/other terms |
|------------|-------------------------|
| 338 | 1790 |
| -5.937299 | -11.049991 |
| 1789 | 3513 |
| -38.349991 | -87.877299 |
| 3125 | 4345 |
| 3957 | 38.040009 |
| 3313 | 4145 |
| 337 | -37.127299 |


```
head(residuals(fit_age))
```


| | | | | | |
|-----------|------------|------------|------------|------------|------------|
| 338 | 1790 | 3125 | 3957 | 3313 | 4145 |
| -5.937299 | -11.049991 | -12.447299 | -71.199991 | -53.847299 | -44.529991 |

5.3 Summary

- we saw that the equation for a straight line boils down to its intercept and slope
- we fit our first linear model with a categorical predictor

Important terms

Learning Objectives

Today we learned...

5.4 Task

We'll use a dataset from Biondo et al. (2022), an eye-tracking reading study exploring the processing of adverb-tense concord in Spanish past and future tenses. Participants read sentences that began with a temporal adverb (e.g., yesterday/tomorrow), and had a verb marked with the congruent or incongruent tense (past/future).

Load in the data.

```
df_tense <-  
  read_csv(here("data", "Biondo.Soilemezidi.Mancini_dataset_ET.csv"),  
           locale = locale(encoding = "Latin1") # for special characters in Spanish  
           ) |>  
  mutate(gramm = ifelse(gramm == "0", "ungramm", "gramm")) |>
```

```
clean_names()
```

5.4.1 Treatment contrasts

We will look at the measure *total reading time* (`tt`) at the *verb* region (`roi == 4`). Subset the data to only include the verb region.

```
df_verb <-  
  df_tense |>  
  filter(roi == 4)
```

1. Run a simple linear model with (log-transformed) total reading time (`tt`) as an independent variable and grammaticality (`gramm`) as a dependent variable. Use treatment contrasts.
2. Inspect your coefficients again. What conclusions do you draw?
3. Run model diagnostics:
 - check model assumptions where relevant (normality, constant variance, collinearity)
 - check model fit (R^2)

5.4.2 Sum contrasts

1. Re-run your model with sum contrasts.
2. Inspect your coefficients again. Do your conclusions change?
3. Re-run your model diagnostics. How does it compare to your first model?

5.4.3 Multiple regression

1. Add verb tense (`verb_t`: past, future) as a predictor, including an interaction term. Use sum contrasts.
2. Inspect your coefficients again. Do your conclusions change?
3. Re-run your model diagnostics. How does it compare to the last models?

Session Info

Developed with Quarto using R version 4.3.0 (2023-04-21) (Already Tomorrow) and RStudio version 2023.9.0.463 (Desert Sunflower), and the following packages:

```
sessionInfo()

R version 4.3.0 (2023-04-21)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Ventura 13.2.1

Matrix products: default
BLAS:      /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
LAPACK:   /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib; 

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: Europe/Berlin
tzcode source: internal

attached base packages:
[1] stats      graphics    grDevices utils      datasets   methods    base

other attached packages:
[1] kableExtra_1.3.4 knitr_1.44       patchwork_1.1.3  languageR_1.5.0
[5] janitor_2.2.0    lme4_1.1-33     Matrix_1.5-4     broom_1.0.5
[9] here_1.0.1       lubridate_1.9.2 forcats_1.0.0   stringr_1.5.0
[13] dplyr_1.1.3     purrr_1.0.2     readr_2.1.4     tidyverse_1.3.0
[17] tibble_3.2.1    ggplot2_3.4.3  tidyverse_2.0.0

loaded via a namespace (and not attached):
[1] gtable_0.3.4      xfun_0.39        lattice_0.21-8   tzdb_0.4.0
[5] vctrs_0.6.3       tools_4.3.0       generics_0.1.3   parallel_4.3.0
[9] fansi_1.0.4       pacman_0.5.1     pkgconfig_2.0.3  webshot_0.5.4
[13] lifecycle_1.0.3   farver_2.1.1     compiler_4.3.0  munsell_0.5.0
[17] carData_3.0-5    snakecase_0.11.0 htmltools_0.5.5  yaml_2.3.7
[21] crayon_1.5.2     car_3.1-2       pillar_1.9.0     nloptr_2.0.3
[25] MASS_7.3-58.4    abind_1.4-5     boot_1.3-28.1   nlme_3.1-162
[29] tidyselect_1.2.0   rvest_1.0.3     digest_0.6.33   stringi_1.7.12
[33] labeling_0.4.3   splines_4.3.0   rprojroot_2.0.3  fastmap_1.1.1
[37] grid_4.3.0       colorspace_2.1-0 cli_3.6.1     magrittr_2.0.3
```

| | | | |
|------------------|------------------|----------------|-------------------|
| [41] utf8_1.2.3 | withr_2.5.0 | scales_1.2.1 | backports_1.4.1 |
| [45] bit64_4.0.5 | timechange_0.2.0 | rmarkdown_2.22 | httr_1.4.6 |
| [49] bit_4.0.5 | hms_1.1.3 | evaluate_0.21 | viridisLite_0.4.2 |
| [53] mgcv_1.8-42 | rlang_1.1.3 | Rcpp_1.0.11 | glue_1.6.2 |
| [57] xml2_1.3.4 | vroom_1.6.3 | svglite_2.1.1 | rstudioapi_0.14 |
| [61] minqa_1.2.5 | jsonlite_1.8.7 | R6_2.5.1 | systemfonts_1.0.4 |

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Part IV

Day 3: Logistic regression

6 Logistic regression

Regression for Linguists

This lecture jumps to chapter 12 'Generalised Linear Models 1: Logistic Regression' (Winter, 2019). We're skipping a few chapters, which I encourage you to go through on your own. However, they cover topics that you presumably have covered in previous courses (namely significance testing, t -values and p -values).

Learning Objectives

Today we will learn...

- how to model binomial data with logistic regression
- how to interpret log-odds and odds ratio

Set-up environment

```
# suppress scientific notation
options(scipen=999)
options(pillar.sigfig = 5)

library(broman)
# function to format p-values
format_pval <- function(x){
  if (x < .001) return(paste('<', '.001'))
  if (x < .01) return(paste('<', '.01'))
  if (x < .05) return(paste('<', '.05'))
  paste('=', myround(x, 3)) # if above .05, print p-value to 3 decimal points
}
```

We'll also need to load in our required packages. Hopefully you've already install the required packages (if not, go to `?@sec-software`).

```
# load libraries
pacman::p_load(
    tidyverse,
    here,
    broom,
    lme4,
    janitor,
    languageR)

# set preferred ggplot2 theme
theme_set(theme_bw() + theme(plot.title = element_text(size = 10)))
```

6.1 Generalised linear models

Logistic regression is a type of generalised linear model (GLM), and is used to model binomial response data. Whereas continuous response variables, such as reaction times, assume a normal distribution (a.k.a., a Gaussian distribution), logistic regression assumes a binomial distribution (a.k.a., Bernoulli distribution). These are formalised in equations 6.1, where μ and σ correspond to the mean and standard deviation, and 6.2, where N and p refer to the number of trials and the probability of y being 1 or 0.

$$y \sim Normal(\mu, \sigma) \tag{6.1}$$

$$y \sim binomial(N = 1, p) \tag{6.2}$$

Don't stress about this for now, I find the math behind everything will start to make more sense the more often you see it. However, *some* math is necessary in order to understand the output of our models, namely the relation between probabilities, odds, and log odds.

6.1.1 Log-odds, odds ratio, and probabilities

In logistic regression, we the probability (p) of observing one outcome or another as a function of a predictor variable. In linguistic research, these outcomes could be the absence or presence of some phenomenon (pause, schwa, etc.) or button responses (yes/no, accept/reject). In logistic regression, we describe the probability, odds, or log-odds of a particular outcome over another.

Table 6.1: Comparison of different values of probabilities/odds/log-odds

| name | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
|----------|------------|------------|------------|------------|-----|-----------|------------|------------|
| prob | 0.0066929 | 0.0229774 | 0.0758582 | 0.2227001 | 0.5 | 0.7772999 | 0.9241418 | 0.9770226 |
| odds | 0.0067379 | 0.0235177 | 0.0820850 | 0.2865048 | 1.0 | 3.4903430 | 12.1824940 | 42.5210820 |
| log_odds | -5.0000000 | -3.7500000 | -2.5000000 | -1.2500000 | 0.0 | 1.2500000 | 2.5000000 | 3.7500000 |

Probability is quite intuitive, and ranges from 0 (no chance) to 1 (certain). A 50% chance corresponds to a probability of 0.5. You're also likely familiar with odds, which can range from 0 to infinity. Odds are often used in betting, such as *the odds that I'll win are 2:1*, which corresponds to $\frac{2}{1} = 2$ in favour of my winning. Conversely, *the odds that you'll win are 1:2*, corresponding to $\frac{1}{2} = 0.5$, meaning it's less likely that you'll win compared to you losing. If the odds are even, then: $\frac{1}{1} = 1$. So, odds of 1 correspond to a probability of 0.5. Log-odds are just the logarithmically-transformed odds: $\log(2) = 0.6931472$; $\log(0.5) = -0.6931472$; $\log(1) = 0$. Probability can also be computed using the odds, as shown in 6.3: $\frac{2}{1+2} = 0.6666667$; $\frac{1}{1+1} = 0.5$; $\frac{0.5}{1+0.5} = 0.3333333$.

We can get the probability from a log odds value using `plogis()`, which performs the following calculation:

$$p = \frac{\exp(\text{log odds})}{1 + \exp(\text{log odds})} = \frac{\text{odds}}{1 + \text{odds}} \quad (6.3)$$

Table 6.1 gives an example of how the three relate to each other. The grey cells are all where chances are 50/50, with increasingly more likely (green) or less likely (red) values/

This relationship is demonstrated in Figure 6.1. Take your time to really understand these plots, as it will help understand the output of our models.

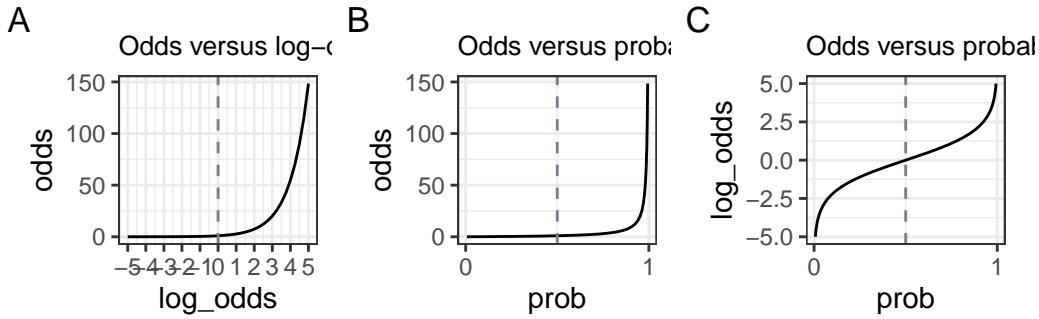


Figure 6.1: Relationship between probability, odds, and log-odds

6.2 Logistic regression

I find the more we talk about the math behind the models before even running a model, the more overwhelmed we become. So, let's run our first logistic regression and then dissect it to understand it. Most relevant to the output of a logistic regression model is Figure 6.1 C, as the model will output log-odds, and we most likely want to interpret them in terms of probabilities.

We'll use a dataset from Biondo et al. (2022), an eye-tracking reading study exploring the processing of adverb-tense concord in Spanish past and future tenses. Participants read sentences that began with a temporal adverb (e.g., yesterday/tomorrow), and had a verb marked with the congruent or incongruent tense (past/future). We will look at the measure *regression in* at the *verb* region.

Let's start by loading in the data:

```
df_tense <-  
  read_csv(here("data", "Biondo.Soilemezidi.Mancini_dataset_ET.csv"),  
           locale = locale(encoding = "Latin1") # for special characters in Spanish  
           ) |>  
  mutate(gramm = ifelse(gramm == "0", "ungramm", "gramm")) |>  
  clean_names() |>  
  filter(roi == 4,  
         adv_type == "Deic")
```

6.2.1 EDA

And conducting a quick EDA: print summaries and plot the response variables.

```
head(df_tense)
```

```
# A tibble: 6 x 13  
  sj      item adv_type adv_t  verb_t gramm    roi label     fp     gp     tt     ri  
  <chr> <dbl> <chr>   <chr> <chr> <chr> <dbl> <chr> <dbl> <dbl> <dbl> <dbl> <dbl>  
1 1       54 Deic    Past    Past   gramm     4 enca~  1027  1027  1027  0  
2 1       4 Deic    Future  Future gramm     4 cole~  562   562   1337  1  
3 1       62 Deic    Past    Past   gramm     4 esqu~  293   1664  1141  0  
4 1       96 Deic    Future  Past   ungramm   4 cons~  713   1963  1868  0  
5 1       52 Deic    Past    Past   gramm     4 desa~  890   890   1707  1  
6 1       90 Deic    Future  Past   ungramm   4 dece~  962   962   962   0  
# i 1 more variable: ro <dbl>
```

Let's look at only our binomial dependent variables, regression in (**ri**) and regression out (**ro**). For each variable, 1 indicates a regression in/out, 0 indicates there was no regression in/out.

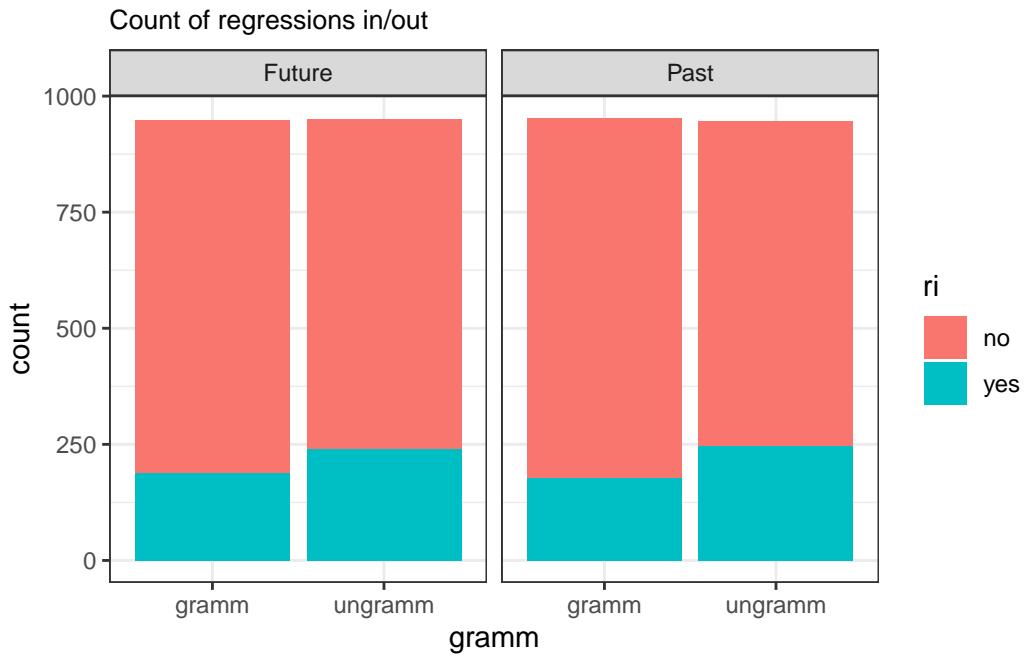
```
df_tense |>
  select(roi, ri, ro) |>
  summary()

      roi          ri          ro
Min.   :4   Min.   :0.0000   Min.   :0.00000
1st Qu.:4   1st Qu.:0.0000   1st Qu.:0.00000
Median :4   Median :0.0000   Median :0.00000
Mean   :4   Mean   :0.2248   Mean   :0.08169
3rd Qu.:4   3rd Qu.:0.0000   3rd Qu.:0.00000
Max.   :4   Max.   :1.0000   Max.   :1.00000
NA's    :45       NA's    :45
```

Let's plot out our dependent variable of interest: regression in.

```
# make grammaticality a factor
df_tense |>
  mutate(gramm = as_factor(gramm))

# A tibble: 3,840 x 13
  sj      item adv_type adv_t verb_t gramm    roi label     fp     gp     tt     ri
  <chr> <dbl> <chr>   <chr> <chr> <fct> <dbl> <chr> <dbl> <dbl> <dbl> <dbl> <dbl>
1 1        54 Deic    Past    Past  gramm     4 enca~  1027  1027  1027  0
2 1        4 Deic    Future  Future gramm     4 cole~  562   562   1337  1
3 1        62 Deic   Past    Past  gramm     4 esqu~  293   1664  1141  0
4 1        96 Deic   Future  Past  ungra~    4 cons~  713   1963  1868  0
5 1        52 Deic   Past    Past  gramm     4 desa~  890   890   1707  1
6 1        90 Deic   Future  Past  ungra~    4 dece~  962   962   962   0
7 1        8 Deic    Future  Future gramm     4 evid~  718   718   718   0
8 1        9 Deic    Future  Future gramm     4 excu~  1453  1453  1453  0
9 1        56 Deic   Past    Past  gramm     4 equi~  769   769   769   0
10 1       11 Deic   Future  Future gramm    4 cena~  778   778   778   0
# i 3,830 more rows
# i 1 more variable: ro <dbl>
```



It looks like there are more regressions in for the grammatical versus ungrammatical conditions in both the future and past tenses. There doesn't seem to be a large difference between the two tenses in overall regressions in, nor in the effect of grammaticality on the proportion of regressions in. We can also see that it was more likely overall for there to *not* be a regression in (versus for there to be a regression in).

6.2.2 Model

Now let's run our model. Verb tense and grammaticality are each two-level factors, so we'll want to set sum coding for each of them. Let's set `past` and `grammatical` to -0.5 , and `future` and `ungrammatical` to $+0.5$.

```
df_tense$verb_t <- as.factor(df_tense$verb_t)
levels(df_tense$verb_t)
```

```
[1] "Future" "Past"
```

```
contrasts(df_tense$verb_t) <- c(+0.5, -0.5)
contrasts(df_tense$verb_t)
```

```
[,1]
```

```

Future  0.5
Past    -0.5

df_tense$gramm <- as.factor(df_tense$gramm)
levels(df_tense$gramm)

[1] "gramm"   "ungramm"

contrasts(df_tense$gramm) <- c(-0.5, +0.5)
contrasts(df_tense$gramm)

[,1]
gramm   -0.5
ungramm  0.5

```

Now that we've set our contrasts (if you have continuous predictors, you would centre and potentially standardise them instead), we can fit our model. We use the `glm()` function to fit a generalised linear model, and use the argument `family = "binomial"` to indicate our data are binomial.

```

fit_tense_ri <-
  glm(ri ~ verb_t*gramm,
     data = df_tense,
     family = "binomial")

```

What do our coefficients look like?

```

tidy(fit_tense_ri) %>%
  mutate(p.value = as.numeric(p.value)) |>
  mutate(p.value = round(p.value*4,10)
        ) |>
  knitr::kable() |>
  kableExtra::kable_styling()

```

Let's first consider the estimates. The intercept is negative, meaning it is below 0. Verb tense is positive, meaning that there are more regressions in for the future compared to the past, holding grammaticality constant. Grammaticality is positive, meaning that there were more regressions in for the ungrammatical than grammatical conditions. But what does zero mean here? Logistic regression gives the estimates in log-odds. This means that a value of 0 means

| term | estimate | std.error | statistic | p.value |
|----------------|------------|-----------|-------------|-----------|
| (Intercept) | -1.2472175 | 0.0392027 | -31.8146220 | 0.0000000 |
| verb_t1 | 0.0209637 | 0.0784053 | 0.2673755 | 3.1567201 |
| gramm1 | 0.3668992 | 0.0784053 | 4.6795205 | 0.0000115 |
| verb_t1:gramm1 | -0.1197221 | 0.1568106 | -0.7634823 | 1.7807033 |

there is an equal probability of a regression in or out for both conditions (as in (**tab-odds?**)), i.e., the slope is flat (or not significantly different from 0). How can we convert our log-odds estimates to something more interpretable, like probabilities? Recall the equation in [6.3](#), which would require a lot of typing. Luckily, we can just use the `plogis()` function, which takes a log-odds value and spits out the corresponding probability. We can also just use the `exp()` function to get the odds ratio from the log-odds.

```
plogis(-1.23) # intercept prob
```

```
[1] 0.2261814
```

```
plogis(0.0277) # tense prob
```

```
[1] 0.5069246
```

```
exp(-1.23) # intercept odds
```

```
[1] 0.2922926
```

```
exp(0.0277) # tense odds
```

```
[1] 1.028087
```

This is great, but a bit tedious. We can also just feed a tibble column through the `plogis()` and `exp()` functions to print a table with the relevant probabilities and odds.

```
tidy(fit_tense_ri) %>%
  mutate(p.value = round(p.value*4,10),
        prob = plogis(estimate),
        odds = exp(estimate))
```

| term | estimate | std.error | statistic | p.value | prob | odds |
|----------------|----------|-----------|-----------|---------|--------|--------|
| (Intercept) | -1.2472 | 0.0392 | -31.8146 | 0.0000 | 0.2232 | 0.2873 |
| verb_t1 | 0.0210 | 0.0784 | 0.2674 | 3.1567 | 0.5052 | 1.0212 |
| gramm1 | 0.3669 | 0.0784 | 4.6795 | 0.0000 | 0.5907 | 1.4433 |
| verb_t1:gramm1 | -0.1197 | 0.1568 | -0.7635 | 1.7807 | 0.4701 | 0.8872 |

```
) |>
mutate_if(is.numeric, round, 4) |>
knitr::kable() |>
kableExtra::kable_styling()
```

We see that the odds of the future tense have a regression in versus the past tense is ~ 1 , with the corresponding probability of 0.51. Unsurprisingly, we see this p -value indicates this effect was not significant ($p > .05$), and the z -value (note: not t -value!) is also low.

i z-values

z -values correspond to the estimate divided by the standard error. It's interpretation is similar to that of the t -value: a z -value of ~ 2 or higher will likely have a p -value below 0.05.

The interaction term is negative, what does this mean? We can interpret this as indicating that the effect of congruence is different in either level of tense. These effects are often more easily interpreted with a visualisation, e.g., using the `plot_model()` function from the `sjPlot` package. This effect is not significant, however.

```
sjPlot::plot_model(fit_tense_ri,
                    type = "eff",
                    terms = c("gramm", "verb_t")) +
geom_line(position = position_dodge(0.1))
```

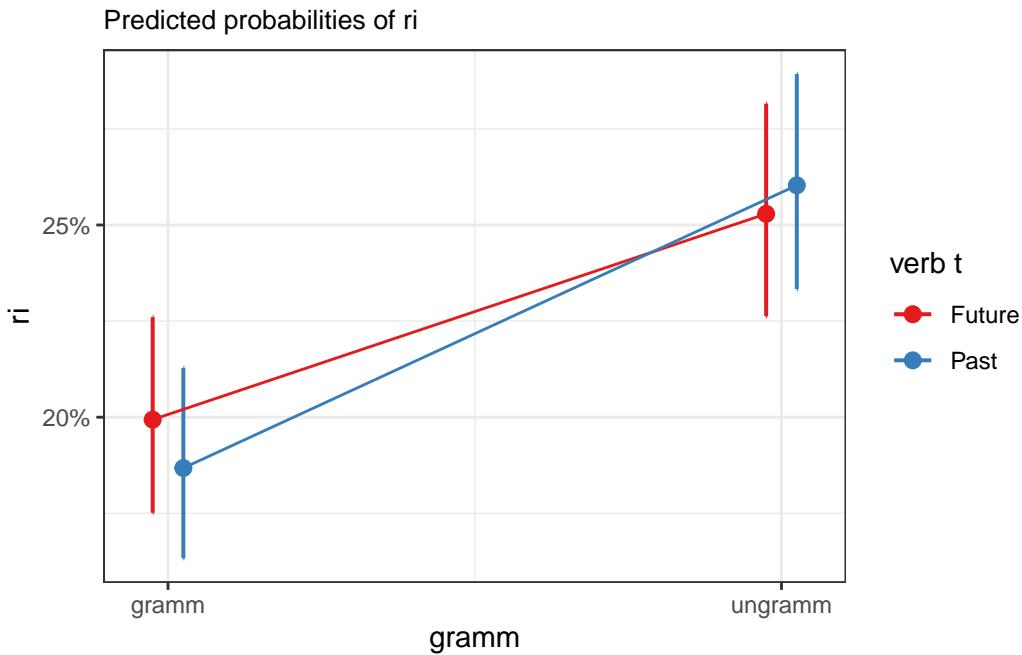


Figure 6.2: Interaction plot of

We can also use the `predict()` function to extract the predicted values for each condition. We could just simply print the predicted values (`predict(fit_tense_ri)`), append the predicted values to the data frame

```
# make sure dataset is the same length as the model data
df_tense_v <-
  df_tense |>
  filter(roi == "4") |>
  drop_na(ri)

# append model estimates
augment(fit_tense_ri, data = df_tense_v) |>
  distinct(verb_t, gramm, .keep_all = T) |>
  arrange(verb_t) |>
  select(verb_t, gramm, .fitted)

# A tibble: 4 x 3
verb_t gramm .fitted
<fct> <fct>   <dbl>
1 Future gramm -1.3903
2 Future ungramm -1.0832
```

```

3 Past    gramm   -1.4711
4 Past    ungramm -1.0443

```

Or we could create a list of the unique conditions.

```

df_sim <-
  tibble(
  verb_t = rep(c('Past', 'Future'), each = 2),
  gramm = rep(c('0', '1'), times = 2))

# alternatively, just extract the relevant factor levels from your datafram
df_sim <-
  df_tense |>
  arrange(verb_t) |>
  distinct(verb_t, gramm)

# and add predicted values
df_sim$fit <- num(predict(fit_tense_ri, df_sim), digits = 5)

df_sim

# A tibble: 4 x 3
  verb_t gramm      fit
  <fct>  <fct>    <num:.5!>
1 Future gramm   -1.39025
2 Future ungramm -1.08322
3 Past    gramm   -1.47108
4 Past    ungramm -1.04432

```

And now if we look at the predicted log-odds values for the future and past tenses:

```

df_sim |>
  summarise(
  mean_tense = mean(fit),
  .by = verb_t)

# A tibble: 2 x 2
  verb_t mean_tense
  <fct>    <num:.5!>
1 Future   -1.23674
2 Past     -1.25770

```

What is the difference between these two numbers (in our model summary)?

```
df_sim |>
  summarise(
    mean_tense = mean(fit),
    .by = gramm)

# A tibble: 2 x 2
  gramm  mean_tense
  <fct>   <num:.5!>
1 gramm    -1.43067
2 ungramm  -1.06377
```

What is the difference between these two numbers (in our model summary)?

So, our slopes for `verb_t` and `gramm` correspond to the predicted difference between the two levels of each factor.

