Fundamentals of Quantitative Analysis

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Overview

Book Name: Fundamentals of Quantitative Analysis.

Summary: Materials for the MSc Conversion Research Methods 1 and 2 courses at the University of Glasgow School of Psychology & Neuroscience.

Authors: James Bartlett and Wil Toivo. This version of the book was adapted from a previous version written by Emily Nordmann and Phil McAleer.

Aim: This course covers data skills such as creating reproducible documents with R Markdown, data wrangling, and data visualisation with the tidyverse family of packages. It also introduces statistical concepts such as Null Hypothesis Significance Testing (NHST), as well as demonstrating how to perform numerous analyses based around the general linear model including regression and ANOVA.

Contact: This book is a living document and will be regularly checked and updated for improvements. Should you have any issues using the book or have any queries, please contact James Bartlett and Wil Toivo.

The online version of the book will always be the most up-to-date version with interactive exercises. Periodically, we create a PDF version of the book if that helps you work offline. We last knitted the book on 2025-09-17.

R Version: We wrote this book using R version 4.4.1 (2024-06-14).

How to use this book

Welcome to the Fundamentals of Quantitative Analysis

We wrote and designed this book to support RM1 and RM2 on the MSc Psychology Conversion programme, where you will learn core quantitative data skills using R and R Studio. In addition to this book, the course team will support you with demonstration videos and we encourage you to use Teams or office hours to ask any questions.

The ability to work with quantitative data is a key skill for psychologists and by using R and R Studio as our tool, we can also promote reproducible research practices. Although at first it may seem like writing a programming script is more time-consuming than other point-and-click approaches, you speed up with practice. Once you have written a script that does what you need it to do, you can easily re-run your analysis without having to go through each step again manually which is easier and less likely to result in errors if you do something slightly different or forget one of the steps.

Crucially, with an analysis script, you can demonstrate to other researchers how you got from the raw data to the statistics you report in your final paper. Sharing analysis scripts alongside published articles on sites such as the Open Science Framework is now an important open science practice. Even if you do not continue with quantitative research yourself, the skills you develop throughout these courses will allow you to evaluate quantitative research and to understand what goes on behind the scenes to produce their numbers and conclusions, allowing you to become a much more confident and competent consumer and user of research.

How to use this book

We follow a scaffolding approach in this book to build your skills from following along to independently being able to apply these skills to new scenarios.

In each chapter, we first guide you through a set of demonstrations focused on different data skills, highlighting key parts of the output and what it means (just keep in mind we focus on the practical side of doing and interpreting in this book, the course lectures cover the conceptual background). We strongly encourage you to type out the code yourself, as this is good practice for learning to code, but remember you can copy and paste from the book if you

need to. Typing the code will seem much slower at first and you will make lots errors, but you will learn much more quickly this way.

As you work through the book, you will see technical terms highlighted like console which link to a glossary we have developed as a team. If you hover the cursor over the highlighted word, it will show you a little definition, and you will be able to see a full list of words we highlighted at the bottom of each chapter. There are also different colour-coded boxes to emphasise different content. These provide information, warn you about something, highlight if something is dangerous and you should really pay attention, and try it yourself boxes when we have activities for you to complete.

> **Note**
>
> These boxes have little interesting - but not critical - bits of information.

> **Important**
>
> These boxes warn you about something important in R / R Studio, so you pay attention when you use it.

> **Warning**
>
> These boxes highlight where you need to be cautious when using or interpreting something, as it might be easy to make an error.

> **Try this**
>
> These boxes will invite you to try something yourself, like complete independent activities or answer questions.

> **Solution**
>
> These boxes will include small hints or solutions to check your understanding. Here we show the explanations by default, but normally they will be collapsed.

After these demonstrations, we give you little activities and independent tasks using a new data set to test your understanding using interactive questions. This gives you instant feedback on whether you could apply the skills or if there is something you need to check again.

Some of these activities are what we call "error mode". You never stop making errors when coding - we still make them all the time - but you get faster at recognising and fixing common sources of error. Hoffman & Elmi (2021) demonstrated incorporating errors in learning materials can be useful to students, so we will give you a few segments of code containing errors

that you need to fix. Seeing errors can be one of the most intimidating parts of learning to code, so this activity will normalise making errors and develop your problem solving skills.

Finally, there are four data analysis journeys we will direct you to at key points throughout the book. We will tell you the end product you are aiming for from a new raw data set we provide, and your job is to break that end product down and identify a list of tasks to get there. Completing an independent data analysis task is the skill set you will need once it comes to assessments and your dissertation, as this is the point where you are the one making decisions.

In contrast to assignments, for all of these activities and data analysis journeys we provide solutions at the end of each chapter. No one is going to check whether you tried to figure out an activity yourself, rather than going straight to the solution, but if you copy and paste without thinking, you will learn nothing. Developing data skills and the knowledge that underpins those skills is like learning a language: the more you practice and the more you use it, the better you become.

Accompanying videos

Most of the chapters of this book have an associated video that you can access via Moodle. These videos are there to support you as you get comfortable in your data skills as you can see how someone else interacts with R / R Studio. However, it is important that you use them wisely. You should always try to work through each chapter of the book on your own first, and only then watch the video if you get stuck, or for extra information.

Finally, this book is a living document. That means occasionally we will make updates to the book such as fixing typos and including additional detail or activities. When we make substantial changes, we will create new support materials such as the videos. However, it would be impossible to record a new video every time we make a minor change to an activity, so you may notice slight differences between the videos and the content of this book. Where there are differences between the book and the video, the book should always be considered the definitive version.

Data set acknowledgements

Almost all the demonstrations and activities in this book use real data from published research to reinforce how these skills are the same ones researchers use behind the scenes of their articles. We use a range of data from our own research, open data that researchers share with their papers, and some we adapted from the Open Stats Lab who created activities using open data.

Intended learning outcomes (ILOs)

By the end of the courses associated with this book, you will be able to:

- Write reproducible reports using R Markdown.
- Clean and wrangle data into appropriate forms for analysis.
- Visualise data using a range of plots.
- Conduct and interpret a core set of statistical tests from the general linear model (regression, ANOVA).

Acknowledgements

We put a lot of effort into creating the resources in this book, but occasionally typos or broken links will slip through. When a student helps us and highlights an error or makes a suggestion, we like to acknowledge it. We would like to thank the following students for helping us:

Andrés Rajiv Arora, Liam Caldwell, John Gleeson, Ria Manwar, Jacquelyn Scott, Yee Lam So.

1 Introduction to programming with R/R Studio

In this chapter, we will cover interacting with R and RStudio. We will provide an overview of basic programming concepts and terminology, common pitfalls, helpful hints, and where to get help. Those of you who have no programming experience should find this chapter particularly helpful, but there should be helpful hints and tips even if you have used R or another programming language before before.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Navigate and interact with RStudio.
- Use an R function and find help documentation.
- Install and load R packages.
- Assign content to an object.
- Know where to find support from online resources and from the course team.

1.1 R and RStudio

R is a programming language that you will write code in and **RStudio** is an Integrated Development Environment (IDE) which makes working with R easier. Think of it as knowing English and using a plain text editor like NotePad to write a book versus using a word processor like Microsoft Word. You could do it, but it would not look as good and it would be much harder without things like spell-checking and formatting.

In a similar way, you can use R without RStudio but we wouldn not recommend it. The key thing to remember is that although you will do all of your work using RStudio for this course, you are actually using two pieces of software. This means that you will need both, you need to keep both up-to-date, and you should cite both in any work you do (see the Appendix on citing R and RStudio when needed).

But first we need to look at starting up R and RStudio. There are two ways you can use R for Psychology as a student here at the University of Glasgow. First, you can use a online version

of R and R through your web browser and we will refer to this as the **R server**. Second, you can download and install R and RStudio for free on your laptop or desktop computer.

1.1.1 Installing R and RStudio on your computer

We recommend wherever possible installing R and RStudio on your own computer. This is known as a local installation as you do not need to be connected to the internet to use it. We find it is easier to save and manage your files, and you can take your computer wherever you go.

However, we appreciate not everyone has a computer that will support R and RStudio. All of our computer lab and library spaces have R and RStudio installed, so you will always be able to access those for working through the materials and your assignments. If you cannot install R and RStudio on your computer and there are accessibility issues preventing you from using the university computers, please come and speak with your course leads who will advise alternative options.

To install R and RStudio on your computer, please see the Installing R/RStudio guide which we use across all of our books. The guide covers installing R/RStudio on a Windows computer, Mac, and accessing the software on one of the university computers. Please install R and RStudio **before** continuing with the chapter.

1.2 Getting to know R Studio

By default, RStudio has four windows:

1. The **console**, where you can type R code in the bottom left (as shown in Figure Figure 1.1).
2. Eventually, there will be a **script** editor in the top left, but you will not see this when you open RStudio for the first time.
3. The **environment** window in top right, where you will see things like data, functions, and objects that you create.
4. Finally, the bottom right window shows files, plots, packages, and help documentation.

You will learn more about how to use the features included in RStudio throughout this course, but we recommend watching the RStudio Essentials 1 series of videos from the Posit team (the company who maintain RStudio). The video we link here lasts around 30 minutes and gives a tour of the main parts of RStudio.

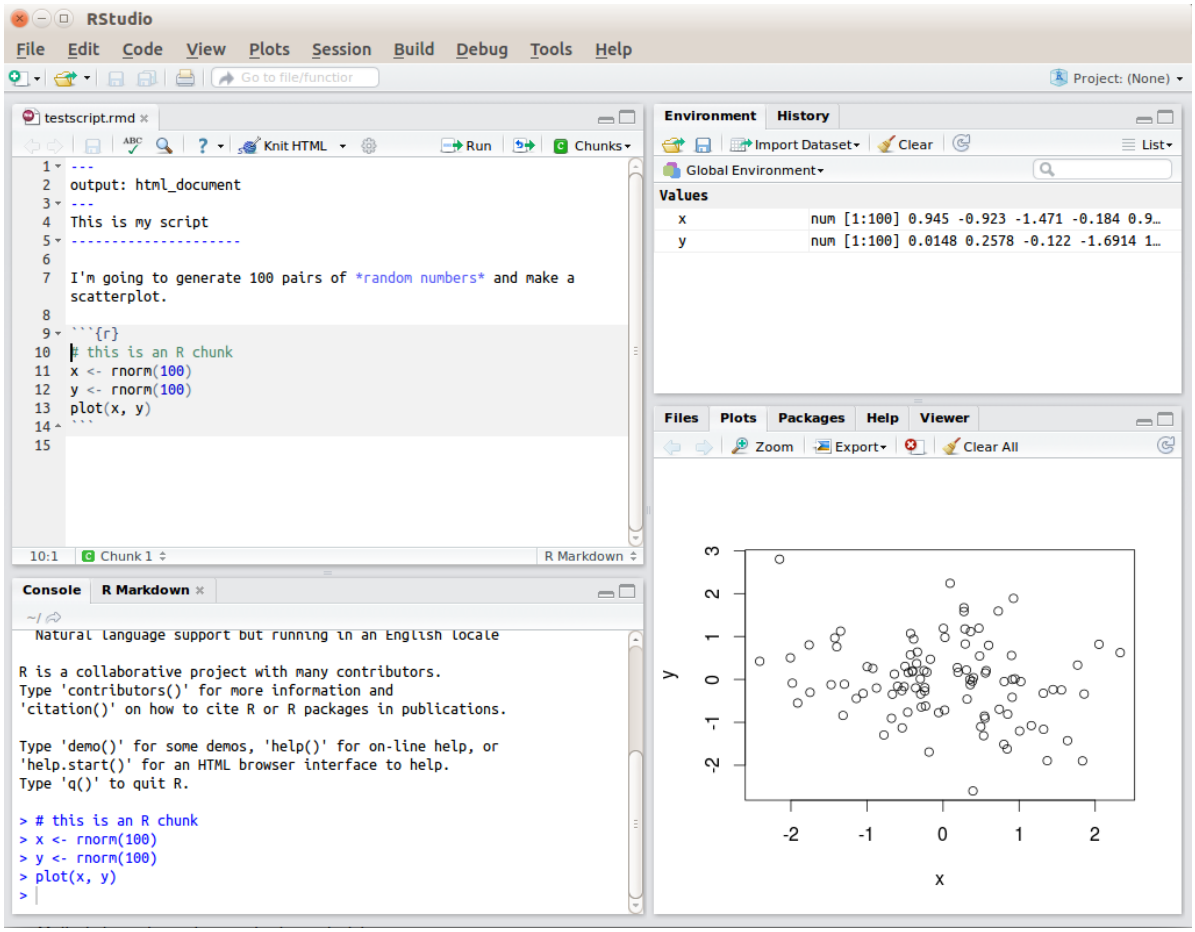


Figure 1.1: RStudio interface

1.2.1 Console vs. scripts

When you first open up RStudio, you will not see an R script like above, there will just be the console window taking up the whole left half. You can write code in the console to test it out, but you cannot save that code anywhere, and you would lose all your code if you closed down RStudio.

For this chapter only, we will use the console window to show you some simple R code, but from Chapter 2 - Creating reproducible documents - we will teach you to work in a type of R script called an **R Markdown** document which ends with the file name .Rmd.

You can open a new file in a number of ways, but the simplest is in the top menu of RStudio, selecting **`File >> New File >> R Markdown`** and clicking OK. You will then be able to see the extra pane in the top left like Figure Figure 1.1.

1.3 Writing code with functions and arguments

R code is made up of **functions** and **arguments** that go into the functions to create outputs. **Functions** in R execute specific tasks and normally take one or more **arguments**. You can think of these concepts like a spoken language as verbs (function) that require a subject and an object (arguments). You could also think of them as a kind of recipe. Some recipes (function) are quite simple and have one or two ingredients (arguments), while other recipes are more complicated with many ingredients (arguments).

You can spot functions as they end in round brackets (known as parentheses, `()`), and the arguments go within the round brackets. They tend to look a bit like this:

```
function_name(argument1 = value, argument2 = value)
```

That would be the layout of a function with two arguments and each argument takes a value. Bare with us as these concepts might feel super abstract until you start using them.

You will learn to use many functions throughout this book and you can look up all the arguments that a function takes in the help documentation by using the format `?function`. You will see some arguments are required while others are optional. Optional arguments will often use what is known as a default setting, value, or option (normally specified in the help documentation) if you do not enter any value.

As an example, let us look at the help documentation for the function `rnorm()` - a function which randomly generates a set of numbers from what is known as the **Normal Distribution**.

1.3.1 Activity 1 - Finding help documentation for functions

Open up RStudio and in the console window (bottom left), type the following code:

```
?rnorm
```

The help documentation for `rnorm()` should appear in the bottom right help panel. In the **Usage** section of the help, we see that `rnorm()` takes the following form:

```
rnorm(n, mean = 0, sd = 1)
```

In the **Arguments** section of the help, there are explanations for each of the arguments:

- `n` is the number of observations/numbers/data points we want to create,
- `mean` is the **mean** of the observations/numbers/data points we will create.
- and `sd` is the **standard deviation** of the observations/numbers/data points we will create.

In the **Details** section of the help, it notes that if no values are entered for `mean` and `sd` it will use a default of 0 for the mean and 1 for the standard deviation. So, these are the values the function will use for its arguments of `mean` and `sd` if you do not state any. However, because there is no **default value** for `n`, this means that you must state a value for the arguments `n`, otherwise the code will not run.

This is all still a little abstract, so let us try an example. Still using `rnorm()` let us set the required argument `n` to ask R to produce 5 random numbers.

1.3.2 Activity 2 - Running your first function

Type the following two lines of code into your console window. Press enter/return on your keyboard at the end of each line to "run" that line. So, type `set.seed(10072024)` and press enter/return and then type `rnorm(n = 5)` and press enter/return. You will now see these numbers in your console window:

```
[1] -0.6773381  2.9686894 -1.0461339 -1.4800300  0.4313315
```

These numbers have a mean close to 0 ($M = 0.039$) and a standard deviation (SD) close to 1 ($SD = 1.784$) - they are not exact because you only sampled a very small set and that sampling is random.

What does set.seed() do?

You can get R to generate seemingly random numbers, but they are not totally random. Computers generate random numbers through a predictable process, but they pick a starting point based on something like the clock time. If you run `rnorm(n = 5)` several times in the console, you will see the five numbers are different each time. However, when you run `set.seed(10072024)` first, you will get the same five numbers every time, which is useful when you want a random but reproducible set of numbers.

Now, we can play with the function and change the additional arguments to produce a different set of numbers. This time we will say we want 5 numbers again (`n = 5`) but we want our mean closer to 10 (`mean = 10`) and our standard deviation closer to 2 (`sd = 2`). We would do that as follows and you should see the output numbers below.

```
set.seed(10072024)

rnorm(n = 5, mean = 10, sd = 2)
```

```
[1]  8.645324 15.937379  7.907732  7.039940 10.862663
```

This time, we created 5 random numbers again, but this set has a mean close to 10 ($M = 10.079$) and a SD close to 2 ($SD = 3.569$). Hopefully, you are starting to get a sense of arguments within functions, how you can change them, and how you can always remember to use the help documentation to understand what arguments a function requires.

Over time, you start to remember which arguments you need within functions you commonly use, but even experienced R users have to regularly check the documentation. Coding is not a memory test, so do not worry if you find yourself needing to constantly look up the name of arguments.

Error mode

One thing that can be intimidating at first is making errors. They have little red marks and produce sometimes vague messages to try and explain what went wrong. You will make many errors as you learn and over time, you do not stop making errors, but you get faster at working out what went wrong and how you can fix it. So, we will introduce you to common errors as we work through the book to help with problem solving.
Try and run the following code in the console:

```
rnorm(mean = 10, sd = 2)
```

You should get an error saying something like `Error in rnorm(mean = 10, sd = 2): argument "n" is missing, with no default`. This error message is useful as it is

telling us we forget to state the `n` argument which has no default value, so the function has no idea how many observations to give you. You would fix this error by adding a value for `n` within the function.

1.3.3 Stating argument names

In the examples above, we have written out the argument names in our code (for example, we wrote `n = 5`, `mean = 10`, `sd = 2`), however, this is not strictly necessary. The following two lines of code would produce very similar outputs with the same number of values and similar means and standard deviations. Remember though: each time you run `rnorm()`, it will produce a slightly different set of numbers unless you set a seed.

```
rnorm(n = 6, mean = 3, sd = 1)
rnorm(6, 3, 1)
```

The main thing is that both lines of code would still work - the code knows what to do with the numbers. Both options work as the code is following a set order of arguments: `n` then `mean` then `sd`. If you do not write out the argument names, the code will use the default order of arguments, which for `rnorm` will assume that the first number you enter is `n`, the second number is `mean`, and the third number is `sd`.

So, you can write the argument names or not, but it is important to know the default order if you choose not to write the argument names. Alternatively, if you write out the argument names, then you can write the arguments in whatever order you like. The code below will still work and produce six numbers with a mean close to 3 and a standard deviation close to 1.

```
rnorm(sd = 1,
      n = 6,
      mean = 3)
```

When you are first learning R, we recommend writing out the argument names every time as it can help you remember and understand what each part of the function is doing. However, as your skills progress you may find it quicker to omit the argument names and you will also see examples of code online that do not use argument names. In this course, we will always write out the argument names the first time we use each function, but afterwards, we may omit them.

> ⚠ Warning
>
> If you do omit argument names, it is important to check the values you use for arguments are the ones you intended to use. The sneakiest errors are the ones that "work" in that

they do not produce an error, but they are doing something different to what you expect. For example, if you wanted five numbers with a mean of 1 and *SD* of 2, `rnorm(5, 2, 1)` would work, but we accidentally entered the mean and SD the wrong way around.

1.3.4 Tab auto-complete

One very useful feature of RStudio is the tab auto-complete for functions (see Figure Figure 1.2). If you write the name of the function and then press the tab key on your keyboard, RStudio will show you the arguments that function takes along with a brief description. If you press enter on the argument name, it will fill in the name for you, just like auto-complete on your phone.

You can also use the tab button when writing a function name to auto-complete that function name or to find functions that start with certain letters. This feature can be really helpful if you cannot quite remember the name of a function or argument.