6.3 Interpreting our coefficients

What do our coefficient estimates reflect, though? Let's remind ourselves of the rate of regressions in at the verb region:

```
df_tense |>
  filter(roi == "4") |>
  drop_na(ri) |>
  summary()

sj          item      adv_type      adv_t
Length:3795     Min.   : 1.00  Length:3795     Length:3795
Class :character 1st Qu.: 25.00  Class :character  Class :character
Mode  :character Median : 52.00  Mode   :character  Mode   :character
                           Mean   : 50.91
                           3rd Qu.: 78.00
                           Max.   :101.00

verb_t      gramm      roi      label      fp
Future:1897  gramm :1901  Min.   :4  Length:3795      Min.   : 81.0
Past   :1898  ungramm:1894  1st Qu.:4  Class :character  1st Qu.: 266.0
                           Median :4  Mode   :character  Median : 371.0
                           Mean   :4                  Mean   : 440.5
```

| gp | tt | ri | ro |
|--------------|----------------|----------------|-----------------|
| Min. : 87 | Min. : 90.0 | Min. :0.0000 | Min. :0.00000 |
| 1st Qu.: 285 | 1st Qu.: 326.5 | 1st Qu.:0.0000 | 1st Qu.:0.00000 |
| Median : 405 | Median : 493.0 | Median :0.0000 | Median :0.00000 |
| Mean : 510 | Mean : 607.4 | Mean :0.2248 | Mean :0.08169 |
| 3rd Qu.: 606 | 3rd Qu.: 747.0 | 3rd Qu.:0.0000 | 3rd Qu.:0.00000 |
| Max. :3877 | Max. :3936.0 | Max. :1.0000 | Max. :1.00000 |


```

ptab_gramm <-
  df_tense |>
  filter(roi == "4") |>
  drop_na(ri) |>
  select(gramm, ri) |>
  table() |>
  prop.table()

ptab_tense <-
  df_tense |>
  filter(roi == "4") |>
  drop_na(ri) |>
  select(verb_t, ri) |>
  table() |>
  prop.table()

df_tense |>
  filter(roi == "4") |>
  drop_na(ri) |>
  tabyl(gramm, ri, verb_t) |>
  adorn_percentages() |>
  adorn_totals()

```


\$Future

| | | |
|---------|-----------|-----------|
| gramm | 0 | 1 |
| gramm | 0.8006329 | 0.1993671 |
| ungramm | 0.7471022 | 0.2528978 |
| Total | 1.5477351 | 0.4522649 |

\$Past

| | | |
|-------|-----------|-----------|
| gramm | 0 | 1 |
| gramm | 0.8132214 | 0.1867786 |

```

ungramm 0.7396825 0.2603175
Total 1.5529039 0.4470961

```

We want to measure how much more likely a regression in ($y = 1$) is for ungrammatical conditions ($x = 1$) than in grammatical conditions ($x = 0$). Si we want to calculate the odds of a regression in for each case, and take their ratio:

```

# odds(y = 1 | x = 0)
odds_ri1_gramm0 <-
  ptab_gramm[1,2] / ptab_gramm[1,1] # in gramm conditions: ri 0/1
odds_ri1_gramm1 <-
  ptab_gramm[2,2] / ptab_gramm[2,1] # in ungramm condititons: ri 0/1

## odds ratio
odds_ri1_gramm1 / odds_ri1_gramm0

```

```
[1] 1.442756
```

```

## log odds
log(odds_ri1_gramm1) - log(odds_ri1_gramm0)

```

```
[1] 0.3665552
```

```

# or
log(odds_ri1_gramm1 / odds_ri1_gramm0)

```

```
[1] 0.3665552
```

```

## probability
plogis(log(odds_ri1_gramm1 / odds_ri1_gramm0))

```

```
[1] 0.5906263
```

So the odds of a regression into the verb region is 1.4 times more likely in ungrammatical versus grammatical conditions.

```

intercept <- tidy(fit_tense_ri)$estimate[1]
tense <- tidy(fit_tense_ri)$estimate[2]
gramm <- tidy(fit_tense_ri)$estimate[3]
interact <- tidy(fit_tense_ri)$estimate[4]

What are the log odds for the past (tense = -0.5) grammatical (gramm = -0.5)?

plogis(intercept)

[1] 0.2231822

plogis(tense)

[1] 0.5052407

plogis(gramm)

[1] 0.5907095

plogis(interact)

[1] 0.4701052

tidy(fit_tense_ri) |>
  mutate(prob = plogis(estimate))

# A tibble: 4 x 6
  term      estimate std.error statistic   p.value     prob
  <chr>       <dbl>     <dbl>     <dbl>        <dbl>    <dbl>
1 (Intercept) -1.2472    0.039203 -31.815 4.0637e-222 0.22318
2 verb_t1      0.020964   0.078405   0.26738 7.8918e- 1 0.50524
3 gramm1       0.36690    0.078405   4.6795  2.8755e- 6 0.59071
4 verb_t1:gramm1 -0.11972  0.15681    -0.76348 4.4518e- 1 0.47011

```

plogis(intercept + tense*-.5 + gramm*-.5)

```
[1] 0.1913675
```

And past ungrammatical (gramm = +0.5)?

```
plogis(intercept + tense*-.5 + gramm*.5)
```

```
[1] 0.2545957
```

And for the future conditions?

```
plogis(intercept + tense*.5 + gramm*-.5)
```

```
[1] 0.1946325
```

And past ungrammatical (gramm = +0.5)?

```
plogis(intercept + tense*.5 + gramm*.5)
```

```
[1] 0.2585946
```

```
plogis(-1.22521)
```

```
[1] 0.2270209
```

```
plogis(-1.22521)
```

```
[1] 0.2270209
```

$$p = \frac{odds}{1 + odds} \quad (6.4)$$

$$odds = \frac{p}{1 - p} \quad (6.5)$$

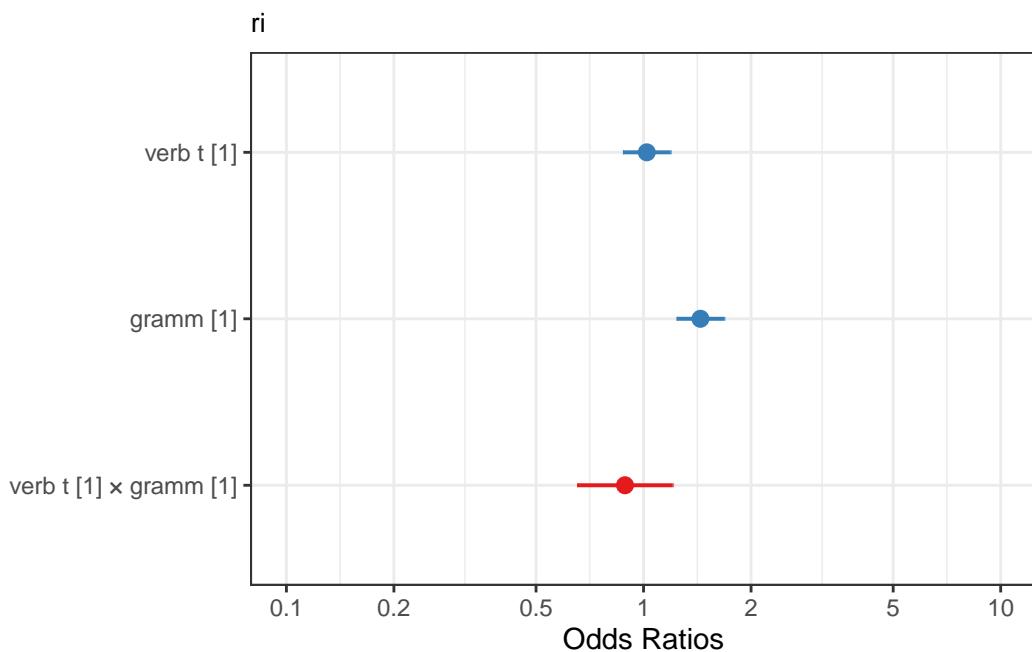
$$\log odds = \exp(odds) \quad (6.6)$$

6.4 Visualising model predictions

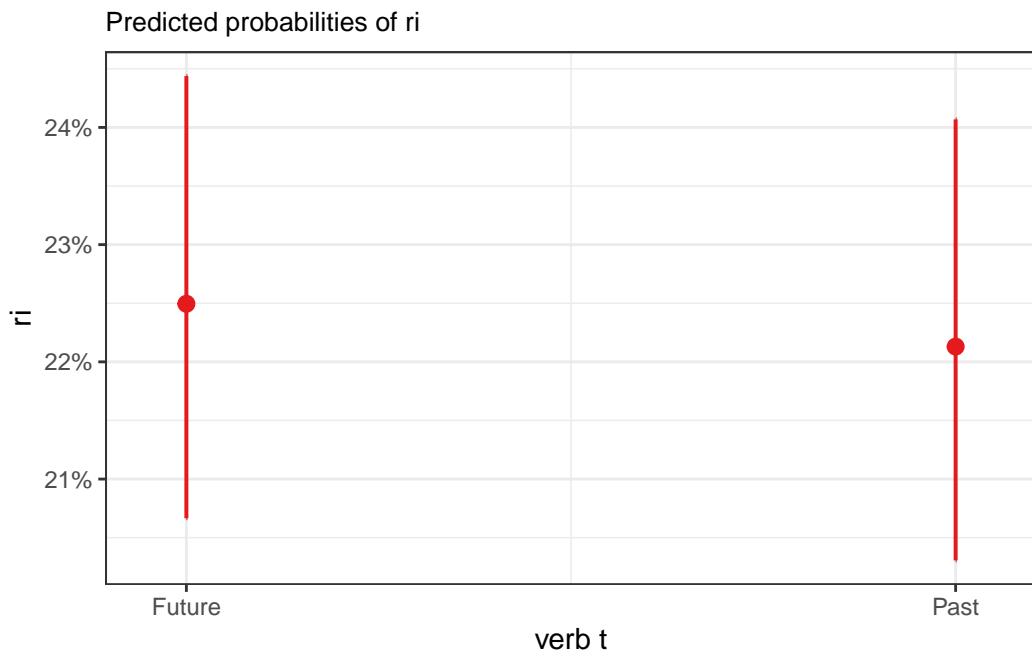
Something we haven't really covered is how to visualise our model predictions. So far we've only visualised the raw data, but when interpreting model results it helps to see the predictions. This is especially true for logistic regression, because our estimates are given in log odds, which are not very intuitive.

We can use the `sjPlot` package, which is very handy:

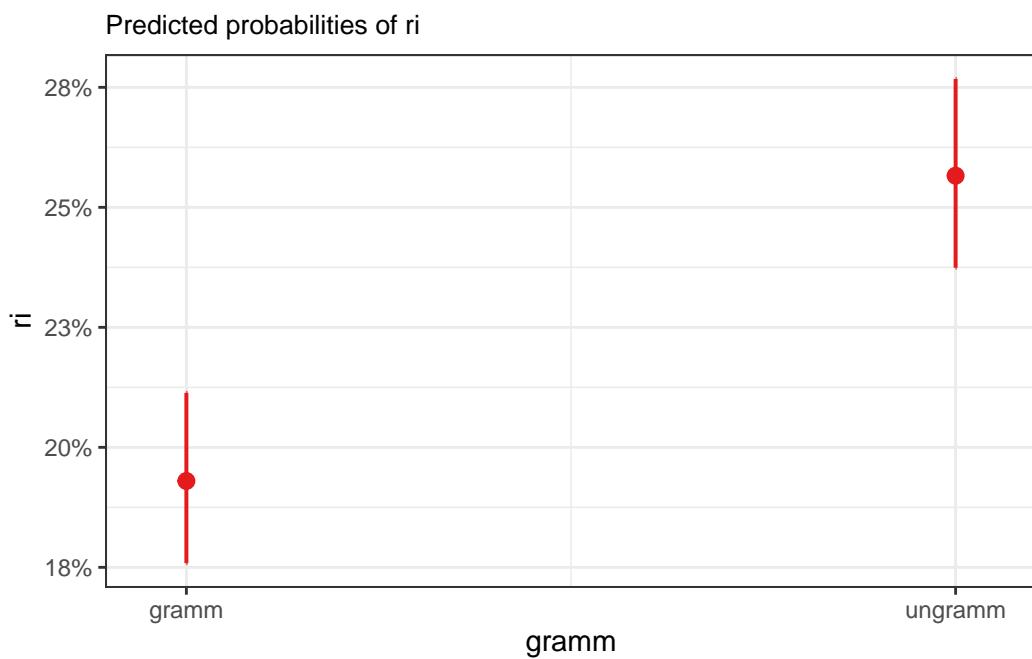
```
library(sjPlot)  
  
plot_model(fit_tense_ri)
```



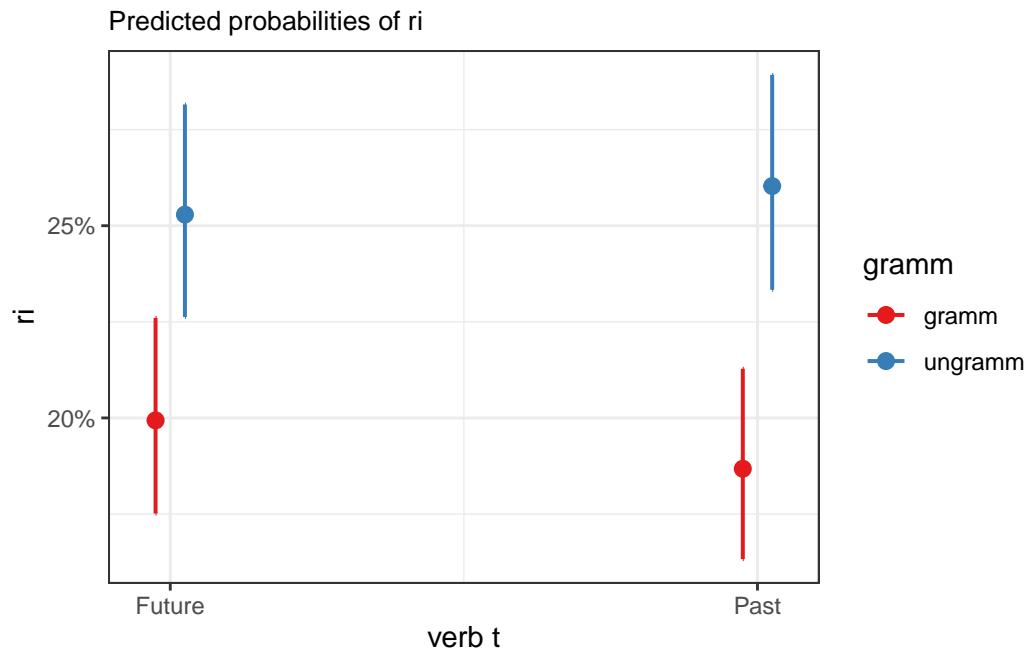
```
plot_model(fit_tense_ri, type = "eff",  
           terms = "verb_t")
```



```
plot_model(fit_tense_ri, type = "eff",
           terms = "gramm")
```



```
plot_model(fit_tense_ri, type = "int")
```



Or we can use the `ggeffects` package to extract summaries of effects, and then feed them into `ggplot2`.

```
library(ggeffects)

ggeffect(fit_tense_ri)

$verb_t
# Predicted probabilities of ri

verb_t | Predicted |      95% CI
-----
Future |      0.22 | [0.21, 0.24]
Past   |      0.22 | [0.20, 0.24]

$gramm
# Predicted probabilities of ri

gramm | Predicted |      95% CI
```

```

-----  

gramm | 0.19 | [0.18, 0.21]  

ungramm | 0.26 | [0.24, 0.28]  

attr("class")  

[1] "ggalleffects" "list"  

attr("model.name")  

[1] "fit_tense_ri"  

ggeffect(fit_tense_ri,  

         terms = c("gramm", "verb_t"))  

# Predicted probabilities of ri  

# verb_t = Future  

gramm | Predicted | 95% CI  

-----  

gramm | 0.20 | [0.18, 0.23]  

ungramm | 0.25 | [0.23, 0.28]  

# verb_t = Past  

gramm | Predicted | 95% CI  

-----  

gramm | 0.19 | [0.16, 0.21]  

ungramm | 0.26 | [0.23, 0.29]

```

6.5 Reporting

Sonderegger (2023a) (Section 6.9) says the following:

Reporting a logistic regression model in a write-up is generally similar to reporting a linear regression model...Reporting a logistic regression model in a write-up is generally similar to reporting a linear regression model: the guidelines and rationale in section 4.6 for reporting individual coefficients and the whole model hold, with some adjustments.

We can produce such a table using the `papaja` package, as in Table 6.2.

Table 6.2: ?(caption)

(a) Model summary for regressions in at the verb region. Estimates are given in log odds.

| Predictor | <i>b</i> | 95% CI | <i>z</i> | <i>p</i> |
|------------------|----------|----------------|----------|----------|
| Intercept | -1.25 | [-1.32, -1.17] | -31.81 | < .001 |
| Verb t1 | 0.02 | [-0.13, 0.17] | 0.27 | .789 |
| Gramm1 | 0.37 | [0.21, 0.52] | 4.68 | < .001 |
| Verb t1 × Gramm1 | -0.12 | [-0.43, 0.19] | -0.76 | .445 |

Table 6.3: ?(caption)

(a)

(b)

| term | estimate | std.error | prob | statistic | p.value |
|----------------|----------|-----------|------|-----------|---------|
| (Intercept) | -1.25 | 0.04 | 0.22 | -31.81 | 0.00 |
| verb_t1 | 0.02 | 0.08 | 0.51 | 0.27 | 0.79 |
| gramm1 | 0.37 | 0.08 | 0.59 | 4.68 | 0.00 |
| verb_t1:gramm1 | -0.12 | 0.16 | 0.47 | -0.76 | 0.45 |

```
library(papaja)

fit_tense_ri |>
  apa_print() |>
  apa_table(caption = "Model summary for regressions in at the verb region. Estimates are")
```

Or by extracting the model summary with `tidy()`, and even adding our probabilities, as in Table 6.3.

```
tidy(fit_tense_ri) |>
  mutate(prob = plogis(estimate)) |>
  relocate(prob, .after = std.error) |>
  apa_table()
```

6.6 Summary

- we saw that the equation for a straight line boils down to its intercept and slope

| term | description/other terms |
|------|-------------------------|
|------|-------------------------|

- we fit our first linear model with a categorical predictor

Important terms

Important terms

| Term | Definition | Equation/Code |
|------------------------|------------|---------------|
| Bernoulli distribution | NA | NA |
| plogis() | NA | NA |
| log odds | NA | NA |

Learning Objectives

Today we learned...

- how to model binomial data with logistic regression
- how to interpret log-odds and odds ratio

Task

6.6.1 Regressions out

Using the same dataset, run a logistic model exploring regressions in (`ri`) at the adverb region (`roi = "2"`). Before you run the model, do you have any predictions? Try plotting the regressions in for this region first, and generate some summary tables to get an idea of the distributions of regressions in across conditions.

6.6.2 Dutch verb regularity

Load in the `regularity` data from the `languageR` package.

```
df_reg <-  
  regularity |>  
  clean_names()
```

Regular and irregular Dutch verbs and selected lexical and distributional properties.

Our relevant variables will be:

- **written_frequency**: a numeric vector of logarithmically transformed frequencies in written Dutch (as available in the CELEX lexical database).
 - **regularity**: a factor with levels irregular (1) and regular (0).
 - **verb**: a factor with the verbs as levels.
1. Fit a logistic regression model to the data which predicts verb regularity by written frequency. Consider: What type of predictor variable do you have, and what steps should you take before fitting your model?
 2. Print the model coefficients, e.g., using `tidy()`.
 3. Interpret the coefficients, either in log-odds or probabilities. Report your findings.

Session Info

Developed with Quarto using R version 4.3.0 (2023-04-21) (Already Tomorrow) and RStudio version 2023.9.0.463 (Desert Sunflower), and the following packages:

```
sessionInfo()
```

```
R version 4.3.0 (2023-04-21)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Ventura 13.2.1

Matrix products: default
BLAS:      /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
LAPACK:    /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: Europe/Berlin
tzcode source: internal

attached base packages:
[1] stats      graphics   grDevices utils      datasets   methods    base
```

```

other attached packages:
[1] papaja_0.1.1.9001   tinylabels_0.2.3    ggeffects_1.2.2
[4] sjPlot_2.8.14       gt_0.9.0          googlesheets4_1.1.0
[7] kableExtra_1.3.4    knitr_1.44        patchwork_1.1.3
[10] languageR_1.5.0    janitor_2.2.0    lme4_1.1-33
[13] Matrix_1.5-4       broom_1.0.5       here_1.0.1
[16] lubridate_1.9.2   forcats_1.0.0    stringr_1.5.0
[19] dplyr_1.1.3         purrr_1.0.2      readr_2.1.4
[22] tidyverse_1.3.0     tibble_3.2.1     ggplot2_3.4.3
[25] tidyverse_2.0.0     broman_0.80

loaded via a namespace (and not attached):
[1] DBI_1.1.3           sandwich_3.0-2    rlang_1.1.3      magrittr_2.0.3
[5] multcomp_1.4-23     snakecase_0.11.0  compiler_4.3.0  systemfonts_1.0.4
[9] vctrs_0.6.3          rvest_1.0.3       pkgconfig_2.0.3 crayon_1.5.2
[13] fastmap_1.1.1      backports_1.4.1  labeling_0.4.3  effectsize_0.8.3
[17] utf8_1.2.3          rmarkdown_2.22    tzdb_0.4.0      haven_2.5.2
[21] nloptr_2.0.3        bit_4.0.5        xfun_0.39       jsonlite_1.8.7
[25] sjmisc_2.8.9        parallel_4.3.0   R6_2.5.1        RColorBrewer_1.1-3
[29] stringi_1.7.12      boot_1.3-28.1   cellranger_1.1.0 estimability_1.4.1
[33] Rcpp_1.0.11          modelr_0.1.11    zoo_1.8-12      parameters_0.21.1
[37] pacman_0.5.1         nnet_7.3-18      splines_4.3.0  timechange_0.2.0
[41] tidyselect_1.2.0     effects_4.2-2   rstudioapi_0.14 yaml_2.3.7
[45] codetools_0.2-19     sjlabelled_1.2.0 curl_5.0.1      lattice_0.21-8
[49] withr_2.5.0          bayestestR_0.13.1 coda_0.19-4    evaluate_0.21
[53] survival_3.5-5      survey_4.2-1   xml2_1.3.4      pillar_1.9.0
[57] carData_3.0-5       insight_0.19.3  generics_0.1.3 vroom_1.6.3
[61] rprojroot_2.0.3     hms_1.1.3       munsell_0.5.0  scales_1.2.1
[65] minqa_1.2.5          xtable_1.8-4   glue_1.6.2      emmeans_1.8.6
[69] tools_4.3.0          webshot_0.5.4  fs_1.6.2       mvtnorm_1.2-3
[73] grid_4.3.0           mitools_2.4    datawizard_0.7.1 colorspace_2.1-0
[77] nlme_3.1-162          performance_0.10.4 googledrive_2.1.0 cli_3.6.1
[81] fansi_1.0.4           gargle_1.4.0    viridisLite_0.4.2 svglite_2.1.1
[85] sjstats_0.18.2        gtable_0.3.4    digest_0.6.33  TH.data_1.1-2
[89] farver_2.1.1          htmltools_0.5.5 lifecycle_1.0.3 httr_1.4.6
[93] bit64_4.0.5           MASS_7.3-58.4

```

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Part V

Report 1

7 Report 1

Linear and logistic regression

The goal of this report is to review and consolidate what we learned together in the first block of the course. You are not required to do anything that we have not already seen.

For students enrolled in this course in the Winter Semester 2023/24: The report is due **January 11, 2024 at 11:59pm**, but I encourage you to submit before the holidays if you have the capacity to do so. Please submit your Quarto script, as well as a rendered copy (preferably HTML, but PDF is also fine) to Moodle (under ‘Reports’).

7.1 Dataset

For this report you will continue using the data from Biondo et al. (2022), an eye-tracking reading study on adverb-tense congruence effects on reading time measures. Participants’ eye movements were recorded as they read Spanish sentences where temporal adverbs and verb tense were either congruent or incongruent. For both sentence regions, the time reference was either past (e.g., *yesterda*, bought) or future (e.g., *tomorrow*, will buy). Example stimuli from this experiment are given in Table 31.1. You will be fitting models to different eye-tracking reading measures from this experiment, with the predictors *verb tense* and *grammaticality*.

Table 7.1: Example stimuli

| sentence | adverb | verb | gramm |
|---|--------|--------|---------|
| A la salida del trabajo, ayer las chicas compraron pan en la tienda. <i>After leaving work yesterday the girls bought bread at the shop</i> | past | past | gramm |
| A la salida del trabajo, ayer las chicas *comprarán pan en la tienda. <i>After leaving work yesterday the girls *will buy bread at the shop</i> | past | future | ungramm |
| A la salida del trabajo, mañana las chicas comprarán pan en la tienda. <i>After leaving work tomorrow the girls will buy bread at the shop</i> | future | future | gramm |
| A la salida del trabajo, mañana las chicas *compraron pan en la tienda. <i>After leaving work tomorrow the girls *bought bread at the shop</i> | future | past | ungramm |

7.2 Set-up

Make sure you begin with a *clear* working environment. To achieve this, you can go to **Session > Restart R**. Your Environment should have no objects in it, and you should not have any packages loaded.

7.2.1 Packages

Load the packages below. Give a short description of why we load in each package, i.e., what these packages help us do (1-2 sentences each). Tip: remember you can type `?tidyverse` into the Console to get an overview of a package or function.

```
pacman::p_load(  
  tidyverse,  
  janitor,  
  here,  
  broom  
)  
  
1. tidyverse:  
2. janitor:  
3. here:
```

7.2.2 Data

Run the code below. Give a short description of what each line of code does (you can skip the `locale` line). Tip: `roi == 2` corresponds to the *temporal adverb* condition.

```
df_tense <-  
  read_csv(here("data", "Biondo.Soilemezidi.Mancini_dataset_ET.csv"),  
           locale = locale(encoding = "Latin1") ## for special characters in Spanish  
           ) |>  
  clean_names() |>  
  mutate(gramm = ifelse(gramm == "0", "ungramm", "gramm")) |>  
  filter(roi == 2,  
         adv_type == "Deic") |>  
  mutate(length = nchar(label))
```

You can write your answer like this, for example:

```
1. df_tense <- :
```

2. `read_csv`:
3. `clean_names`:
4. `mutate`:
5. `filter`:

7.3 How to report your models

You will be running linear and logistic regression models. Our variables of interest will be:

| variable | description | type | class |
|---------------------|--|-------------|-------------|
| <code>fp</code> | first-pass reading time (summation of fixations from when a reader first fixates on a region to when they first leave that region) | dependent | continuous |
| <code>tt</code> | total reading time (summation of all fixations within a region during a trial) | dependent | continuous |
| <code>ri</code> | regressions in (whether there was at least one regression into a region) | dependent | binomial |
| <code>ro</code> | regressions out (whether there was at least one regression out of a region) | dependent | binomial |
| <code>verb_t</code> | verb tense: past or future | independent | categorical |
| <code>gramm</code> | grammaticality: grammatical or ungrammatical | independent | categorical |
| <code>length</code> | region length in letters | independent | continuous |

7.3.1 Example model report

Imagine we fit a linear model, called `fit_verb_tt`, to log-transformed total reading times at the verb region. Our fixed effects (i.e., predictors) are verb tense, grammaticality, and their interaction. Below I report the findings of the model, which is what you should aim to do with the models you run.

The model summary is given in `?@tbl-fit_verb_tt`, with back-transformed model predictions visualised in Figure 7.1. A main effect of grammaticality was found in total reading times at the verb region, with ungrammatical conditions eliciting longer total reading times than grammatical conditions ($\text{Est} = -0.06$, $t = -2.4$, $p < 0.05$). A main effect of tense was also found, with the future condition eliciting longer total reading times than the past condition ($\text{Est} = 0.07$, $t = 2.48$, $p < .05$). An interaction of tense and grammaticality was not significant ($\text{Est} = 0.04$, $t = 1$).

```
library(papaja)

fit_verb_tt |>
```

Table 7.3: Model summary for (log-transformed) total reading times at the verb region.

| Predictor | <i>b</i> | 95% CI | <i>t</i> | <i>df</i> | <i>p</i> |
|---------------------------|----------|----------------|----------|-----------|----------|
| Intercept | 6.22 | [6.19, 6.26] | 332.72 | 3791 | < .001 |
| Verb tPast | -0.06 | [-0.11, -0.01] | -2.38 | 3791 | .017 |
| Grammungramm | 0.07 | [0.01, 0.12] | 2.47 | 3791 | .013 |
| Verb tPast × Grammungramm | 0.04 | [-0.04, 0.11] | 1.01 | 3791 | .312 |

```

apa_print() |>
  apa_table(label = "tbl-fit_verb_tt",
             caption = "Model summary for (log-transformed) total reading times at the verb region")

library(sjPlot)
plot_model(fit_verb_tt, type = "int") +
  geom_line(position = position_dodge(0.1)) +
  labs(title = "Predicted total reading times at the verb region",
       x = "Verb tense",
       y = "Reading time (ms)") +
  theme_bw()

```

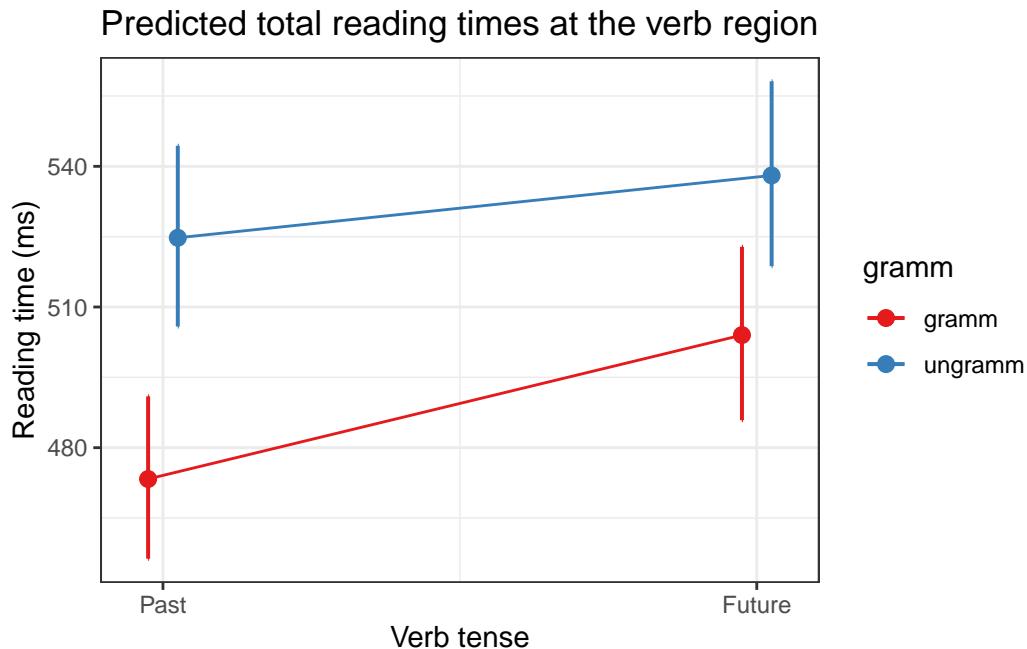


Figure 7.1: Back-transformed model predictions for total reading time at the verb region (with 95% confidence intervals).

7.4 Variable prep

We need to prepare our predictors: centering continuous variables and sum contrast coding categorical variables.

7.4.1 Centring continuous variables

Create a new variable `length_c` which contains the centred values of `length` (just centre, you don't need to standardise). Centre using the *median* rather than the mean (hint: there is a function `median()`).

7.4.2 Contrast coding

Set sum contrast coding for `tense` and `gramm`. You might need to first use the `as.factor()` function to save the variables as factors. Your contrasts should look like this:

```
contrasts(df_tense$gramm)
```

```

[,1]
gramm -0.5
ungramm 0.5

contrasts(df_tense$verb_t)

[,1]
Future 0.5
Past -0.5

```

7.5 Linear regression

We run linear regression when we have a continuous dependent variable. You will be fitting a model to first-pass reading time.

7.5.1 Fitting our model

Fit a model of *log-transformed* first-pass reading times with verb tense, grammaticality, and their interaction as fixed effects (hint: you might want to use * in your model).

7.5.2 Assessing assumptions

Visually assess the model assumptions of normality and homoscedasticity and write 1-2 sentences about each assumption, referring to the figures you produced.

7.5.3 Extracting predictions

1. Create objects `intercept`, `b1` (`verb_t`), and `b2` (`gramm`) that contain the corresponding model coefficient estimate for each term (hint: each object should contain a single value, which corresponds to the *estimate* for this term in your model summary output).
2. Generate the fitted values for each of our four conditions. We covered a number of ways to do this in class:
 - (a) Using our model formula (7.1) and the sum contrast values for each level of `verb_t` and `gramm` (i.e., +/-0.5, given in Table 7.4), compute the *back-transformed* predicted total reading time for each condition. Recall: b_0 is our intercept, b_1 is our slope for `verb_t` (i.e., the value of the object you just named `verb_t`), and b_2 is our slope (estimate) for `gramm` (i.e., the value of the object you just named `gramm`).

- (b) The `ggeffects` package: we used the `ggeffect()` function, but the `ggpredict()` function back-transforms the estimates for us.

$$fp = \exp(b_0 + b_1 * \text{verb_t} + b_2 * \text{gramm}) \quad (7.1)$$

Table 7.4: Corresponding value of factor levels to be plugged into equation ef{eq-fp}

| | -0.5 | +0.5 |
|--------|-------|---------|
| verb_t | past | future |
| gramm | gramm | ungramm |

7.5.4 Report model

Write a short report of the model findings. Produce a table and plot like in the example above to supplement your report.

7.6 Logistic regression

We run logistic regression when we have a binomial dependent variable. You will be fitting a logistic regression model to regression in.

7.6.1 Fit model

Fit a generalised linear model (logistic regression) to the regression in data, with the same fixed effects as your linear model above (`verb_t`, `gramm`, and their interaction). Remember, you will need a different function (not `lm`), and to add another argument (`family = ...`).

7.6.2 Interpretation

Write a short report of the model findings. Produce a table and plot like in the example above to supplement your report. Recall that our coefficient estimates are in *log odds*.

Part VI

Mixed models

8 Independence

Motivating mixed models



Under construction

This chapter is not fully translated from bullet points (from my slides) to prose. This will happen eventually (hopefully by spring 2024).

This lecture covers Winter & Grice (2021) (Sections 1 and 2), Chapter 14 'Mixed Models 1: Conceptual Introduction (Sections 14.1-14.3; Winter, 2019), and Sections 8.1-8.2 from Ch. 8 (Mixed-effects models I: Linear Regression) in Sonderegger (2023b).

Learning Objectives

Today we will learn about...

- the independence assumption
- types of non-independence in linguistic data
- the history of mixed models in linguistics

9 Independence assumption

- we already learned about some model assumptions
 - assumption of *normality* of residuals
 - *homoscedasticity* (constant variance) of residuals
 - absence of *collinearity* of predictors
- there another, arguably more important assumption
 - assumption of *independence*

9.1 (Non-)Independence

- non-independence: any possible link or connection between groups of data points
 - e.g., two observations from the same participant will tend to be more similar than to completely independent observations
 - any case where you might expect some clustering of observations by some grouping factor
- the independence assumption assumes that our data points are *not* linked
 - i.e., the value of one observation is completely independent from another
- violations of this assumption have major implications for Type I (alpha) error
 - i.e., the chances of observing an effect where there is none (false positive)
- it also artificially inflates sample size, which affects statistical power

9.2 Repeated measures design

- the reason most (experimental) linguistic data is non-independent is the use of the repeated-measures design
 - collecting multiple data points from e.g., the same participant and for the same item

- increases statistical power, needing fewer participants (more data points, lower variance due to control in variability between subjects)
- saves resources (fewer subjects)

9.3 Other sources of non-independence

- non-independence is prevalent in other fields of linguistics, e.g.,
 - corpus studies: text, author, language, dialect, register
 - phonetic experiments: speaker, listener, exact repetitions
 - socio-phonetics: dialect/geographical proximity, register, speaker

10 Pseudoreplication

Pseudoreplication refers to the treatment of dependent observations as independent data points, which causes an overabundance of erroneously significant results.

— Winter (2011), p. 2137

- analysing nonindependent data as if they were independent
- essentially, violating the independence assumption
 - very (*very*) common in older publications
- can also result in Type M (magnitude) and S (sign) error
- is one contributor (out of many) to the so-called replication crisis

10.1 Problem: Generalizability

- beyond spurious results, how researchers interpret the implications of their findings is problematic

Unfortunately, outside of a few domains such as psycholinguistics, it remains rare to see psychologists model stimuli as random effects – despite the fact that most inferences researchers draw are clearly meant to generalize over populations of stimuli.

— Yarkoni (2022), p. 4

- if we don't include grouping factors in our models, our findings are not generalisable beyond our sample
 - it could be that our findings are due to a few participants or experimental items who deviate from the rest
- we need to take this by-grouping factor variation into account, but how?

10.2 Solution 1: Averaging

- e.g., repeated measures ANOVA
 - separate models for by-participant and by-item variance (with averaging) interpreted together
- PRO: takes both by-participant and -item variance into account
- CONs: not flexible or appropriate for complex designs, and:
 - loses information regarding the variation across the grouped observations
 - lowers N
 - * e.g., if we average over participants, we'd have 1 only data point per participant!
 - therefore loses statistical power (Type II error)
 - inflates Type I error (chance of a false positive)
- in sum: not optimal

10.3 Solution 2: Single observations

- run an experiment without repeated measures
 - but this lowers statistical power
 - and drastically reduces generalizability
- e.g., we could present 60 participants with a single item
 - or we could present 1 participant with 60 trials
 - but these findings also can't be generalised beyond that one item or one participant...
- in sum: not optimal

10.4 Solution 3: Linear mixed models

- best available solution: use repeated-measures design and mixed models
- a.k.a. mixed (effects) models/LM(E)Ms, multi-level models, hierarchical models
- “mixed” because they contain:
 - **fixed effects:** usually predictors; describe systematic variation in our data that we wish to explain
 - **random effects:** unsystematic variation that are due to random sampling
- random effects take dependence between observations into account

- contain varying intercepts and slopes per level of a **grouping factor**
- fixed effects estimates are usually qualitatively unchanged
 - what is affected in the measures of *variance*

11 History of mixed-effects models

11.1 1973: Language-as-fixed-effect-fallacy

- none of these ideas are new to linguistics
- Clark (1973):
 - without including dependencies between repeated observations from the same **linguistic items** in our models, we cannot generalise our findings beyond our stimuli
 - our results are relevant only for the subset of the population from which we sampled

The remedies for the language-as-fixed-effect fallacy are for the most part obvious. They include doing the right statistics, choosing the appropriate experimental design, and selecting a random or representative sample of language.

— Clark (1973), p. 347

11.2 ANOVAs: aggregation

- repeated measures ANOVAs were commonly used to take dependence between observations into account (and are still common in some fields today)
 - require aggregation (i.e., averaging) over items *or* subjects, not both simultaneously
 - drastically reduces our number of observations
 - loss of information in the variance of observed data
 - i.e., a loss of power (Type II error) and inflated Type I error (false positive)

11.3 2008: Baayen et al. (2008) and lme4

- enter mixed models with *crossed* random effects
- Journal of Memory and Language, Special Issue: Emerging Data Analysis
 - Baayen et al. (2008): introduction of **lme4** package for linear mixed models
 - Jaeger (2008): overview of generalised linear mixed models

- in addition, Baayen (2008) was published, a textbook for analysing linguistic data with R with an emphasis on LMMs with `lme4`

Learning Objectives

Today we learned about...

- the independence assumption
- types of non-independence in linguistic data
- the history of mixed models in linguistics

12 Task

Discuss the following questions.

1. What is the independence assumption?
2. What happens when the independence assumption is violated?
3. What is the language-as-fixed-effect-fallacy?
4. What other sources of variance might be present in language research?
5. Why are repeated measures ANOVAs sub-optimal?

Session Info

Developed with Quarto using R version 4.3.0 (2023-04-21) (Already Tomorrow) and RStudio version 2023.9.0.463 (Desert Sunflower), and the following packages:

```
R version 4.3.0 (2023-04-21)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Ventura 13.2.1

Matrix products: default
BLAS:    /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
LAPACK:  /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib; 

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: Europe/Berlin
tzcode source: internal

attached base packages:
[1] stats      graphics   grDevices  utils      datasets   methods    base

loaded via a namespace (and not attached):
[1] compiler_4.3.0  fastmap_1.1.1   cli_3.6.1      tools_4.3.0
[5] htmltools_0.5.5 rstudioapi_0.14  yaml_2.3.7     rmarkdown_2.22
```

```
[9] knitr_1.44      jsonlite_1.8.7   xfun_0.39       digest_0.6.33
[13] rlang_1.1.3    evaluate_0.21
```

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13 Random intercepts

What, why, when, and how?

This chapter covers Chapter 14 'Mixed Models 1: Conceptual Introduction' (until Section 14.8; Winter, 2019), Winter (2014) (until page 16), and Sections 8.1-8.3 in Sonderegger (2023a). We will be using the data from Biondo et al. (2022).

Learning Objectives

Today we will learn...

- how to run our fixed mixed effects model with random intercepts
- how to interpret random intercepts

Set-up environment

Our first steps are to set-up our environment. The next two chunks are not necessary, but I use them to set some preferences, such as supressing scientific notation, and establishing a function to nicely format *p*-values.

```
# suppress scientific notation
options(scipen=999)
options(pillar.sigfig = 5)

library(broman)
# function to format p-values
format_pval <- function(pval){
  dplyr::case_when(
    pval < .001 ~ "< .001",
    pval < .01 ~ "< .01",
```

```
    pval < .05 ~ "< .05",
    TRUE ~ broman::myround(pval, 3)
  )
}
```

Load packages

We'll also need to load in our required packages. Hopefully you've already install the required packages (if not, go to [?@sec-software](#)).

```
# load libraries
pacman::p_load(
  tidyverse,
  here,
  broom,
  janitor,
  ggeffects,
  sjPlot,
  # new packages:
  lme4,
  lmerTest,
  broom.mixed,
  lattice)
```

Here I also globally set my preferred `ggplot2` theme so that all of my plots are formatted how I like them, without have to repeat the code for each plot. This is completely optional.

```
# set preferred ggplot2 theme
theme_set(theme_bw() + theme(plot.title = element_text(size = 10)))
```

Resolve conflicts

Sometimes different packages have functions with the same name. In these cases, when you call such a function the package that was last loaded will be used. Both `lme4` and `lmerTest` have a function `lmer()`, but for now we want to use the `lme4` version. We'll discuss the differences later, but for now let's make sure that `lme4` is used. We could also do this each time we call the function by using `lme4::lmer()`, but this can become cumbersome. Instead, let's explicitly define `lme4::lmer()` as the function version that should be used.

```
lmer <- lme4::lmer
```

Load data

Now let's load in our dataset from Biondo et al. (2022).

```
df_biondo <-  
  read_csv(here("data", "Biondo.Soilemezidi.Mancini_dataset_ET.csv"),  
            locale = locale(encoding = "Latin1") ## for special characters in Spanish  
            ) |>  
  clean_names() |>  
  mutate(gramm = ifelse(gramm == "0", "ungramm", "gramm"))
```

And take a look at the data:

```
head(df_biondo)
```

```
# A tibble: 6 x 13  
#> sj      item adv_type adv_t verb_t gramm   roi label      fp     gp     tt     ri  
#> <chr> <dbl> <chr>    <chr> <chr> <chr> <dbl> <chr>    <dbl> <dbl> <dbl> <dbl> <dbl>  
1 1       54 Deic     Past    Past    gramm    1 En la c~ 1173 1173 1173 0  
2 1       54 Deic     Past    Past    gramm    2 ayer te~ 474 474 474 0  
3 1       54 Deic     Past    Past    gramm    3 los car~ 910 910 910 0  
4 1       54 Deic     Past    Past    gramm    4 encarga~ 1027 1027 1027 0  
5 1       54 Deic     Past    Past    gramm    5 muchas ~ 521 521 521 0  
6 1       54 Deic     Past    Past    gramm    6 al prov~ 1029 1029 1029 0  
# i 1 more variable: ro <dbl>
```

?@tbl-data_dictionary gives an overview of the variables in the dataset. Relevant for this chapter are the variables **fp**, **verb_t**, **gramm**, and **roi**. For the tasks at the end of the chapter, you'll also be working with **tt** and **adv_t**.

| variable | description | type | class |
|----------|---|-------------|----------------|
| sj | participant ID | grouping | factor |
| item | item ID | grouping | factor |
| adv_type | adverb type: Deictic (e.g., on Monday), Non-deictic (e.g., last Monday) | independent | factor |
| adv_t | adverb tense: Past, Future | independent | factor |
| verb_t | verb tense: Past, Future | independent | factor |
| gramm | grammaticality: grammatical or ungrammatical | independent | categorical |
| roi | sentence region (Region Of Interest); 2 = adverb, 4 = verb | independent | ordered factor |
| label | sentence region text | independent | string |

| variable | description | type | class |
|----------|--|-----------|------------|
| fp | first-pass reading time (summation of fixations from when a reader first fixates on a region to when they first leave that region) | dependent | continuous |
| gp | regression path duration/go-past time | dependent | continuous |
| tt | total reading time (summation of all fixations within a region during a trial) | dependent | continuous |
| ri | regressions in (whether there was at least one regression into a region) | dependent | binomial |
| ro | regressions out (whether there was at least one regression out of a region) | dependent | binomial |

13.1 Review

Up until now, we've learned about the equation of a line (Section 1.3), simple ([?@sec-simple-regression](#)) and multiple linear regression ([?@sec-multiple-regression](#)), and logistic regression ([?@sec-logistic-regression](#)). We've also learned about centering and standardizing continuous predictors ([?@sec-continuous-predictors](#)), and contrast coding categorical predictors ([?@sec-contrast-coding](#)). We discussed non-linear transformations for dependent variables in linear regression, such as log-transforming data with a positive skew ([?@sec-log-transformation](#)), and how to interpret the coefficients of logistic regressions in log-odds, odds, and probabilities ([?@sec-log-odds](#)). If any of these topics don't sound familiar to you, I suggest going back and reviewing the relevant chapter. If you feel you have a somewhat good handle on these topics, then proceed.

13.1.1 Model equation

Recall the equation of multiple linear regression model, given in Equation 13.1.

$$y_i = b_0 + b_1 x_i + b_2 x_1 + \dots + e_i \quad (13.1)$$

Where the value of some value y (indexed by i) equals the intercept (b_0) plus the corresponding value x (indexed by i) of our first predictor (b_1) plus that of our second predictor (b_2), plus the corresponding error e (indexed by i), which is simply the difference between the predicted value and the observed value (i.e., residual). Here, i indicates values corresponding to the same observation i . Such a model assumes that all possible groups within our data have the same intercept and the same slope.

The estimated parameters, i.e., our coefficients (b_0 , b_1 , b_2), are our **fixed effects**. The estimated values model the mean/population-level effects in our data. Mixed models try to model some of the variance, i.e., residual error (e_i), by including **random effects**. Though we will

never completely get rid of the unexplained variance in our model (e), we can try to minimise it by including some expected variation present in our data. When, why, and how we can do that is the topic of this chapter.

13.2 Mixed models: why, when, and how?

Mixed models are ‘mixed’ in that they have both fixed and random effects. **Fixed effects** are our predictors (i.e., independent variables), the variance in the data we are trying to explain and generalise beyond our data. We would expect the model estimates of our fixed effects to be similar if we were to re-run our experiment with different participants, and even with different linguistic items that contain the same manipulation.

Random effects take into account the random variance, i.e., the variance in our data we are not trying to explain and that we would not expect to replicate across experiments. This is because they are dependent on e.g., the participants or specific linguistic items we collected our data from. Whether or not we have non-independence in our data depends on how/from where we collected our data. It’s common for experiments to involve multiple observations per participant and for the same stimuli (i.e., items) to be presented across participants. In production studies for example, participants may be asked to read the same sentences or words out loud. In corpus studies, data may be collected from several sources with multiple data points collected from the same text and/or author.

Take participants for example: different people will tend to have different reading speeds, fundamental frequencies, and even different effects of our critical manipulations. That is to say, data points from a certain participant will tend to be grouped together since one participant might tend to be a faster reader than another participant, or have a higher fundamental frequency than another. The same can be said for experimental items: one item (e.g., *Yesterday/Tomorrow, the workers went/will go to the bakery*) might tend to have longer reading times or a larger effect of grammaticality than another item for one reason or another.

Of course, participant and item are not the only sources of non-independence in linguistic data. Winter & Grice (2021) provides a description of other possible sources of non-independence in language research, such as phonetic production studies (speaker, exact repetitions), and corpora (author, text, register). In essence, random effects are **grouping factors** in our data across beyond which we want to *generalise* our observed effects.

13.2.1 Why?

Simply put, because of the independence assumption and Type I (alpha) error! The “sexy” answer: Not accounting for non-independence in our data can lead to unreliable p -values.

13.2.2 When?

Whenever you have observations (i.e., data points) that are somehow linked. One such case is when you have a repeated measures design, as is often the case in linguistic experiments: each participant sees the same experimental items. Therefore, we have multiple (non-independent) observations per participant, and also multiple (non-independent) observations per item. See Section 3 in Winter & Grice (2021) for a discussion of sources of dependence beyond participant and item in different subfields of language research.

Let's look at an example. We previously used the data from from Biondo et al. (2022), which contains data from an eye-tracking during reading experiment with a repeated measures design. We're interested in whether reading times were affected by adverb-tense congruence (grammaticality) and tense (past vs. future). Let's review your model from Report 1.

13.2.2.1 An example: report 1 model

In the first report for this class, you fit a model of first-pass reading times from Biondo et al. (2022) with the predictors (i.e., *fixed effects*) grammaticality, tense, and their interaction. The resulting coefficients should look something like Table 13.2.

```
# prep data for model
df_deic_verb <-
  df_biondo |>
  # filter for verb region (roi = 4) and Deictic adverbs
  filter(roi == 4,
         adv_type == "Deic") |>
  # set predictors as factors for contrast coding
  mutate(gramm = as_factor(gramm),
        verb_t = as_factor(verb_t))

# sum contrast coding: gramm and Past = -0.5
contrasts(df_deic_verb$gramm) <- c(-0.5, 0.5)
contrasts(df_deic_verb$verb_t) <- c(-0.5, 0.5)

# check contrasts
# contrasts(df_deic_verb$gramm)
# contrasts(df_deic_verb$verb_t)

fit_lm_fp <-
  lm(log(fp) ~ gramm*verb_t,
     data = df_deic_verb)
```

Table 13.2: Output from report 1 model of first-pass reading times

| term | estimate | std.error | statistic | p.value |
|----------------|----------|-----------|-----------|---------|
| (Intercept) | 5.957 | 0.008 | 741.568 | 0.000 |
| gramm1 | 0.003 | 0.016 | 0.193 | 0.847 |
| verb_t1 | 0.061 | 0.016 | 3.809 | 0.000 |
| gramm1:verb_t1 | -0.015 | 0.032 | -0.474 | 0.635 |

Table 13.3: Predicted values from our lm() model back-transformed into milliseconds

| tense | gramm | predicted | std.error | conf.low | conf.high |
|--------|---------|-----------|-----------|----------|-----------|
| Past | gramm | 372.892 | 0.016 | 361.354 | 384.798 |
| Past | ungramm | 376.912 | 0.016 | 365.202 | 388.998 |
| Future | gramm | 399.460 | 0.016 | 387.069 | 412.249 |
| Future | ungramm | 397.658 | 0.016 | 385.329 | 410.382 |

```
# model
# print model coefficients only
tidy(fit_lm_fp) |>
  kable(digits = 3) |>
  kable_styling()
```

We see there is a significant effect of verb tense ($Est = 0.06$, $t = 3.9$, $p < .001$), where the slope (and therefore the t -value) is positive. Since we coded **Past** as -0.5 and **Future** as $+0.5$, a positive slope means there were longer first-pass reading times for the **Future** condition, which we also saw when we plotted the raw data. So, this means that future-tensed verbs elicited longer first-pass reading times, and that the congruence of the verb with a preceding temporal adverb did not affect first-pass reading times. When we back-transform the log-transformed predicted values per condition into milliseconds we get Table 13.3.

```
ggpredict(fit_lm_fp, terms = c("verb_t", "gramm")) |>
  as_tibble() |>
  rename(
    tense = x,
    gramm = group
  ) |>
  relocate(tense, gramm) |>
  knitr::kable(digits = 3) |>
  kableExtra::kable_styling()
```

But if we look at each participants observations, e.g., their first-pass reading times for past versus future tensed verbs, we see there is quite some variation in their means and in the effect

of tense. Figure 14.2 shows by-participant variation in first-pass reading times for past and future tenses from seven example participants, in raw milliseconds (A) and log-transformed first-pass reading times (B). In each plot, the vertical grey dotted line indicates $x = 0$ (because we used sum contrast coding $x = 0$ is smack dab in the middle between past and future), the blue line represents the by-participant intercept and slope, while the black line represents the intercept and slope from our model. The black line therefore represents the population-level values, i.e., the mean of all first-pass reading times and the mean effect of tense.

```

fig_biondo_sj_ms <-
  df_biondo |>
  filter(sj %in% c(1,10,2,35,46,57,63)) |>
  mutate(verb_t = factor(verb_t, levels = c("Past", "Future"))) |>
  ggplot() +
  aes(x = verb_t, y = fp,
      colour = verb_t,
      shape = verb_t) +
  facet_wrap("sj", nrow = 1) +
  # Put the points on top of lines
  geom_point(position = position_jitter(0.2),
             alpha = .2) +
  stat_smooth(aes(group = 1), method = "lm") +
  # geom_boxplot(colour = "black", alpha = 0) +
  labs(y = "First-pass RT (ms)",
       x = "Tense") +
  geom_vline(xintercept = 1.5, colour = "grey", linetype = "dashed")+
  theme(legend.position = "none") +
  geom_abline(
    intercept = exp(coef(fit_lm_fp)[1]-(coef(fit_lm_fp)[3]*1.5)) ,
    slope = (exp(coef(fit_lm_fp)[1]+(coef(fit_lm_fp)[3]*0.5)) - exp(coef(fit_lm_fp)[1]+(co
      )
    )

fig_biondo_sj_log <-
  df_biondo |>
  mutate(verb_t = factor(verb_t, levels = c("Past", "Future"))) |>
  filter(sj %in% c(1,10,2,35,46,57,63)) |>
  ggplot() +
  aes(x = verb_t, y = log(fp),
      colour = verb_t,
      shape = verb_t) +
  facet_wrap("sj", nrow = 1) +
  # Put the points on top of lines
  geom_point(position = position_jitter(0.2),

```

```

alpha = .2) +
stat_smooth(aes(group = 1), method = "lm") +
labs(y = "First-pass RT (log)", x = "Tense") +
geom_vline(xintercept = 1.5, colour = "grey", linetype = "dashed") +
theme(legend.position = "none") +
geom_abline(
  intercept = coef(fit_lm_fp)[1]-(coef(fit_lm_fp)[3]*1.5),
  slope = coef(fit_lm_fp)[3])

# print
fig_biondo_sj_ms / fig_biondo_sj_log + theme(legend.position = "none") +
plot_annotation(tag_levels = "A")

```

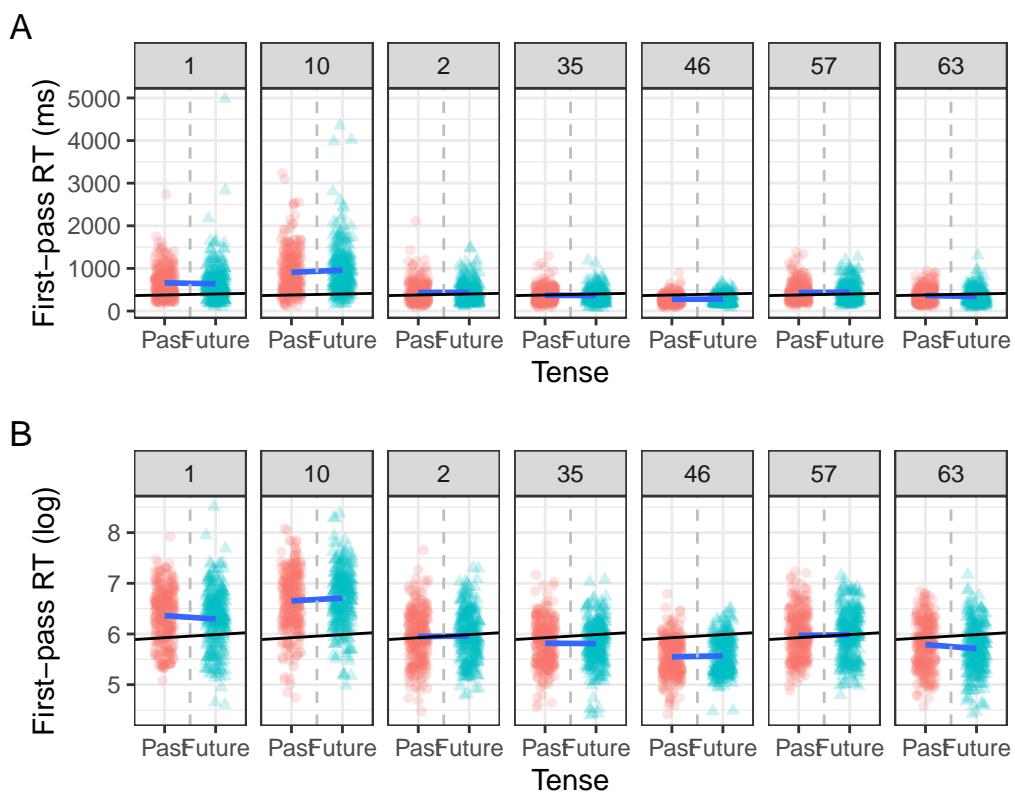


Figure 13.1: Demonstration of by-participant variation in intercept and slope (blue line) versus fixed-effects-only model intercept and slope (black line) for seven example participants. Grey dashed line indicates $x = 0$. Points represent single observations.

Note in Figure 14.2 that there is variation in the central tendency of observations per participant. For example, Participant 10 had overall longer first-pass reading times than the other

participants, as did Participant 1. Conversely, some participants had overall faster first-pass reading times, such as Participants 46 and 63. Meanwhile, some participants were pretty near the grand mean, like Participants 2 and 57. This is not to mention the differences in the slopes: some participants have a flatter slope than the model's fitted slope (e.g., Participants 35 and 46), while some even have a slope in the opposite direction (e.g., Participants 1 and 63).

Figure 13.2 shows the same trend across a sample of seven experimental items. Some by-item intercepts were similar to the model intercept (e.g., items 1 and 85), while some deviated (e.g., item 10 and 26).

```

fig_biondo_item_ms <-
  df_biondo |>
  filter(item %in% c(1,10,26,33,58,101,85)) |>
  mutate(verb_t = factor(verb_t, levels = c("Past", "Future"))) |>
  ggplot() +
  aes(x = verb_t, y = fp,
      colour = verb_t,
      shape = verb_t) +
  facet_wrap("item", nrow = 1) +
  # Put the points on top of lines
  geom_point(position = position_jitter(0.2),
             alpha = .2) +
  stat_smooth(aes(group = 1), method = "lm") +
  # geom_boxplot(colour = "black", alpha = 0) +
  labs(y = "First-pass RT (ms)",
       x = "Tense") +
  geom_vline(xintercept = 1.5, colour = "grey", linetype = "dashed")+
  theme(legend.position = "none") +
  geom_abline(
    intercept = exp(coef(fit_lm_fp)[1]-(coef(fit_lm_fp)[3]*1.5)) ,
    slope = (exp(coef(fit_lm_fp)[1]+(coef(fit_lm_fp)[3]*0.5)) - exp(coef(fit_lm_fp)[1]+(co
      )

fig_biondo_item_log <-
  df_biondo |>
  mutate(verb_t = factor(verb_t, levels = c("Past", "Future"))) |>
  filter(item %in% c(1,10,26,33,58,101,85)) |>
  ggplot() +
  aes(x = verb_t, y = log(fp),
      colour = verb_t,
      shape = verb_t) +
  facet_wrap("item", nrow = 1) +

```

```

# Put the points on top of lines
geom_point(position = position_jitter(0.2),
           alpha = .2) +
stat_smooth(aes(group = 1), method = "lm") +
labs(y = "First-pass RT (log)", x = "Tense") +
geom_vline(xintercept = 1.5, colour = "grey", linetype = "dashed") +
theme(legend.position = "none") +
geom_abline(
  intercept = coef(fit_lm_fp)[1]-(coef(fit_lm_fp)[3]*1.5),
  slope = coef(fit_lm_fp)[3])

# print
fig_biondo_item_ms / fig_biondo_item_log + theme(legend.position = "none") +
plot_annotation(tag_levels = "A")

```

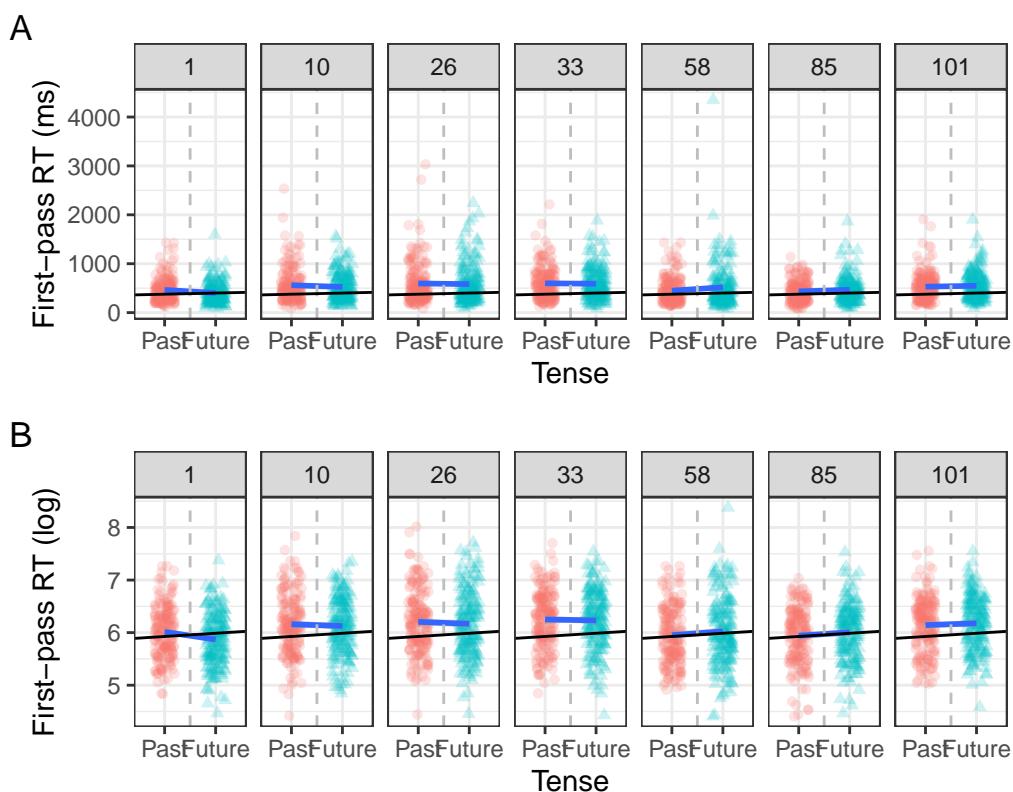


Figure 13.2: Demonstration of by-item variation in intercept and slope (blue line) versus fixed-effects-only model intercept and slope (black line) for seven example items. Grey dashed line indicates $x = 0$. Points represent single observations.