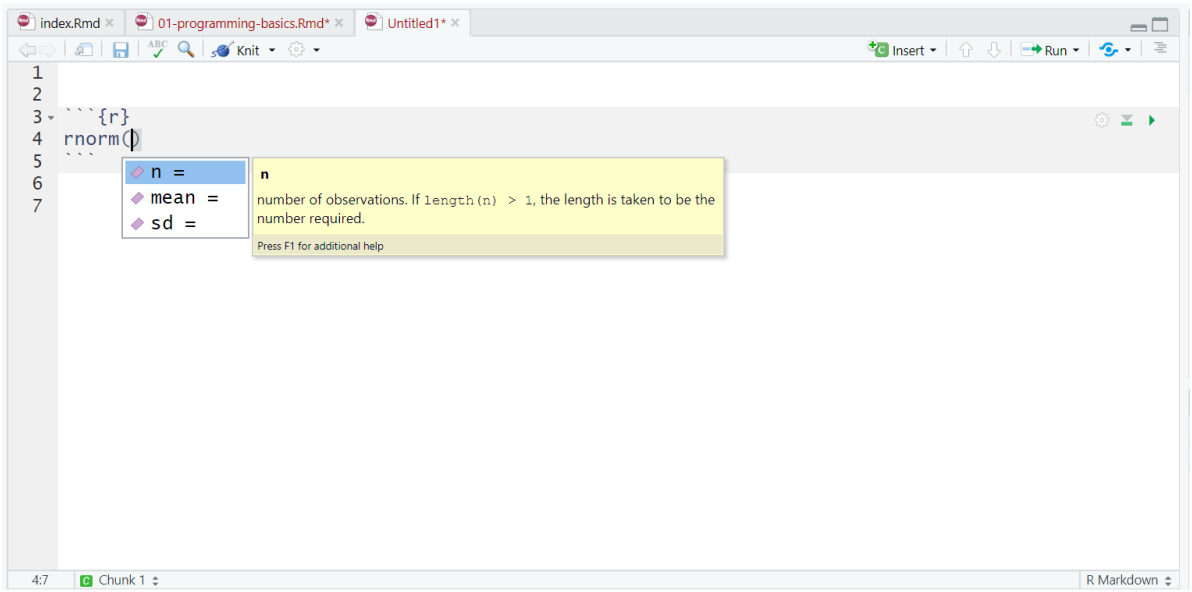


Figure 1.2: Tab auto-complete

1.4 Base R and packages

When you install R, you will have access to a range of functions including options for data wrangling and statistical analysis. The functions that are included in the default installation of R are typically referred to as **Base R** and there is a useful cheat sheet that shows many

Base R functions about halfway down this page under Contributed Cheatsheets here, along with a host of other cheatsheets you might find useful.

However, the power of R is that it is extendable and open source. If a function does not exist or does not work very well, anyone can create a new **package** that contains data and/or code to allow you to perform new tasks. You can think of **Base R** as the default apps that come on your phone and other packages as additional apps; the ones that you really want to use to make the phone your own, but you need to download them separately.

1.4.1 Activity 3 - Install the tidyverse to your own computer

To use a package, you must first install it. The following code installs the package `tidyverse`, a package we will use extensively throughout this course and introduce in the next chapter.

> ⚠ Warning
>
> **Please do not complete this activity if you are working on the online R server or if you are using the computers in a University lab or Boyd Orr Building.** You should only complete this activity on your own device. The university computers and server already have a version of all the packages we introduce you to, and installing a new version can cause problems by having a conflict between one version on your user profile and another version on the system profile.

If you are working on your own computer, use the code below to install the **tidyverse** and typing it into the console and pressing enter/return. Remember: if you are using the online R server or using a university computer, then skip this activity.

```
install.packages("tidyverse")
```

> ❗ Important
>
> If you have a Windows computer and get an error message that says something like "WARNING: Rtools is required to build R packages" you may need to download and install an extra bit of software called Rtools. This was part of the R/RStudio installation instructions, so please see Installing R for more detailed instructions.

You only need to install a package once, but each time you start R / RStudio, you must load the packages you want to use. This is like how you need to install an app on your phone once, but you need to open it every time you want to use it.

To load packages, we use the function `library()` which loads packages into your working library. Typically, you would start any analysis script by loading all of the packages you need, but we will come back to that in the next chapter.

1.4.2 Activity 4 - Load the tidyverse

Run the code below to load the tidyverse into your working library. You must complete this activity regardless of whether you are using your own computer or the university computers / online server.

```
library(tidyverse)
```

Often when you load packages you get information in your console window. Some packages will provide little messages to tell you what it has done or warn you about something. Sometimes these messages can look like errors and make you panic, but try and read over what it is saying first. For example, you should have something that looks like Figure Figure 1.3 when you load `tidyverse`. You might think you have done something wrong as it has little red crosses, but it is just telling you that it has loaded a set of packages and there are some **conflicts**.

```
> library(tidyverse)
── Attaching core tidyverse packages ──────────────────────────────────────── tidyverse 2.0.0 ──
✔ dplyr     1.1.3     ✔ readr     2.1.4
✔ forcats   1.0.0     ✔ stringr   1.5.1
✔ ggplot2   3.4.4     ✔ tibble    3.2.1
✔ lubridate 1.9.3     ✔ tidyr     1.3.0
✔ purrr     1.0.2
── Conflicts ────────────────────────────────────────────────────────── tidyverse_conflicts() ──
✖ dplyr::filter() masks stats::filter()
✖ dplyr::lag()    masks stats::lag()
ℹ Use the conflicted package to force all conflicts to become errors
```

Figure 1.3: Example loading message from tidyverse.

Now that we have loaded the `tidyverse` package, we can use any of the functions it contains but remember, you must run the `library()` function every time you start R.

1.4.3 Package updates

In addition to updates to R and R Studio, the creators of packages also update their code. This can be to add additional functions to a package, or it can be to fix errors.

One thing to avoid is unintentionally updating an installed package. When you run `install.packages()`, it will always install the latest version of the package and it will overwrite any older versions you may have installed. Often this is not a problem, but sometimes you will find that the update means your code no longer works as the package has changed substantially. It is possible to revert back to an older version of a package but try to avoid updating a package unintentionally.

> ⚠ Warning
>
> To avoid accidentally overwriting a package with a later version, you should **never** include `install.packages()` in your analysis scripts in case you, or someone else runs the code by mistake. Remember, the online server and university computers will already have all of the packages you need for this course, so you only need to install packages if you are using your own computer.

1.4.4 Package conflicts

There are thousands of different R packages and each package has many functions. Unfortunately, different people develop different packages and sometimes they use the same name for different functions. For example, the packages `dplyr` and `MASS` both have a function called `select()`. **Do not run the below code**, but if you did you would see a warning telling you that there is a conflict.

```
library(dplyr)
```

```
Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

```
library(MASS)
```

```
Attaching package: 'MASS'

The following object is masked from 'package:dplyr':

    select
```

You would see a warning that `The following object is masked from 'package:dplyr': select`.

In this case, R is telling you that the function `select()` in the `dplyr` package is being hidden (or 'masked') by another function with the same name from the `MASS` package. If you were to try and use `select()`, R would use the function from the package that was loaded most recently - in this case it would use the function from `MASS`. This can be an issue because you think you are using one function but really you are using another. They often work differently and you get odd issues in your code that you do not expect.

There are various solutions but one simple one - if you already know of the clash - is to specify which package you want to use for a particular function by writing the code in the format `package::function`, meaning "use the function from the package", for example:

```
dplyr::select()
MASS::select()
```

Clashes are inevitable in your learning and when you see one, you will probably not spot it at first but you will learn to resolve them quickly.

1.5 Objects

So far, you have learnt about packages, and functions and arguments. Earlier we said functions give us outputs and another name for outputs - or at least specific types of outputs - are **objects**.

Objects are the output of functions but you can also create objects without functions. Most of your coding will involve creating and manipulating objects. Objects contain stuff, which could be numbers, words, or the result of functions, operations, and analyses.

The first key thing to know about objects is how to create them and to give them content. You assign content to an object using `<-` - often called the "left arrow" or the **assignment operator** which you can read as "assigned to". Note that we do not use the `=` symbol as an assignment operator. There is a large discussion on why objects are assigned content and not equal to content but that is for another time. For now, just remember that we assign (`<-`) content, be it words, numbers, or function output, to objects.

1.5.1 Activity 5 - Create some objects

Type the following code into the console window and run each line. You should see that `name`, `age`, `today`, `new_year`, and `data` appear in the environment pane like Figure Figure 1.4.

```r
name <- "James"
age <- 16 + 14
today <- Sys.Date()
new_year <- as.Date("2025-01-01")
data <- rnorm(n = 10, mean = 15, sd = 3)
```

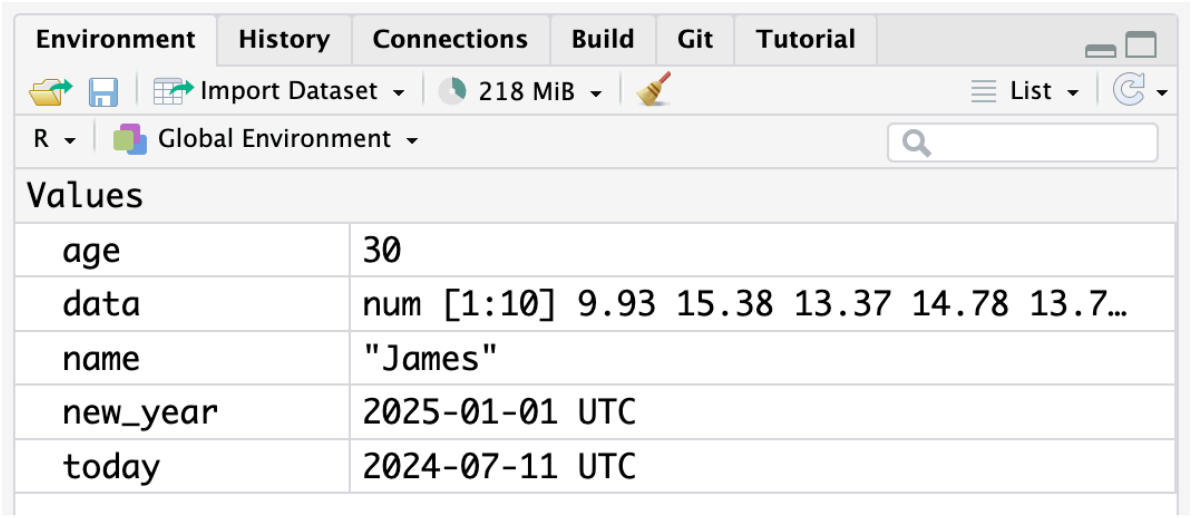


Figure 1.4: Objects in the environment. Feel free to change your numbers and check that they match the environment!

Note that in these examples, `name`,`age`, and `new_year` would always contain the values `James`, 30, and the date of New Year's Day 2025, but `today` will draw the date from the operating system on the day you are using the computer, and `data` will be a randomly generated set of data - as we saw earlier - so the values of these objects will not be static.

> **Try this**
>
> Try changing the name to your name and the age to your age, and seeing if they update in the environment window.

Importantly, for what we will learn in future chapters, you can use different objects in calculations and interact with each other. For example:

```r
age + 10
```

```
[1] 40
```

```
new_year - today
```

```
Time difference of -259 days
```

```
mean(data)
```

```
[1] 14.41643
```

Finally, you can store the result of these operations on objects in a new object as below:

```
decade <- age + 10
```

Remember that you may find it helpful to read `<-` as `contains` or `assigned to`, e.g., `name` contains the text `James` or `James` is assigned to the object `name`.

You will constantly be creating objects throughout this course and you will learn more about them and how they behave as we go along. For now, it is enough to understand that they are a way of saving values, that these values can be numbers, text, or the result of operations, and that you can use objects in further operations to create new objects.

> **i** What should I call objects?
>
> In coding, we are trying to balance keeping objects names as short as possible to be easy to type repeatedly, while being informative enough that you know what they represent days, weeks, or months later when they are not fresh in your memory.
> For example, `dob` might save time now, but `birth_date` will be easier to understand in future.

1.5.2 Looking after the environment

Now that you are starting to learn about the other windows in RStudio like the environment window, if you have been writing a lot of code, you may find that the environment window (or workspace) becomes cluttered with many objects. This can make it difficult to figure out which object you need and you run the risk of using the wrong value or data frame. If you are working on a new dataset, or if you have tried lots of different code before getting the final version, it is good practice to remember to clear the environment to avoid using the wrong object. You can do this in several ways.

1. To remove individual objects, you can type `rm(object_name)` in the console. Try this now to remove one of the objects you created in the previous section. For example, you would remove the object `age` by writing `rm(age)`.

2. To clear all objects from the environment, run `rm(list = ls())` in the console.
3. To clear all objects from the environment, you can also click the broom icon in the environment pane like Figure Figure 1.5.

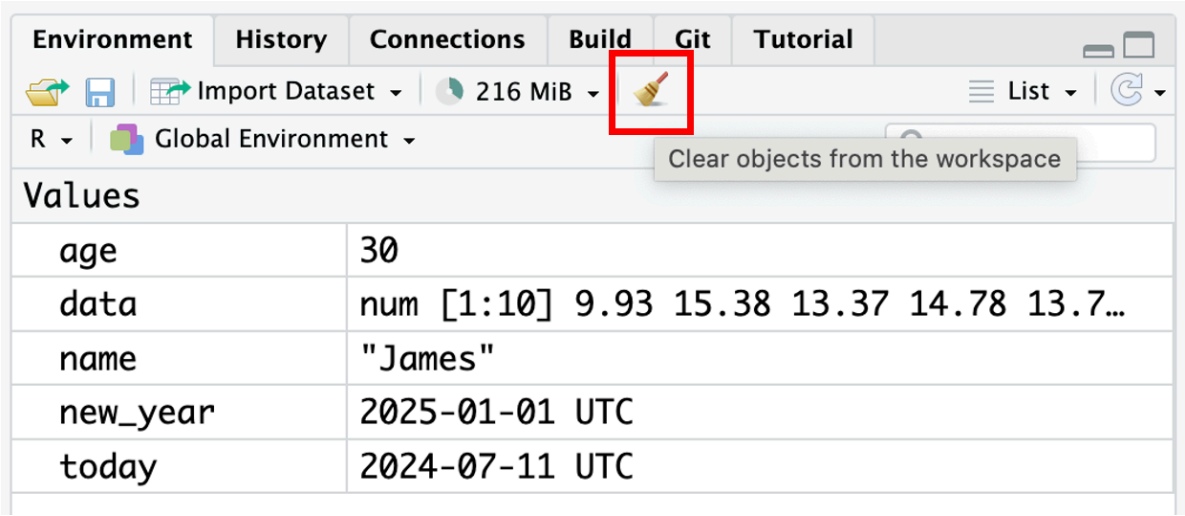


Figure 1.5: Clearing the workspace.

1.6 Global options

When you open RStudio, it will show you what you were last working on, including your code and any objects you have created, assuming this is not the first time you have used RStudio. This might sound helpful, but it can cause more problems than it is worth because it means that you risk accidentally using an old version of an object.

For example, you might have `Date` in the environment from the last time you did some work and you start working on the wrong `Date` without realising. In reality, we recommend changing the settings so that each time you start RStudio, it opens a fresh new environment.

You can do this by clicking on the top menu **`Tools >> Global Options...`** and then deselecting boxes so that your General box looks like Figure Figure 1.6 and applying the changes to save your selections.

That should save a lot of hassle going forward. You will still encounter issues of course, so we are going to end this chapter by outlining where you can get help.

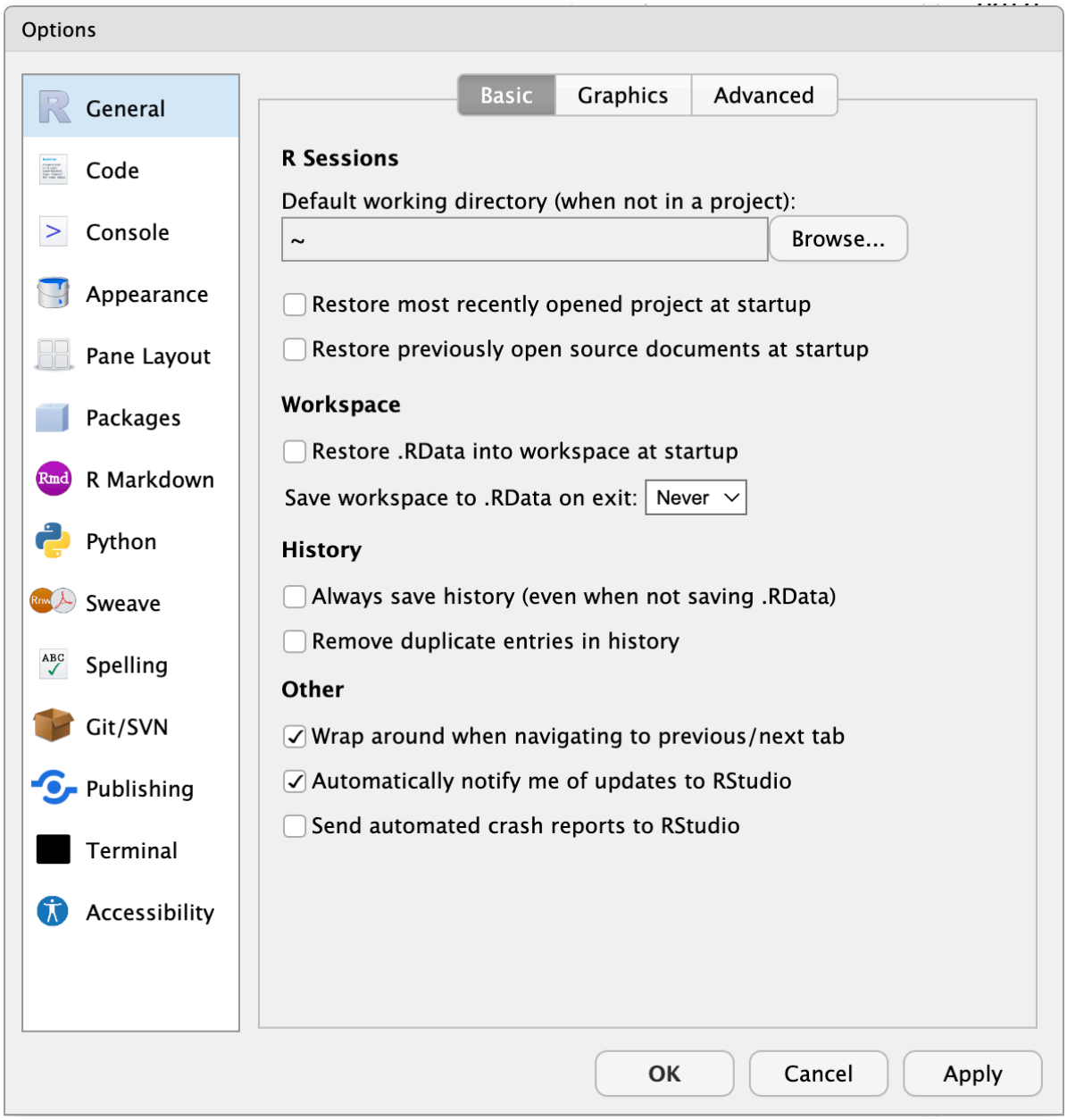


Figure 1.6: Global options - you want to make your global options look similar, in terms of what is ticked, to the above. The main thing is to make sure that you untick Restore RData into workspace at startup, and set Save workspace to .RData on exit to Never. Unticking the History options are optional but can help. The update option is really just in case you want to.

1.7 Getting Help

1.7.1 Help and additional resources

Learning to code really means trying stuff out, searching for help online when it does not work, and finding examples of code to adapt to your own needs.

If you are having difficulty with any of the content in this book, then you can of course ask for help from the course team but learning to problem solve effectively is a key skill that you will develop throughout this course and beyond.

There are a wealth of additional resources in the Appendix of this book, so it might be worth checking them out, but here are four approaches we take to resolving an issue when we hit a problem.

- Use the help documentation. If you are struggling to understand how a function works or what the arguments are, remember the `?function` command.
- Think about when you last had to use this function or code successfully. Look back on what you did then and see what is the difference.
- If you get an error message, copy and paste it into Google. It is very likely someone else has had the same problem.
- Trying Googling your question in the style of the package name or function name and what you want to do. For example, **arrange data tidyverse** or maybe **sort data in R**.

If those approaches do not work, in addition to these course materials and the other PsyTeachR books from other courses we run, there are many excellent online resources for learning data skills that can serve as quick guides:

- Individual package cheat sheets which you can find via the top menu: **`Help >> Cheat Sheets`**.
- R Cookbook.
- StackOverflow.
- R for Data Science.

1.7.2 Debugging tips

Another top skill for resolving issues is what is known as debugging - fixing your coding mistakes. A large part of coding is trying to figure why your code does not work and this is true whether you are a novice or an expert. As you progress through this course, try and keep a record of mistakes you make and how you fixed them. We will highlight common mistakes to look out for throughout the book but you will undoubtedly make (and fix) new mistakes yourself.

You never stop making mistakes, you just get better at problem solving and having a list of strategies that worked in the past. That is why we include **error mode** as a set of activities to develop your problem solving skills and normalise making errors.

As a short list of suggestions when you come across an error, keep in mind:

- Have you loaded the correct packages for the functions you are trying to use? One common mistake is to write the code to load the package, e.g., `library(tidyverse)` but then forget to press enter/return to run it.
- Have you made a typo? Coding has to be specific on spelling and `data` is not the same as `DATA`, and `t.test` is not the same as `t_test`.
- Is there a package conflict? Have you tried specifying the package and function with `package::function`?
- Is it definitely an error? Not all red text in R / RStudio means an error. Sometimes it is just giving you a message with information.

1.7.3 Activity 6 - Reset your R session

Finally, if you find that your code is not working and you cannot figure out why, it might be worth starting a new session. This will clear the environment and detach all loaded packages. Think of it like restarting your phone.

When you open up R and start writing code, loading packages, and creating objects, you are typically doing so in a new **session**. In addition to clearing your environment workspace, it can sometimes be useful to start a new session. This will happen automatically each time you start RStudio on your computer, although sessions can persist if you use the online server.

This last activity shows a quick way to restart R from inside RStudio. On the Top Menu, click **`Session >> Restart R`** like Figure Figure 1.7.

Try not to worry about making mistakes. Accept that you will make them and learn from them. We are always here to help if you are struggling, so reach out to the course team, post on Teams, or attend a graduate teaching assistant (GTA) session.

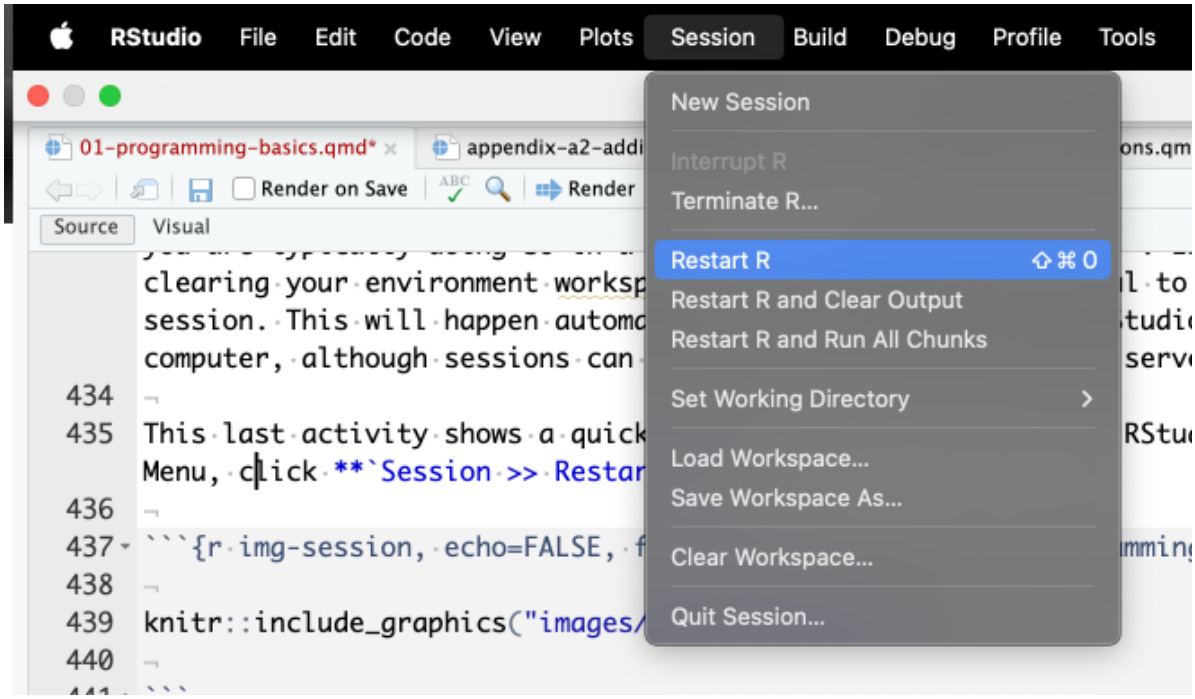


Figure 1.7: Restarting your R session from within RStudio.

1.8 Test yourself

Throughout the book, you will find additional questions and activities like these to help you check your understanding. Some will have blanks to fill in, some will be multiple choice, but the chapters include the answers and explanations to check your understanding against. You are always welcome to ask further questions to the course team though.

1.8.1 Knowledge check

Question 1. Why should you never include the code `install.packages()` in your analysis scripts?

- (A) You should use library() instead
- (B) Packages are already part of Base R
- (C) You (or someone else) may accidentally install a package update that stops your code working
- (D) You already have the latest version of the package

Explain this answer

Remember, when you run `install.packages()` it will always install the latest version of the package and it will overwrite any older versions of the package you may have installed.

Question 2. What will the following code produce?