If we were to gather by-participant and by-item slopes from all participants and items and plotted them together, we would get Figure 13.3 (where colour indicates direction of slope: positive or negative).

```
fig_item_sj_fp_means
```

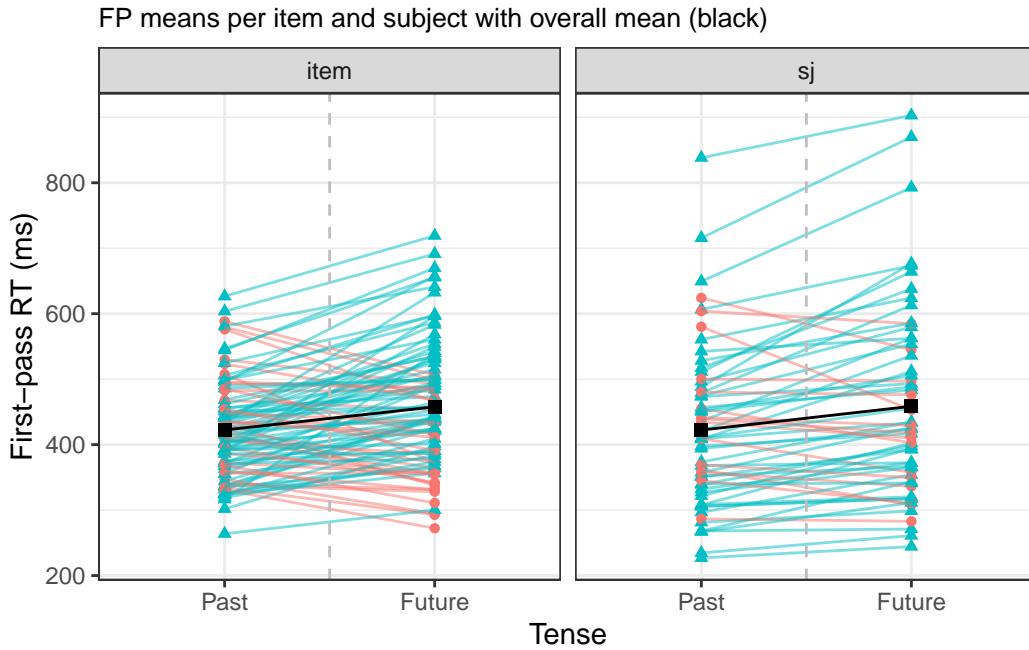


Figure 13.3: Means per condition per item (left) and subject (right) with overall mean in black

We see saw in seven examples in Figure 14.2 and (**fit-pooling_item?**), and across all participants and items in Figure 13.3, that there is a lot of variability in terms of the overall mean (intercept, which would correspond to the grey dotted line) across items and participants, as well and in the differences between past and future verbs. Firstly, focusing on the intercept (values crossing the vertical grey dotted line), there is a range of approximately 300 to 675 ms between items, and a range of 250 and 875 between participants. Compared to the overall mean of 440.5ms, this is quite some variation. Looking now at the effect of tense, i.e. the *slope*, we see not only differences in the magnitude of effects between items and participants (i.e., how steep the slope is), but also in the *direction* of the effect: There are quite a few items and participants that have a slope in the opposite direction of the overall mean in black, which is positive.

So why does it matter that there's variability by item and by participant? All of this data was already included in our model, and so it was taken into consideration when calculating standard error and confidence intervals, so why should this matter? The answer is simply: dependence of data points affects the number of observations, which in turn affects our degrees of freedom

and measures like standard error and confidence intervals. In essence, it alters our measures of uncertainty in the presence or absence of a reliable effect.

To drive this point home, let's look at an ordered plot of by-item and -participant intercepts with 95% confidence intervals (Figure 13.4) and boxplots of the raw observations of first-pass reading times at the verb region (Figure 13.5). In Figure 13.4, we see the intercept value on the x-axis, again highlighting the range of varying intercept values for across items and participants. In Figure 13.5, we see the range in the spread of values, with wider inter-quartile ranges especially for participants with higher a median first-pass reading time. This was also represented in Figure 13.4 by wider 95% confidence intervals for both items and participants with higher intercepts.

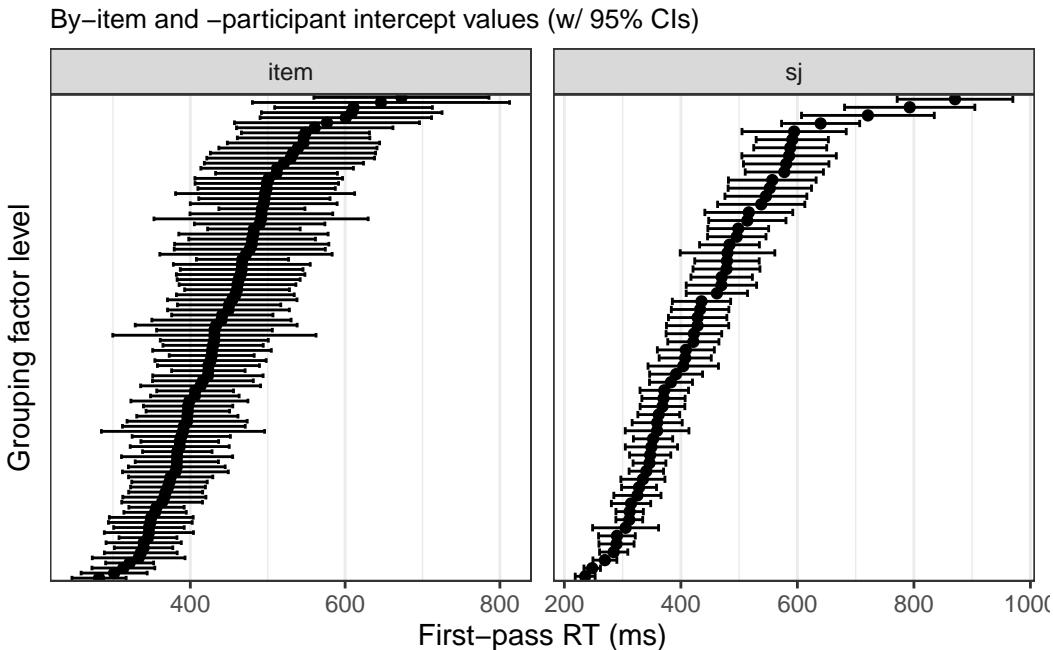


Figure 13.4: By-item (left) and -participant (right) varying intercepts (x-axis) per grouping factor level (i.e., per item and per participant). Errorbars indicate 95% confidence intervals.

```
fig_sj_boxplot <-
  df_deic_verb |>
  mutate(sj_median = median(fp, na.rm = T), .by=sj) |>
  ggplot() +
  aes(x = reorder(sj, sj_median), y = fp) +
  labs(title = "By-participant boxplot of first-pass reading times at the verb",
       y = "First-pass RT (ms)") +
  geom_boxplot() +
```

```

theme(
  axis.ticks.x = element_blank(),
  axis.text.x = element_blank(),
  axis.title.x = element_blank()
)

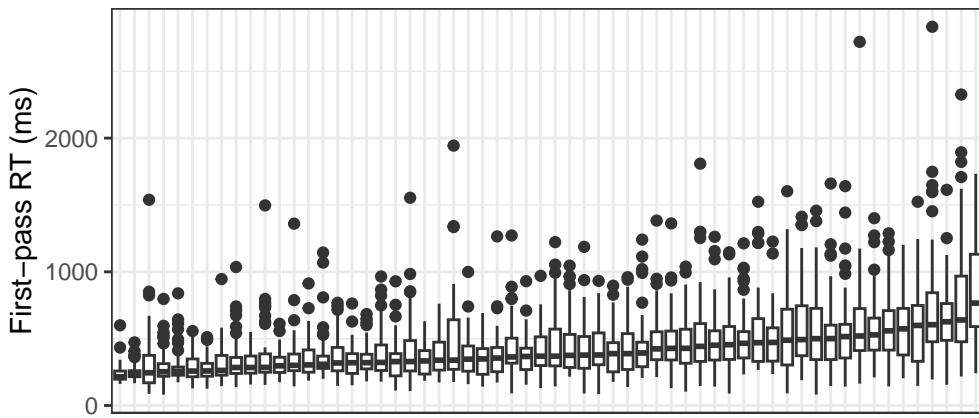
fig_item_boxplot <-
df_deic_verb |>
  mutate(item_median = median(fp, na.rm = T), .by=item) |>
  ggplot() +
  aes(x = as_factor(reorder(item, item_median)), y = fp) +
  labs(title = "By-item boxplot of first-pass reading times at the verb",
       y = "First-pass RT (ms)") +
  geom_boxplot() +
  theme(
    axis.ticks.x = element_blank(),
    axis.text.x = element_blank(),
    axis.title.x = element_blank()
  )

fig_sj_boxplot / fig_item_boxplot +
  plot_annotation(tag_levels = "A")

```

A

By-participant boxplot of first-pass reading times at the verb



B

By-item boxplot of first-pass reading times at the verb

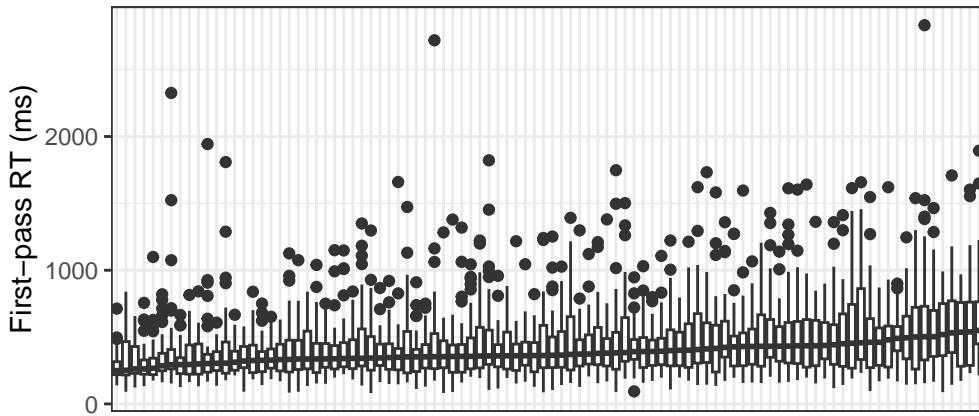


Figure 13.5: Boxplots of first-pass reading times per participant (A) and item (B)

In order for our model to take this by-participant and by-item variance into account, we can add by-participant and by-item random terms in a mixed model.

13.2.3 How?

We can add random intercepts and random slopes per grouping factor. Random intercepts would correspond to the average y -value (if we're using sum contrast coding) per level of a grouping factor, e.g., per participant. Random slopes would give us the fitted effect per level of a grouping factor, e.g., per participant. So, if we fit a model with by-participant random intercepts and slopes, our model will also fit an intercept and slope per participant, thereby taking the by-participant variance into account. Importantly, each grouping factor

must be a factor (i.e., categorical), and each level of this grouping factor must have sufficient observations. In this chapter we'll focus on random intercepts, and we will be running what's called *random-intercept-only* or *intercept-only* random effects models. A word of warning: such models can lead to inflated Type I (alpha) error, i.e., a false positive result (Barr et al., 2013b). Mixed models with intercept-only random effects are often the final model reported because of something called convergence issues, meaning the model cannot be fit because of a lack of computational power or too few observations "per cell".

The `lme4` ([lme4-package?](#)) or `lmerTest` ([lmerTest-package?](#)) packages are commonly used to produce mixed models in R. The main difference between the two is that `lmerTest` produces *p*-values while `lme4` does not. The coefficients from the two packages should be otherwise identical. For a more in-depth discussion on *p*-values in mixed models, see for example Section 8.5.1.3 (*t/F-tests with approximate df*) in Sonderegger (2023a). We'll be using the `lme4` package to start off with to fit mixed models with the `lmer()` function, which uses similar syntax to the `lm()` function:

$$dv \sim 1 + iv, data = data_name \quad (13.2)$$

$$dv \sim 1 + iv + (1 + iv|gf), data = data_name \quad (13.3)$$

Where `dv` is our dependent variable (measure, outcome variable), `iv` is our independent variable(s) (predictor variable), and `gf` refers to a grouping factor. The `1`s stand-in for intercept, so `1 + iv` means fit an intercept (1) and slope (`iv`). Recall that the `1` is optional, and we often don't write it in our models. We see a `1` in the random effects structure, however: `(1 + iv|gf)`. This represents random effects for a grouping factor (`gf`): We are fitting an intercept and slope *per level* of this grouping factor. Basically, this model is a mixed model fit to **some dependent variable with an independent variable(s) as fixed effect, and by-grouping factor random intercepts and slopes for our fixed effect iv**. You could replace the highlighted terms in the last sentence with the names of your own variables in a model to describe your formula.

This might all sound abstract at the moment, but it helps to see it in action. For the rest of the chapter we'll focus on random intercepts, and we will get to random slopes in the next chapter. Let's now fit and explore some mixed models.

13.3 By-participant random intercepts

Recall the equation in Equation 13.1. To model first-pass reading times as a function of verb tense and grammaticality, we would get Equation 13.5. Adding random intercepts for a single grouping factor would give us Equation 13.5.

$$fp = \beta_0 + \beta_{verb_t}x + \beta_{gramm}x \quad (13.4)$$

$$fp_i = \beta_0 + \alpha_{j[i]} + \beta_{verb_t}x + \beta_{gramm}x + e_i \quad (13.5)$$

Where α represents the deviation of some level $[i]$ in some group j from the population-level intercept (β_0). In other words, we assume here that there is some grouping factor within our data structure and that each level of this grouping factor will have an intercept value that deviates somewhat from the population-level intercept. As we saw above, the data from Biondo et al. (2022) contains non-independent observations from 60 participants. If we wanted to take that into consideration

A simplified version in Equation ?? is the model for the average participant in our data, where the intercept is the average first-pass reading time across all participants, and the slopes for tense and grammaticality are also the average effect of each across all participants. [Equation 13.7](#) models the first-pass reading time with varying intercepts for participant (sj), where $\beta_0 + \alpha_{sj[i]}$ represents the intercept for participants. [Equation 13.7](#) models the first-pass reading time for participant (sj) 60, where $\beta_0 + \alpha_{sj[60]}$ represents the intercept for participant 60.

$$fp = \beta_0 + \alpha_{sj[i]} + \beta_1x + \beta_2x \quad (13.6)$$

$$fp = \beta_0 + \alpha_{sj[60]} + \beta_1x + \beta_2x \quad (13.7)$$

Let's continue with our model from Report 1, with log-transformed first-pass reading times (`fp`) as dependent variable, grammaticality (`gramm`), verb tense (`verb_t`), and their interaction as fixed effects, and by-participant (`sj`) random intercepts:

```
fit_lmm_fp_sj <-
  lmer(log(fp) ~ gramm*verb_t +
    (1|sj),
    data = df_deic_verb)
```

We see the only difference between this code and that above is that we are using `lmer()` instead of `lm()`, and that we have added `+ (1|sj)` to the model equation.

What happens if we try to run this model without `+ (1|sj)`?

```
fit_lmm_fp_sj <-
  lmer(log(fp) ~ gramm*verb_t,
    data = df_deic_verb)
```

```
Error: No random effects terms specified in formula
```

We get an informative error message: `Error: No random effects terms specified in formula.` The `lmer()` function requires a random effects structure, so if it is missing a model will not be fit.

13.3.1 Inspecting your model output

The `summary()` function also worth `lmer()` models, but there are some differences in the output.

```
summary(fit_lmm_fp_sj)

Linear mixed model fit by REML ['lmerMod']
Formula: log(fp) ~ gramm * verb_t + (1 | sj)
Data: df_deic_verb

REML criterion at convergence: 4479.1

Scaled residuals:
    Min      1Q  Median      3Q     Max 
-4.0560 -0.6427 -0.0419  0.6168  4.0901 

Random effects:
 Groups   Name        Variance Std.Dev. 
 sj       (Intercept) 0.06573  0.2564  
 Residual           0.18030  0.4246  
 Number of obs: 3795, groups: sj, 60

Fixed effects:
            Estimate Std. Error t value
(Intercept) 5.957102  0.033809 176.199
gramm1       0.003466  0.013787   0.251
verb_t1      0.062209  0.013787   4.512
gramm1:verb_t1 -0.015741  0.027573  -0.571

Correlation of Fixed Effects:
          (Intr) gramm1 vrb_t1
gramm1    0.000
verb_t1   0.000 -0.002
grmm1:vrb_1 0.000  0.000  0.002
```

Similar to the model output from a `lm()` model, we have the model formula at the top. We also have have the distribution of the residuals, which look quite normally distributed. Our fixed

Table 13.4: broom.mixed::tidy(fit_lmm_fp_sj)

| effect | term | estimate | std.error | statistic |
|--------|----------------|------------|-----------|-------------|
| fixed | (Intercept) | 5.9571020 | 0.0338089 | 176.1991812 |
| fixed | gramm1 | 0.0034662 | 0.0137866 | 0.2514208 |
| fixed | verb_t1 | 0.0622091 | 0.0137873 | 4.5120666 |
| fixed | gramm1:verb_t1 | -0.0157409 | 0.0275733 | -0.5708757 |

effects are under **Fixed Effects** (instead of **Coefficients** in `lm()` output). Here you might notice we don't have any p-values, we'll talk about why below. Lastly, instead of information about model fit (e.g., R^2), we have **Correlation of Fixed Effects**, which is exactly what the title suggests: the correlation between fixed effects. This corresponds to the assumption of multicollinearity, and should have small values.

There are two other main differences near the top: **REML criterion at convergence: ...**, and our **Random effects**. We won't be getting into REML in this course, but know that it is important when doing model comparisons.

💡 REML: restricted maximum likelihood

Sonderegger (2023a), Section 8.5 and Box 8.4

We can use the `broom.mixed` package to extract tidy coefficient summaries from `lmer()` models, similar to the `broom` package for `lm()` models. The `broom.mixed` package also has a function `tidy()` for this purpose. This function also has an optional argument `effects` which can be used to control what information you extract from your model:

- `effects = "fixed"`: fixed-effect parameters
- `effects = "ran_pars"`: random effects of our model (standard deviations of our random effect terms)

```
tidy(fit_lmm_fp_sj, effects = "fixed") |>
  kable() |>
  kable_styling()

tidy(fit_lmm_fp_sj, effects = "ran_pars") |>
  kable() |>
  kable_styling()
```

We can also use the `VarCorr()` function from `lme4` to extract the variance components (i.e., random effects) from our model summary:

Table 13.5: broom.mixed::tidy(fit_lmm_fp_sj)

| effect | group | term | estimate |
|----------|----------|----------------|-----------|
| ran_pars | sj | sd_(Intercept) | 0.2563809 |
| ran_pars | Residual | sd_Observation | 0.4246230 |

```
print(VarCorr(fit_lmm_fp_sj), comp=c("Variance", "Std.Dev.))
```

| Groups | Name | Variance | Std.Dev. |
|--------|-------------|----------|----------|
| sj | (Intercept) | 0.065731 | 0.25638 |
| | Residual | 0.180305 | 0.42462 |

But what exactly do these random effect parameters mean? We see the estimated degree of by-participant intercept variability is approximately 0.07 has a standard deviation of approximately 0.26.

13.3.2 lmerTest

```
fit_lmm_fp_sj <-  
  lmerTest::lmer(log(fp) ~ gramm*verb_t +  
    (1|sj),  
    data = df_deic_verb)
```

13.3.3 Comparing to simple regression

Visualise both models' coefficients

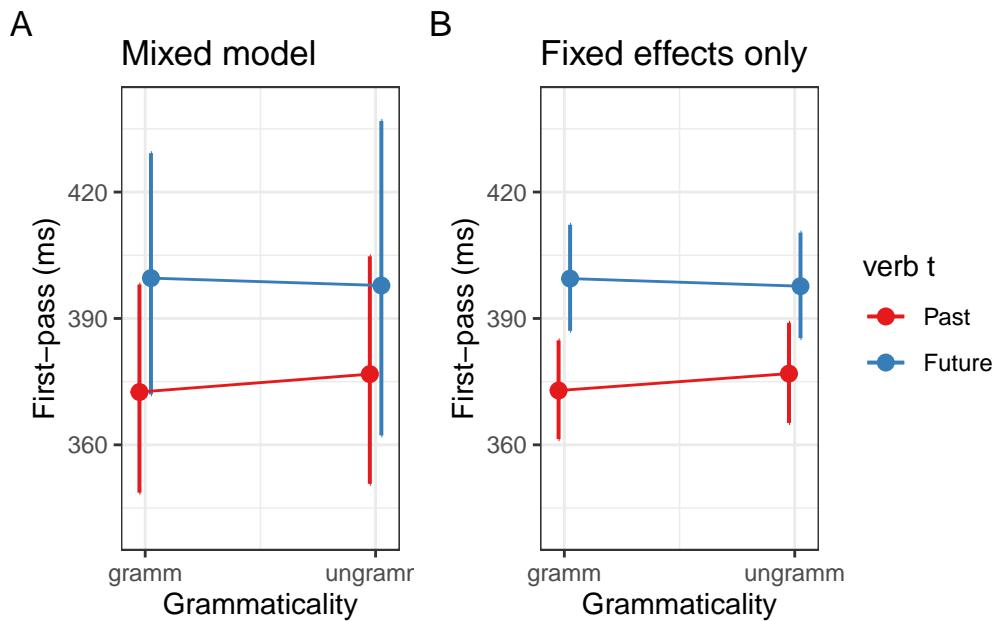
```
fig_lmer <- plot_model(fit_lmm_fp_sj, type = "int") +  
  geom_line(position = position_dodge(0.1)) +  
  labs(title = "Mixed model",  
    x = "Grammaticality",  
    y = "First-pass (ms)") +  
  theme_bw() +  
  ylim(340, 440)  
  
fig_lm <- plot_model(fit_lm_fp, type = "int") +  
  geom_line(position = position_dodge(0.1)) +  
  labs(title = "Fixed effects only",  
    x = "Grammaticality",
```

```

y = "First-pass (ms)" +
theme_bw() +
ylim(340, 440)

fig_lmer + fig_lm + plot_annotation(tag_levels = "A") +
plot_layout(guides = "collect")

```



13.4 Adding another grouping factor

So far we've fit the data using one grouping factor: participant. The experimental design in (**biondo_tomorrow_2022?**) used repeated measures, however. This means that each participant was presented items from multiple items. In other words, each item (`item`) was presented to multiple participants (`sj`). This is a crossed-design, also called a factorial design, where both participant and item are grouping factors. We should be using crossed random effects, i.e., two grouping factors. We can do this by simply adding another `+ (1|gf)` to our model syntax.

```

fit_lmm_fp_sj_item <-
lmer(log(fp) ~ gramm*verb_t +
  (1|sj) +
  (1|item),
  data = df_deic_verb)

```

This is now a model with by-participant and by-item random intercepts. Let's inspect this model as we did with our model with by-participant random intercepts. This amounts to Equation 14.1, where we have varying intercepts (α) for two grouping variables, j and k .

$$fp_i = \beta_0 + \alpha_{j[i]} + \alpha_{k[i]} + \beta_{verb_t}x + \beta_{gramm}x + e_i \quad (13.8)$$

If we take j to represent participants and k to represent items, then the j in $\alpha_{j[i]}$ has 60 levels (1-60, because we have 60 participants), and k in $\alpha_{k[i]}$ has 96 levels (1-96, because we have 96 items). And i has 3795 levels, because there are 3795 observations in our model (which we will see in a moment).

13.5 Exploring our random effects estimates

- what we saw in our model summary were the variance components
 - a description of the variance of our by-item and by-participant random intercepts
- our model also contains intercept estimates for each level of item and participant
 - we can extract the intercept estimates
 - or we extract their deviance from the model intercept

13.5.1 Extracting fixed effects

- we've already used `coef()` to extract fixed effect estimates from `lm` objects

```
coef(fit_lm_fp)
```

| | (Intercept) | gramm1 | verb_t1 | gramm1:verb_t1 |
|--|-------------|-------------|-------------|----------------|
| | 5.957251870 | 0.003101061 | 0.061204153 | -0.015245374 |

- to extract our fixed effect estimates from `lmer` objects we need `fixef()`

```
fixef(fit_lmm_fp_sj_item)
```

| | (Intercept) | gramm1 | verb_t1 | gramm1:verb_t1 |
|--|-------------|------------|------------|----------------|
| | 5.95640363 | 0.00321152 | 0.06189237 | -0.01431578 |

- or we can append `$coefficients` to the model summary

```

summary(fit_lmm_fp_sj_item)$coefficients |>
  as_tibble()

# A tibble: 4 x 3
  Estimate `Std. Error` `t value`
  <dbl>       <dbl>      <dbl>
1  5.9564     0.036790  161.90
2  0.0032115  0.013025   0.24657
3  0.061892   0.013025   4.7517
4 -0.014316   0.026049  -0.54956

```

13.5.1.1 Extract random intercept estimates

- `coef()` behaves very differently with `lmer` objects, extracting the random effects estimates per level

```
coef(fit_lmm_fp_sj_item) |> pluck("item") |> head()
```

| | (Intercept) | gramm1 | verb_t1 | gramm1:verb_t1 |
|---|-------------|------------|------------|----------------|
| 1 | 6.022184 | 0.00321152 | 0.06189237 | -0.01431578 |
| 2 | 5.761268 | 0.00321152 | 0.06189237 | -0.01431578 |
| 3 | 5.854873 | 0.00321152 | 0.06189237 | -0.01431578 |
| 4 | 6.056862 | 0.00321152 | 0.06189237 | -0.01431578 |
| 5 | 6.138213 | 0.00321152 | 0.06189237 | -0.01431578 |
| 6 | 6.331058 | 0.00321152 | 0.06189237 | -0.01431578 |

- which outputs a `list` object, with one data frame for `item` and one for `sj`
- we can extract just one or the other (`head()` is for presentation purposes):

```
coef(fit_lmm_fp_sj_item) |> pluck("item") |>
  rownames_to_column(var = "item") |> head()
```

| item | (Intercept) | gramm1 | verb_t1 | gramm1:verb_t1 |
|------|-------------|------------|------------|----------------|
| 1 | 6.022184 | 0.00321152 | 0.06189237 | -0.01431578 |
| 2 | 5.761268 | 0.00321152 | 0.06189237 | -0.01431578 |
| 3 | 5.854873 | 0.00321152 | 0.06189237 | -0.01431578 |
| 4 | 6.056862 | 0.00321152 | 0.06189237 | -0.01431578 |
| 5 | 6.138213 | 0.00321152 | 0.06189237 | -0.01431578 |
| 6 | 6.331058 | 0.00321152 | 0.06189237 | -0.01431578 |

```
coef(fit_lmm_fp_sj_item) |> pluck("sj") |>  
rownames_to_column(var = "sj") |> head()
```

```
sj (Intercept) gramm1 verb_t1 gramm1:verb_t1  
1 07 5.869627 0.00321152 0.06189237 -0.01431578  
2 09 5.782527 0.00321152 0.06189237 -0.01431578  
3 1 6.401777 0.00321152 0.06189237 -0.01431578  
4 10 6.621081 0.00321152 0.06189237 -0.01431578  
5 11 5.913712 0.00321152 0.06189237 -0.01431578  
6 12 6.153031 0.00321152 0.06189237 -0.01431578
```

- why do our intercepts vary by participant, but not verb_t1, gramm1, or verb_t1:gramm1?