```
rnorm(6, 50, 10)
```

- (A) A dataset with 10 numbers that has a mean of 6 and an SD of 50
- (B) A dataset with 6 numbers that has a mean of 50 and an SD of 10
- (C) A dataset with 50 numbers that has a mean of 10 and an SD of 6
- (D) A dataset with 50 numbers that has a mean of 10 and an SD of 6

Explain this answer

The default form for `rnorm()` is `rnorm(n, mean, sd)`. If you need help remembering what each argument of a function does, look up the help documentation by running `?rnorm`.

Question 3. If you have two packages that have functions with the same name and you want to specify exactly which package to use, what code would you use?

- (A) package::function
- (B) function::package
- (C) library(package)
- (D) install.packages(package)

Explain this answer

You should use the form `package::function`, for example `dplyr::select`. Remember that when you first load your packages R will warn you if any functions have the same name - remember to look out for this!

Question 4. Which of the following is most likely to be the input to an argument?

- (A) read_csv()
- (B) 35
- (C) <-

Explain this answer

read_csv() looks like a function as it has the round brackets at the end and the <- is the assignment symbol, so it is most likely that 35 might be the input to an argument as it is just a value.

Question 5. An easy way to spot functions is to look for

- (A) round brackets
- (B) computers
- (C) numbers

Explain this answer

Remember that functions tend to have round brackets or parentheses at the end of their name and the arguments and values go inside the parentheses.

Question 6. The job of `<-` is to send the output from the function to a/an

- (A) object
- (B) assignment
- (C) argument

Explain this answer

This is the assignment operator (`<-`) and we use it to assign content such as the output of functions to an object.

1.8.2 Error mode

The following questions are designed to introduce you to making and fixing errors. Try and run the code, look at the error message, and see if you can fix it before checking the answer.

Consider keeping a note of what kind of error messages you receive and how you fixed them, so you have a bank of solutions when you tackle errors independently.

Question 7. Type the following code into the console and press enter/return: `rnorm(n = 10, meen = 5, sd = 1)`. You should get an error saying something like `Error in rnorm(n = 10, meen = 5, sd = 1) : unused argument (meen = 5)`. How can you fix it?

Explain this answer

We accidentally spelt one of the arguments incorrectly. If you look closely, you will see that we typed `meen` spelt with two es instead of one e when we should have typed `mean`.

Question 8. To end on a sneaky one that we have not covered in this chapter, type the following code into the console and press enter/return: `rnorm(n = 10, mean = 5, sd = 1`. What happened and how can you fix it? Before checking the explain this answer box below, maybe try and Google what happens to see if you can describe it and find a solution.

Explain this answer

We missed the final bracket, so we start the function name `rnorm(`, enter our arguments, but there is no closing bracket. You will see in the console like Figure Figure 1.8, there is a little `+` symbol and you can enter new code, but there is no output.

```
> rnorm(n = 10, meen = 5, sd = 1
+
```

Figure 1.8: An R function without a closing bracket in the console.

This can be really frustrating as it looks like nothing is happening, but when you did not add a closing bracket, R is just sitting there waiting for you to add something else. To fix it, you can either type `)` and press enter/return to finish the function and it should work, or you can press the escape (esc) key to cancel the code and start again.

1.9 Words from this Chapter

Below, you will find a list of words that we used in this chapter that might be new to you in case you need to refer back to what they mean. The links in this table take you to the entry for the words in the PsyTeachR Glossary. Note that numerous members of the team wrote

entries in the Glossary and as such the entries may use slightly different terminology from what we used in the chapter.

term	definition
argument	A variable that provides input to a function.
assignment-operator	The symbol <-, which functions like = and assigns the value on the right to the object on the left
base-r	The set of R functions that come with a basic installation of R, before you add external packages.
conflict	Having two packages loaded that have a function with the same name.
console	The pane in RStudio where you can type in commands and view output messages.
default-value	A value that a function uses for an argument if it is skipped.
environment	A data structure that contains R objects such as variables and functions
function	A named section of code that can be reused.
mean	A descriptive statistic that measures the average value of a set of numbers.
normal-distribution	A symmetric distribution of data where values near the centre are most probable.
object	A word that identifies and stores the value of some data for later use.
package	A group of R functions.
r-markdown	The R-specific version of markdown: a way to specify formatting, such as headers, paragraphs, lists, bolding, and links, as well as code blocks and inline code.
rstudio	An integrated development environment (IDE) that helps you process R code.
script	A plain-text file that contains commands in a coding language, such as R.
session	When you start R/RStudio and executive code to fill the workspace until you close R/RStudio
standard-deviation	A descriptive statistic that measures how spread out data are relative to the mean.
tidyverse	A set of R packages that help you create and work with tidy data

1.10 End of chapter

Well done on reaching the end of the first chapter! This was one of the longest chapters in the book to introduce you to several foundational concepts of coding in R and RStudio. The next chapter builds on these skills to produce something a little more concrete by showing you how to create reproducible documents.

2 Creating Reproducible Documents

In this chapter, we introduce you to using code to create **reproducible research**. Creating reproducible research means you will write text and code that completely and transparently performs an analysis from start to finish in a way that produces the same result for different people using the same software on different computers. We will cover things such as file structure and setting a working directory, using **R Markdown** files, and writing code chunks.

As well as improving transparency with others researchers, reproducible research benefits **you**. When you return to an analysis or task after days, weeks, or months, you will thank past you for doing things in a transparent, reproducible way, as you can easily pick up right where you left off.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Understand and set your working directory, either manually or through creating an R project.
- Create a knit an R Markdown file to create a reproducible document.
- Use inline code to combine text and code output in your reproducible documents.
- Identify and fix common errors in knitting R Markdown files.

2.1 File structure, working directories, and R Projects

In chapter 1, we never worked with files, so you did not have to worry about where you put things on your computer. Before we can start working with R Markdown files, we must explain what a **working directory** is and how your computer knows where to find things.

Your working directory is the folder where your computer starts to look for files. It would be able to access files from within that folder and within sub-folders in your working directory, but it would not be able to access folders outside your working directory.

In this course, we are going to prescribe a way of working to support an organised file system, helping you to know where everything is and where R will try to save things on your computer and where it will try to save and load things. Once you become more comfortable working with

files, you can work in a different way that makes sense to you, but we recommend following our instructions for at least RM1 as the first course.

2.1.1 Activity 1: Create a folder for all your work

In your documents or OneDrive, create a new folder called `ResearchMethods1_2`. This will be your highest level folder where you will save everything for Research Methods 1 and 2.

> **Top tip**
>
> When you are a student at the University of Glasgow, you have access to the full Microsoft suite of software. One of those is the cloud storage system OneDrive. We heavily recommend using this to save all your work in as it backs up your work online and you can access it from multiple devices.

Within that folder, create two new folders called `Assessments` and `Quant_Fundamentals`. In `Assessments`, you can save all your assessments for RM1 and RM2 as you come to them. In `Quant_Fundamentals`, that is where you will save all your work as you progress through this book.

Within `Quant_Fundamentals`, create a new folder called `Chapter_02_reproducible_docs`. As you work through the book, you will create a new chapter folder each time you start a new chapter and the sub-folders will always be the same. Within `Chapter_02_reproducible_docs`, create two new folders called `data` and `figures`. As a diagram, it should look like Figure 2.1.

> **How to name files and folders**
>
> You might notice in the folder names we avoided using spaces by adding things like underscores _ or capitalising different words. Historically, spaces in folder/file names could cause problems for code, but now it's just slightly easier when file names and folder names do not have spaces in them.
> For naming files and folders, try and choose something sensible so you know what it refers to. You are trying to balance being as short as possible, while still being immediately identifiable. For example, instead of fundamentals of quantitative analysis, we called it `Quant_Fundamentals`.

> **Warning**
>
> When you create and name folders to use with R / RStudio, whatever you do, do not call the folder "R". If you do this, sometimes R has an identity crisis and will not save or load your files properly. It can also really damage your setup and require you to reinstall everything as R tends to save all the packages in a folder called R. If there is another

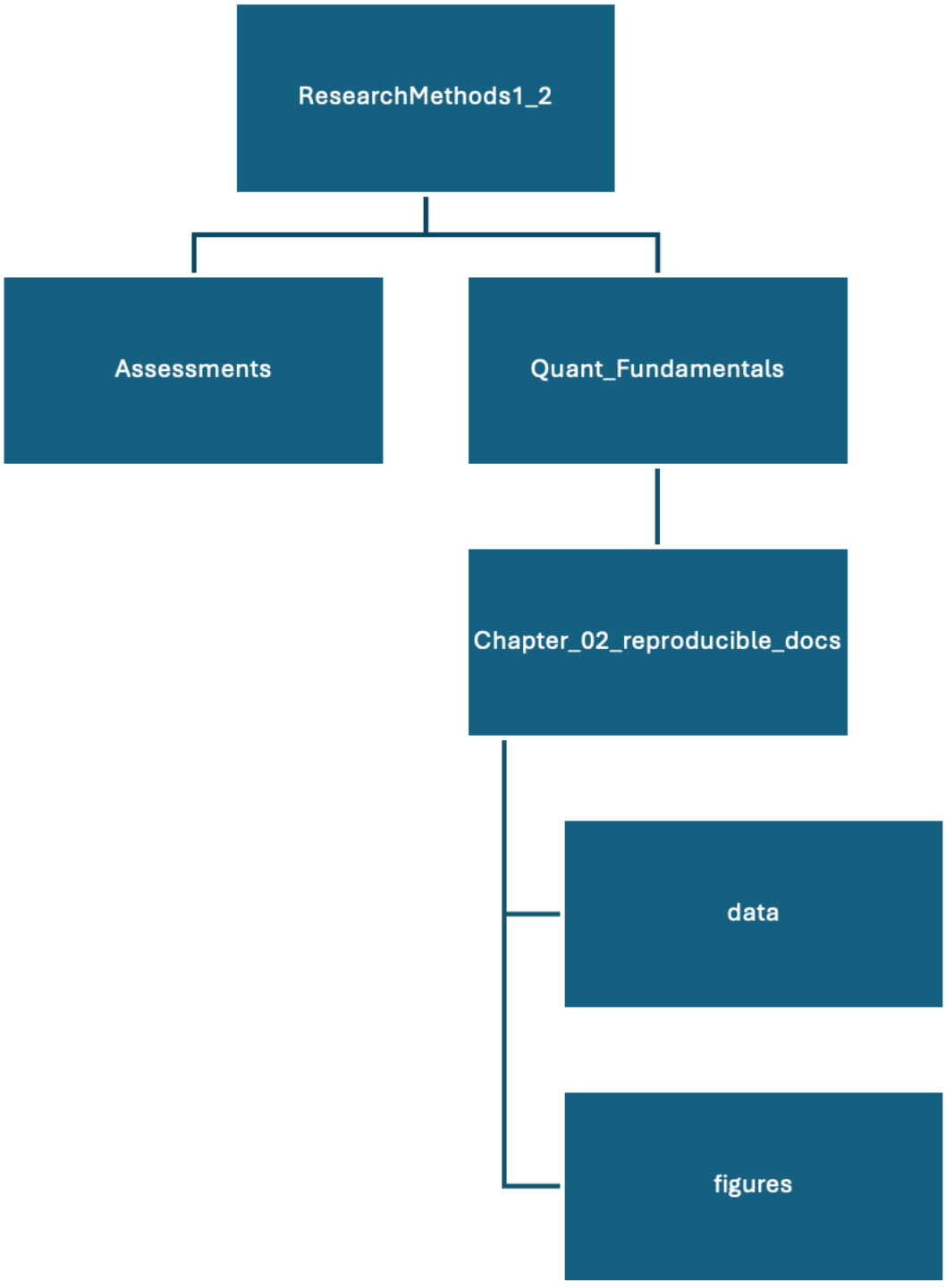


Figure 2.1: Prescribed file structure for RM 1 and RM 2.

folder called R, then it gets confused and stops working properly.

File management when using the online server

If we support you to use the online University of Glasgow **R Server**, working with files is a little different. If you downloaded R / RStudio to your own computer or you are using one of the library/lab computers, please ignore this section.
The main disadvantage to using the R server is that you will need create folders on the server and then upload and download any files you are working on to and from the server. Please be aware that **there is no link between your computer and the R server**. If you change files on the server, they will not appear on your computer until you download them from the server, and you need to be very careful when you submit your assessment files that you are submitting the right file. This is the main reason we recommend installing R / RStudio on your computer wherever possible.
Going forward throughout this book, if you are using the server, you will need to follow an extra step where you also upload them to the sever. As an example:

1. Log on to the **R server** using the link we provided to you.
2. In the file pane, click `New folder` and create the same structure we demonstrated above.
3. Download `ahi-cesd.csv` and `participant-info.csv` into the `data` folder you created for chapter 2. To download a file from this book, right click the link and select "save link as". Make sure that both files are saved as ".csv". Do not open them on your machine as often other software like Excel can change setting and ruin the files.
4. Now that the files are stored on your computer, go to RStudio on the server and click `Upload` then `Browse` and choose the folder for the chapter you are working on.
5. Click `Choose file` and go and find the data you want to upload.

2.1.2 Manually setting the working directory

Now that you have a folder structure that will keep everything nice and organised, we will demonstrate how you can manually **set the working directory**. If you open RStudio, you can check where the current working directory is by typing the function `getwd()` into the console and pressing enter/return. That will show you the current file path R is using to navigate files. If you look at the Files window in the bottom right, this will also show you the files and folders available from your working directory.

If you click on the top menu `Session >> Set Working Directory >> Choose Directory...`,

(Figure 2.2) you can navigate through your documents or OneDrive until you can select `Chapter_02_reproducible_docs`. Click open and that will set the folder as your working directory. You can double check this worked by running `getwd()` again in the console.

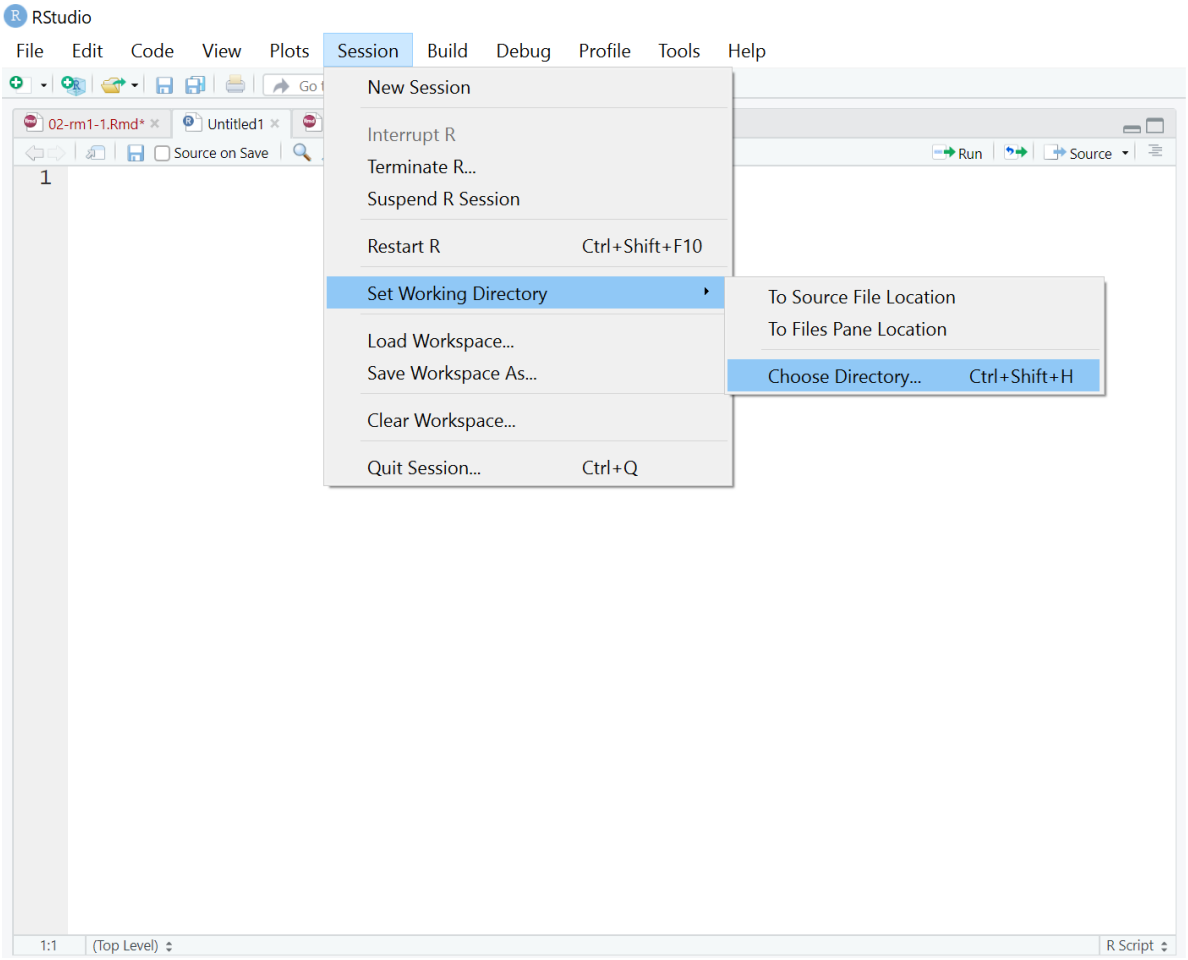


Figure 2.2: Manually setting the working directory.

2.1.3 Activity 2 - Creating an R Project

Knowing how to check and manually set your working directory is useful, but there is a more efficient way of setting your working directory alongside organised file management. You are going to create something called an **R Project**.

To create a new project for the work you will do in this chapter (Figure 2.3):

1. Click on the top menu and navigate to `File >> New Project...`.

2. You have the option to select from New Directory, Existing Directory, or Version Control. You already created a folder for `Chapter_02_reproducible_docs`, so select Existing Directory.

3. Click Browse... next to Project working directory to select the folder you want to create the project in.

4. When you have navigated to `Chapter_02_reproducible_docs` for this chapter, click Open and then Create Project.

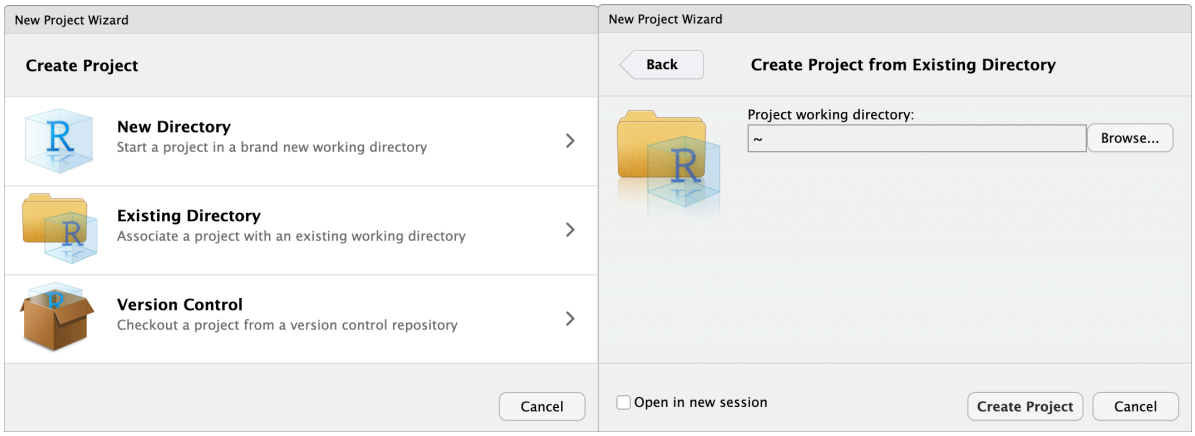


Figure 2.3: Starting a new project.

RStudio will restart itself and open with this new project directory as the working directory. You should see something like Figure 2.4.

In the files tab in the bottom right window, you will see all the contents in your project directory. You can see your two sub-folders for data and figures and a file called `Chapter_02_reproducible_docs.Rproj`. This is a file that contains all of the project information. When you come back to this project after closing down RStudio, if you double click on the .Rproj file, it will open up your project and have your working directory all set up and ready to go.

> **Warning**
>
> In each chapter, we will repeat these instructions at the start to prescribe this file structure, but when you create your own folders and projects, do not ever save a new project **inside** another project. This can cause some hard to resolve problems. For example, it would be fine to create a new project within the `Quant_Fundamentals` folder as we will do for each new chapter, but should never create a new project within the `Chapter_02_reproducible_docs` folder.

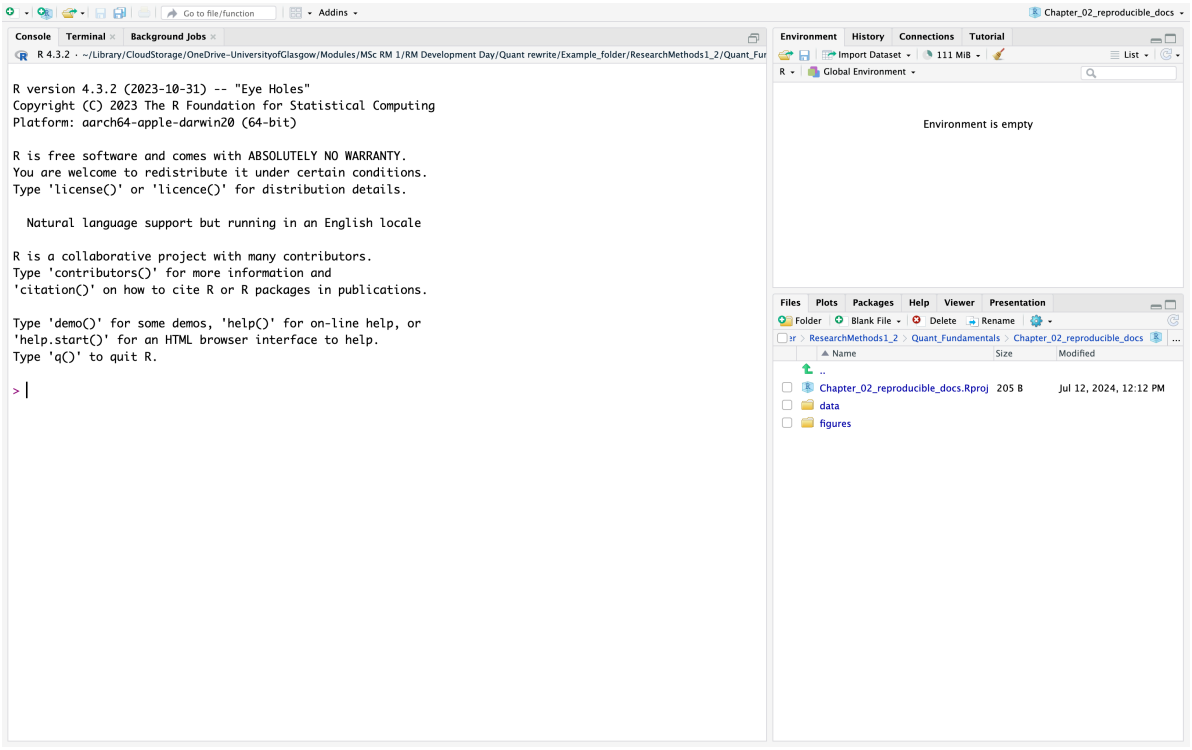


Figure 2.4: RStudio screen in a new project in your chapter 2 folder.

2.2 Creating and navigating R Markdown documents

Now you know how to navigate files and folders on your computer, we can start working with R Markdown files.

Throughout this data skills book and related assignments, you will use a file format called R Markdown (abbreviated as .Rmd) which is a great way to create dynamic documents combining regular text and embedded code chunks.

R Markdown documents are self-contained and fully reproducible, meaning if you have the necessary data, you should be able to run someone else's analyses. This is an important part of your open science training as one of the reasons we teach data skills this way is that it enables us to share open and reproducible information.

Using these worksheets enables you to keep a record of all the code you write as you progress through this book (as well as any notes to help yourself), for data skills assessments we can give you a task to add required code, and in your research reports you can independently process, visualise, and analyse your data all from one file.

For more information about R Markdown, feel free to have a look at their main webpage http://rmarkdown.rstudio.com, but for now the key advantage to know about is that it allows you to write code into a document, along with regular text, and then **knit** it to create your document as either a webpage (**html**), a PDF, or Word document (.docx).

2.2.1 Activity 3: Open, save, and knit a new R Markdown document

Open a new R Markdown document by clicking the 'new item' icon and then click 'R Markdown' like Figure 2.5.

After selecting R Markdown, there are different format options you can explore in time, but Select Document and there are four boxes to complete:

- Title: This is the title for the document which will appear at the top of the page. For this chapter, enter `02 Creating Reproducible Documents`.
- Author: This is where you can add your name or names for multiple people. For this chapter, enter your GUID as this will be good practice for the data skills assignments.
- Date: By default, it adds today's date, so it will update every time you knit the document. Leave the default so you know when you completed the chapter, but if you untick, you can manually enter a static date.
- Default Output Format: You have the option to select from html, PDF, and Word. We will demonstrate how to change output format in a later chapter, so keep html for now as it's the most flexible format.

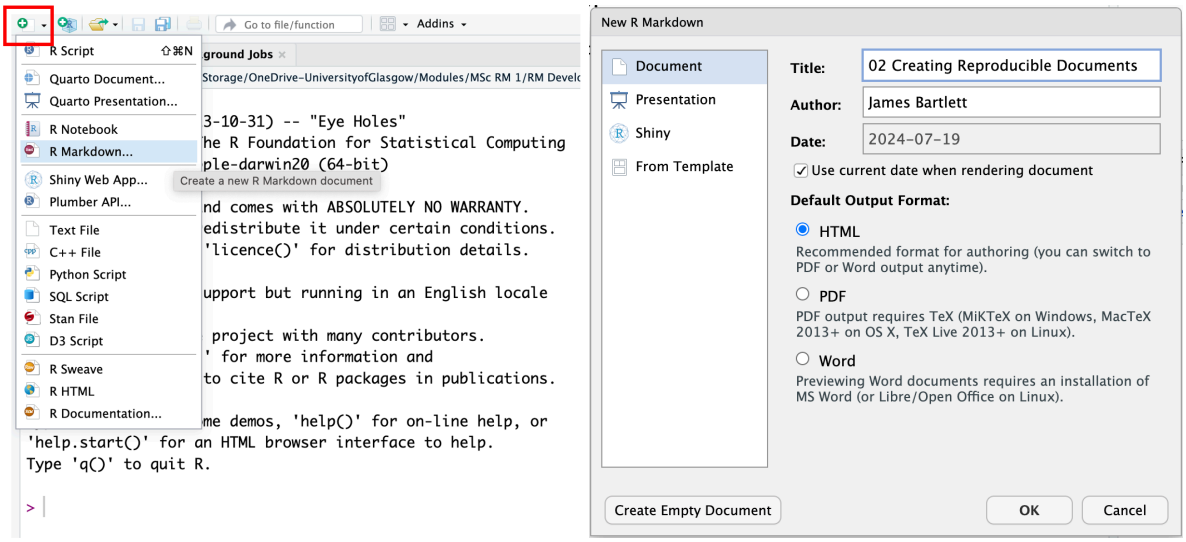


Figure 2.5: Creating a new R Markdown document from the menu (left) and setting title, author, date, and output (right).

Once you click **OK**, this will open a new R Markdown document.

Save this R Markdown document by clicking **`File >> Save as`** from the top menu, and name this file "`02_reproducible_docs`". Note the document title and file name are separate, so you still have to name the file when you save it.

If you have set the working directory correctly, you should now see this file appear in your Files window in the bottom right hand corner like Figure 2.6, alongside your .Rproj file and two folders.

Now you have the default version of the R Markdown file, you have a bunch of text and code to show its capabilities (Figure 2.7).

We will now demonstrate what it looks like to **knit** a document. This means that we are going to compile (i.e., turn) our code into a document that is more presentable. This way, you can check it knits and there are no errors. So, as we add changes in the following activities, you can identify if and when any errors appear and fix them quicker.

At the top of your R Markdown window, you should see a Knit button next to a little ball of yarn (Figure 2.8). If you click that, the document will knit and produce a html file.

You will see a small version of the knitted document appear in the Viewer tab in the bottom right of your screen. You will also see it has created a new file in your working directory. It will have the same name as your R Markdown file, but with .html as the file ending. You can view the knitted document by clicking the "Show in new window" button or opening the file

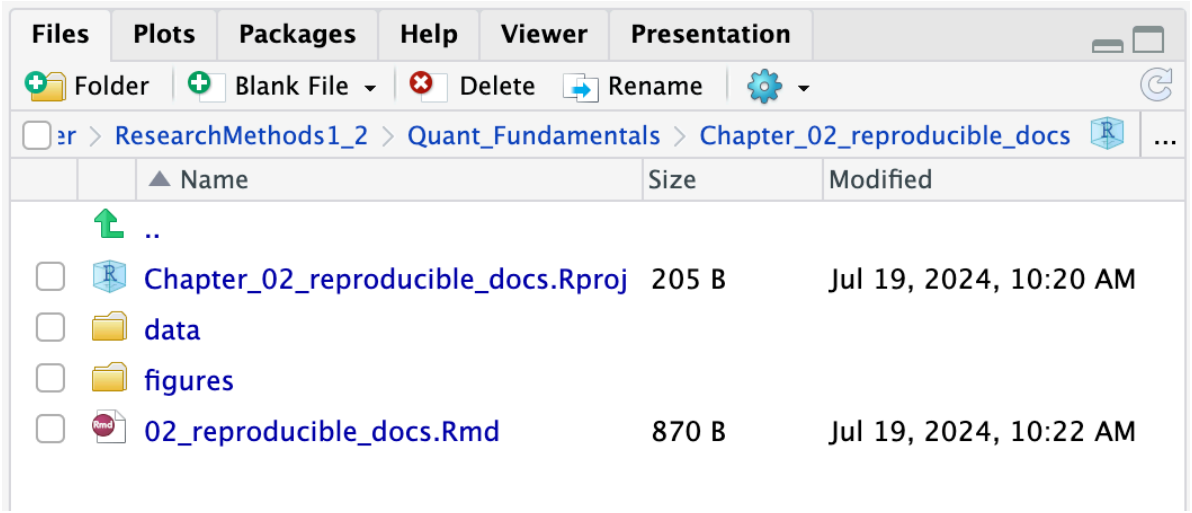


Figure 2.6: New .Rmd file in your working directory.

from your folder (Figure 2.9). This should open the document in your default internet browser as websites are created in html.

Now everything is working and knitting, we can start editing the R Markdown file to add new content.

2.2.2 Activity 4: Create a new code chunk

Let's start using your new R Markdown document to combine code and text. Follow these steps:

1. Delete **everything** below line 10.

> **i** What does the {r setup} chunk do?
>
> At the moment, you do not need to worry about the code chunk between lines 8 and 10. We are slowly introducing you to different features in R Markdown as it's easier to understand by doing, rather than giving you a list of explanations.
> If you are really curious though, this setting forces R Markdown to show both the code and output for all code chunks. When we add code shortly, if you change it to `echo = FALSE`, it will only show the output and not the code.

2. On line 12, type "## About me".

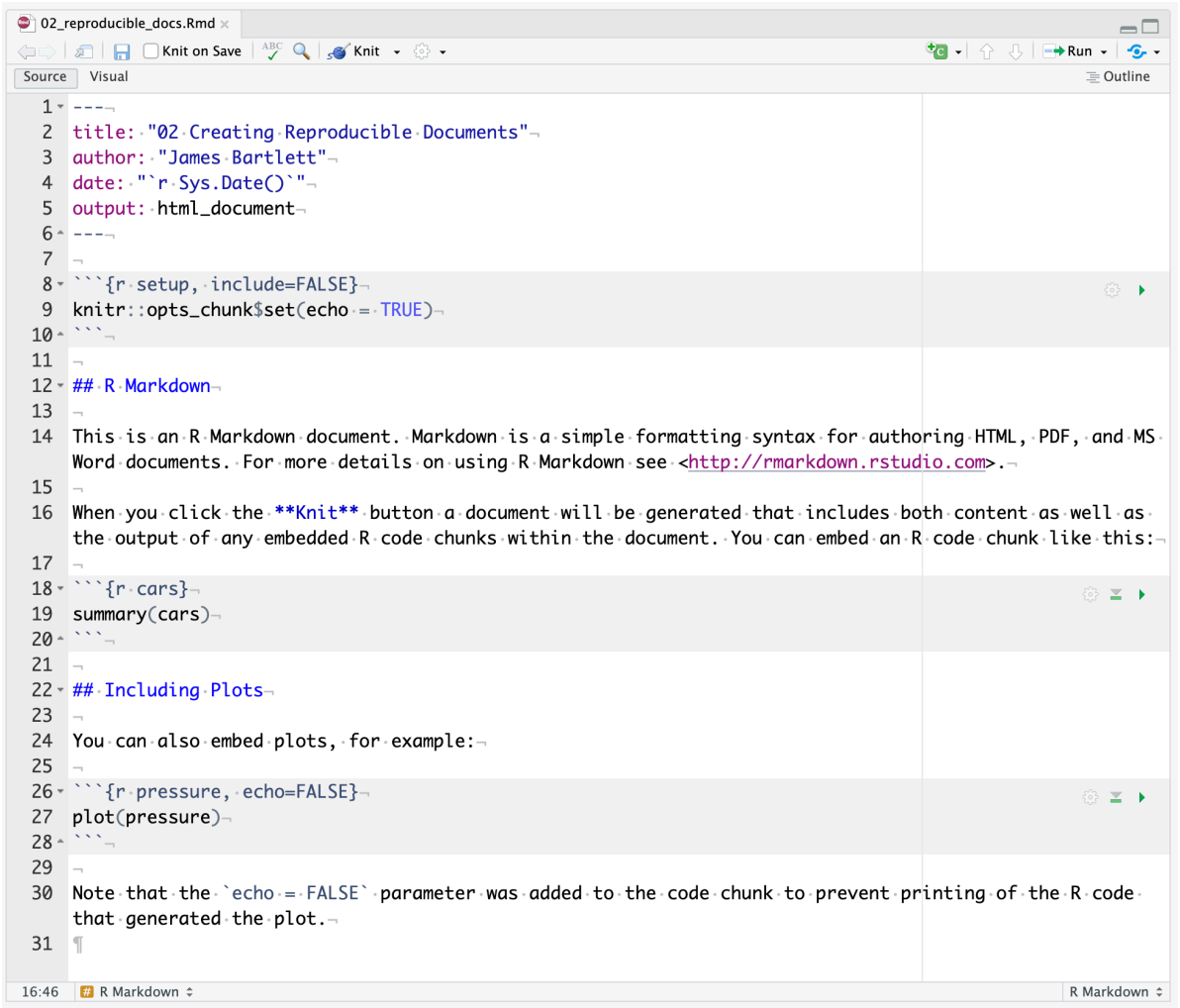


Figure 2.7: Default text and code in a new R Markdown document.

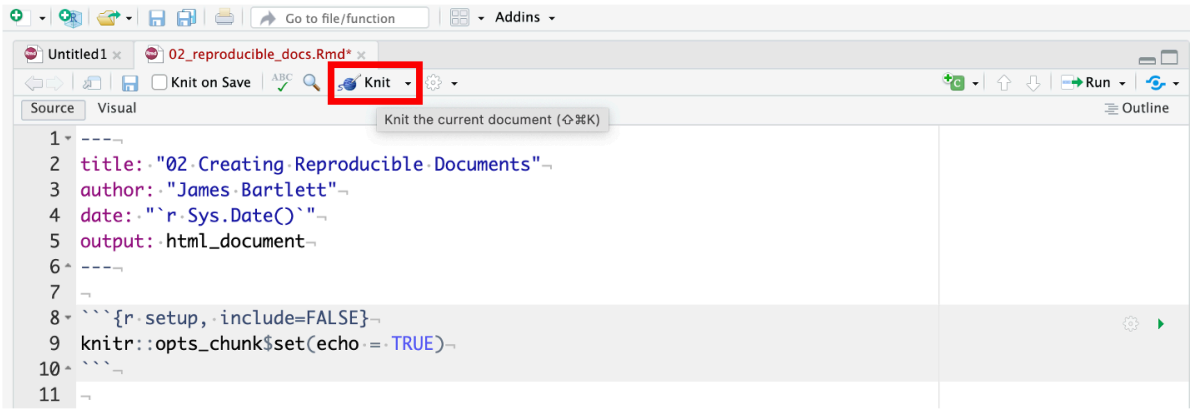


Figure 2.8: Clicking the knit button on a .Rmd document.

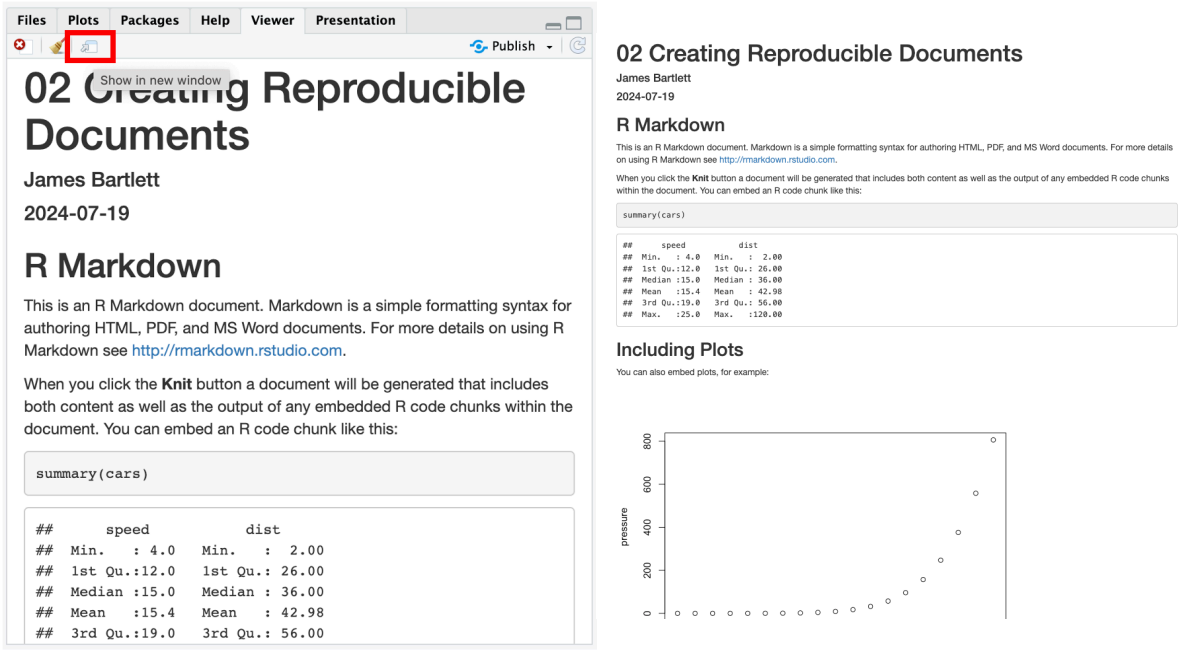


Figure 2.9: On the left, you can see a small version of the knitted document in the Viewer tab. On the right, you can see the full version open in your internet browser.

3. With your cursor on line 14, insert a blank code chunk by clicking on the top menu **`Code >> Insert Chunk`** or using the shortcut at the top of the R Markdown window that looks like a small green c and select R.

Your document should now look something like Figure 2.10.

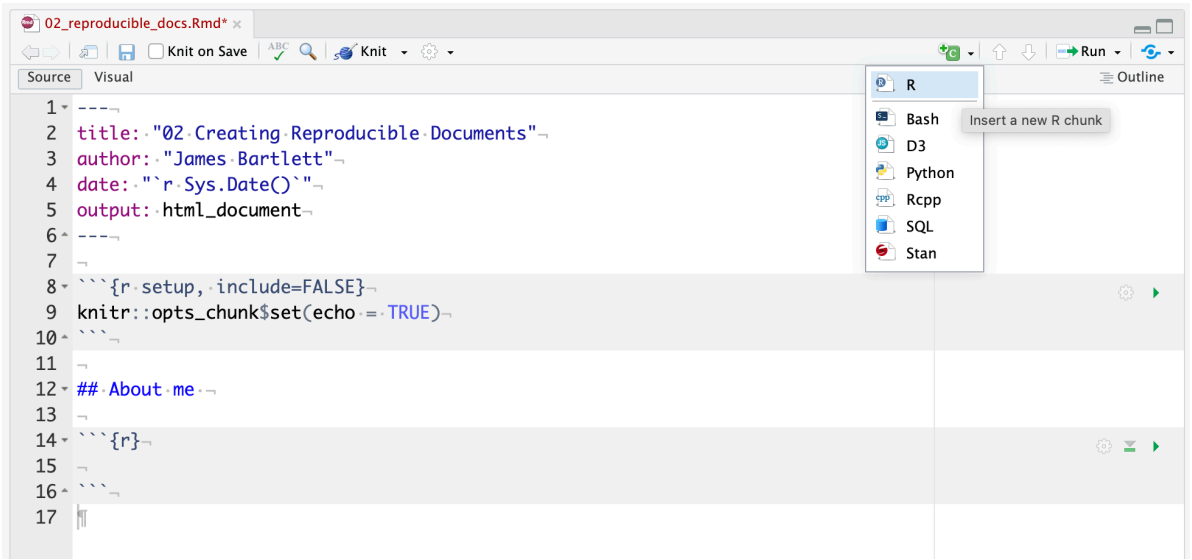


Figure 2.10: Creating a new R chunk in your blank R Markdown document

What you have created is called a **code chunk**. R Markdown assumes anything written outside of a code chunk is just normal text, just like you would have in a text editor like Word. It assumes anything written inside the code chunk is R code. This makes it easy to combine both text and code in one document.

> **!** Error mode
>
> When you create a new code chunk, you should notice that the grey box starts and ends with three back ticks (```), followed by the {r}, and then it ends with three back ticks again. This is the structure that creates a code chunk. You could actually just type this structure instead of using the `Insert` approach but we are introducing you to some shortcuts
> One common mistake is to accidentally delete one or more of these back ticks. A useful thing to notice is that code chunks tend to have a different color background - in the default appearance of RStudio a code chunk is grey and the normal text is white. You can use this to look for mistakes. If the colour of certain parts of your Markdown does not look right, check that you have not deleted the backticks.
> Remember it is backticks (i.e. this ‘) and not single quotes (i.e. not this ’).

Markdown language

When you typed "## About me", you might notice the two hashes. You will see the effect of this shortly, but this is using **Markdown** language to add document formatting. Markdown is a type of formatting language, so instead of using buttons to add features like you would in Word, you add symbols which will produce different features when you knit the document.
The hashes create headers. One (#) creates a first level header (larger text), two (##) creates a second level header, and so on. Make sure there is a space between the text and hash or it will not knit properly.
As we progress through the book, we will slowly introduce you to different Markdown features, but you can see the RStudio Markdown Basics page if you are interested.

2.2.3 Activity 5: Write some code

Now we are going to use the code examples you read about in Chapter 1 - Introduction to programming with R/R Studio - to add some code to our R Markdown document.

In your code chunk, write the code below but replace the values of name/age/birthday with your own details). Remember that the four lines of code should all be inside the code chunk.

Note: Text and dates need to be contained in quotation marks, e.g., "my name". Numerical values are written without quotation marks, e.g., 45.