13.5.1.2 Extract deviations from the intercept

- the ranef() function provides the deviance from the model intercept and each random intercept estimate
 - the output is a list with a one element per grouping factor

```
ranef(fit_lmm_fp_sj_item) |> pluck("item") |>  
rownames_to_column(var = "item") |> head(10)
```

```
item (Intercept)  
1 1 0.06578061  
2 2 -0.19513572  
3 3 -0.10153080  
4 4 0.10045812  
5 5 0.18180978  
6 6 0.37465425  
7 7 0.09281920  
8 8 0.13695475  
9 9 0.05810287  
10 10 -0.05426568
```

- ranef()\$grouping_factor or pluck("grouping_factor") selects the relevant grouping factor

```
ranef(fit_lmm_fp_sj_item)$sj |>  
head()
```

```

(Intercept)
07 -0.08677692
09 -0.17387701
1   0.44537367
10  0.66467739
11 -0.04269124
12  0.19662767

ranef(fit_lmm_fp_sj_item) |>
  pluck("sj") |> head()

```

```

(Intercept)
07 -0.08677692
09 -0.17387701
1   0.44537367
10  0.66467739
11 -0.04269124
12  0.19662767

```

13.5.1.3 Compare estimates and deviances

- the values extracted by `ranef()` (`sj_dev` in Table 13.6) equal the difference (`difference`) between the model intercept (`model_intercept`) and the by-participant random intercept estimates (`sj_est`)
- so we can either look at each participant's (or item's) estimate, or look at how much it deviates from the model intercept

13.6 Visualising your random effects

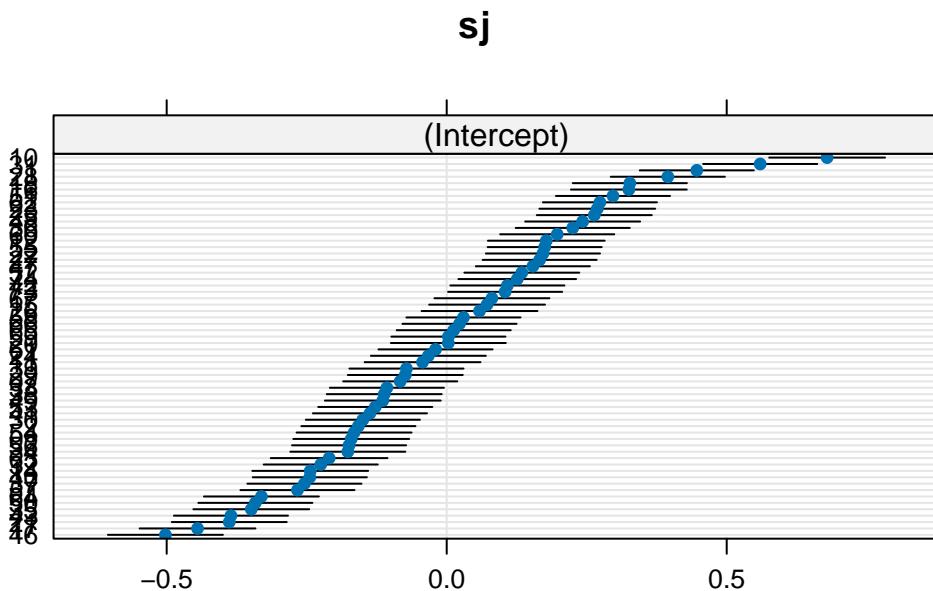
The simplest method to visualise your random effects is to use the `dotplot()` function from the `lattice` package. This prints out a caterpillar plot with a dot indicating the deviance of the intercept value per grouping factor level (here: per participant) from the model intercept, with 95% confidence intervals.

```
dotplot(ranef(fit_lmm_fp_sj))
```

```
$sj
```

Table 13.6: Random intercept estimates versus deviance

| sj | sj_est | sj_dev | est_minus_dev | model_intercept |
|----|--------|--------|---------------|-----------------|
| 07 | 5.870 | -0.087 | 5.956 | 5.956 |
| 09 | 5.783 | -0.174 | 5.956 | 5.956 |
| 1 | 6.402 | 0.445 | 5.956 | 5.956 |
| 10 | 6.621 | 0.665 | 5.956 | 5.956 |
| 11 | 5.914 | -0.043 | 5.956 | 5.956 |
| 12 | 6.153 | 0.197 | 5.956 | 5.956 |



We can also produce this plot ourselves by extracting our random effects per participant by using the `broom.mixed::tidy()` function with the argument `effects = "ran_vals"` and `conf.int = TRUE`. This will give us the intercept value, rather than the deviance from the model intercept. However, you can easily calculate the deviance by subtracting the model intercept value from each participant's intercept value (Figure 13.6 A). If we want the actual by-participant intercept values, we can simply add the model intercept to get each by-participant estimate, i.e., the values we get with `coef()` (Figure 13.6 B). Notice that in comparison to Figure 13.6, nothing has changed except the values along the x-axis. This is because we've

performed a *linear transformation*: adding the model intercept value to the by-participant deviance. The x-axis ticks in Figure 13.6 B equal values as those in Figure 13.6 A (-0.5, 0, 0.5), but with the model intercept value (5.957102) added.

```

fig_res_dev <-
  broom.mixed::tidy(fit_lmm_fp_sj, effects = "ran_vals", conf.int = TRUE) |>
  filter(group == "sj") |>
  ggplot() +
  aes(x = estimate, y = reorder(level, estimate)) +
  labs(title = "By-participant intercept deviance (log)",
       y = "Participant ID",
       x = "Deviance (log)") +
  geom_vline(xintercept = 0, colour = "red", linetype = "dashed") +
  geom_point(colour = "blue") +
  geom_errorbar(
    aes(xmin = conf.low,
        xmax = conf.high)
  ) +
  scale_x_continuous(breaks = c(-0.5,0,0.5)) +
  facet_grid(~term)

fig_res_est <-
  broom.mixed::tidy(fit_lmm_fp_sj, effects = "ran_vals", conf.int = TRUE) |>
  filter(group == "sj") |>
  # back-transform to ms
  mutate(across(c(estimate,conf.low,conf.high),~.+fixef(fit_lmm_fp_sj)[1])) |>
  # mutate(across(c(estimate,conf.low,conf.high),exp)) |>
  # plot
  ggplot() +
  aes(x = estimate, y = reorder(level, estimate)) +
  labs(title = "By-participant intercept estimates (ms)",
       y = "Participant ID",
       x = "Estimate (log)") +
  geom_vline(xintercept = fixef(fit_lmm_fp_sj)[1], colour = "red", linetype = "dashed") +
  geom_point(colour = "blue") +
  geom_errorbar(
    aes(xmin = conf.low,
        xmax = conf.high)
  ) +
  scale_x_continuous(breaks = c(5.457102,5.957102 ,6.457102)) +
  facet_grid(~term)

```

```
fig_res_dev + fig_res_est +
  plot_annotation(tag_levels = "A")
```

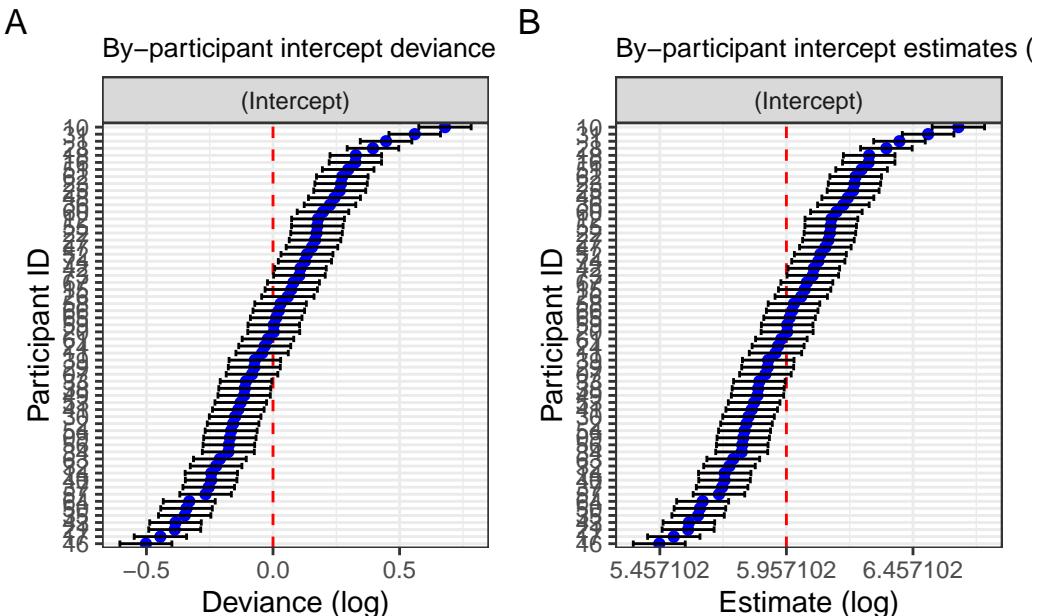


Figure 13.6: By-participant intercept deviances (A) and estimates (B) in log scale

If we wanted to back-transform these values to milliseconds to facilitate interpretation, we simply exponentiate these estimates (Figure 13.7 A). Lastly, we can back-transform the deviances by subtracting the exponentiating model estimate from the back-transformed estimates (Figure 13.7 B).

```
fig_res_est_ms <-
  broom.mixed::tidy(fit_lmm_fp_sj, effects = "ran_vals", conf.int = TRUE) |>
  filter(group == "sj") |>
  # back-transform to ms
  mutate(across(c(estimate,conf.low,conf.high),~.+fixef(fit_lmm_fp_sj)[1])) |>
  mutate(across(c(estimate,conf.low,conf.high),exp)) |>
  # plot
  ggplot() +
  aes(x = estimate, y = reorder(level, estimate)) +
  labs(title = "By-participant intercept estimates (ms)",
       y = "Participant ID",
       x = "Estimate (ms)") +
  geom_vline(xintercept = exp(fixef(fit_lmm_fp_sj)[1]), colour = "red", linetype = "dashed")
```

```

geom_point(colour = "blue") +
geom_errorbar(
  aes(xmin = conf.low,
      xmax = conf.high)
) +
scale_x_continuous(breaks = c(186.4884, 386.4884, 586.4884, 786.4884)) +
facet_grid(~term)

fig_res_dev_ms <-
broom.mixed::tidy(fit_lmm_fp_sj, effects = "ran_vals", conf.int = TRUE) |>
filter(group == "sj") |>
# back-transform to ms
mutate(across(c(estimate,conf.low,conf.high),~.+fixef(fit_lmm_fp_sj)[1])) |>
mutate(across(c(estimate,conf.low,conf.high),exp)) |>
mutate(across(c(estimate,conf.low,conf.high),~-exp(fixef(fit_lmm_fp_sj)[1]))) |>
# plot
ggplot() +
aes(x = estimate, y = reorder(level, estimate)) +
labs(title = "By-participant intercept deviance (ms)",
     y = "Participant ID",
     x = "Deviance (ms)") +
geom_vline(xintercept = 0, colour = "red", linetype = "dashed") +
geom_point(colour = "blue") +
geom_errorbar(
  aes(xmin = conf.low,
      xmax = conf.high)
) +
# scale_x_continuous(breaks = c(-0.5,0,0.5)) +
facet_grid(~term)

fig_res_est_ms + fig_res_dev_ms +
plot_annotation(tag_levels = "A")

```

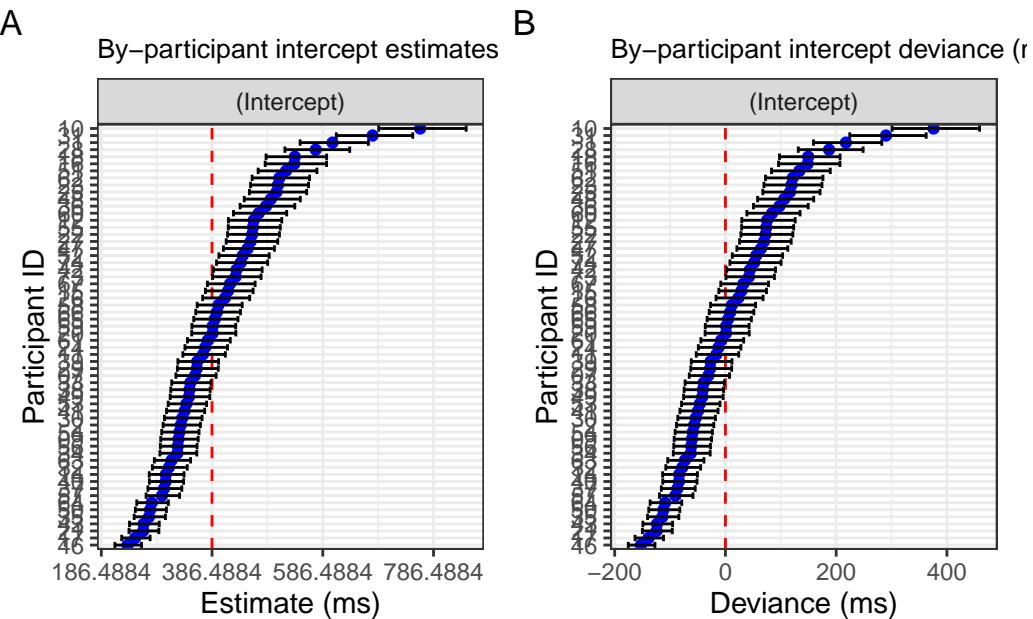


Figure 13.7: By-participant estimates back-transformed to milliseconds

These plots should seem somewhat familiar given our exploration of the by-participant variance in the dataset above. Now we see how this variance is modelled and including in our model, but what does including it actually *change*? Let's take a look at the difference between our mixed model with by-participant varying intercepts and our fixed-effects only model.

13.7 Reporting your model

According to Sonderegger (2023a) (p. 297), we should report:

1. model definition (sometimes in ‘Data Analysis’ section)
2. Fixed effects
3. Random effects
4. Sample size (number of observations, number of levels for each grouping factor)
5. one or more quantitative summaries of the model, e.g., AIC, BIC, or logLik (although they’re only informative in comparison to another model fit to the same data)

13.7.1 Model definition

Below is an example of a write-up of a model definition from Biondo et al. (2022) (p. 9). Note that I’ve highlighted some aspects that we’ve already covered, which you should remember to define in write ups.

We conducted the analysis by fitting `linear mixed-effect models` to our data, using the R package `lme4` (Bates et al., 2014). We included Time Reference (past, future), and Verb Match (match, mismatch) as `fixed-effect factors` [...] by adopting `sum contrast coding` (Schad et al., 2020): past and match conditions were `coded as -.5.` while future and mismatch conditions were `coded as .5.` [...] Moreover, we included `crossed random intercepts` and random slopes for all fixed-effect parameters `for subject and item` grouping factors (Barr et al., 2013) in all models. [...] Logit mixed-effect models were employed (Jaeger, 2008) for the analysis of the probability of regression measure. [...] P-values were derived by using the `lmerTest` package (Kuznetsova et al., 2017).

But this is missing the explicit mention of the method used to compute the *p*-values. For example, Troyer & Kutas (2020) (p. 9) included the following:

P-values for individual predictors were computed using `lmerTest`, with the `Satterthwaite` option for denominator degrees of freedom for F statistics.

But here they don't cite the package. So you see, there's always something you miss! The aim is to be as descriptive as you can be. The aim in describing your model is to enable reproducibility. If you don't fully describe your analysis steps it can be difficult (or impossible) to reproduce your analyses. Ideally, your analysis scripts should also be shared alongside your data (`laurinavichyute_share_2022?`), but your analysis steps should still be explicitly and unambiguously described to the best of your ability in your data analysis/results section.

Citing packages

To get a package's citation, run `citation("package")` in the Console with the name of the relevant package in quotes. This will produce the APA-style formatted citation, as well as the BibTex citation (in case you're writing using Quarto or LaTeX, for example).

13.7.2 Results

When reporting your results a combination of tables, figures, and in-text coefficient estimates is always key. In-line descriptions of your results should include the *t*- and *p*-values at minimum. The estimate and standard error (*Est* = ..., *SE* = ...) could also be included in-line, but must at the very least be included in a table. Figures will typically only show the distribution of raw observations and model predictions for fixed effects, and so don't differ much from what we saw in previous chapter.

13.7.2.1 In-line text

An example of what we could write:

Table 13.7: Table of fixed effects from fit_lmm_fp_sj

| Coefficient | $\hat{\beta}$ | SE | t | df | p |
|----------------|---------------|-------|---------|--------|--------|
| Intercept | 5.957 | 0.034 | 176.199 | 59.0 | < .001 |
| Grammticality | 0.003 | 0.014 | 0.251 | 3732.0 | 0.802 |
| Tense | 0.062 | 0.014 | 4.512 | 3732.1 | < .001 |
| gramm1:verb_t1 | -0.016 | 0.028 | -0.571 | 3732.0 | 0.568 |

A main effect of tense was found in first-pass reading times at the verb region ($Est = 0.062$, $t = 4.8$, $p < .001$), with the future tense ($M = 449\text{ms}$, $SD = 266\text{ms}$) eliciting longer first-pass reading times than the past tense.

13.7.2.2 Tables

We should include tables of all fixed effects, as we saw in previous chapters. In addition, a description of random effects is a good idea, but isn't often done in practice.

13.7.2.2.1 Fixed effects

```
tidy(fit_lmm_fp_sj,
      effects = "fixed") |>
  as_tibble() |>
  select(-effect) |>
  mutate(p.value = format_pval(p.value),
         across(c(estimate, std.error, statistic), round, 3),
         df = round(df, 1)) |>
  mutate(term = fct_recode(term,
                           "Intercept" = "(Intercept)",
                           "Tense" = "verb_t1",
                           "Grammticality" = "gramm1",
                           "Tense x Gramm" = "verb_t1:gramm1"
  )) |>
  kable(
    col.names = c("Coefficient", "$\\hat{\\beta}$", "SE", "t", "df", "p")) |>
  kable_styling()
```

13.7.2.2.2 Random effects

Table 13.8: Table of random effects from fit_lmm_fp_sj

| Group | Term | Variance | SD |
|----------|-------------|----------|-------|
| sj | (Intercept) | 0.066 | 0.256 |
| Residual | NA | 0.180 | 0.425 |

```
as.data.frame(VarCorr(fit_lmm_fp_sj),comp=c("Variance","Std.Dev."))
  |>
  as_tibble() |>
  select(-var2) |>
  # mutate(var1 = ifelse(var1 == "NA", " ", var1)) |>
  kable(digits = 3,
        col.names = c("Group", "Term", "Variance", "SD")) |>
  kable_styling()
```

13.7.2.3 Figures

Random effect visualisations aren't typically included in publications, but these can be useful for model exploration and can be included in supplementary materials. When individual differences are of interest, these can also be useful. You can use either the `lattice::dotplot()` function or a combination of `broom.mixed::tidy()` and `ggplot()` that we saw above. I would suggest always starting with `dotplot()` though to make sure that the visualisations you produce have the same values.

13.8 Summary

- we saw that the equation for a straight line boils down to its intercept and slope
- we fit our first linear model with a categorical predictor

Learning Objectives

Today we learned...

- how to model binomial data with logistic regression
- how to interpret log-odds and odds ratio

Important terms

| Term | Definition | Equation/Code |
|------------------------------|------------|---------------|
| linear mixed (effects) model | NA | NA |

Task

Repeat the steps we took here, but on Ö

- regression path duration at the verb region, and
- regressions in at the adverb region (`roi == 2`)

13.8.1 Random-intercepts

Using the same dataset,

13.8.2 Dutch verb regularity

Session Info

Developed with Quarto using R version 4.3.0 (2023-04-21) (Already Tomorrow) and RStudio version 2023.9.0.463 (Desert Sunflower), and the following packages:

```
sessionInfo()
```

```
R version 4.3.0 (2023-04-21)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Ventura 13.2.1
```

```
Matrix products: default
BLAS:    /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
LAPACK:  /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib
```

```
locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: Europe/Berlin
```

```

tzcode source: internal

attached base packages:
[1] stats      graphics   grDevices utils      datasets  methods   base

other attached packages:
[1] gt_0.9.0           googlesheets4_1.1.0 kableExtra_1.3.4
[4] knitr_1.44          patchwork_1.1.3    lattice_0.21-8
[7] broom.mixed_0.2.9.4 lmerTest_3.1-3    lme4_1.1-33
[10] Matrix_1.5-4       sjPlot_2.8.14     ggeffects_1.2.2
[13] janitor_2.2.0      broom_1.0.5      here_1.0.1
[16] lubridate_1.9.2    forcats_1.0.0     stringr_1.5.0
[19] dplyr_1.1.3         purrr_1.0.2      readr_2.1.4
[22] tidyverse_1.3.0     tibble_3.2.1     ggplot2_3.4.3
[25] tidyverse_2.0.0     broman_0.80

loaded via a namespace (and not attached):
[1] sandwich_3.0-2      rlang_1.1.3      magrittr_2.0.3
[4] multcomp_1.4-23     snakecase_0.11.0 furrr_0.3.1
[7] compiler_4.3.0      mgcv_1.8-42     systemfonts_1.0.4
[10] vctrs_0.6.3         rvest_1.0.3      crayon_1.5.2
[13] pkgconfig_2.0.3     fastmap_1.1.1    backports_1.4.1
[16] labeling_0.4.3      utf8_1.2.3      rmarkdown_2.22
[19] tzdb_0.4.0          haven_2.5.2      nloptr_2.0.3
[22] bit_4.0.5           xfun_0.39       jsonlite_1.8.7
[25] sjmisc_2.8.9        parallel_4.3.0   R6_2.5.1
[28] RColorBrewer_1.1-3  stringi_1.7.12   parallelly_1.36.0
[31] boot_1.3-28.1       cellranger_1.1.0 numDeriv_2016.8-1.1
[34] estimability_1.4.1  Rcpp_1.0.11     modelr_0.1.11
[37] zoo_1.8-12          pacman_0.5.1    splines_4.3.0
[40] timechange_0.2.0    tidyselect_1.2.0  rstudioapi_0.14
[43] yaml_2.3.7          codetools_0.2-19 sjlabelled_1.2.0
[46] curl_5.0.1          listenv_0.9.0    plyr_1.8.8
[49] withr_2.5.0         bayestestR_0.13.1 coda_0.19-4
[52] evaluate_0.21        future_1.32.0   survival_3.5-5
[55] xml2_1.3.4          pillar_1.9.0    insight_0.19.3
[58] generics_0.1.3       vroom_1.6.3     rprojroot_2.0.3
[61] hms_1.1.3           munsell_0.5.0   scales_1.2.1
[64] minqa_1.2.5         globals_0.16.2  xtable_1.8-4
[67] glue_1.6.2           emmeans_1.8.6   tools_4.3.0
[70] webshot_0.5.4       fs_1.6.2       mvtnorm_1.2-3
[73] grid_4.3.0           colorspace_2.1-0 nlme_3.1-162
[76] Rmisc_1.5.1          performance_0.10.4 googledrive_2.1.0

```

```
[79] cli_3.6.1          fansi_1.0.4        gargle_1.4.0
[82] viridisLite_0.4.2  svglite_2.1.1      sjstats_0.18.2
[85] gtable_0.3.4       digest_0.6.33      TH.data_1.1-2
[88] farver_2.1.1       htmltools_0.5.5    lifecycle_1.0.3
[91] httr_1.4.6         bit64_4.0.5       MASS_7.3-58.4
```

14 Random slopes

Including varying intercepts and slopes

⚠ Under construction

This chapter is not fully translated from bullet points (from my slides) to prose. This will happen eventually (hopefully by spring 2024).

This chapter covers Chapter 14 'Mixed Models 1: Conceptual Introduction' (from Section 14.8) and Ch 15 (Section 15.4) in Winter (2019), Winter (2014) (from page 16), and Ch. 14 (from Section 8.4) in Sonderegger (2023a). We will be using the data from Biondo et al. (2022).

Learning Objectives

Today we will learn...

- how and why to add random slopes
- how to interpret random slopes

Set-up environment

Our first steps are to set-up our environment. The next two chunks are not necessary, but I use them to set some preferences, such as supressing scientific notation, and establishing a function to nicely format *p*-values.

```
# suppress scientific notation
options(scipen=999)
options(pillar.sigfig = 5)
```

```

library(broman)
# function to format p-values
format_pval <- function(pval){
  dplyr::case_when(
    pval < .001 ~ "< .001",
    pval < .01 ~ "< .01",
    pval < .05 ~ "< .05",
    TRUE ~ broman::myround(pval, 3)
  )
}

```

Load packages

We'll also need to load in our required packages. Hopefully you've already install the required packages (if not, go to [?@sec-software](#)).

```

# load libraries
pacman::p_load(
  tidyverse,
  here,
  broom,
  janitor,
  ggeffects,
  sjPlot,
  # new packages:
  lme4,
  lmerTest,
  broom.mixed,
  lattice)

```

Here I also globally set my preferred `ggplot2` theme so that all of my plots are formatted how I like them, without have to repeat the code for each plot. This is completely optional.

```

# set preferred ggplot2 theme
theme_set(theme_bw() + theme(plot.title = element_text(size = 10)))

```

Here I set the `lmer()` function to be the `lmerTest` version.

```

lmer <- lmerTest::lmer

```

Load data

Now let's load in our dataset from Biondo et al. (2022).

```
df_biondo <-  
  read_csv(here("data", "Biondo.Soilemezidi.Mancini_dataset_ET.csv"),  
            locale = locale(encoding = "Latin1") ## for special characters in Spanish  
            ) |>  
  clean_names() |>  
  mutate(gramm = ifelse(gramm == "0", "ungramm", "gramm")) |>  
  mutate_if(is.character, as_factor) |> # all character variables as factors  
  droplevels() |>  
  filter(adv_type == "Deic")
```

For a reminder of what the variables mean, refer to [?@tbl-data_dictionary](#).

Let's also prepare our data for our models. This means transforming our predictors accordingly. In our case, we want to ensure that `verb_t` and `gramm` are factors with sum contrast coding (`Past` and `gramm = -0.5`), and that our grouping factors (`sj` and `item`) are factors.

```
# sum contrast coding  
df_biondo$verb_t <- as_factor(df_biondo$verb_t)  
contrasts(df_biondo$verb_t) <- c(-0.5,0.5)  
  
df_biondo$gramm <- as_factor(df_biondo$gramm)  
contrasts(df_biondo$gramm) <- c(-0.5,0.5)  
  
# check  
contrasts(df_biondo$verb_t)  
  
[,1]  
Past   -0.5  
Future  0.5  
  
contrasts(df_biondo$gramm)  
  
[,1]  
gramm   -0.5  
ungramm  0.5
```

```
# grouping factors as factors
df_biondo$sj <- as_factor(df_biondo$sj)
df_biondo$item <- as_factor(df_biondo$item)
```

14.1 Review

In the last chapter we learned how to add random intercepts, which represent variance in the intercept value per level of a grouping factor. We include by-participant and by-item varying intercepts, and found that there was more variance by-participants than by-items. This is quite typical. We also saw how to plot the varying intercepts in caterpillar plots.

14.1.1 Model equation: random intercepts

Recall the equation of linear mixed model with varying intercepts (α) for two grouping factors (j and k), given in Equation 14.1.

$$fp_i = \beta_0 + \alpha_{j[i]} + \alpha_{k[i]} + \beta_{verb_t}x + \beta_{gramm}x + e_i \quad (14.1)$$

If we take j to represent participants and k to represent items, then the j in $\alpha_{j[i]}$ has 60 levels (1-60, because we have 60 participants), and k in $\alpha_{j[i]}$ has 96 levels (1-96, because we have 96 items). And i has 3795 levels, because there are 3795 observations in our model (which we will see in a moment). Why then does 3795 not correspond to 60 participant \times 96 items? This is because we have filtered the data to not include trials with *non-deictic* adverbs, which were presented in one third of the items ($n = 32$). So, we actually have 64 observations per each participant in the *deictic* condition. So we should have 60 participants \times 64 items = 3840 observations. Whenever our number of observations is less than we would expect, this will be due to missing observations, which are quite common. Here the missing 45 amounts to a loss of 1.2% of the data, which is not problematic.

My reason for pointing out these values is to highlight the importance of understanding your experimental design and applying it to your model. It's also important to be able to interpret the model summary, including the reported number of observations and grouping levels per grouping factor.

14.2 Random slopes

Let's return to our plots of by-participant and by-item variance.

14.2.1 By-participant varying intercepts and slopes

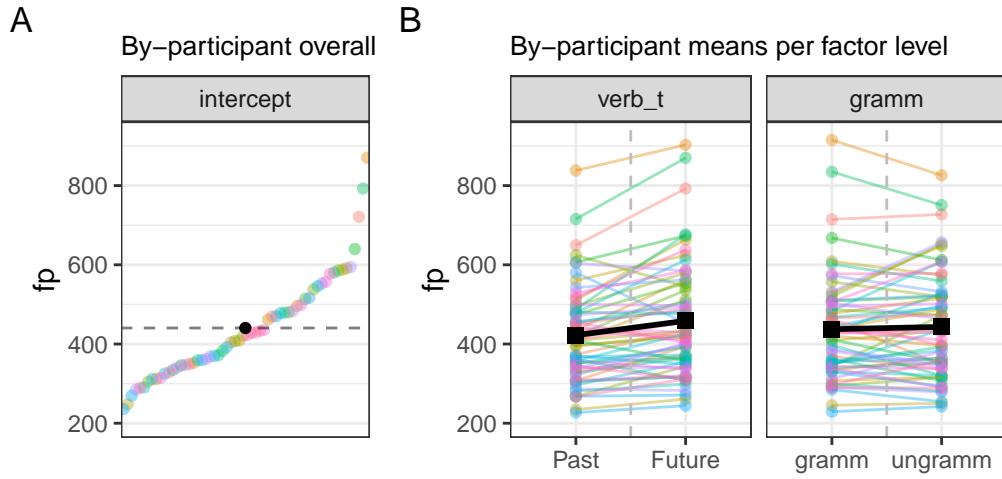


Figure 14.1: Predicted by-participant varying intercepts (A) and slopes (B) with overall effects in black

Let's take a look at a subset of participants and items:

```
fig_biondo_sj_ms <-
  df_biondo |>
  filter(sj %in% c(1,10,2,35,46,57,63)) |>
  mutate(verb_t = factor(verb_t, levels = c("Past", "Future"))) |>
  ggplot() +
  aes(x = verb_t, y = fp,
      colour = verb_t,
      shape = verb_t) +
  facet_wrap("sj", nrow = 1) +
  # Put the points on top of lines
  geom_point(position = position_jitter(0.2),
             alpha = .2) +
  stat_smooth(aes(group = 1), method = "lm") +
  # geom_boxplot(colour = "black", alpha = 0) +
  labs(y = "First-pass RT (ms)",
       x = "Tense") +
  geom_vline(xintercept = 1.5, colour = "grey", linetype = "dashed")+
  theme(legend.position = "none") +
  geom_abline(
    intercept = exp(coef(fit_lm_fp)[1]-(coef(fit_lm_fp)[3]*1.5)) ,
    slope = (exp(coef(fit_lm_fp)[1]+(coef(fit_lm_fp)[3]*0.5)) - exp(coef(fit_lm_fp)[1]+(coef(fit_lm_fp)[3]*1.5))/2)
```

```

    )

fig_biondo_sj_log <-
df_biondo |>
  mutate(verb_t = factor(verb_t, levels = c("Past", "Future"))) |>
  filter(sj %in% c(1,10,2,35,46,57,63)) |>
ggplot() +
  aes(x = verb_t, y = log(fp),
      colour = verb_t,
      shape = verb_t) +
  facet_wrap("sj", nrow = 1) +
# Put the points on top of lines
  geom_point(position = position_jitter(0.2),
             alpha = .2) +
  stat_smooth(aes(group = 1), method = "lm") +
  labs(y = "First-pass RT (log)", x = "Tense") +
  geom_vline(xintercept = 1.5, colour = "grey", linetype = "dashed") +
  theme(legend.position = "none") +
  geom_abline(
    intercept = coef(fit_lm_fp)[1]-(coef(fit_lm_fp)[3]*1.5),
    slope = coef(fit_lm_fp)[3])

```

Here we see that, again, the means (intercepts) for some participants and items are above the population-level mean, some are below, and some are about the same. This should come as no surprise, because a mean is a compromise between all values. Including by-participant and -item varying intercepts takes this variation into account, and quantifies the extent of the variation. This was the standard deviation and variance values we saw in our random effects structures in the last chapter.