```
name <- "James"
age <- 30
today <- Sys.Date()
next_birthday <- as.Date("2025-02-18") # Year, month, day format
```

Error mode

Missing and/or unnecessary quotation marks are a common cause of code not working. For example, if you try and type `name <- James`, R will try and look for an object called `James` and throw an error since there is not an object called that. When you add quotation marks, R recognises you are storing a character.

2.2.4 Activity 6: Run your code

We now have code in our code chunk and now we are going to **run** the code. Running the code just means making it do what you told it, such as creating objects or using functions. Remember you need to write the code first, then tell RStudio to run the code.

When you are working in an R Markdown document, there are several ways to run your lines of code.

1. One option is you can highlight the code you want to run and then click **`Run >> Run Selected Line(s)`** (Figure 2.11).

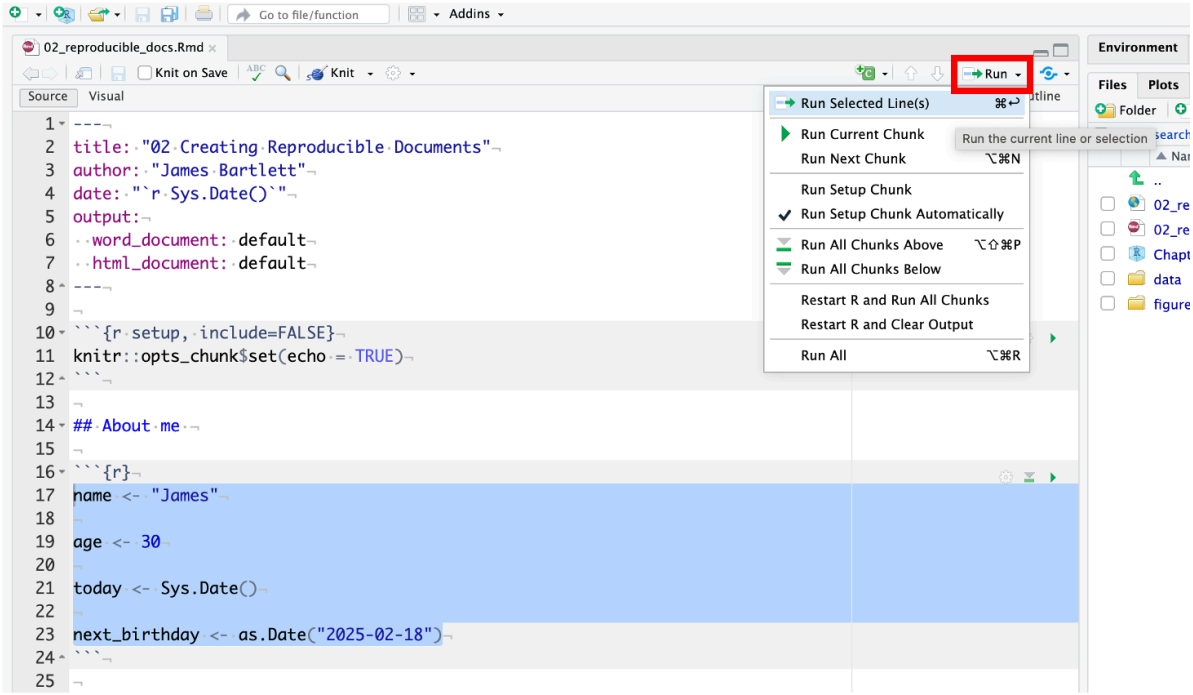


Figure 2.11: Slower method of running code by highlighting and clicking Run Selected Line(s).

2. You can press the green "play" button at the top-right of the code chunk and this will run **all** lines of code in that chunk (Figure 2.12).

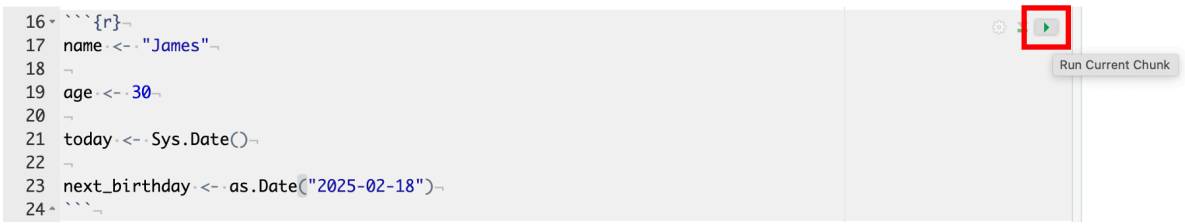


Figure 2.12: Slightly faster method of running all code in a chunk by clicking the green "play" button.

3. There are keyboard shortcuts to run code which will be the fastest as you learn and use RStudio more frequently. For example, to run a single line of code, make sure that the

cursor is in the line of code (it can be anywhere on the line) you want to run and press `ctrl + enter` (`command + return` on a Mac).

> **Keyboard shortcuts**
>
> There are loads of keyboard shortcuts, but you might only use a handful to speed up your day-to-day tasks. For a full list, look in the top menu `Help >> Keyboard shortcuts help`.

Now run your code using one of the methods above. You should see the variables `name`, `age`, `today`, and `next_birthday` appear in the environment pane in the top right corner.

> **Try this**
>
> Clear out the environment using the broom handle approach we saw in Chapter 1 and try a different method to see which works best for you.

2.2.5 Activity 7: Inline code

Your code works and you now know how to run it, but one of the incredible benefits we said about R Markdown is that you can mix text and code. Even better is the ability to combine code with text to put specific outputs of your code, like a value, using **inline code**.

Think about a time you have had to copy and paste a value or text from one file into another and you will know how easy it can be to make mistakes or find the origin of your mistake. Inline code avoids this. It is easier to show you what inline code does rather than to explain it so let us have a go.

First, copy and paste this text exactly (do not change *anything*) to underneath and outside your code chunk:

```
My name is `r name` and I am `r age` years old.

It is `r next_birthday - today` days until my birthday.
```

Your .Rmd should look like Figure 2.13 but nothing will happen yet. Unlike code chunks, you cannot run inline code. You need to knit your document for it to do it's magic.

> **How does inline code work?**
>
> Inline code has the following form:

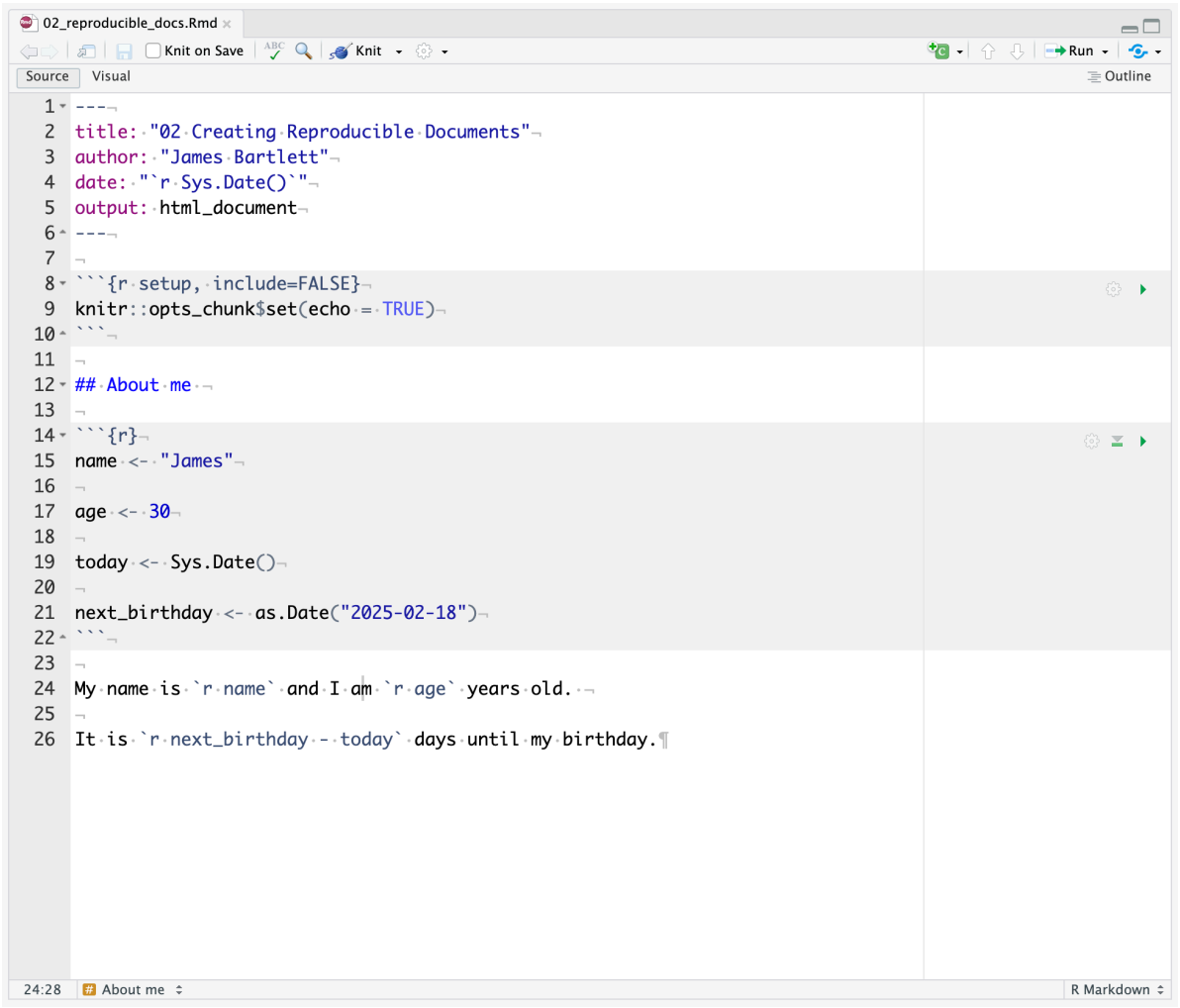


Figure 2.13: Complete .Rmd file with your about me section and inline code.

```
`r object`
```

or

```
`r function(...)`
```

Here, we are using the first version where we are referencing an object we already created. This is normally a good idea if you have a long function to run as it's easier to spot mistakes in a code chunk than inline code.
You will see it has the form of a backtick (`), `r` and a space, the object/function you want to reference, and a final backtick. When the R Markdown file knits, it sees the `r` and recognises it as inline code and uses the object or function.
If you just write the two backticks without the `r`, it will just add code formatting and not produce inline code.

2.2.6 Activity 8: Knitting your file

As our final step in this part, we are going to knit our file again to see how it looks now. So, click the Knit button to regenerate your knitted .html version.

If you look at the knitted .html document in the Viewer tab or in your browser, you should see the sentence we copied in from Activity 7. As if by magic, that slightly odd bit of text you copied and pasted now appears as a normal sentence with the values pulled in from the objects you created:

My name is **James** and I am **30** years old. It is **-211** days until my birthday.

R Markdown is an incredibly powerful and flexible format, we wrote this whole book using it! There are a few final things to note about knitting that will be useful going forward for your data skills learning and assessments:

- R Markdown will only knit if your code works. If you have an error, it will stop and tell you to fix the error before you can click knit and try again. This is a good way of checking whether you have written functioning code in your assessments.
- When you knit an R Markdown document, it runs the code from the start of the document to the end in order, and in a fresh session. This means it cannot access your environment, just the objects you create within that R Markdown. One common error can be writing and running code as you work on the document, but the code chunks are in the wrong order, or you created an object in the console but not in the code chunks. This means R Markdown would not know the object exists yet, or it does not have access to it at all.

- You can choose to knit to a Word document rather than HTML. This can be useful for sharing with others or adding further edits, but you might lose some functionality. By default, html looks good and is accessible, so that will be our default throughout this book, but look out for our instructions on what output format we want your assessments in.
- You can choose to knit to PDF, however, unless you are using the server this requires a **LaTeX** installation and can be quite complicated. If you do not already know what LaTeX is and how to use it, we do not recommend trying to knit to PDF just yet. If you do know how to use LaTeX, you probably do not need us to give you instructions!

We will test some of these warnings in error mode in the test yourself section, but we have one final demonstration for how R Markdown files support reproducibility.

2.3 Demonstrating reproducibility

At the start of this chapter, we plugged the benefits of reproducible research as the ability to produce the same result for different people using the same software on different computers. We are going to end the chapter on a demonstration of this by giving you an R Markdown document and data. You should be able to click knit and see the results without editing anything. We do not expect you to understand the code included in it, we are previewing the skills you will develop over the next four chapters on visualisation and data wrangling.

2.3.1 Activity 9 - Knit the reproducibility demonstration document

Please follow these steps and you should be able to knit the document without editing anything. Make sure you are still in your `Chapter_02_reproducible_docs` folder. If you are coming back to this activity, remember to set your working directory by opening the .Rproj file.

1. If you are working on your own computer, make sure you installed the `tidyverse` package. Please refer to Chapter 1 - Activity 3 if you have not completed this step yet. If you are working on a university computer or the online server, you **do not** need to complete this step as `tidyverse` will already be installed.
2. Download the R Markdown document through the following link: 02_reproducibility_demo.Rmd. To download a file from this book, right click the link and select "save link as", or just clicking the link will save the file to your Downloads. Save or copy the file to your `Chapter_02_reproducible_docs` folder.
3. Download these two data files. Data file one: ahi-cesd.csv. Data file two: participant-info.csv. Right click the links and select "save link as", or clicking the links will save the files to your Downloads. Make sure that both files are saved as ".csv". Do not open them

on your machine as often other software like Excel can change setting and ruin the files. Save or copy the file to your `data/` folder within `Chapter_02_reproducible_docs`.

At this point, you should have "**02_reproducibility_demo.Rmd**" within your `Chapter_02_reproducible_docs` folder. You should have "**ahi-cesd.csv**" and "**participant_info.csv**" in the `data/` folder within `Chapter_02_reproducible_docs`.

If you open "02_reproducibility_demo.Rmd" and followed all the steps above, you should be able to click knit. This will turn the R Markdown file into a knitted html file, showing some data wrangling, summary statistics, and two graphs (Figure 2.14). In the next chapter, you will learn how to write this code yourself, starting with creating graphs.

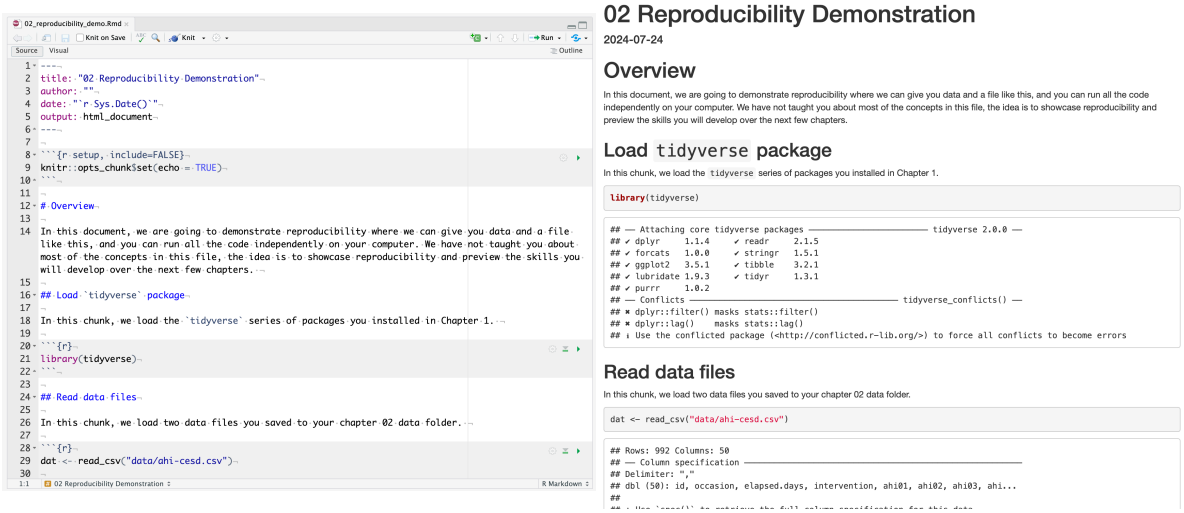


Figure 2.14: You should see the reproducibility demonstration as the .Rmd (left) and be able to knit it into a html file (right).

If you have any questions or problems about anything contained in this chapter, please remember you are always welcome to post on the course Teams channel, attend a GTA support session, or attend the office hours of one of the team.

2.4 Test yourself

To end the chapter, we have some knowledge check questions to test your understanding of the concepts we covered in the chapter. We then have some error mode tasks to see if you can find the solution to some common errors in the concepts we covered in this chapter.

2.4.1 Knowledge check

Question 1. One of the key first steps when we open RStudio is to:

- (A) set your working directory/open a project
- (B) put on some music as we will be here a while
- (C) check out the news
- (D) make a coffee

Explain this answer

One of the most common issues we see where code does not work the first time is because people have forgotten to set the working directory. The working directory is the starting folder on your computer where you want to save any files, any output, or contains your data. R/RStudio needs to know where you want it to look, so you must either manually set your working directory, or open a .Rproj file.

Question 2. When using the default environment color settings for RStudio, what color would the background of a code chunk be in R Markdown?

- (A) white
- (B) red
- (C) green
- (D) grey

Question 3. When using the default environment color settings for RStudio, what color would the background of normal text be in R Markdown?

- (A) white
- (B) red
- (C) green
- (D) grey

Explain this answer

Assuming you have not changed any of the settings in RStudio, code chunks will tend to have a grey background and normal text will tend to have a white background. This is a good way to check that you have closed and opened code chunks correctly.

Question 4. Code chunks start and end with:

- (A) three single quotes
- (B) three backticks
- (C) three double quotes
- (D) three single clefs

Explain this answer

Code chunks always take the same general format of three backticks followed by curly parentheses and a lower case r inside the parentheses (`{r}`). People often mistake these backticks for single quotes but that will not work. If you have set your code chunk correctly using backticks, the background color should change to grey from white

Question 5. Inline code is:

- (A) where you nicely organise your code in a line.
- (B) where you make sure all the code is nicely indented from the side.
- (C) a fancy way of saying you have written good code.
- (D) an approach of integrating code and text in a sentence outside of a code chunk.

Explain this answer

Inline coding is an incredibly useful approach for merging text and code in a sentence outside of a code chunk. It can be really useful for when you want to add values from your code directly into your text. If you copy and paste values, you can easily create errors, so it's useful to add inline code where possible.

2.4.2 Error mode

The following questions are designed to introduce you to making and fixing errors. For this topic, we focus on R Markdown and potential errors in using code blocks and inline code. Remember to keep a note of what kind of error messages you receive and how you fixed them, so you have a bank of solutions when you tackle errors independently.

Create and save a new R Markdown file by following the instructions in activity 3 and activity 4. You should have a blank R Markdown file below line 10. Below, we have several variations of a code chunk and inline code errors. Copy and paste them into your R Markdown file, click knit, and look at the error message you receive. See if you can fix the error and get it working before checking the answer.

Note: For all of our error mode activities, the error is based on clicking knit so it applies to inline code examples. If you try and run the code instead of clicking knit on the whole document, you might see a different error message to what we report.

Question 6. Copy the following text/code/code chunk into your R Markdown file and press knit. You should receive an error like `Line 18 Execution halted` in the Render tab.

````
city <- "Glasgow"

```{r}

```
`r city` is a city in Scotland.
````

Explain the solution

Here, we wrote `city <- "Glasgow"` outside the code chunk. So, when we try and knit, it is not evaluated as code, and city does not exist as an object to be referenced in inline code. If you copy `city <- "Glasgow"` into the code chunk and press knit, it should work.

Question 7. Copy the following text/code/code chunk into your R Markdown file and press knit. You should receive an error like `Error in parse(): ! attempt to use zero-length variable name` which is not very helpful for diagnosing the problem.

````
```{r}
city <- "Glasgow"
```

`r city` is a city in Scotland.
````

Explain the solution

Here, we missed a final backtick in the code chunk. You might have noticed all the text had a grey background, so R Markdown thought everything was code. So, when it reached the inline code and text, it tried interpreting it as code and caused the error. If you add the final backtick to the code chunk, you should be able to click knit successfully.

Question 8. Copy the following text/code/code chunk into your R Markdown file and press knit. You should receive an error like `Line 12 Execution halted` in the Render tab.

````
`r city` is a city in Scotland.

```{r}
city <- "Glasgow"
```
````

Explain the solution

Here, we tried using inline code before the code chunk. R Markdown runs the code from start to finish in a fresh environment. We tried referencing `city` in inline code, but R Markdown did not know it existed yet. To fix it, you need to move the inline code below the code chunk, so you create `city` before referencing it in inline code.

Question 9. Copy the following text/code/code chunk into your R Markdown file and press knit. This…works?

````
```{r}
city <- "Glasgow"
```

`city` is a city in Scotland.
````

Explain the solution

Here, we have a sneaky kind of "error" where it knits, but it is not doing what we wanted it to do. In the inline code part, we only added code formatting `city`, we did not add the r to get R Markdown to interpret it as R code:

```
`r city`
```

If you add the `r` after the first backtick, it should knit and add the city object in.

2.5 Words from this Chapter

Below, you will find a list of words that we used in this chapter that might be new to you in case you need to refer back to what they mean. The links in this table take you to the entry for the words in the PsyTeachR Glossary. Note that numerous members of the team wrote entries in the Glossary and as such the entries may use slightly different terminology from what we used in the chapter.

term	definition
chunk	A section of code in an R Markdown file
html	Hyper-Text Markup Language: A system for semantically tagging structure and information on web pages.
inline-code	Directly inserting the result of code into the text of a .Rmd file.
knit	To create an HTML, PDF, or Word document from an R Markdown (Rmd) document
latex	A typesetting program needed to create PDF files from R Markdown documents.
markdown	A way to specify formatting, such as headers, paragraphs, lists, bolding, and links.
r-markdown	The R-specific version of markdown: a way to specify formatting, such as headers, paragraphs, lists, bolding, and links, as well as code blocks and inline code.
r-project	A project is simply a working directory designated with a .RProj file. When you open an R project, it automatically sets the working directory to the folder the project is located in.
reproducible-research	Research that documents all of the steps between raw data and results in a way that can be verified.
working-directory	The filepath where R is currently loading files from and saving files to.

2.6 End of chapter

Well done on reaching the end of the second chapter! This was another long chapter as we had to cover a range of foundational skills to prepare you for learning more of the coding element in future chapters.

The next chapter builds on all the skills you have developed so far in R programming and creating reproducible documents to focus on something more tangible: data visualisation in R to create plots of your data.

3 Introduction to Data Visualisation

In this chapter, we introduce you to data visualisation. Visualising our data and the relationships between our variables is an incredibly useful and important skill.

It is important for **you** before you conduct any statistical analyses or present any summary statistics. We should always visualise our data as it is a quick and easy way to check our data make sense and identify any unusual trends. It is also important for **others** who read your work. Data visualisation can honestly present the features of our data to anyone who reads our research and provides a faster overview of our findings than reading a wall of numbers.

Across several chapters, we introduce you to the extremely flexible `ggplot2` package for data visualisation as part of the `tidyverse` family. In two or three lines of code, you can create plots like Figure 3.1 for exploratory data analysis. With a few extra lines, you can create publication quality plots that could go into a report.

In this chapter, we introduce you to the `ggplot2` system of creating plots and cover histograms and bar plots. In future chapters, we cover different types of plot to communicate more complex data and analyses.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Read data files into R/RStudio.
- Understand the `ggplot2` layering system of creating plots.
- Create and edit histograms to visualise the frequency of observations collated into bins.
- Create and edit barplots to visualise the frequency of different categories.
- Save plots as an image to use in reports or presentations.

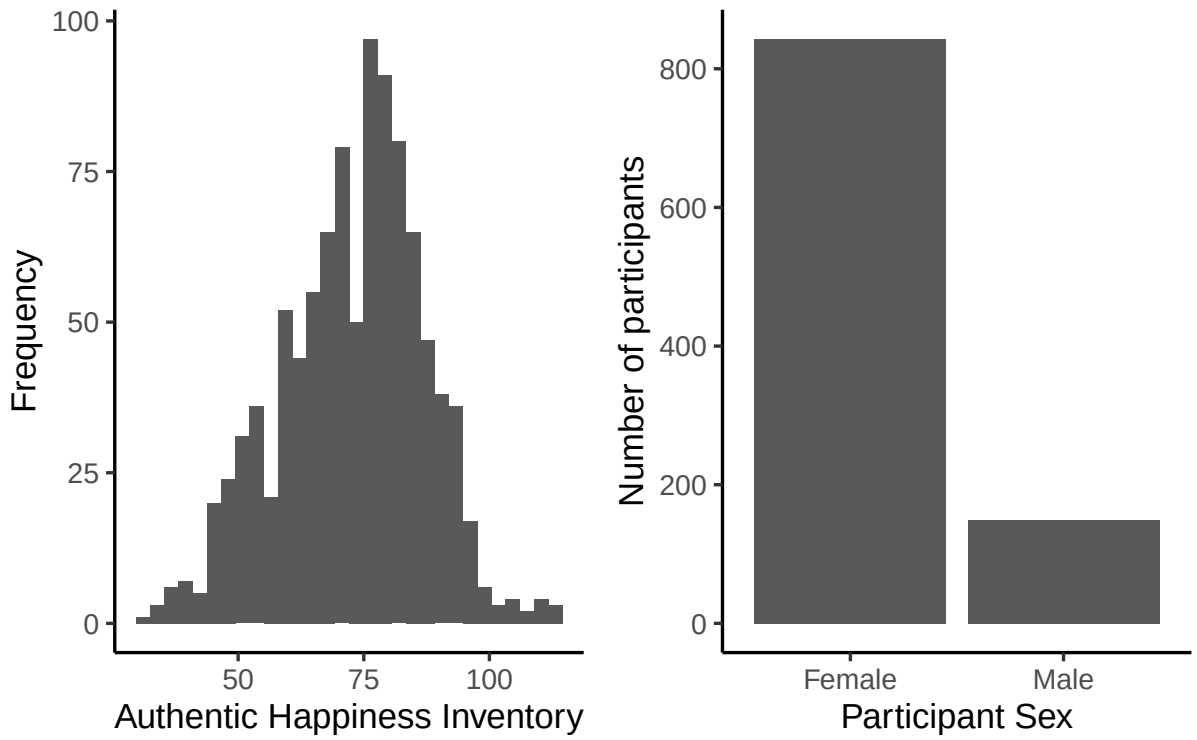


Figure 3.1: Preview of the kind of plots you can quickly create using the ggplot2 package. On the left, a histogram of responses to a happiness questionnaire. On the right, a bar plot showing the frequency men and women in the study.

3.1 Chapter preparation

3.1.1 Introduction to the data set

From now on, we are going to use different data sets from psychology to develop and practice your data skills. This will prepare you for working with different kinds of psychology data and introduce you to different kinds of research questions they might ask. For this chapter, we are using open data from Woodworth et al. (2018). The abstract of their article is:

> We present two datasets. The first dataset comprises 992 point-in-time records of self-reported happiness and depression in 295 participants, each assigned to one of four intervention groups, in a study of the effect of web-based positive-psychology interventions. Each point-in-time measurement consists of a participant's responses to the 24 items of the Authentic Happiness Inventory and to the 20 items of the Center for Epidemiological Studies Depression (CES-D) scale. Measurements were sought at the time of each participant's enrolment in the study and on five subsequent occasions, the last being approximately 189 days after enrolment. The second dataset contains basic demographic information about each participant.

In summary, we have two files containing demographic information about participants and measurements of two scales on happiness and depression:

- The Authentic Happiness Inventory (AHI),
- The Center for Epidemiological Studies Depression (CES-D) scale.

3.1.2 Organising your files and project for the chapter

Before we can get started, you need to organise your files and project for the chapter, so your working directory is in order. If you need a refresher of this process, you can look back over Chapter 2 - File structure, working directories, and R Projects.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, create a new folder called `Chapter_03_intro_data_viz`. Within `Chapter_03_intro_data_viz`, create two new folders called `data` and `figures`.
2. Create an R Project for `Chapter_03_intro_data_viz` as an existing directory for your chapter folder. This should now be your working directory.
3. Create a new R Markdown document and give it a sensible title describing the chapter, such as `03 Introduction to Data Visualisation`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Chapter_03_intro_data_viz` folder.

4. Download these two data files which we used at the end of Chapter 2. Data file one: ahi-cesd.csv. Data file two: participant-info.csv. Right click the links and select "save link as", or clicking the links will save the files to your Downloads. Make sure that both files are saved as ".csv". Do not open them on your machine as often other software like Excel can change setting and ruin the files. Save or copy the file to your `data/` folder within `Chapter_03_intro_data_viz`.

You are now ready to start working on the chapter!

> **i** Reminder of file management if you use the online server
>
> If we support you to use the online University of Glasgow R Server, working with files is a little different. If you downloaded R / RStudio to your own computer or you are using one of the library/lab computers, please ignore this section.
> The main disadvantage to using the R server is that you will need create folders on the server and then upload and download any files you are working on to and from the server. Please be aware that **there is no link between your computer and the R server**. If you change files on the server, they will not appear on your computer until you download them from the server, and you need to be very careful when you submit your assessment files that you are submitting the right file. This is the main reason we recommend installing R / RStudio on your computer wherever possible.
> Going forward throughout this book, if you are using the server, you will need to follow an extra step where you also upload them to the sever. As an example:
>
> 1. Log on to the **R server** using the link we provided to you.
> 2. In the file pane, click `New folder` and create the same structure we demonstrated above.
> 3. Download these two data files which we used at the end of Chapter 2. Data file one: ahi-cesd.csv. Data file two: participant-info.csv. Save the two files into the `data` folder you created for chapter 3. To download a file from this book, right click the link and select "save link as". Make sure that both files are saved as ".csv". Do not open them on your machine as often other software like Excel can change setting and ruin the files.
> 4. Now that the files are stored on your computer, go to RStudio on the server and click `Upload` then `Browse` and choose the folder for the chapter you are working on.
> 5. Click `Choose file` and go and find the data you want to upload.

3.2 Loading the `tidyverse` and reading data files

3.2.1 Activity 1 - Loading the `tidyverse` package

For everything we do in this chapter and almost every chapter from now, we need to use the **tidyverse** package. The `tidyverse` is a package of packages, containing a kind of ecosystem of functions that work together for **data wrangling**, **descriptive** statistics, and visualisation. So let's load that package into our library using the `library()` function.

To load the `tidyverse`, below line 10 of your RMarkdown document, create a code chunk, type the following code into your code chunk, and run the code:

```
library(tidyverse)
```

Remember that sometimes in the **console** or below your code chunk, you will see information about the package you have loaded. If you see an error message, be sure to read it and try to identify what the problem is. For example, if you are working on your own computer, have you installed `tidyverse` so R/RStudio can access it? Are there any spelling mistakes in the function or package?

Remember though, not all messages are errors, `tidyverse` explains what packages it loaded and highlights function name clashes. See activity 3 and 4 from Chapter 1 if you need a refresher.

3.2.2 Activity 2 - Reading data files using `read_csv()`

Now we have loaded `tidyverse`, we can read in the data we need for the remaining activities. "Read" in this sense just means to bring the data into RStudio and store it in an **object**, so we can work with it.

We will use the function `read_csv()` that allows us to read in **.csv files**. There are also functions that allow you to read in Excel files (e.g. .xlsx) and other formats, but in this course we will only use .csv files as they are not software specific, meaning they are more accessible to share, promoting our open science principles.

> **i** Where does `read_csv()` come from?
>
> When we describe tidyverse as a package of packages, the `read_csv()` function comes from a package called `readr`. This is one of the packages that tidyverse loads and contains several functions for reading different kinds of data.

Create a new code chunk below where you loaded `tidyverse`, type the following code, and run the code chunk:

```
dat <- read_csv("data/ahi-cesd.csv")

pinfo <- read_csv("data/participant-info.csv")
```

To break down the code:

- First, we create an object called `dat` that contains the data in the `ahi-cesd.csv` file within `data/`.
- Next, we create an object called `pinfo` that contains the data in the `participant-info.csv` file within `data/`.
- Both lines have the same format of `object <- function("folder/datafile_name.csv")`
- Remember that `<-` is called the **assignment operator** but we can read it as "assigned to". For example, the first line can be read as the data in `data/ahi-cesd.csv` is assigned to the object called `dat`.

> **!** Error mode
>
> There are several common mistakes that can happen here, so be careful how you are typing the code to read in the data.
>
> - You need the double quotation marks around the data file name, so R recognises you are giving it a file path.
> - Computers are literal, so you must spell the data file name correctly. For example, R would not know what `data/participant-inf.csv` is. This is where pressing the tab key on your keyboard can be super helpful, as you can search and auto-complete your files and avoid spelling mistakes.
> - For the same reason as spelling mistakes, you must add the .csv part on the end to tell R the specific file you want.
> - You must point R to the right folder relative to your working directory. If you typed `ahi-cesd.csv`, you would receive an error as R would look in your chapter folder where `ahi-cesd.csv` does not exist, rather than within the `data/` folder you stored it in.

If you have done this activity correctly, you should now see the objects `dat` and `pinfo` in the **environment** window in the top right of RStudio. If they are not there, check there are no error messages, check the spelling of the code and file names, and check your working directory is `Chapter_03_intro_data_viz`.

⚠ Be careful to use the right `read_csv()` function

There is also a function called `read.csv()`. Be very careful **not** to use this function instead of `read_csv()` as they have different ways of naming columns. For the activities and the assignments in RM1 and RM2, we will **always** ask and expect you to use `read_csv()`. This is really a reminder to watch spelling on functions and to be careful to use the right functions, especially when the names are so close.

3.2.3 Activity 3 - Wrangling the two data sets

For this final preparation step, we would like you to add the following code. We are not tackling data wrangling until the next chapter, so we are not going to fully explain the code just yet. Copy the code (if you hover over the code, there is a copy to clipboard icon in the top right) and paste it into a code chunk below where you read the two data files, then run the code again.