The focus of this chapter is on the difference in the slopes, i.e., the magnitude and direction of the effect of our fixed effects. We see in Figure 14.2 that the population-level slope for tense is positive, with longer first-pass reading times for the future versus past condition. We see this is also the case for some participants (e.g., participants 1 and 10), but that some participants have a negative slope (e.g., participants 35 and 63). This is a difference in the direction, or sign (+ or -), of the effect. But there is also a difference in the magnitude, or strength, of the effect: participant 10 seems to have a “steeper” slope than participant 46, who has a somewhat flatter slope (meaning a smaller, or no, difference between the past and future conditions). Let’s see this in action.

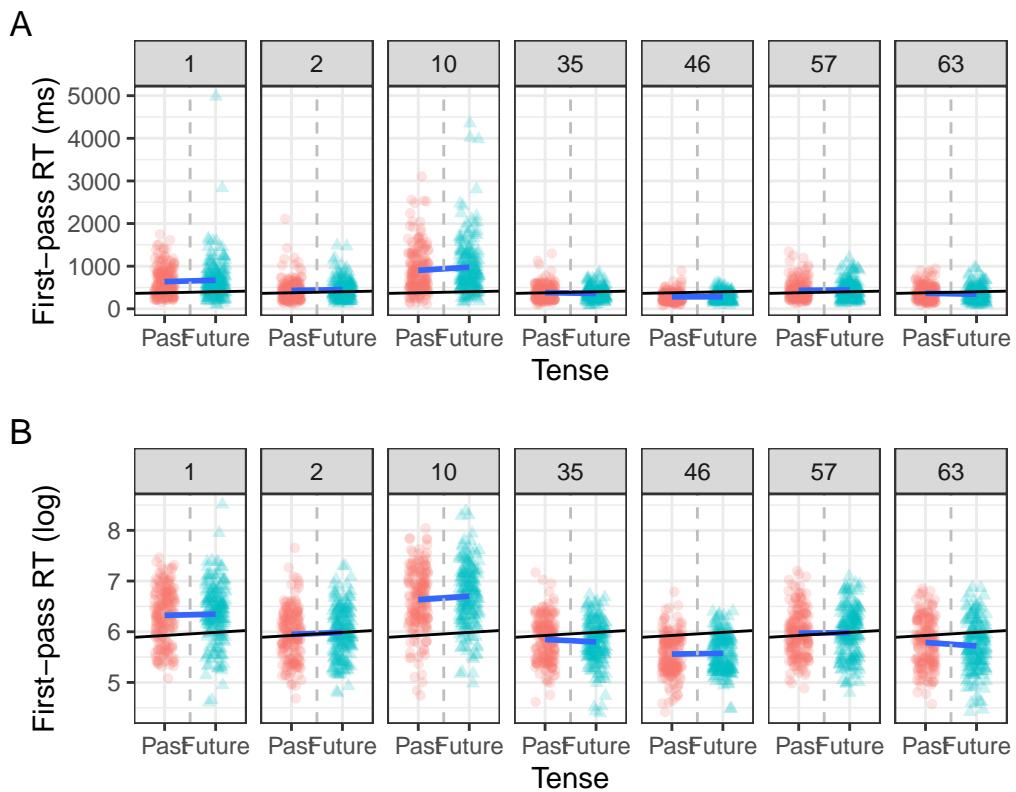


Figure 14.2: Demonstration of by-participant variation in intercept and slope (blue line) versus fixed-effects-only model intercept and slope (black line) for seven example participants. Grey dashed line indicates $x = 0$. Points represent single observations.

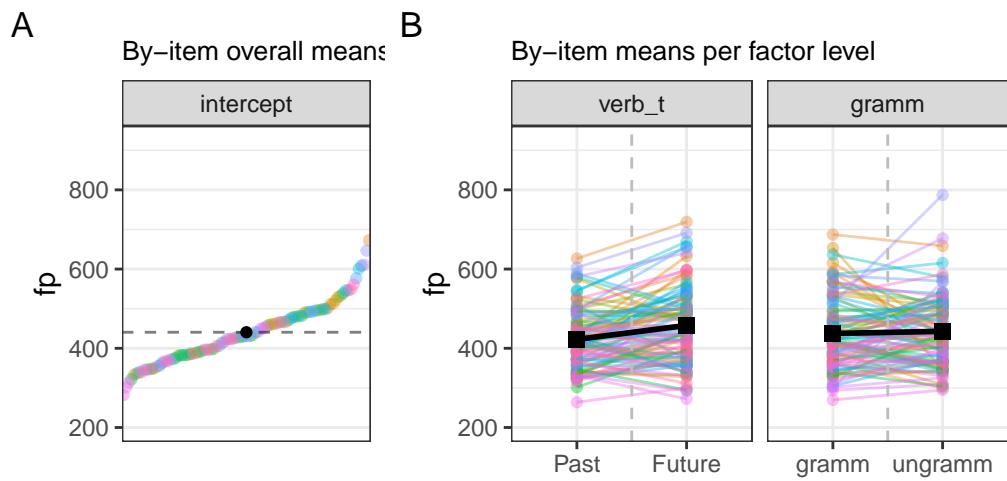


Figure 14.3: By-item varying intercepts (A) and slopes (B) with overall effects in black

14.2.2 By-item varying intercepts and slopes

14.2.3 By-participant random slopes

```
fit_lmm_sj_slope <-
  lmer(log(fp) ~ verb_t +
    (1 + verb_t|sj) +
    (1 + verb_t| item),
  data = df_biondo,
  subset = roi == 4)

summary(fit_lmm_sj_slope)

Linear mixed model fit by REML. t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: log(fp) ~ verb_t + (1 + verb_t | sj) + (1 + verb_t | item)
Data: df_biondo
Subset: roi == 4

REML criterion at convergence: 4202.5

Scaled residuals:
    Min      1Q  Median      3Q     Max
-4.1490 -0.6092 -0.0207  0.6106  4.0719

Random effects:
  Groups   Name        Variance Std.Dev. Corr
  item     (Intercept) 0.0193662 0.13916
            verb_t1     0.0025019 0.05002  0.55
  sj       (Intercept) 0.0664211 0.25772
            verb_t1     0.0003073 0.01753  1.00
  Residual           0.1601193 0.40015
Number of obs: 3795, groups: item, 96; sj, 60

Fixed effects:
            Estimate Std. Error    df t value    Pr(>|t|)
(Intercept) 5.95639   0.03676 79.18686 162.055 < 0.0000000000000002 ***
verb_t1     0.06175   0.01414 91.57724   4.366      0.0000332 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

Correlation of Fixed Effects:
  (Intr)
verb_t1  0.221
optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see help('isSingular')

```

14.2.4 By-item random slopes

Let's not log-transform first-pass reading times just yet.

```

fit_lmm_sj_slope <-
  lmer(fp ~ verb_t*gramm +
    (1 | sj) +
    (1 + verb_t | item),
  data = df_biondo,
  subset = roi == 4)

```

Let's ignore the warning we get for now and take a look at our model summary output.

```
summary(fit_lmm_sj_slope)
```

```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: fp ~ verb_t * gramm + (1 | sj) + (1 + verb_t | item)
Data: df_biondo
Subset: roi == 4

```

REML criterion at convergence: 51655.4

Scaled residuals:

| Min | 1Q | Median | 3Q | Max |
|---------|---------|---------|--------|---------|
| -3.0458 | -0.5638 | -0.1308 | 0.3505 | 10.0116 |

Random effects:

| Groups | Name | Variance | Std.Dev. | Corr |
|----------|-------------|----------|----------|------|
| item | (Intercept) | 4968.7 | 70.49 | |
| | verb_t1 | 303.1 | 17.41 | 1.00 |
| sj | (Intercept) | 16187.1 | 127.23 | |
| Residual | | 43834.3 | 209.37 | |

Number of obs: 3795, groups: item, 96; sj, 60

```

Fixed effects:
            Estimate Std. Error      df t value      Pr(>|t|)
(Intercept) 440.069    18.251   80.092 24.112 < 0.0000000000000002 ***
verb_t1      35.937     7.027   546.900   5.114      0.000000437 ***
gramm1       5.675     6.799  3637.459   0.835      0.404
verb_t1:gramm1 -7.192    13.597  3637.376  -0.529      0.597
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
          (Intr) verb_t1 gramm1
verb_t1    0.100
gramm1     0.000 -0.002
vrb_t1:grm1 0.000  0.002  0.000
optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see help('isSingular')

```

The main difference to our random-intercepts-only models is the addition of random slope for `verb_t` under `Name` and a `Correlation` terms in our random effects. We refer to this as the variance-covariance matrix. Let's first focus on the by-item varying slope. We again see that we have `Variance` and `Std.Dev.` values. Recall that standard deviation is just the square root of variance, and that the standard deviation in particular can be used to conclude the range within which our by-item varying slopes will fall into using the 68% and 95% rule, assuming a perfect normal distribution (which we almost certainly don't have because we haven't logged our dependent variable). Our population-level tense slope is approximately 35.9ms, so 68% of the by-item varying slopes for tense should be 35.9 ± 30 , meaning 5.9 and 65.9, and 95% falls between $35.9 \pm 30 \times 2$ (more specifically 1.96, but we round up to 2), meaning -24.1 and 95.9. If we look at Figure 14.4, we see this isn't quite true. The red lines show the true range of the middle 95% of the data (the red area between Q2.5 () and Q97.5) and the middle 68% of the data (the blue area between Q16 and Q84).

```

item_verb <- coef(fit_lmm_sj_slope) |>
  pluck("item") |>
  rownames_to_column(var = "item") |>
  rename(intercept = `"(Intercept)``)

# set quantiles
q5 <- quantile(item_verb$verb_t1,.025)
q95 <- quantile(item_verb$verb_t1,.975)
q16 <- quantile(item_verb$verb_t1,.16)
q84 <- quantile(item_verb$verb_t1,.84)

```

```

x.dens <- density(item_verb$verb_t1)
df.dens <- data.frame(x = x.dens$x, y = x.dens$y)

# plot

fig_res_density <-
  item_verb |>
  ggplot() +
  aes(x = verb_t1) +
  labs(title = "By-item varying slopes (verb_t) density",
       x = "Intercept",
       y = "Density") +
  geom_density() +
  geom_area(data = subset(df.dens, x >= q5 & x <= q95),
            aes(x=x,y=y), fill = 'red',
            alpha = .4) +
  geom_area(data = subset(df.dens, x >= q16 & x <= q84),
            aes(x=x,y=y), fill = 'blue',
            alpha = .4) +
  geom_vline(colour = "black",
             linetype = "dashed",
             aes(xintercept = fixef(fit_lmm_sj_slope)[2])) +
  geom_vline(colour = "blue",
             linetype = "dashed",
             aes(xintercept = q16)) +
  geom_vline(colour = "blue",
             linetype = "dashed",
             aes(xintercept = q84)) +
  geom_vline(colour = "red",
             linetype = "dashed",
             aes(xintercept = q5)) +
  # add labels
  geom_text(label = "Q2.5",
            x = q5, y = 0.02, angle = 90,
            vjust = -.35,
            colour = "red") +
  geom_vline(colour = "red",
             linetype = "dashed",
             aes(xintercept = q95)) +
  geom_text(label = "Q97.5",
            x = q95, y = 0.02,

```

```

        colour = "red", angle = 90,
        vjust = -.35) +
geom_text(label = "Q16",
  x = q16, y = 0.02,
  colour = "blue", angle = 90,
  vjust = -.35) +
geom_text(label = "Q84",
  x = q84, y = 0.02,
  colour = "blue", angle = 90,
  vjust = -.35) +
geom_text(aes(x = mean(verb_t1)), y = 0.02, label = "verb_t", angle = 90,
  vjust = -.35)

```

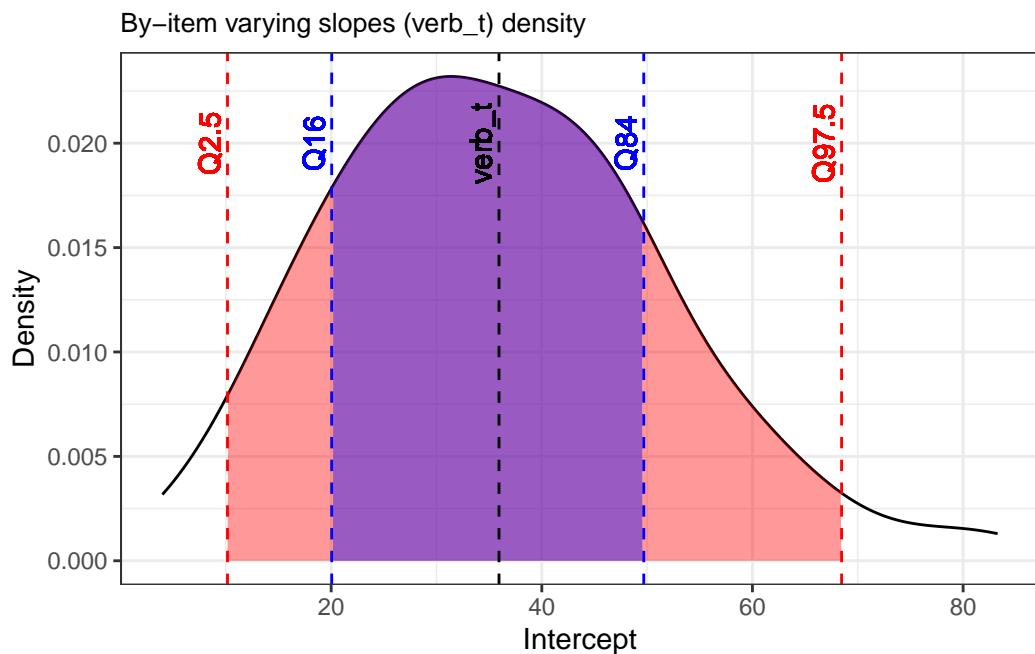


Figure 14.4: Density plot of by-item varying slopes for tense with 95% (+/-SD*1.96, red) and 68% (+/-SD, blue) ranges around the population-level slope (black ‘verb_t’ line)

```

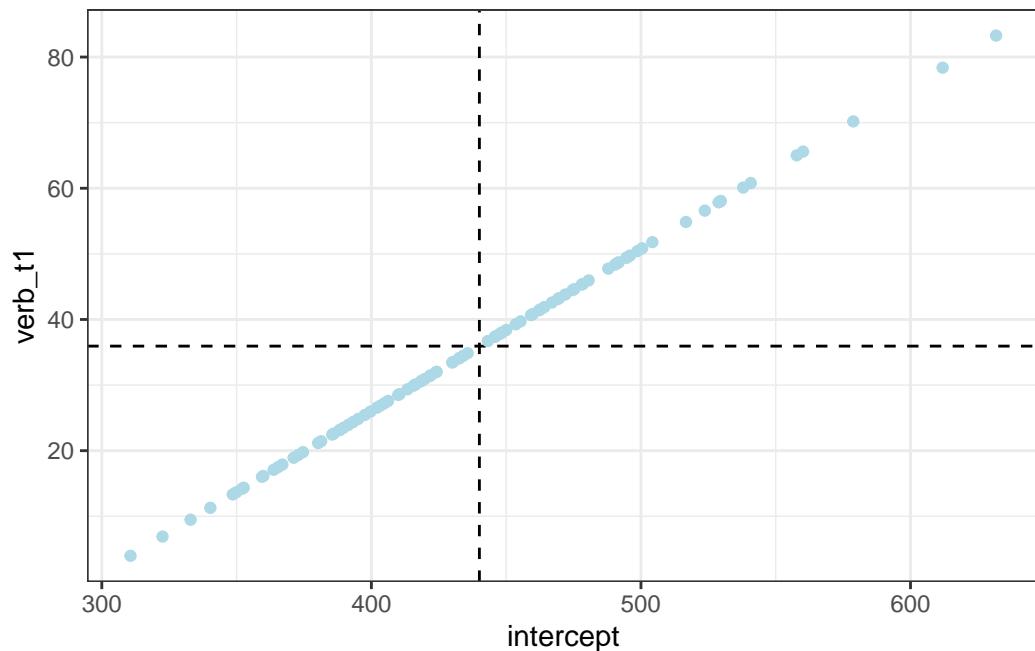
item_verb |>
  ggplot() +
  aes(x = intercept, y = verb_t1) +
  geom_vline(colour = "black",
    linetype = "dashed",
    aes(xintercept = fixef(fit_lmm_sj_slope)[1])) +

```

```

geom_hline(colour = "black",
           linetype = "dashed",
           aes(yintercept = fixef(fit_lmm_sj_slope)[2])) +
geom_point(colour = "lightblue")

```



```

# pop-level

pop_level <-
  tibble(
    intercept = fixef(fit_lmm_sj_slope)[1],
    verb_t1 = fixef(fit_lmm_sj_slope)[2],
    item = "200",
    past = intercept + verb_t1 * -.5,
    future = intercept + verb_t1 * .5
  ) |> pivot_longer(
    cols = c(past, future),
    names_to = "tense",
    values_to = "time"
  )

fig_item_verb <-
  item_verb %>%

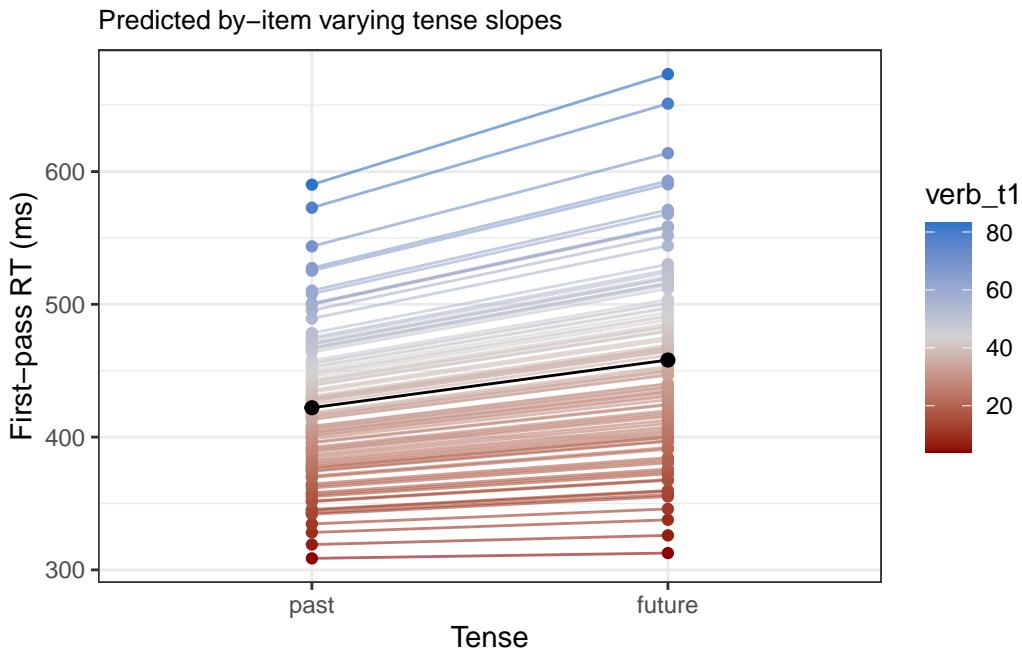
```

```

arrange(verb_t1) |> # arrange in ascending order of slope
# slice(which(row_number() %% 12 == 1)) |> # take every 12th participant
mutate(past = intercept + (verb_t1*-0.5),
       future = intercept + (verb_t1*0.5),
       dev = verb_t1 - fixef(fit_lmm_sj_slope)[2]) |>
pivot_longer(
  cols = c(past, future),
  names_to = "tense",
  values_to = "time"
) |>
mutate(tense = factor(tense, levels = c("past", "future"))) |>
ggplot() +
  aes(x = tense, y = time,
      colour = verb_t1) +
  labs(title = "Predicted by-item varying tense slopes",
       x = "Tense",
       y = "First-pass RT (ms)") +
# facet_wrap(~item, nrow = 2) +
  geom_point() +
  geom_line(aes(group = item),
            alpha = .6) +
  scale_colour_gradientn(colours = c("darkred", "lightgrey", "#2C74C9")) +
  geom_point(data = pop_level, colour = "black", size = 2) +
  geom_line(data = pop_level, colour = "black", group = 1)

```

`fig_item_verb`



Going back to the variance-covariance matrix, each value tells in the first row tells use the correlation between the relevant parameter (e.g, by-item `verb_t` slopes) with the by-participant intercept. We see that `verb_t1` has a correlation of 1.00 with the intercepts (this is a sign of a problem, which we'll come back to later), `adv_type1` has a correlation of .23, and the interaction of `verb_t:adv_type` has a correlation of -0.48. What do these values mean? Firstly,

We get a warning: `boundary (singular) fit: see help('isSingular')`. This tells us that our model is “overfit”, i.e., all variance-covariance terms cannot be estimated. To inspect our variance-covariance matrix, we can run:

```
VarCorr(fit_lmm_sj_slope)
```

| Groups | Name | Std.Dev. | Corr |
|----------|-------------|----------|-------|
| item | (Intercept) | 70.489 | 1.000 |
| | verb_t1 | 17.409 | |
| sj | (Intercept) | 127.229 | |
| Residual | | 209.366 | |

14.3 Mixed model with varying slopes

```
fit_lmm_sj_slope <-
  lmer(log(fp) ~ verb_t*gramm +
    (1 | sj) +
    (1 + verb_t + gramm| item),
  data = df_biondo,
  subset = adv_type == "Deic" & roi == 4)

summary(fit_lmm_sj_slope)

Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: log(fp) ~ verb_t * gramm + (1 | sj) + (1 + verb_t + gramm | item)
Data: df_biondo
Subset: adv_type == "Deic" & roi == 4

REML criterion at convergence: 4215.4

Scaled residuals:
    Min      1Q  Median      3Q     Max
-4.1677 -0.6069 -0.0211  0.6064  4.0416

Random effects:
Groups   Name        Variance Std.Dev. Corr
item     (Intercept) 0.0194226 0.13937
          verb_t1     0.0031136 0.05580  0.49
          gramm1      0.0004218 0.02054 -0.10 -0.92
sj       (Intercept) 0.0663835 0.25765
Residual           0.1599961 0.40000
Number of obs: 3795, groups: item, 96; sj, 60

Fixed effects:
            Estimate Std. Error      df t value Pr(>|t|)
(Intercept) 5.956396  0.036755 79.245291 162.059 < 0.0000000000000002
verb_t1     0.061692  0.014183 107.904449   4.350  0.000031
gramm1      0.003348  0.013157 558.238407   0.254  0.799
verb_t1:gramm1 -0.014422  0.025978 3546.179061  -0.555  0.579

(Intercept) ***
verb_t1      ***
```

```

gramm1
verb_t1:gramm1
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) verb_t1 gramm1
verb_t1      0.075
gramm1     -0.006 -0.061
verb_t1:grm1 0.000  0.002  0.000
optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see help('isSingular')

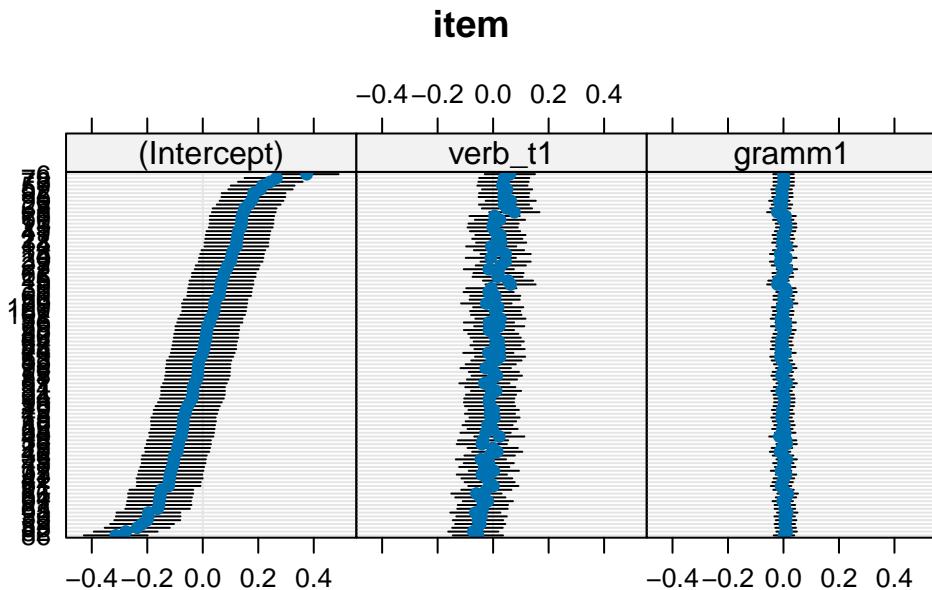
```

```

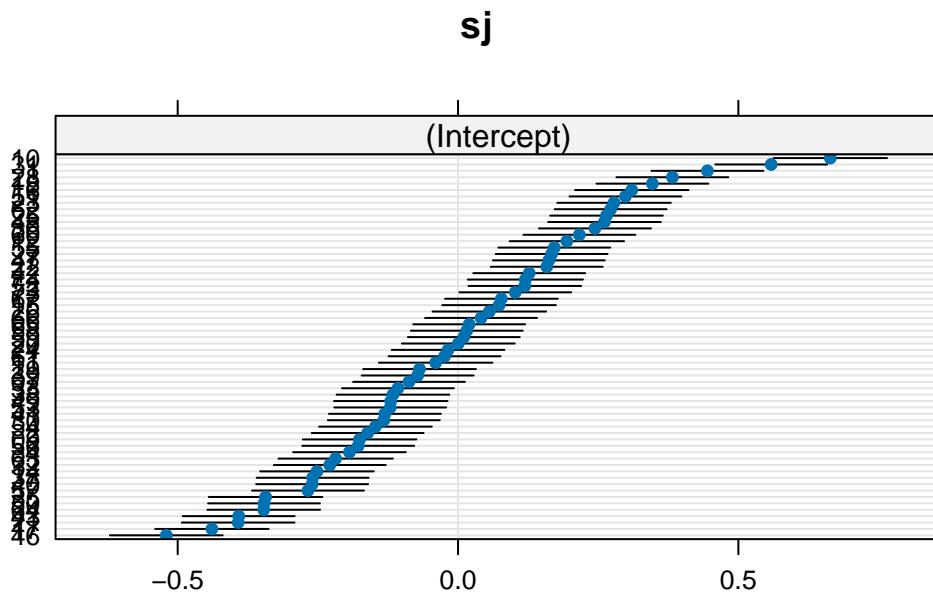
lattice::dotplot(ranef(fit_lmm_sj_slope))

```

\$item



\$sj



What do we mean with “less explanatory power”? Well, if we plot our random effects, we can see that more variance seems to be explained by verb tense: the range of values is larger (the ‘caterpillar’ is on more of an angle) and the confidence intervals (horizontal black bars which represent a measure uncertainty) are wider. This tells us that `verb_t` slopes seem to have more by-participant variance than `gramm` does.

15 Review

15.1 Fixed-effects only models

- do not include any grouping factors
 - can be dangerously unconservative if violating independence assumption

15.1.1 Fixed-effects only equation

$$fp_i = \beta_0 + \beta_{verb_t}x_i + \beta_{gramm}x_i + e_i \quad (15.1)$$

- Equation 15.1 shows the equation for such a model using first-pass reading times as a function of verb tense (`verb_t`) and grammaticality (`gramm`)
 - where i represents an observation ($i = 1:N$)
 - β_0 = intercept value
 - $\beta_{verb_t}x$ = tense slope multiplied by the corresponding level (+/- 0.5)
 - $\beta_{gramm}x$ = grammaticality slope multiplied by the corresponding level (+/- 0.5)
 - e_i = residual error for this observation

15.2 Random intercepts only models

- random intercepts: varying intercepts per e.g., participant
 - intercept = mean when your predictor is centred (continuous) or sum contrast coded (categorical)
- explains some additional variance (i.e., should reduce our residual error)

15.2.1 Random intercepts model equation

- Equation 15.2 includes two additional terms:
 - $\alpha_{j[i]}$ = random intercept (α) for some grouping factor j
 - * e.g., participants, where $i = 1 : 60$
 - $\alpha_{k[i]}$ = random intercept (α) for some grouping factor k
 - * e.g., items, where $i = 1 : 96$

$$fp_i = \beta_0 + \alpha_{j[i]} + \alpha_{k[i]} + \beta_{verb_t}x_i + \beta_{gramm}x_i + e_i \quad (15.2)$$

- $\alpha_{j[16]}$ = random intercept for participant 16
- $\alpha_{j[7]}$ = random intercept for item 1

15.3

💡 Missing values and subsetting conditions

N.B., because we subsetted the data to include only `adv_type == "Deic"`, each participant did not contribute 96 data points to our current dataset, but 64.

So, our overall N observations should be $64*60$, minus however many missing observations we have + so i in fp_i has a value of 1:3840, minus missing values.

We can use the `nobs()` function to find out the number of observations in a model. For example our random-intercepts only model from the last class had 3795 observations, meaning we had $3840 - 3795 = 45$ missing observations. This amounts to 1.17% of trials, which is fine (something around 5% of trials is not out of the ordinary).

```
nobs(fit_fp_1)
```

```
[1] 3795
```

Why do we have missing values? This can depend on a lot of things, such as incorrect attention-check responses (not relevant for this data), measurement error, or pre-processing steps (likely the cause for this data, which is eye-tracking during reading).

15.3.1 Interpreting random effects

- how can we interpret this output from a model, without knowing anything else about the model?

| Groups | Name | Std.Dev. |
|----------|-------------|----------|
| Word | (Intercept) | 38.201 |
| Subject | (Intercept) | 91.004 |
| Residual | | 127.258 |

15.3.2 Formulating a model

- can you formulate a model based on this output in the `lmer()` syntax?
 - let's call the dependent variable `rt` for reaction time

| Groups | Name | Std.Dev. |
|----------|-------------|----------|
| Word | (Intercept) | 38.201 |
| Subject | (Intercept) | 91.004 |
| Residual | | 127.258 |

| | Estimate | Std. Error | t value |
|-----------------|----------|------------|-----------|
| (Intercept) | 619.6160 | 20.761039 | 29.845135 |
| NativeLanguage1 | 106.2954 | 40.622552 | 2.616659 |
| freq_c | -29.4397 | 4.168753 | -7.061990 |

15.3.3 Interpreting random effects

| Groups | Name | Std.Dev. |
|----------|-------------|----------|
| Word | (Intercept) | 38.201 |
| Subject | (Intercept) | 91.004 |
| Residual | | 127.258 |

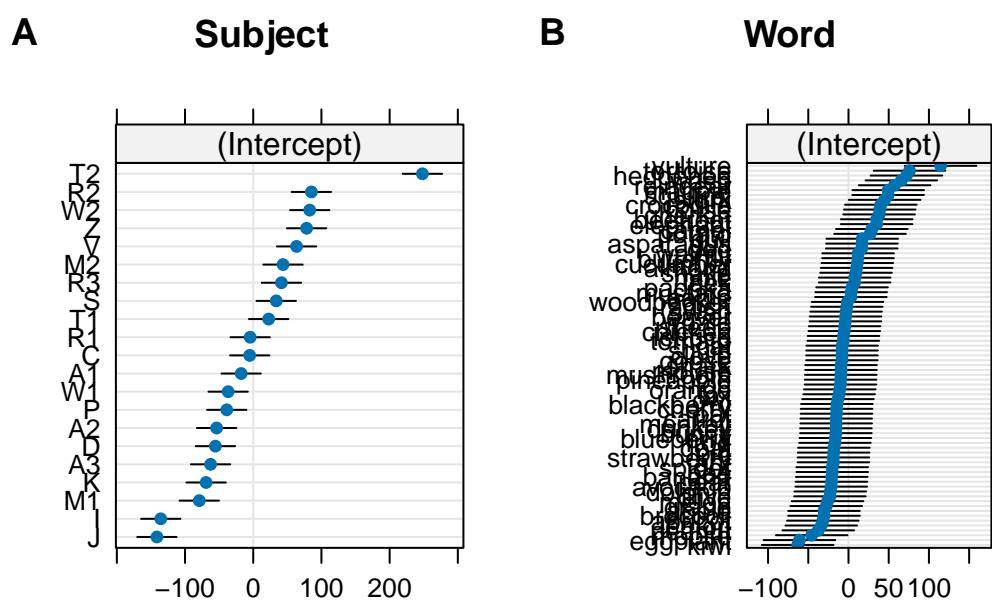


Figure 15.1: lattice::dotplot(ranef(model))

16 Random slopes

- random slopes: varying slopes
 - allows for different magnitude/sign of effects per e.g., participant
- recall that our model still produces by-participant and -item slopes
 - but they don't *vary*

```
fixef(fit_fp_1)
```

```
(Intercept)      verb_t1      gramm1 verb_t1:gramm1
5.95640363     0.06189237    0.00321152   -0.01431578
```

```
coef(fit_fp_1)$item |>
  rownames_to_column(var = "item") |>
  head()
```

```
item (Intercept)      verb_t1      gramm1 verb_t1:gramm1
1     1     6.022184 0.06189237 0.00321152   -0.01431578
2     2     5.761268 0.06189237 0.00321152   -0.01431578
3     3     5.854873 0.06189237 0.00321152   -0.01431578
4     4     6.056862 0.06189237 0.00321152   -0.01431578
5     5     6.138213 0.06189237 0.00321152   -0.01431578
6     6     6.331058 0.06189237 0.00321152   -0.01431578
```

16.1 A short history of varying slopes

A lot of people construct random intercept-only models but conceptually, it makes hella sense to include random slopes most of the time. After all, you can almost always expect that people differ with how they react to an experimental manipulation!

— Winter (2014), p. 17

- after Baayen et al. (2008), linguists who adopted mixed models typically used random-intercepts only models
 - but these have been shown time and again to drastically inflate Type I error rate (false positive) (e.g., Barr et al., 2013b)
 - Barr et al. (2013b) began the credo “keep it maximal”, meaning include all random slopes justified by your design and existing theories
 - let’s focus on adding just one varying slope for now

16.2 Random intercepts and slopes equation

- Equation 16.1 gives an example of a model with by-participant varying slopes for grammaticality

$$fp_i = \beta_0 + \alpha_{j[i]} + \alpha_{k[i]} + \beta_{verb_t}x_i + (\beta_{gramm} + \gamma_{j[i]})x_i + e_i \quad (16.1)$$

- we’ve changed $\beta_{grammt}x_i$ to $(\beta_{grammt} + \gamma_j[i])x_i$
 - where $\gamma_j[i]$ is our by-participant varying slope for gramm for participant i
- imagine observation 163 comes from participant (j) 6, item (k) 38, which is a Future-grammatical condition
 - how could we plug these into the equation?

16.2.1 Visualising varying intercepts and slopes

16.3 Comparing participant and item effects

- we’ve already noted that there’s more variation between participants in the overall first-pass reading times
 - some tend to have higher, others lower, reading times
 - this is taken into consideration with the by-participant and -item varying intercepts
 - and we saw in our random effects parameters that the standard deviation for participant intercepts was larger
- today we will focus on varying slopes
 - there seems to be comparable inter-group slope variation in both participants and items

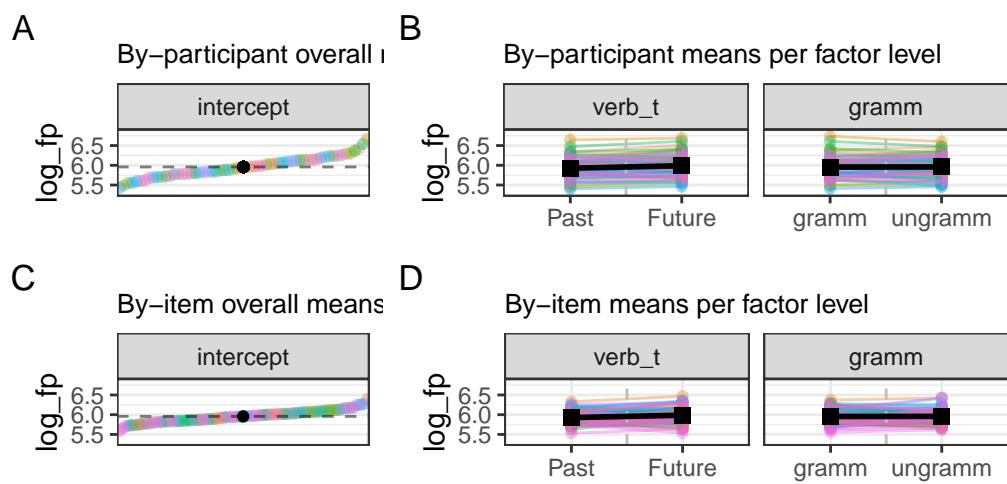


Figure 16.1: Mean effects by-participant overall (A) and per condition (B) with population-level effects in black, with the same plots by-item (C and D)

17 Random intercepts and slopes model

- random slopes = taking group-level variance in effect direction/magnitude into account
 - i.e., some participants might have a stronger effect, weaker effect, or effect in the opposite direction compared to the population-level

17.1 Disclaimer!!!

⚠ Model building

Today we are *exploring* the random effects of our model by adding and subtracting random slopes to ‘see what happens’. You typically would NOT do this!

Generally, you would start with a pre-defined random effects structure justified by your experimental design and theory (your “maximal” model (Barr et al., 2013b)). We will get into model selection in the next (and last) session. Today we will be adding and removing varying slopes willy-nilly, which can amount to p-hacking, data dredging, or HARKing (Hypothesisng After the Results are Known).

17.2 Random intercept-only model

- recall our random intercept-only model

```
fit_fp_1 <-  
  lmer(log(fp) ~ verb_t*gramm +  
        (1 |sj) +  
        (1|item),  
        data = df_biondo,  
        subset = roi == 4)
```

- and inspect the random effects parameters

```
# an alternative to VarCorr(fit_fp_1):  
summary(fit_fp_1)$varcor
```

| Groups | Name | Std.Dev. |
|----------|-------------|----------|
| item | (Intercept) | 0.13929 |
| sj | (Intercept) | 0.25795 |
| Residual | | 0.40111 |

- what does this tell us?

17.3 Adding a slope

- let's look at by-item varying slopes for tense to start

```
fit_fp_item <-  
  lmerTest::lmer(log(fp) ~ verb_t*gramm +  
    (1 | sj) +  
    (1 + verb_t | item),  
    data = df_biondo,  
    subset = roi == 4)
```

- we've just added + gramm to (1|sj)
 - this reads as “*fit varying intercepts (1) per participant (|sj)...*”
 - “...and by-item varying intercepts (1) and tense slopes (+ verb_t) per item (|item) ”

17.4 summary()

```
summary(fit_fp_item)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
lmerModLmerTest]  
Formula: log(fp) ~ verb_t * gramm + (1 | sj) + (1 + verb_t | item)  
Data: df_biondo  
Subset: roi == 4  
  
REML criterion at convergence: 4216.2
```

```

Scaled residuals:
    Min     1Q Median     3Q    Max
-4.1758 -0.6096 -0.0227  0.6060  4.0568

Random effects:
Groups   Name        Variance Std.Dev. Corr
item     (Intercept) 0.019424 0.13937
          verb_t1      0.002513 0.05012  0.54
sj       (Intercept) 0.066414 0.25771
Residual           0.160252 0.40032
Number of obs: 3795, groups: item, 96; sj, 60

Fixed effects:
            Estimate Std. Error      df t value Pr(>|t|)
(Intercept) 5.956384  0.036763 79.249351 162.023 < 0.0000000000000002
verb_t1     0.061733  0.013970 93.398427   4.419  0.0000267
gramm1      0.003298  0.012999 3544.431926   0.254  0.80
verb_t1:gramm1 -0.014380  0.025998 3544.742546  -0.553  0.58

(Intercept) ***
verb_t1      ***
gramm1
verb_t1:gramm1
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
  (Intr) verb_t1 gramm1
verb_t1  0.077
gramm1   0.000 -0.002
vrb_t1:grm1 0.000  0.002  0.000

```

17.5 Fixed effects

Random intercept only

```

round(
  summary(fit_fp_1)$coefficients,
  5)

```

| | Estimate | Std. Error | df | t value | Pr(> t) |
|----------------|----------|------------|------------|-----------|----------|
| (Intercept) | 5.95640 | 0.03679 | 79.20081 | 161.90252 | 0.00000 |
| verb_t1 | 0.06189 | 0.01303 | 3637.13315 | 4.75172 | 0.00000 |
| gramm1 | 0.00321 | 0.01302 | 3637.18338 | 0.24657 | 0.80526 |
| verb_t1:gramm1 | -0.01432 | 0.02605 | 3637.10235 | -0.54956 | 0.58265 |

Random intercept and slope

```
round(
  summary(fit_fp_item)$coefficients,
  5)
```

| | Estimate | Std. Error | df | t value | Pr(> t) |
|----------------|----------|------------|------------|-----------|----------|
| (Intercept) | 5.95638 | 0.03676 | 79.24935 | 162.02259 | 0.00000 |
| verb_t1 | 0.06173 | 0.01397 | 93.39843 | 4.41890 | 0.00003 |
| gramm1 | 0.00330 | 0.01300 | 3544.43193 | 0.25367 | 0.79977 |
| verb_t1:gramm1 | -0.01438 | 0.02600 | 3544.74255 | -0.55312 | 0.58021 |

- the uncertainty around the effect of tense in `fit_fp_item` has changed
 - slightly larger standard error
 - much fewer degrees of freedom
 - slightly smaller t-value value
 - slightly larger larger p-value

17.6 Random effects

```
summary(fit_fp_1)$varcor # or VarCorr(fit_fp_1)
```

| Groups | Name | Std.Dev. |
|----------|-------------|----------|
| item | (Intercept) | 0.13929 |
| sj | (Intercept) | 0.25795 |
| Residual | | 0.40111 |

```
summary(fit_fp_item)$varcor
```

| Groups | Name | Std.Dev. | Corr |
|--------|-------------|----------|------|
| item | (Intercept) | 0.139371 | |

```

verb_t1      0.050125 0.542
sj          (Intercept) 0.257710
Residual           0.400315

```

- variance components are qualitatively unchanged
- residual error is slightly lower
- but we have a new row under the `item` group: `verb_t1`
 - we see the standard deviation of by-participant varying slopes by tense (0.05)
 - and we see a new columns: `Corr`

17.6.1 Correlation parameter

- this is now what we call a variance-covariance matrix
 - but we only have one correlation term, that of by-item intercepts with by-item tense slopes
 - their correlation is 0.54
 - * this is a positive correlation, meaning the *higher* a participant's intercept (overall first-pass reading times), the stronger the effect of tense

17.6.2 Plotting

- to make life simple, let's use `lattice::dotplot()`: what do these plots tell us?

```

fig_item <- lattice::dotplot(ranef(fit_fp_item))$item
fig_sj <- lattice::dotplot(ranef(fit_fp_item))$sj

cowplot::plot_grid(fig_item, fig_sj, rel_widths = c(2,1), labels = c("A", "B"))

```

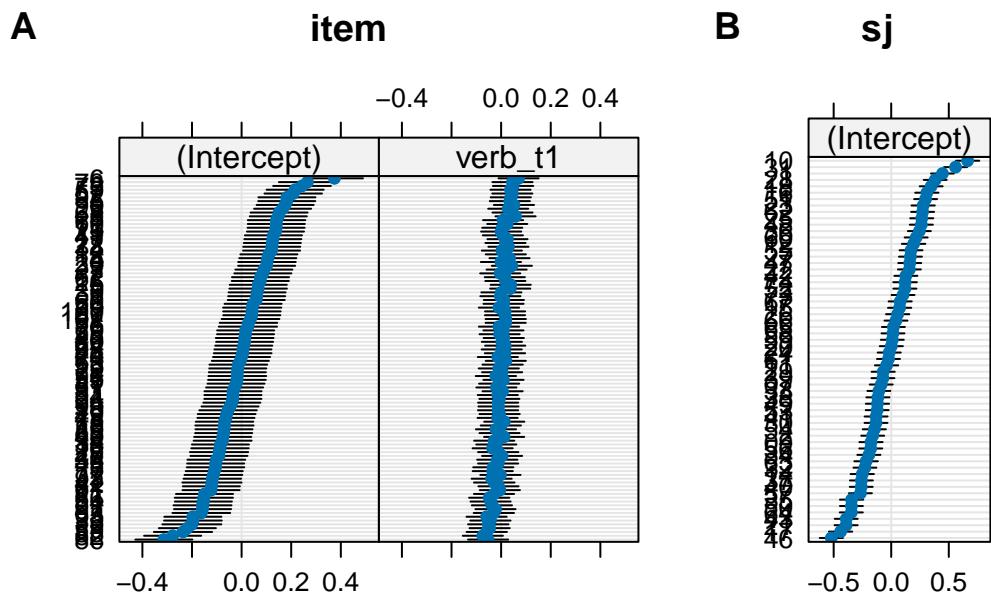


Figure 17.1: By-item varying intercepts and slopes (A), by-participant varying intercepts (B)

17.7 Correlation parameter

- we can plot this relationship by extracting the intercept and slope values with `coef()`
 - or `raneef` to get their deviances from the population-level intercept/slope

```
coef(fit_fp_item)$item |>
  rownames_to_column(var = "item") |>
  rename(intercept = `"(Intercept)"`) |>
  # head()
  ggplot() +
  aes(x = verb_t1, y = intercept) +
  geom_point() +
  labs(
    title = "Correlation of slopes and intercepts"
  )
```

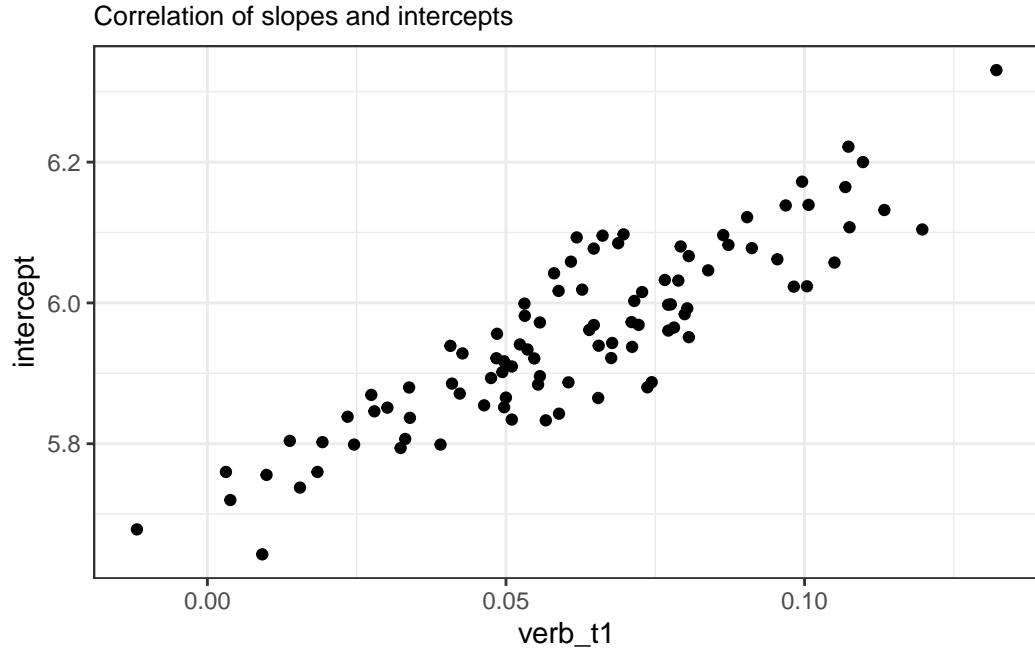


Figure 17.2: Correlation of by-participant gramm1 slopes (x-axis) and intercepts (y-axis)

- participants with higher intercepts had a stronger effect of grammaticality
 - with most participants estimated to have a positive effect

17.8 Model comparison

- does including by-participant slopes for adverb type improve our model fit?

```
anova(fit_fp_1, fit_fp_item)
```

```
Data: df_biondo
Subset: roi == 4
Models:
fit_fp_1: log(fp) ~ verb_t * gramm + (1 | sj) + (1 | item)
fit_fp_item: log(fp) ~ verb_t * gramm + (1 | sj) + (1 + verb_t | item)
npar   AIC   BIC  logLik deviance Chisq Df Pr(>Chisq)
fit_fp_1     7 4210.3 4254.0 -2098.2    4196.3
fit_fp_item  9 4210.4 4266.5 -2096.2    4192.4 3.9796  2      0.1367
```

- not really

- log likelihood is slightly higher (“smaller” negative number) for `fit_fp_item`
- but $p > 0.05$
- recall from our plots that there seemed to be by-participant variance in the slopes
 - what if we add by-participant slopes?

18 Adding another slope

- here we've added + verb_t to (1|sj)

```
fit_fp_sj_item <-
  lmerTest::lmer(log(fp) ~ verb_t*gramm +
    (1 + verb_t|sj) +
    (1 + verb_t|item),
    data = df_biondo,
    subset = roi == 4)
```

boundary (singular) fit: see `help('isSingular')`

- and we get a message about singular fit

18.1 Singular fit

- boundary (singular) fit: see `help('isSingular')`
 - follow this advice: run `help('isSingular')` in the Console and see what you find
- you should *never* ignore such messages, nor report models with singular fit or convergence warnings!
 - let's explore the model to see what went wrong

18.2 Fixed effects

```
round(
  summary(fit_fp_item)$coefficients,
  5)
```

| | Estimate | Std. Error | df | t value | Pr(> t) |
|----------------|----------|------------|------------|-----------|----------|
| (Intercept) | 5.95638 | 0.03676 | 79.24935 | 162.02259 | 0.00000 |
| verb_t1 | 0.06173 | 0.01397 | 93.39843 | 4.41890 | 0.00003 |
| gramm1 | 0.00330 | 0.01300 | 3544.43193 | 0.25367 | 0.79977 |
| verb_t1:gramm1 | -0.01438 | 0.02600 | 3544.74255 | -0.55312 | 0.58021 |

```
round(
  summary(fit_fp_sj_item)$coefficients,
  5)
```

| | Estimate | Std. Error | df | t value | Pr(> t) |
|----------------|----------|------------|------------|-----------|----------|
| (Intercept) | 5.95641 | 0.03676 | 79.17933 | 162.05485 | 0.00000 |
| verb_t1 | 0.06173 | 0.01415 | 91.56777 | 4.36365 | 0.00003 |
| gramm1 | 0.00329 | 0.01300 | 3544.45970 | 0.25349 | 0.79990 |
| verb_t1:gramm1 | -0.01434 | 0.02599 | 3544.77121 | -0.55150 | 0.58133 |

- we see again that the effect of tense is slightly changed, with an increase in the uncertainty around the effect

18.3 Random effects

```
summary(fit_fp_item)$varcor # or VarCorr(fit_fp_1)
```

| Groups | Name | Std.Dev. | Corr |
|----------|-------------|----------|-------|
| item | (Intercept) | 0.139371 | |
| | verb_t1 | 0.050125 | 0.542 |
| sj | (Intercept) | 0.257710 | |
| Residual | | 0.400315 | |

```
summary(fit_fp_sj_item)$varcor
```

| Groups | Name | Std.Dev. | Corr |
|----------|-------------|----------|-------|
| item | (Intercept) | 0.139147 | |
| | verb_t1 | 0.050010 | 0.549 |
| sj | (Intercept) | 0.257726 | |
| | verb_t1 | 0.017519 | 1.000 |
| Residual | | 0.400240 | |

- we see that by-participant tense has a comparatively smaller variance than the other terms
 - and the correlation with by-item intercepts is 1
 - this is a red flag: 1 or -1 correlation terms are an indication of convergence failure

18.3.1 Plotting

- in Figure 18.1 we see by-participant varying tense slopes
 - but the confidence intervals are tiny and hard to see
 - and they constantly increase
 - this is because of the erroneous perfect correlation between them and the intercepts

```
fig_item <- lattice::dotplot(ranef(fit_fp_sj_item))$item
fig_sj <- lattice::dotplot(ranef(fit_fp_sj_item))$sj

cowplot::plot_grid(fig_item, fig_sj, labels = c("A", "B"))
```

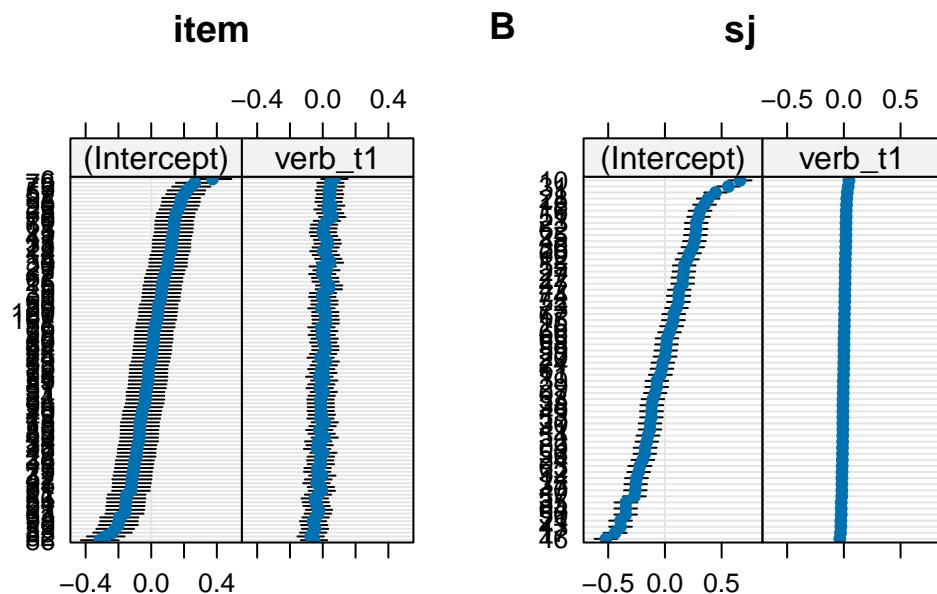


Figure 18.1: By-item (A) and by-participant (B) varying intercepts and slopes

18.4 Convergence warnings

- convergence warnings should not be ignored

- they are a sign that a reliable line fit could not be found (this is an oversimplification...)
- there can be many reasons for this:
 - * impossible random effects structure (e.g., adding slopes that don't make sense)
 - * sparse data
 - * overfitting
- these are topics that we can address next week when discussion model selection

18.5 Dealing with convergence issues

- getting a convergence warning is an invitation to explore your random effects
 - a first step is to remove terms that are giving you Correlation terms +/-1
- so for now we would stick with `fit_fp_item`

```
# extract formula
formula(fit_fp_item)
```

```
log(fp) ~ verb_t * gramm + (1 | sj) + (1 + verb_t | item)
```

19 Reporting your model

- an example for this particular model:

A linear-mixed model was fit to log-transformed first-pass reading times at the verb region with grammaticality, tense, and their interaction as fixed effects, and by-participant intercepts and by-item varying intercepts and tense slopes. Tense and grammaticality were sum contrast coded (past and grammatical = -0.5, future and ungrammatical = 0.5).

- however, we've made a grave misstep in coming to our final model
 - we did not start with a “maximal” model
- we'll talk about model selection and reduction next

Learning objectives

Today we learned...

- how to fit a random-intercepts and slopes model
- how to inspect and interpret random slopes ## Important terms {unnumbered .smaller}

| Term | Definition | Equation/Code |
|------------------------------|------------|---------------|
| linear mixed (effects) model | NA | NA |

Task

Repeat the steps we took here, but on Ö

- regression path duration at the verb region, and
- regressions in at the adverb region (`roi == 2`)

19.0.1 Random-intercepts

Using the same dataset,

19.0.2 Dutch verb regularity

Session Info

Developed with Quarto using R version 4.3.0 (2023-04-21) (Already Tomorrow) and RStudio version 2023.9.0.463 (Desert Sunflower), and the following packages:

```
sessionInfo()
```

```

R version 4.3.0 (2023-04-21)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Ventura 13.2.1

Matrix products: default
BLAS:      /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
LAPACK:    /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: Europe/Berlin
tzcode source: internal

attached base packages:
[1] stats      graphics   grDevices utils      datasets   methods    base

other attached packages:
[1] gt_0.9.0           googlesheets4_1.1.0 kableExtra_1.3.4
[4] knitr_1.44         patchwork_1.1.3   lattice_0.21-8
[7] broom.mixed_0.2.9.4 lmerTest_3.1-3   lme4_1.1-33
[10] Matrix_1.5-4       sjPlot_2.8.14    ggeffects_1.2.2
[13] janitor_2.2.0     broom_1.0.5     here_1.0.1
[16] lubridate_1.9.2   forcats_1.0.0    stringr_1.5.0
[19] dplyr_1.1.3        purrr_1.0.2     readr_2.1.4
[22] tidyr_1.3.0        tibble_3.2.1    ggplot2_3.4.3
[25] tidyverse_2.0.0    broman_0.80

loaded via a namespace (and not attached):
[1] sandwich_3.0-2      rlang_1.1.3       magrittr_2.0.3
[4] multcomp_1.4-23    snakecase_0.11.0 furrr_0.3.1
[7] compiler_4.3.0      mgcv_1.8-42      systemfonts_1.0.4
[10] vctrs_0.6.3        rvest_1.0.3      crayon_1.5.2
[13] pkgconfig_2.0.3    fastmap_1.1.1    backports_1.4.1
[16] labeling_0.4.3     utf8_1.2.3       rmarkdown_2.22
[19] tzdb_0.4.0         nloptr_2.0.3     bit_4.0.5
[22] xfun_0.39          jsonlite_1.8.7   sjmisc_2.8.9
[25] parallel_4.3.0     R6_2.5.1        stringi_1.7.12
[28] parallelly_1.36.0   boot_1.3-28.1  cellranger_1.1.0
[31] numDeriv_2016.8-1.1 estimability_1.4.1 Rcpp_1.0.11
[34] modelr_0.1.11      zoo_1.8-12      pacman_0.5.1
[37] splines_4.3.0       timechange_0.2.0 tidyselect_1.2.0
[40] rstudioapi_0.14    yaml_2.3.7      codetools_0.2-19

```

```
[43] sjlabelled_1.2.0      curl_5.0.1          listenv_0.9.0
[46] plyr_1.8.8           withr_2.5.0         bayestestR_0.13.1
[49] coda_0.19-4          evaluate_0.21       future_1.32.0
[52] survival_3.5-5       xml2_1.3.4          pillar_1.9.0
[55] insight_0.19.3        generics_0.1.3       vroom_1.6.3
[58] rprojroot_2.0.3       hms_1.1.3           munsell_0.5.0
[61] scales_1.2.1          minqa_1.2.5         globals_0.16.2
[64] xtable_1.8-4          languageR_1.5.0     glue_1.6.2
[67] emmeans_1.8.6         tools_4.3.0          webshot_0.5.4
[70] fs_1.6.2              mvtnorm_1.2-3        cowplot_1.1.1
[73] grid_4.3.0             colorspace_2.1-0     nlme_3.1-162
[76] Rmisc_1.5.1            performance_0.10.4   googledrive_2.1.0
[79] cli_3.6.1              fansi_1.0.4          gargle_1.4.0
[82] viridisLite_0.4.2      svglite_2.1.1        sjstats_0.18.2
[85] gtable_0.3.4            digest_0.6.33        TH.data_1.1-2
[88] farver_2.1.1           htmltools_0.5.5      lifecycle_1.0.3
[91] httr_1.4.6              bit64_4.0.5          MASS_7.3-58.4
```

20 Shrinkage and Partial Pooling

Shrinkage of random Complete, No, Partial Pooling

 Under construction

This chapter is not fully translated from bullet points (from my slides) to prose. This will happen eventually (hopefully by spring 2024).