```
all_dat <- inner_join(dat,
                      pinfo,
                      by= c("id", "intervention"))

summarydata <- select(.data = all_dat,
                      id,
                      occasion,
                      elapsed.days,
                      intervention,
                      ahiTotal,
                      cesdTotal,
                      sex,
                      age,
                      educ,
                      income)
```

For a brief overview, we are joining the two data files by common columns ("id" and "intervention") to create the object `all_dat`. We are then selecting 10 columns from the original 54 to make the data easier to work with in `summarydata`.

This final object `summarydata` is the source of the data we will be working with for the rest of this chapter.

3.2.4 Activity 4 - Exploring the data set

Before we start plotting, it is a good idea to explore the data set you are working with. There is a handy function called `glimpse()` which provides an overview of the columns and responses in your data set.

Create a new code chunk below where you read and wrangled the data, and type and run the following code:

```
glimpse(summarydata)
```

```
Rows: 992
Columns: 10
$ id           <dbl> 12, 162, 162, 267, 126, 289, 113, 8, 185, 185, 246, 185, ~
$ occasion     <dbl> 5, 2, 3, 0, 5, 0, 2, 2, 2, 4, 4, 0, 4, 0, 1, 4, 0, 5, 4, ~
$ elapsed.days <dbl> 182.025139, 14.191806, 33.033831, 0.000000, 202.096887, 0~
$ intervention <dbl> 2, 3, 3, 4, 2, 1, 1, 2, 3, 3, 3, 3, 1, 2, 2, 2, 3, 2, 2, ~
$ ahiTotal     <dbl> 32, 34, 34, 35, 36, 37, 38, 38, 38, 38, 39, 40, 41, 41, 4~
$ cesdTotal    <dbl> 50, 49, 47, 41, 36, 35, 50, 55, 47, 39, 45, 47, 33, 27, 3~
$ sex          <dbl> 1, 1, 1, 1, 1, 1, 2, 1, 2, 2, 1, 2, 1, 2, 2, 1, 1, 1, 1, ~
$ age          <dbl> 46, 37, 37, 19, 40, 49, 42, 57, 41, 41, 52, 41, 52, 58, 5~
$ educ         <dbl> 4, 3, 3, 2, 5, 4, 4, 4, 4, 4, 5, 4, 5, 5, 5, 4, 3, 4, 3, ~
$ income       <dbl> 3, 2, 2, 1, 2, 1, 1, 2, 1, 1, 2, 1, 3, 2, 2, 3, 2, 2, 2, ~
```

> **i** Where does `glimpse()` come from?
>
> The `glimpse()` function comes from a package called `dplyr`, which is part of the tidyverse. This package contains many functions for wrangling data like joining data sets and selecting columns. We will explore loads of functions within `dplyr` in the next few chapters on data wrangling.

This function provides a condensed summary of your data. You can see there are 992 rows and 10 columns. You see all the column names for each variable in the data set. You can also see that all the variables are automatically considered as numeric (in this case double represented by `<dbl>`). Treating categorical variables like "sex" and "income" as numbers will cause us problems later, but it is fine for the variables we will be working on now.

3.3 `ggplot2` and the layer system

There are multiple approaches to data visualisation in R but we will use `ggplot2` which uses a layered grammar of graphics where you build up plots in a series of layers. You can think of it as building a picture with multiple elements that sit over each other.

Figure 3.2 from Nordmann et al. (2022) demonstrates the idea of building up a plot by adding layers. One function creates the first layer, the basic plot area, and you add functions and arguments to add additional layers such as the data, the labels, the colors etc. If you are used to making plots in other software, this might seem a bit odd at first, but it means that you can customise each layer separately to make complex and beautiful figures with relative ease.

You can get a sense of what plots are possible from the website data-to-viz, but we will build up your data visualisation skills over the RM1 and RM2 courses.

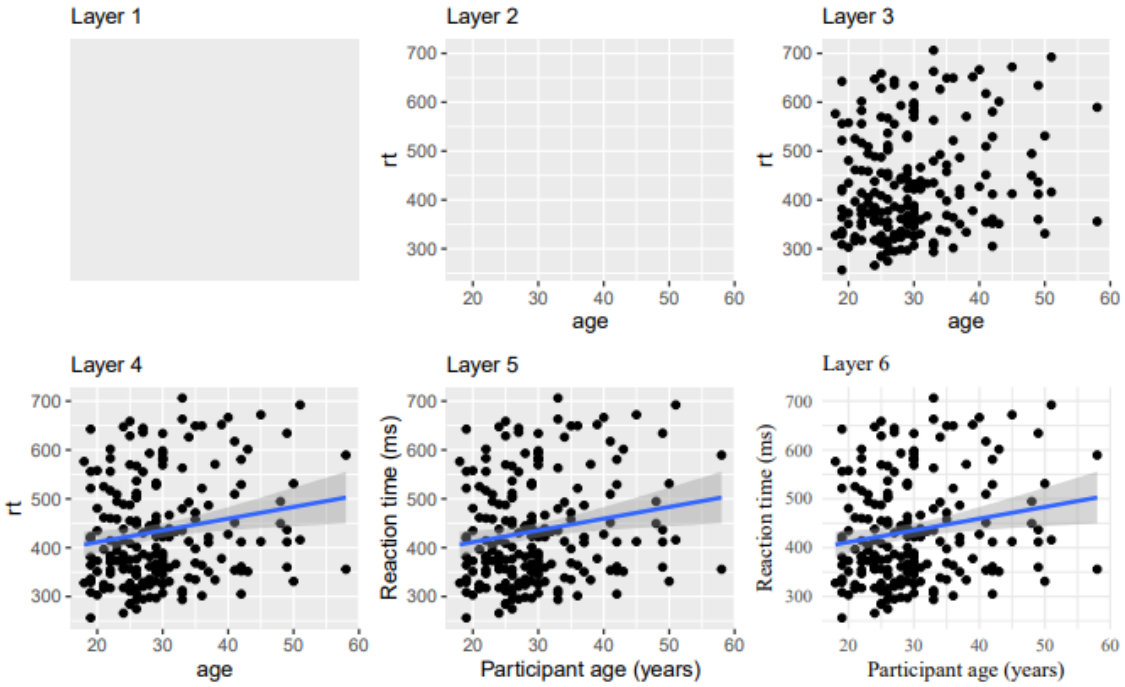


Figure 3.2: Building a figure using the ggplot2 layering system from Nordmann et al. (2022).

3.4 Histograms and density plots

We are going to start by plotting the distribution of participant age in a histogram, and add layers to demonstrate how we build the plot step-by-step.

3.4.1 Step 1: Start with the `ggplot` function

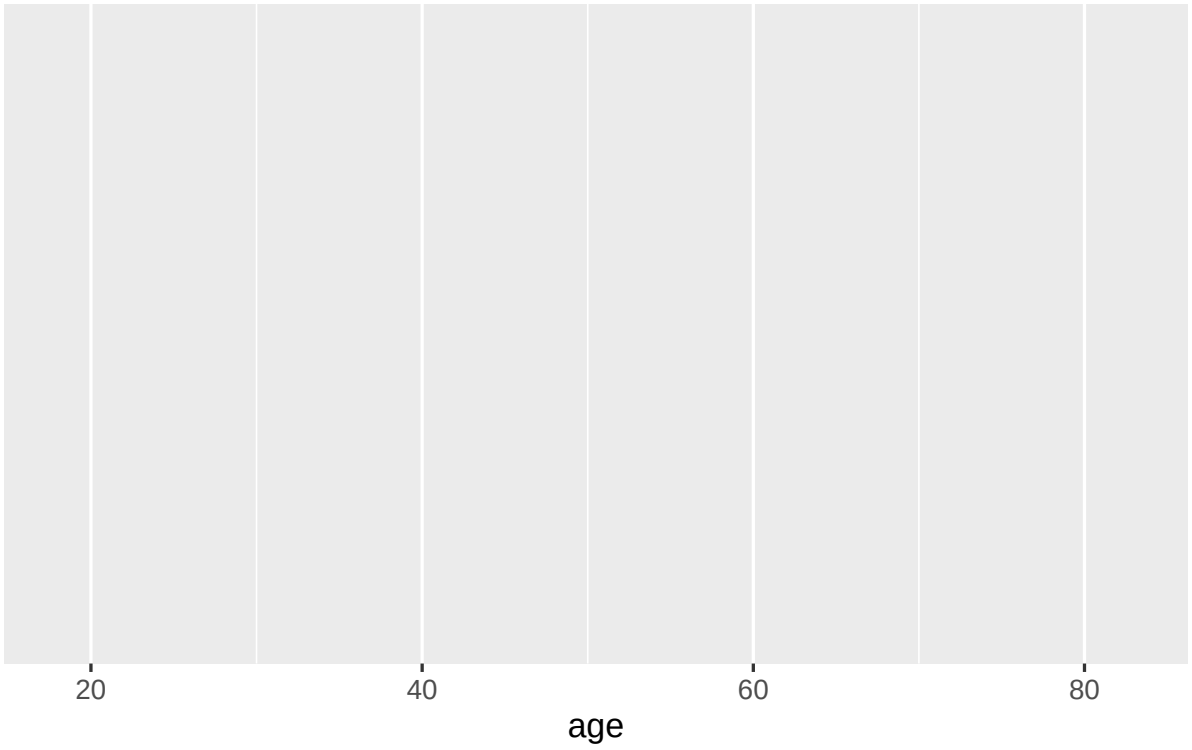
This first layer tells R to access the `ggplot` function.

The first argument tells R to plot the `summarydata` dataframe. In the `aes` function, you specify the aesthetics of the plot, such as the axes and colours. What you need to specify depends on the plot you want to make (you will learn more about this later).

For a basic histogram, you only need to specify the x-axis (the y-axis will automatically be counts).

For each step, type the code in a new code chunk and run it after we add each layer to see it's effect.

```
# Plot the variable age from summarydata
ggplot(summarydata, aes(x = age)) # Plot age on the x axis
```



R Markdown tip of the chapter: Add code comments

After we introduced you to R Markdown to create reproducible documents in Chapter 2, we are going to add a tip in every chapter to demonstrate extra functionality.
In the code chunk above, we added a code comment by adding a hash (`#`). In code chunks and scripts, you can add a comment which R will ignore, so you can explain to yourself what the code is doing. In R Markdown, you can combine adding notes to

yourself outside and inside the code chunks.
Code comments help explain what the code is doing and why you added certain values. It might seem redundant for simple functions, but as your code becomes more complex, you will forget what it is doing when you return to it after days, months, or years. Future you will thank past you.

3.4.2 Step 2: Add the geom_histogram layer

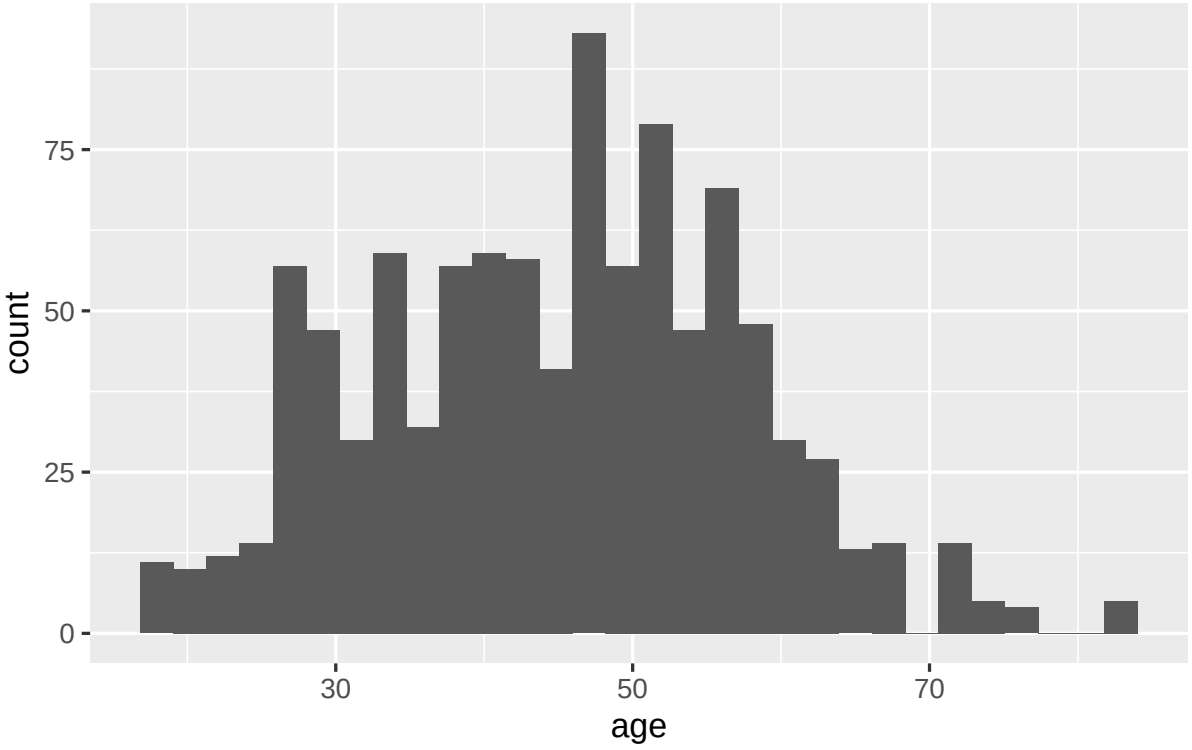
You can see that the code above produces an empty plot, because we have not specified which type of plot we want to make.

We will do this by adding another layer: `geom_histogram()`. A geom is an expression of the type of plot you want to create. For this variable, we want to create a histogram which is a type of plot showing the frequency of each observation.

You will see that you add the layers by adding a `+` at the end of each layer. As you read new code, try and read it line by line to walk through what it is doing. You can interpret `+` as "and then". So, you could describe the plot as currently saying "plot the age variable from summary data, and then add a histogram".

```
# Plot the variable age from summarydata
ggplot(summarydata, aes(x = age)) +  # Plot age on the x axis
  geom_histogram()
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



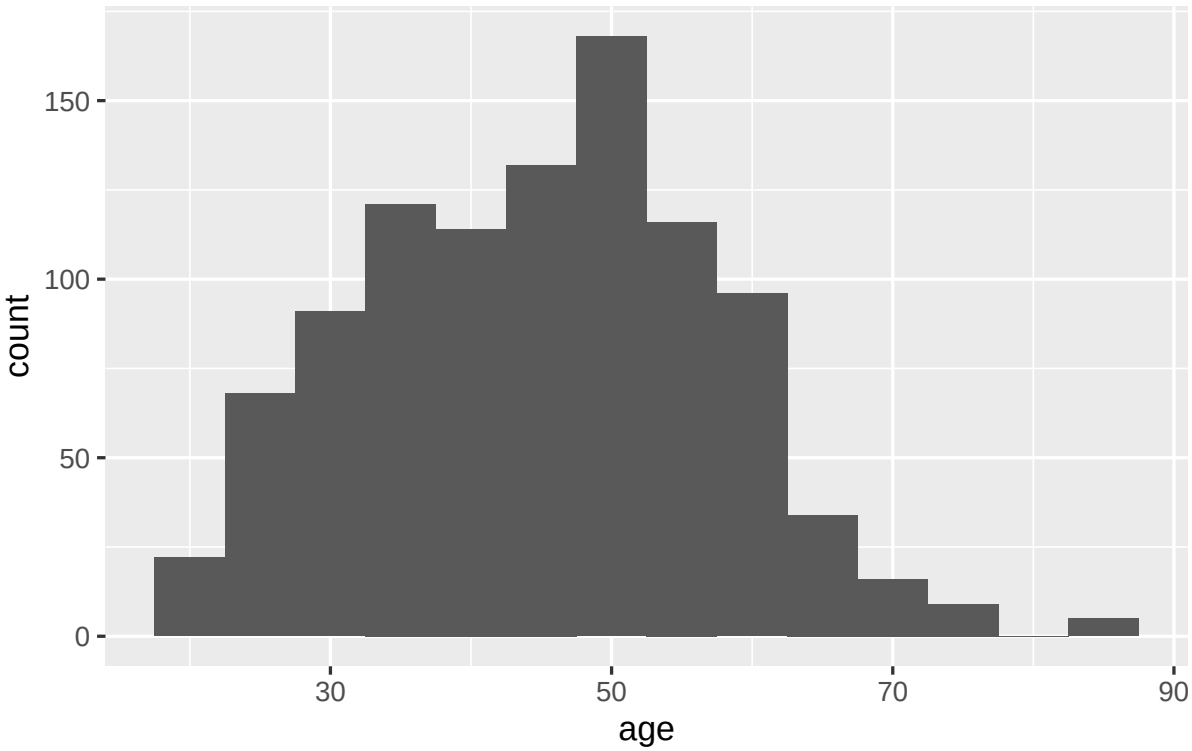
3.4.3 Step 3: Edit the histogram bins

In just two lines of code, we have a histogram! For exploratory data analysis, this is how `ggplot2` is such a flexible and quick tool to get a visual overview of your data.

After running the last code chunk, you might have noticed a message warning you about the bin width: `stat_bin() using bins = 30`. A histogram describes the frequency of values within your variable. To do so, it must collect the values into "bins". By default - the warning `ggplot2` gives you - it uses 30 bins, meaning it tries to plot 30 bars. Depending on the granularity of your data, you might want more or fewer bins.

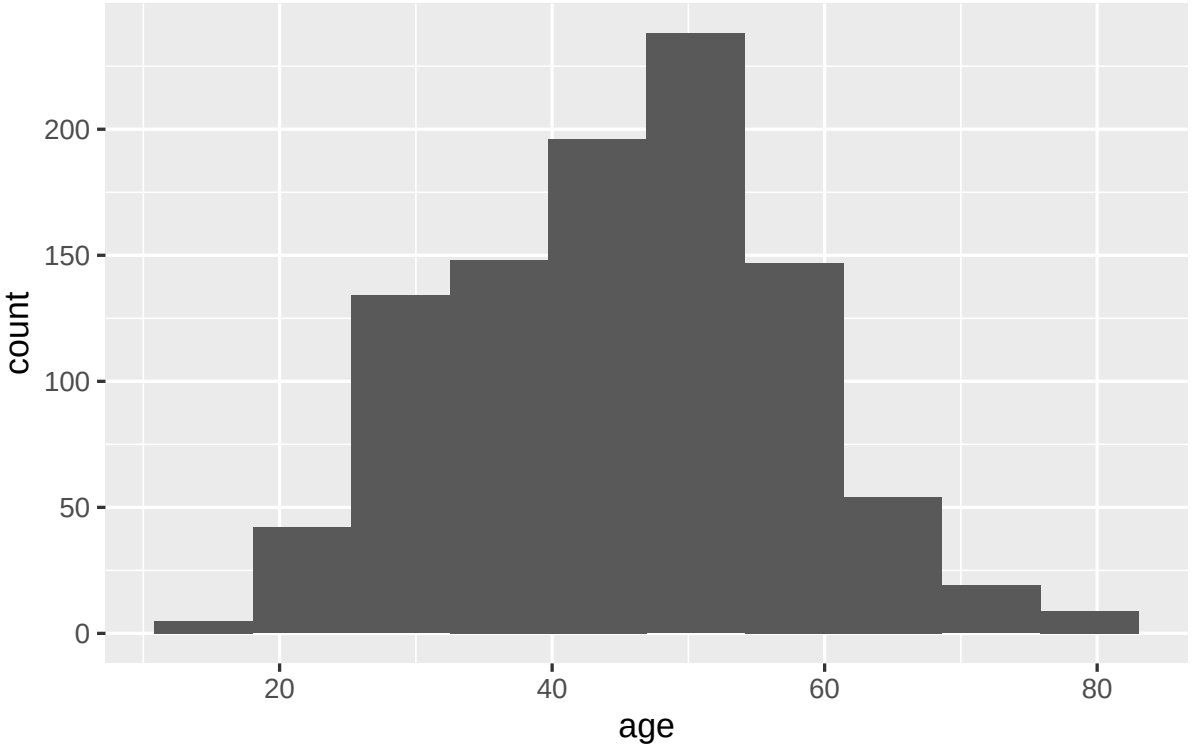
You can control this using one of two arguments. First, you can add an argument called `binwidth` which sets the bins by how wide you want the bars on your x-axis scale. For example, we can plot the data for every 5 years:

```
# Plot the variable age from summarydata
ggplot(summarydata, aes(x = age)) +  # Plot age on the x axis
  geom_histogram(binwidth = 5) # collate bins into a 5-year span
```



Alternatively, you can control precisely how many bars the histograms uses through the `bins` argument. For example, we can plot age by collecting the observations into 10 bars:

```
# Plot the variable age from summarydata
ggplot(summarydata, aes(x = age)) +  # Plot age on the x axis
  geom_histogram(bins = 10) # Plot age using 10 bars
```



Try this

Play around with the `bin` and `binwidth` arguments to see what effect it has on the plot. One of the best ways of learning is through trial and error to see what effect your changes have on the result.

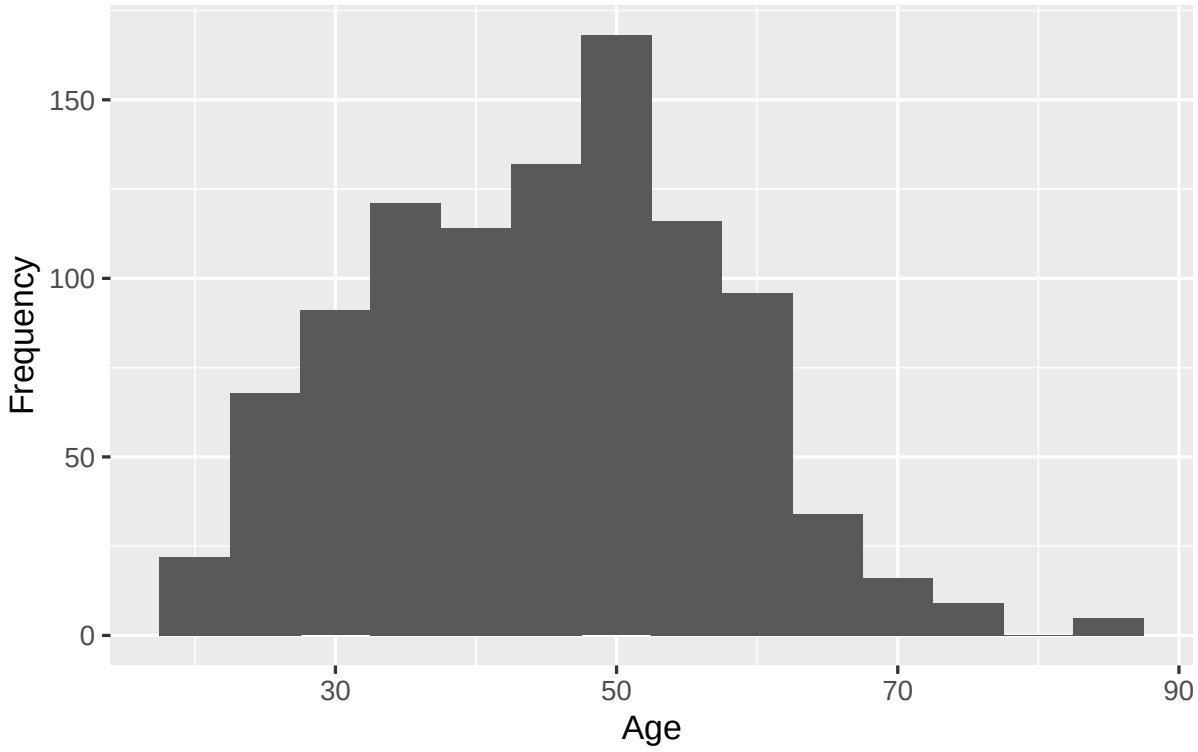
3.4.4 Step 4: Edit the axis names

By default, the axis names come from the variable names in your data. When you are making quick plots for yourself, you rarely need to worry about this. However, as you edit your plot for a report to show other people, it is normally a good idea to edit the names so they clearly communicate what they represent.