This chapter presents figures from the [blog post](#) “Plotting partial pooling in mixed-effects models” from Tristin Mahr (2017). You can also read Section 15.9 ‘Shrinkage and Individual Differences’ in Winter (2019) and Box 8.2 ‘Broader Context: Shrinkage and Partial Pooling’ in Sonderegger (2023b) for a short overview of the topics of shrinkage and partial pooling. We will be using the data from Biondo et al. (2022).

Learning Objectives

Today we will learn...

- about no/complete/partial pooling
- about shrinkage

Set-up

```
# suppress scientific notation
options(scipen=999)
```

Load packages

```
# load libraries
pacman::p_load(
    tidyverse,
    janitor,
    here,
    lmerTest)

lmer <- lmerTest::lmer
```

Load data

- data from Biondo et al. (2022)

```
df_biondo <-
  read_csv(here("data", "Biondo.Soilemezidi.Mancini_dataset_ET.csv"),
           locale = locale(encoding = "Latin1") ## for special characters in Spanish
           ) |>
  clean_names() |>
  mutate(gramm = ifelse(gramm == "0", "ungramm", "gramm")) |>
  mutate_if(is.character, as_factor) |> # all character variables as factors
  droplevels() |>
  filter(adv_type == "Deic")
```

20.1 Set contrasts

```
contrasts(df_biondo$verb_t) <- c(-0.5,+0.5)
contrasts(df_biondo$gramm) <- c(-0.5,+0.5)
contrasts(df_biondo$adv_type) <- c(-0.5,+0.5)
```

```
contrasts(df_biondo$verb_t)
```

```
[,1]
Past   -0.5
Future  0.5
```

```
contrasts(df_biondo$gramm)
```

```
[,1]
gramm  -0.5
ungramm 0.5
```

```
contrasts(df_biondo$adv_type)
```

```
[,1]
Deic   -0.5
Non-deic 0.5
```

20.2 Run models

- random-intercepts only

```
fit_fp_1 <-
  lmer(log(fp) ~ verb_t*gramm +
    (1 |sj) +
    (1|item),
    data = df_biondo,
    subset = roi == 4)
```

- by-item varying tense slopes

```
fit_fp_item <-
  lmerTest::lmer(log(fp) ~ verb_t*gramm +
    (1 |sj) +
    (1 + verb_t|item),
    data = df_biondo,
    subset = roi == 4)
```

21 Pooling

- do the random effects represent the exact average of participants?
 - below we see the mean logged first-pass reading time per participant (`mean`) and the by-participant intercepts from `fit_fp_1` and `fit_fp_item`
- to understand what's happening, we first have to understand pooling

```
sum_shrinkage <- df_biondo |>
  filter(roi == 4) |>
  summarise(mean = mean(log(fp), na.rm = T),
            .by = "sj") |>
  mutate(population_mean = mean(mean, na.rm = T)) |>
  left_join(coef(fit_fp_1)$sj[["(Intercept)"]] |> rownames_to_column(var = "sj")) |>
  rename(intercept_1 = `^(Intercept)` |>
  left_join(coef(fit_fp_item)$sj[["(Intercept)"]] |> rownames_to_column(var = "sj")) |>
  rename(intercept_item = `^(Intercept)`)

sum_shrinkage |>
  head()

# A tibble: 6 x 5
  sj      mean population_mean intercept_1 intercept_item
  <chr> <dbl>        <dbl>       <dbl>        <dbl>
1 1       6.42        5.96       6.40        6.40
2 2       5.79        5.96       5.79        5.80
3 07      5.87        5.96       5.87        5.87
4 09      5.78        5.96       5.78        5.78
5 10      6.67        5.96       6.62        6.62
6 11      5.91        5.96       5.91        5.92
```

21.1 No pooling

- no pooling refers to separate regression lines fit e.g., per participant

- each regression line is fit ignoring the population-level information
- the intercepts are the true mean from each participant

```
head(df_no_pooling)
```

| | model | sj | intercept | verb_t1 | gramm1 | verb_t1:gramm1 |
|---|------------|----|-----------|------------|-------------|----------------|
| 1 | No pooling | 1 | 6.422811 | 0.16094962 | 0.07844247 | 0.12950513 |
| 2 | No pooling | 2 | 5.792669 | 0.10115512 | -0.10571656 | -0.23199316 |
| 3 | No pooling | 07 | 5.870556 | 0.15344172 | -0.25264603 | -0.29866189 |
| 4 | No pooling | 09 | 5.780839 | 0.16938275 | 0.14074977 | -0.07324559 |
| 5 | No pooling | 10 | 6.664530 | 0.04786447 | -0.13824470 | 0.21824110 |
| 6 | No pooling | 11 | 5.912309 | 0.07573670 | -0.06469794 | 0.35318406 |

```
sum_shrinkage |> head(6)
```

| | # A tibble: 6 x 5 | sj | mean | population_mean | intercept_1 | intercept_item |
|---|-------------------|-------|-------|-----------------|-------------|----------------|
| | <chr> | <dbl> | <dbl> | <dbl> | <dbl> | |
| 1 | 1 | 6.42 | 5.96 | 6.40 | 6.40 | |
| 2 | 2 | 5.79 | 5.96 | 5.79 | 5.80 | |
| 3 | 07 | 5.87 | 5.96 | 5.87 | 5.87 | |
| 4 | 09 | 5.78 | 5.96 | 5.78 | 5.78 | |
| 5 | 10 | 6.67 | 5.96 | 6.62 | 6.62 | |
| 6 | 11 | 5.91 | 5.96 | 5.91 | 5.92 | |

21.2 Complete pooling

- complete pooling refers to ignoring grouping factors
 - i.e., fixed-effects only models (e.g., with `lm()` or `glm()`)
 - one regression line fit ignoring the individual-level information
 - the intercepts are the same as the population-level mean

```
head(df_pooled)
```

| | # A tibble: 6 x 6 | model | sj | intercept | verb_t1 | gramm1 | `verb_t1:gramm1` |
|---|-------------------|-------|-------|-----------|---------|--------|------------------|
| | <chr> | <fct> | <dbl> | <dbl> | <dbl> | <dbl> | |
| 1 | | | | | | | |
| 2 | | | | | | | |
| 3 | | | | | | | |
| 4 | | | | | | | |
| 5 | | | | | | | |
| 6 | | | | | | | |

```

1 Complete pooling 1      5.96  0.0612 0.00310   -0.0152
2 Complete pooling 2      5.96  0.0612 0.00310   -0.0152
3 Complete pooling 07     5.96  0.0612 0.00310   -0.0152
4 Complete pooling 09     5.96  0.0612 0.00310   -0.0152
5 Complete pooling 10     5.96  0.0612 0.00310   -0.0152
6 Complete pooling 11     5.96  0.0612 0.00310   -0.0152

```

```
sum_shrinkage |> head(6)
```

```

# A tibble: 6 x 5
  sj      mean population_mean intercept_1 intercept_item
  <chr> <dbl>        <dbl>       <dbl>        <dbl>
1 1       6.42        5.96       6.40        6.40
2 2       5.79        5.96       5.79        5.80
3 07      5.87        5.96       5.87        5.87
4 09      5.78        5.96       5.78        5.78
5 10      6.67        5.96       6.62        6.62
6 11      5.91        5.96       5.91        5.92

```

21.3 Complete vs. no pooling

- complete pooling (green solid line) and no pooling (orange dotted line) of grammaticality effects for 10 participants
 - describe what you see in terms of intercept and slopes across the participants

21.4 Partial pooling: mixed models

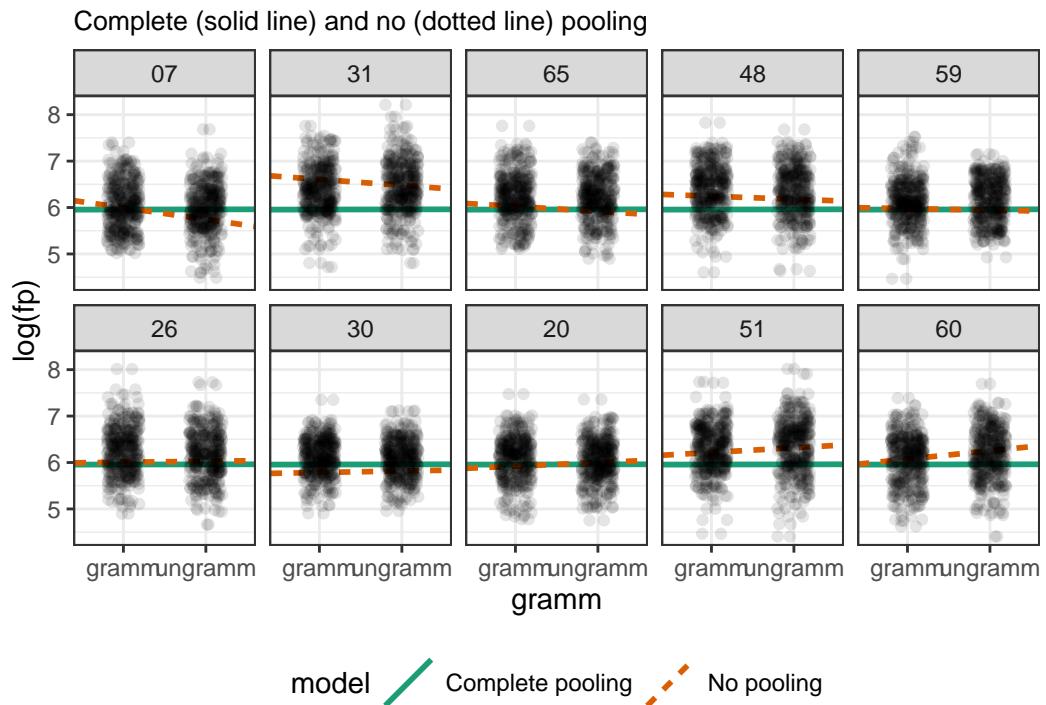


Figure 21.1: Observations (black dots) with complete pooling regression line (solid green) and no pooling line (dotted orange) per 10 participants

22 Shrinkage

- turns out the estimates are pulled towards the population-level estimates
 - all the information in the model is taken into account when fitting varying intercepts and slopes



Figure 22.1: Elaine Benes learns about shrinkage of random effect estimates towards the population-level estimates

22.1 Shrinkage

22.2 Centre of gravity

- why are some points not being pulled directly to the ‘centre of gravity’?
 - they’re being pulled to a higher confidence region

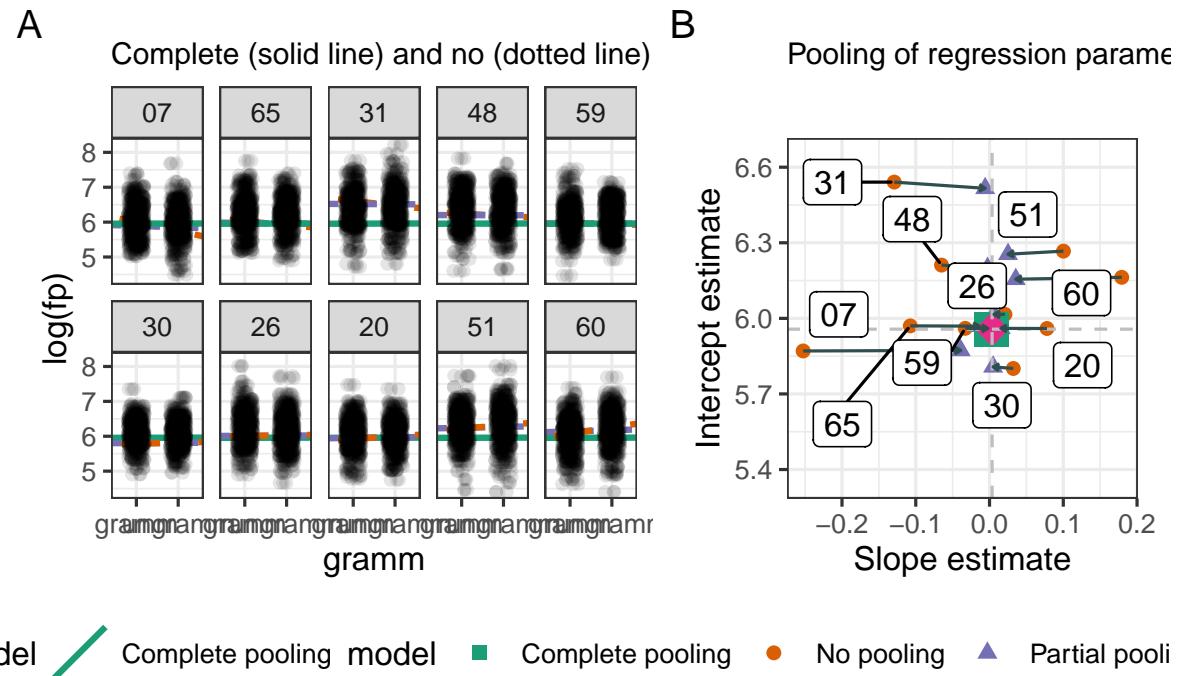


Figure 22.2: Shrinkage of 10 participants

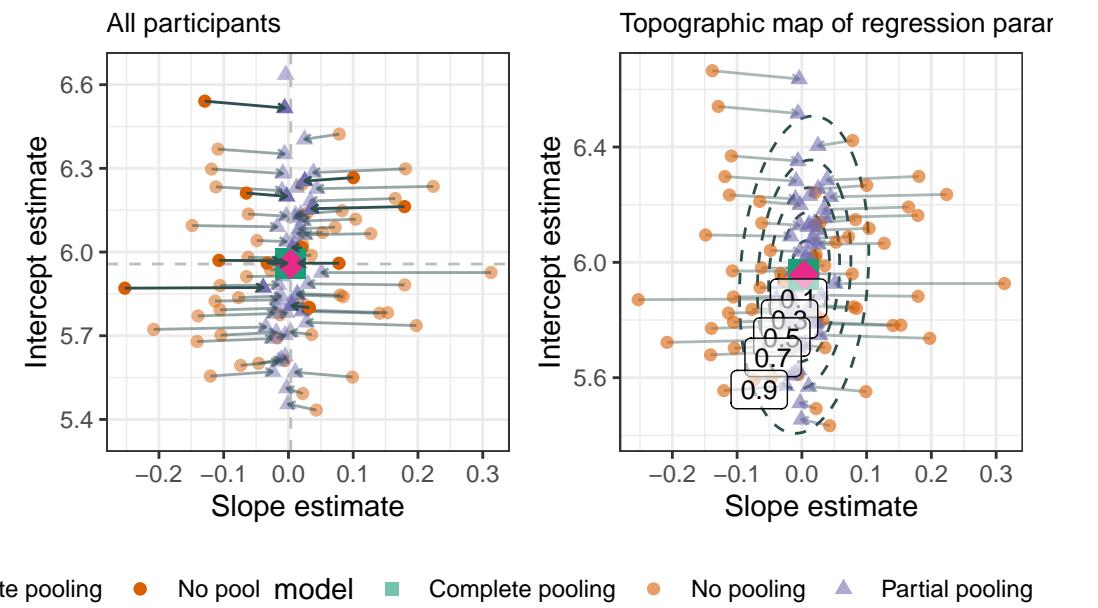


Figure 22.3: Shrinkage for all participants: each ellipsis represents a confidence level (really, a quantile: q1, q3, q5, q7, and q9); The inner ellipsis contains the centre 10% of the data, the outer ellipsis 90%

23 Why shrinkage?

- with partial pooling, each random effect is like a weighted average
 - it takes into account the effect for one group level (e.g., one participant) *and* the population-level estimates
 - the empirical effect for a group level is weighted by the number of observations
 - so if one participant has fewer observations than another, then more weight is given to the population-level estimates, and vice versa
- the implications (benefits) of this:
 - imbalanced data are not a problem for linear mixed models
 - the model can make predictions for unseen levels, i.e., it can generalise to new data

Learning objectives

Today we learned...

- what linear mixed models are
- how to fit a random-intercepts model
- how to inspect and interpret a mixed effects model

Important terms

| Term | Definition | Equation/Code |
|------------------------------|------------|---------------|
| linear mixed (effects) model | NA | NA |

References

- Baayen, R. H. (2008). *Analyzing Linguistic Data: A Practical Introduction to Statistics using R*.
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24 Model selection

Strolling through the garden of forking paths



Under construction

This chapter is not fully translated from bullet points (from my slides) to prose. This will happen eventually (hopefully by spring 2024).

Learning Objectives

Today we will learn about...

- the history of mixed models (again)
- strategies for model selection
- variability in model selection

Resources

- relevant papers for this topic
 - Barr et al. (2013b)
 - Bates et al. (2015)
 - Matuschek et al. (2017)
 - Brauer & Curtin (2018)
 - Meteyard & Davies (2020)

25 Review: random intercepts and slopes

- violation of independence assumption → increased Type I error (false positive)
 - include random effects per plausible grouping factor (herein “unit,” à la Barr et al., 2013b)
- random-intercepts only models → increased Type I error (false positive)
 - add random slopes per within-unit manipulation, i.e., “maximal” models (Barr et al., 2013b)
- but such models often fail to “converge”
 - and have been shown to increase Type II error (false negative) (Bates et al., 2015; Matuschek et al., 2017)
- some questions remain:
 - how to define our maximal model
 - how to handle convergence issues

26 History of LMMs revisited

- recall Clark (1973)’s language-as-fixed-effect fallacy and the issue of generalisability (see also Winter & Grice, 2021; Yarkoni, 2022)
- Baayen et al. (2008) motivated LMM’s for linguistic data in the JML special issue
 - effect: everybody adopted random-intercepts only models
- Barr et al. (2013b): random-intercepts only models are overconfident, “keep it maximal!”
 - effect: everybody adopted maximal models
- Matuschek et al. (2017) and Bates et al. (2015): maximal models are underconfident and lower statistical power! Use data-driven model selection to find a “parsimonious” model!
 - effect: some people adopt this method, but many psycholinguists just want a “recipe” to follow

26.1 2013: Keep it maximal

A maximal model should optimize generalization of the findings to new subjects and new items.

- Barr et al. (2013b), p. 261
- random-intercepts-only models tend to be underpowered
- for this reason, Barr et al. (2013b) suggested using a maximal random effects structure justified by the experimental design

26.2 2015 & 2017: Parsimonious models

[W]hile the maximal model indeed performs well as far as Type I error rates were concerned, power decreases substantially with model complexity.

— Matuschek et al. (2017), p. 310-311

- there is a trade-off between Type I (overconfidence) and Type II error (underconfidence)

- i.e., maximal models can lead to over-fitting
 - lowers statistical power, which increases Type II error (false rejection)
- but we should strive for the most *parsimonious* model
 - parsimonious models are a compromise between the maximal model justified by your design and theory, and a given data set
- best way to maintain low Type I and II error: collect lots of data

27 Model building

Every statistical model is a description of some real or hypothetical state of affairs in the world.

– Yarkoni (2022), p. 2

- our models reflect not only our hypotheses or effects of interest, but any other plausible or known co-variates
- our predictors should reflect our research questions or theories tested
 - plus any plausible or previously motivated co-variates (e.g., trial order)
 - plus known sources of nonindependence, i.e., our random effects

27.1 Choosing predictors

- your model should be defined *a priori*
 - i.e., you should define what predictors you will include and any covariates
 - e.g., if you have a prediction about the effect of phonological neighbours on vowel duration
 - * define what phonological characteristics you will include (e.g., place of articulation? manner?)
 - * these should be related to specific hypotheses/research questions

27.2 Choosing a maximal random effects structure (RES)

- how do we define our maximal model? Some tips from Barr et al. (2013b)
 - between-unit factor (e.g., age): include random intercept only
 - within-unit factor with multiple observations per unit-level (e.g., age in longitudinal data): include random slopes
- all factors in an interaction are within-unit: include by-unit random slopes for interaction terms

27.2.1 Example: Biondo et al. (2022)

- Biondo et al. (2022): 2x2 design
 - verb-tense (past, future) and grammaticality (grammatical, ungrammatical)
 - repeated-measures: within-participant and -item design
 - * so we should have by-participant and -item random intercepts (multiple observations per unit level)
 - each participant and item contributed multiple data points *per condition* (i.e., tense and grammaticality were manipulated within each unit level)
 - * so we should have varying tense and grammaticality slopes by- item and - participant

```
fit_verb_fp_mm <- lmer(log(fp) ~ verb_t*gramm +
                         (1 + verb_t*gramm|sj) +
                         (1 + verb_t*gramm|item),
                         data = df_biondo,
                         subset = roi == 4)
```

27.3 Observations per cell

- if there is only a single observation per cell, e.g., you collected one observation from each participant per condition, then you can't fit random intercepts or slopes
- ideally you would have at least 5 observations per cell (per unit level per condition, e.g., each participant has at least 5 observations per condition)
- this is also a question of statistical power

```
# obvz per sj per condition
df_biondo |>
  filter(roi == 4) |>
  count(sj, verb_t, gramm) |>
  count(n)
```

```
# A tibble: 1 x 2
      n     nn
  <int> <int>
1    16    240
```

```

# obvz per item per condition
df_biondo |>
  filter(roi == 4) |>
  count(item, verb_t, gramm) |>
  arrange(desc(n)) |>
  count(n)

# A tibble: 1 x 2
  n     nn
  <int> <int>
1    10   384

```

27.4 Data structure

- random effects must be factors/categorical
- single observation per row
 - generally speaking, there should be $n(\text{participants}) * n(\text{items})$ rows
 - every fixed or random effect in your model should correspond to a column in your dataset

28 Variability in methods

- Meteyard & Davies (2020)
 - survey of (psychology) researchers
 - review of papers using LMMs
- insecurity in researchers re: choosing models
- great variation in papers in how models are built and reported

28.1 Researcher degrees of freedom

What we hope to make clear is that there is no single correct way in which LMM analyses should be conducted, and this has important implications for how the reporting of LMMs should be approached.

— Meteyard & Davies (2020), p. 9

- the problem:
 - ‘researcher degrees of freedom’ (Simmons et al., 2011), or ‘the garden of forking paths’ (Gelman & Loken, 2013)
 - the same data can be analysed in a variety of ways
- this leads to insecurity for many researchers

28.2 Justify and document

Replicability and reproducibility are critical for scientific progress, so the way in which researchers have implemented LMM analysis must be entirely transparent. We also hope that the sharing of analysis code and data becomes widespread, enabling the periodic re-analysis of raw data over multiple experiments as studies accumulate over time.

— Meteyard & Davies (2020), p. 9

- the (partial) solution:

- make model building/selection decisions a priori
- be transparent
- share your data and code

29 Moving forward

- other alternatives that have fewer convergence issues:
 - Julia
 - * e.g., in VS Code IDE
 - Bayesian framework (e.g., `brms` R package)
 - * also run (G)LMMs, but abandons arbitrary p-values
 - * instead quantifies uncertainty
- both are more more computationally powerful
 - they are not (yet) as widely used in the field

Learning objectives

Today we learned...

- the history of mixed models (again)
- strategies for model selection
- variability in model selection

Important terms

References

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Part VII

Report 2

30 Report 2

(Generalised) linear mixed models

The goal of this report is to review and consolidate what we learned together in the second block of the course. You are not required to do anything that we have not already seen.

For students enrolled in this course in the Winter Semester 2023/24: The report is due **March 29, 2024 at 11:59pm**. Please submit your Quarto script, as well as a rendered copy in HTML and PDF to Moodle (under ‘Reports’).

31 Dataset

For this report you will continue using the data from Biondo et al. (2022), an eye-tracking reading study on adverb-tense congruence effects on reading time measures. Participants' eye movements were recorded as they read Spanish sentences where temporal adverbs and verb tense were either congruent or incongruent. For both sentence regions, the time reference was either past (e.g., yesterday, bought) or future (e.g., tomorrow, will buy). Example stimuli from this experiment are given in Table 31.1.

Table 31.1: Example stimuli

| sentence | adverb | verb | gramm |
|---|--------|--------|---------|
| A la salida del trabajo, ayer las chicas compraron pan en la tienda. <i>After leaving work yesterday the girls bought bread at the shop</i> | past | past | gramm |
| A la salida del trabajo, ayer las chicas *comprarán pan en la tienda. <i>After leaving work yesterday the girls *will buy bread at the shop</i> | past | future | ungramm |
| A la salida del trabajo, mañana las chicas comprarán pan en la tienda. <i>After leaving work tomorrow the girls will buy bread at the shop</i> | future | future | gramm |
| A la salida del trabajo, mañana las chicas *compraron pan en la tienda. <i>After leaving work tomorrow the girls *bought bread at the shop</i> | future | past | ungramm |

You will be fitting models to different eye-tracking reading measures from this experiment, with the predictors *adverb*, *time* and *grammaticality*.

32 Set-up

Make sure you begin with a *clear* working environment. To achieve this, you can go to **Session > Restart R**. Your Environment should have no objects in it, and you should not have any packages loaded.

32.1 Quarto YAML

Make sure your YAML looks something like this:

```
---
```

```
title: "Report 2"
name: "My Name"
format:
  html: default
  pdf: default
toc: true
number-sections: true
---
```

 Render often

I suggest you render your document frequently, e.g., after every substantial code chunk/task achieved. This will ensure earlier detection of broken code and makes it easier to fix problems. Do this for both HTML and PDF.

32.2 Packages

Load the following packages, however you prefer (i.e., you don't have to use `pacman::p_load()`):

- tidyverse
- janitor
- here
- broom.mixed

- lattice
- lme4
- lmerTest

Describe what each of the following packages is used for (in our experience, they have many more useful functions than we've tried).

1. broom.mixed:
2. lattice:
3. lme4:
4. lmerTest:

32.3 Data

Load in the Biondo et al. (2022) data by running the following code chunk.

```
df_biondo <-
  read_csv(here("data", "Biondo.Soilemezidi.Mancini_dataset_ET.csv"),
            locale = locale(encoding = "Latin1") ## for special characters in Spanish
            ) |>
  clean_names() |>
  mutate(gramm = ifelse(gramm == "0", "ungramm", "gramm")) |>
  mutate_if(is.character, as_factor) |> # all character variables as factors
  filter(adv_type == "Deic") |>
  droplevels() |>
  mutate(
    roi_length = str_length(label)
  ) |>
  relocate(roi_length, .after = label)
```

The last few lines add a new variable (`roi_length`) that contains region length (in letters). We will use this as a covariate in one of our models.

33 Model set up

You will be asked to run two models, one linear mixed model (`lmer()` from the `lme4` or `lmerTest` package) and one generalised (logistic) linear mixed model (`glmer(family = "binomial")` from the `lme4` package).

33.1 Variable transformations

For each model, consider whether you need to implement the following steps:

- centre (sum contrast code) categorical predictors
- standardize continuous predictors (e.g., using the `scale()` function)
- log-transform continuous dependent variables if skewed
- model selection: begin with a maximal model
 - simplify in case of nonconvergence or singular fit

33.2 Model selection

For each model, start with a “maximal” model justified by the design. If you encounter convergence issues, begin by first implementing “unintrusive” remedies. If you still have convergence issues (as indicated by warning messages and/or e.g., inspecting the variance-covariance matrix), reduce the random effects structure as you see fit. Be sure to document and justify your decisions step-by-step. N.B., the equivalent of `lmerControl` argument (for `lmer()` models) is `glmerControl` for `glmer()` models.

If you choose to use the `lme4::allFit()` function, beware that it can take a long time to run, especially on ‘maximal’ models. I suggest you (i) save the output as an object (e.g., `allFit_model1 <- allFit(model1)`) and (ii) plan another task that doesn’t involve running code when you run this function.

I am not expecting any particular model/random effects structure that is correct, but am looking for explanations on how you made decisions regarding what to remove or keep in your model.

34 Linear mixed model

Fit a linear mixed model to total reading times (`tt`) at the adverb region (`roi == 2`). Your fixed effects are adverb type (`adv_t`), grammaticality (`gramm`), their interaction, and (standardized) region length in characters as a covariate without any interaction. Include by-participant and -item random effects.

34.1 Fit a model

Start by defining your most maximal model justified by your design, and simplify accordingly. Remember to not delete the code for nonconverging models, instead set the code chunk to not run when you render your document, as in the code chunk below (`#| eval: false`).

```
```{r}
#| eval: false

fit_some_maximal_model <-
 lmer(dependent_variable ~ predictor1*predictor2 + covariate +
 (1 + predictor1*predictor2|participant) +
 data = my_data,
 subset = some_factor == "some_level")
informative comment, e.g., "didn't converge"
````
```

34.2 Report results

Once you've landed on a final model that converges, inspect the fixed and random effects (some useful functions we've already seen: `summary()`, `broom.mixed::tidy()`, `fixef()`, `ranef()`, `coef()`, `lattice::dotplot()`).

35 Generalised linear mixed model

We didn't cover how to implement logistic mixed regression, however the relationship between `lm()` and `glm()` is the same in mixed models (`lmer()` and `glmer()`).

35.1 Fit a model

Fit a generalised linear mixed model (`glmer()` from the `lme4` package, `lmerTest` does not have this function) to the regressions in (`ri`) to the adverb region (`roi == 2`). Your fixed effects are adverb time reference (`adv_t`), grammaticality (`gramm`), and their interaction. Remember to use `eval: false` in your code chunk options to stop Quarto from running all your non-final models when rendering.

35.2 Report results

Once you've landed on a final model that converges, inspect the fixed and random effects (some useful functions we've already seen: `summary()`, `broom.mixed::tidy()`, `fixef()`, `ranef()`, `coef()`, `lattice::dotplot()`)

Recall that our coefficient estimates are in *log odds*. The interpretation of your coefficient estimates (fixed effects) is identical to that in generalised linear models (i.e., without random effects).

36 Interpretation

Write a short report of the findings from the two models. Produce a table and plot like in the example above to supplement your report.

37 Render

Render your Quarto finished script. Upload the `.qmd`, `.pdf`, and `.html` files to Moodle. N.B., you need to have `tinytex` installed to be able to render PDFs.