There are different layers to control the axes depending on the type of variable you use. Both the x- and y-axis here are continuous numbers, so we can use the `scale_x_continuous` and `scale_y_continuous` layers to control them.

There are many options available in `ggplot2` for controlling the axes, but you will learn through experience and searching what you need in different scenarios.

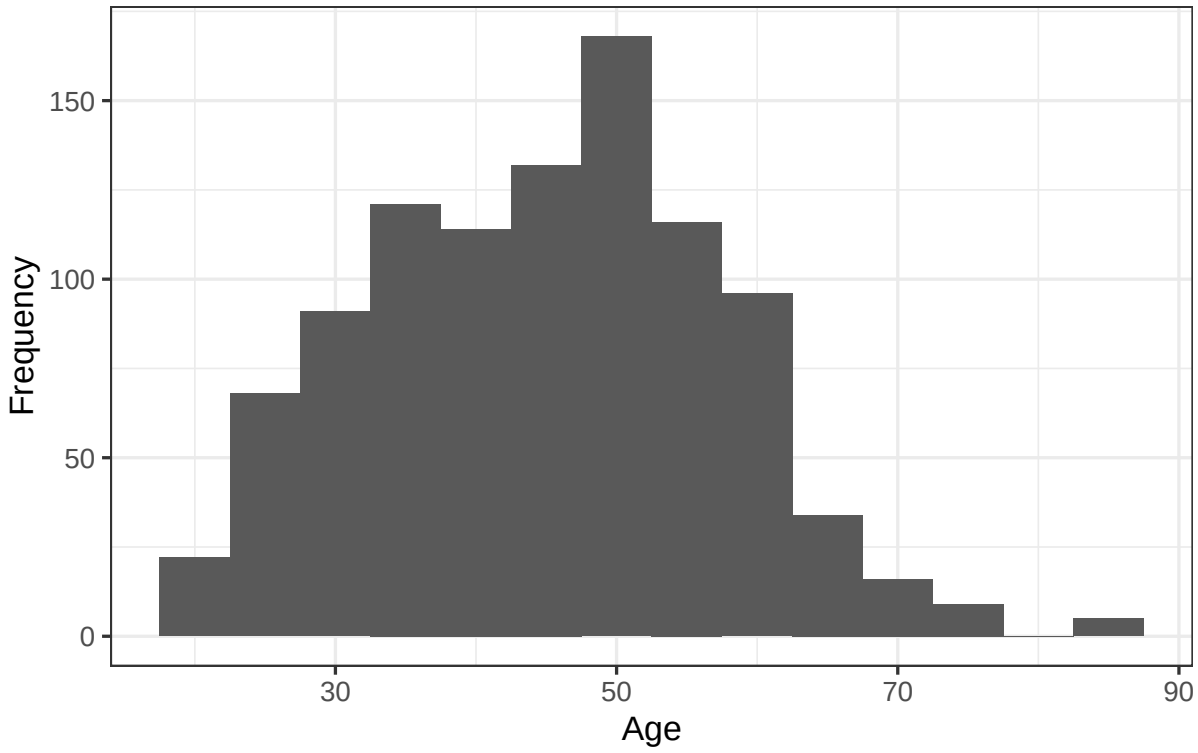
```
# Plot the variable age from summarydata
ggplot(summarydata, aes(x = age)) +  # Plot age on the x axis
  geom_histogram(binwidth = 5) + # collate bins into a 5-year span
  scale_x_continuous(name = "Age") +
  scale_y_continuous(name = "Frequency")
```



3.4.5 Step 5: Change the plot theme

So far, we used the default plot theme which has the grey gridlines as a background. This looks pretty ugly, so we can edit the plot them by adding a `theme_` layer. For example, we can add a black-and-white theme:

```
# Plot the variable age from summarydata
ggplot(summarydata, aes(x = age)) +  # Plot age on the x axis
  geom_histogram(binwidth = 5) + # collate bins into a 5-year span
  scale_x_continuous(name = "Age") +
  scale_y_continuous(name = "Frequency") +
  theme_bw()
```



Try this

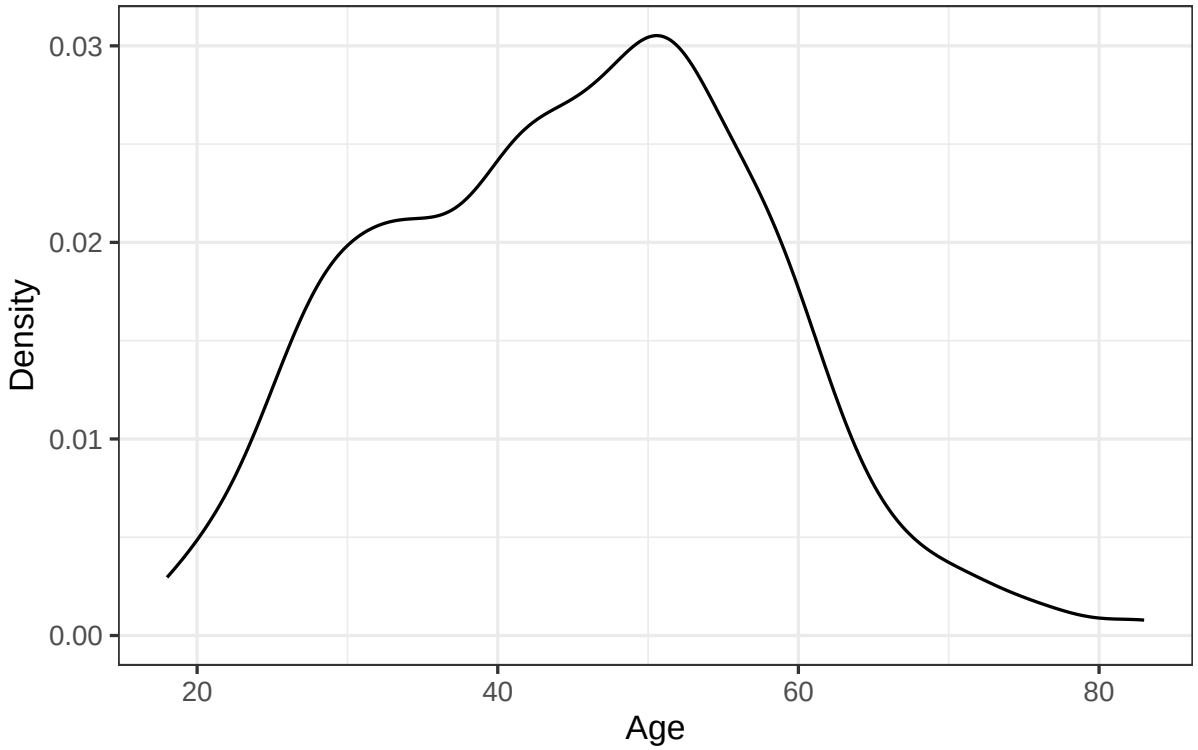
There are loads of themes available. As you start typing `theme_`, you should see the full range appear as a drop-down to autocomplete. Try one or two alternatives such as `theme_classic()` or `theme_minimal()` to see how they look.

3.4.6 Switch the geom layer

The layer system makes it easy to create new types of plots by adapting existing recipes. For example, rather than creating a histogram, we can create a smoothed density plot by calling `geom_density()` rather than `geom_histogram()`. Apart from the name of the y-axis, the rest of the code remains identical to demonstrate how easy it is to customise your `ggplot2` layers.

```
# Plot the variable age from summarydata
ggplot(summarydata, aes(x = age)) +  # Plot age on the x axis
  geom_density() + # summarise age as a smoothed density plot
  scale_x_continuous(name = "Age") +
```

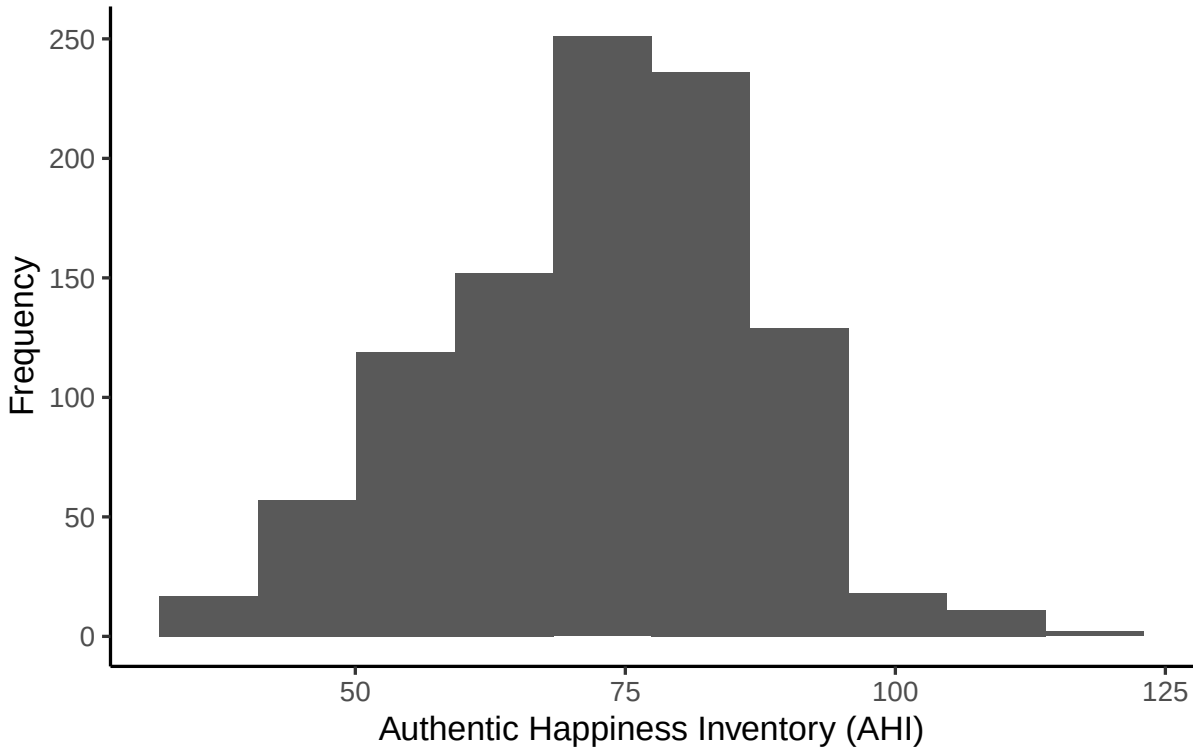
```
  scale_y_continuous(name = "Density") +
  theme_bw()
```



3.4.7 Activity 5 - Apply your plotting skills to a new variable

Before we move on to barplots, an important learning step is being able to apply or transfer what you learnt in one scenario to something new.

In the data set, there is a variable for The Authentic Happiness Inventory (AHI): `ahiTotal`. Plot the new variable and try to recreate the customisation layers before checking the solution below. It might take some trial-and-error to get some features right, so do not worry if it does not immediately look the same.



Show me the solution code

To recreate the plot, this is the code:

```
# Plot the variable ahi total from summarydata
ggplot(summarydata, aes(x = ahiTotal)) +  # Plot ahi total on the x axis
  geom_histogram(bins = 10) +
  scale_x_continuous(name = "Authentic Happiness Inventory (AHI)") +
  scale_y_continuous(name = "Frequency") +
  theme_classic()
```

We were a little sneaky with using the classic theme to get you exploring.

3.5 Barplots

In the next section, we are going to cover making barplots - potentially the most common type of visualisation you will see in published research. A barplot shows counts of categorical data, or factors, where the height of each bar represents the count of that particular variable.

You will see people use them to represent continuous outcomes, such as showing the mean on the y-axis, but there is good reason to never use bar plots to communicate continuous data we will cover in the course materials (see Weissgerber et al., 2019 if you are interested). We will cover more advanced plots for continuous data in Chapter 7 - Building your data visualisation skills.

3.5.1 Activity 6 - Convert to factors

Earlier, we highlighted that all the variables were processed as numbers. This was fine for most of the variables, but `sex`, `educ`, and `income` should be categories or what we call **factors**.

To get around this, we need to convert these variables into factors. This is relates to data wrangling, so this is one final time we would like you to copy and run code, before we fully explain how to write this kind of code independently in the next chapter.

Copy and run the following code in your R Markdown document, at least below where you read and wrangled the data:

```
# Overwrite summary data
summarydata <- mutate(summarydata, # mutate to change columns
         sex = as.factor(sex), # save sex as a factor
         educ = as.factor(educ),
         income = as.factor(income))
```

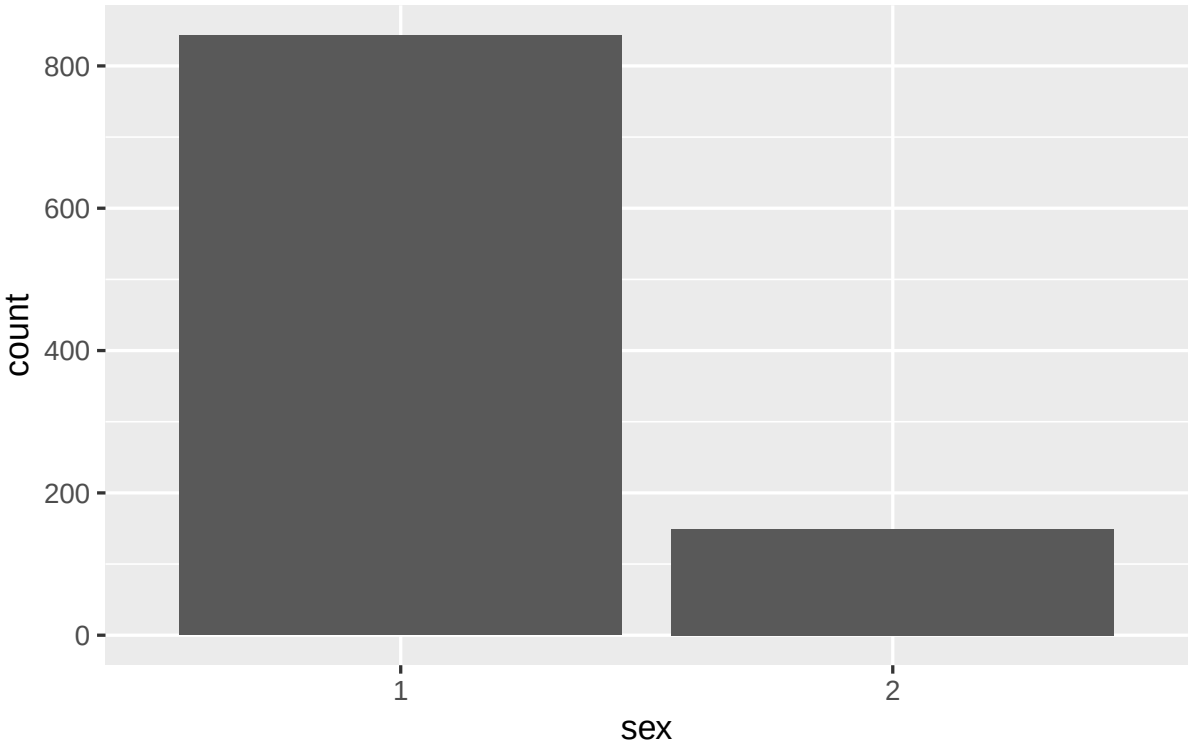
You can interpret this code as "overwrite `summarydata` and transform three columns (`sex`, `educ`, and `income`) into the same values but now considered factors and not doubles".

> **!** Error mode
>
> If you do not do convert numbers to factors when they should represent distinct categories, you can get some weird looking figures. Instead of treating the numbers as categories, it will try and plot the full range of numerical values. If you notice this, just go back and convert your variables to factors (which we will break down in the next chapter).

3.5.2 Activity 7 - Create a bar plot

Now you are familiar with the layering system, we will jump straight into creating the barplot. As before, type and run the code in each step, making notes to yourself either in the R Markdown document outside the code chunks, or using code comments.

```r
# Plot the variable sex from summarydata
ggplot(summarydata, aes(x = sex)) +
  geom_bar()
```



Compared to the histogram plot, the only difference here is using the `geom_bar()` as the layer instead. Rather than plot the frequency of your variable in bins, we plot the frequency of each unique category.

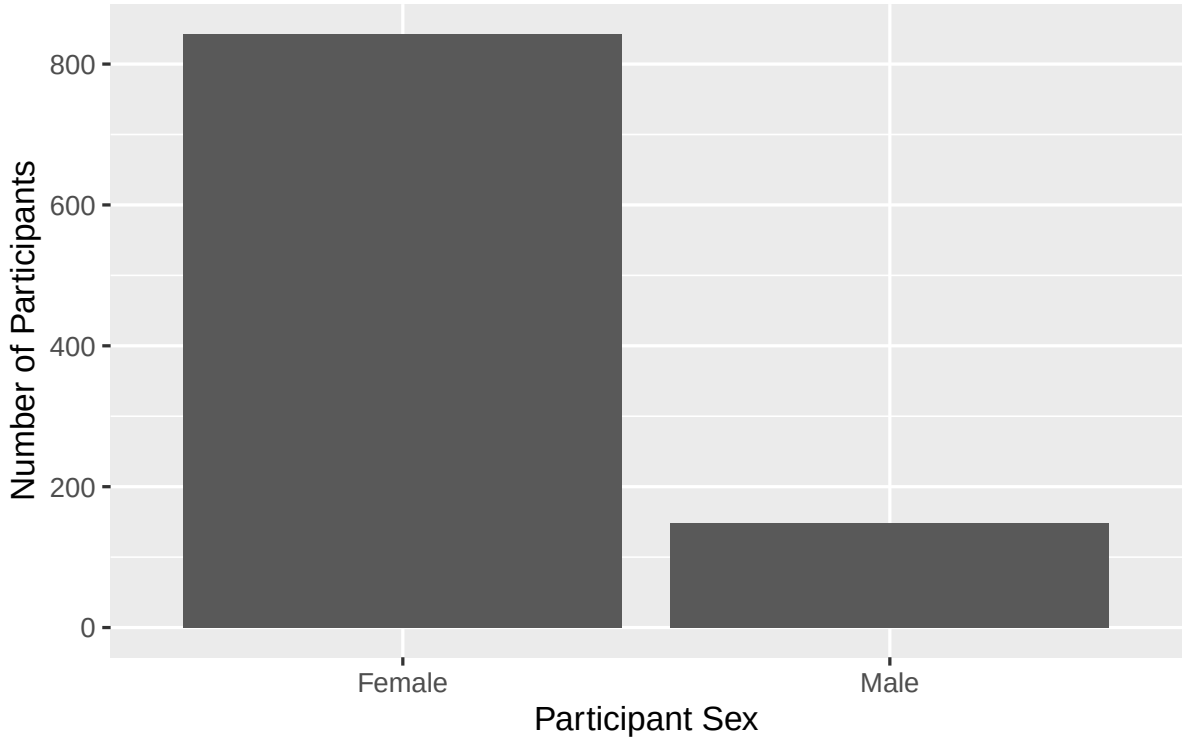
We can see 1s are way more frequent than 2s, but for this to make sense to you and your reader, we need to edit the axis labels.

3.5.3 Activity 8 - Edit the axis labels

In the histogram section, we demonstrated how to edit the axis labels. We used `scale_y_continuous` and `scale_x_continuous` as we had two continuous variables for the x-axis range and the y-axis frequency. This time, we need a slightly different layer since the x-axis now represents distinct groups: `scale_x_discrete`.

Type and run the following code:

```r
# Plot the variable sex from summarydata
ggplot(summarydata, aes(x = sex)) +
  geom_bar() +
  scale_x_discrete(name = "Participant Sex",
                   labels = c("Female", # 1 = Female
                              "Male")) + # 2 = Male
  scale_y_continuous(name = "Number of Participants")
```



Within `scale_x_discrete`, we have a new argument called "labels". This is where we can edit the labels for each category. Instead of 1 and 2, we labelled the x-axis clearer as "Female" and "Male", making it easier to understand there are way more female participants compared to male.

What does `c()` mean in labels?

When we specified the labels, you might have noticed the `c("Female", "Male")` format. `c()` stands for concatenate and you will see it a lot in R. When we give a value to a function argument, we must provide one "value". However, in scenarios like this, we want to apply multiple values since we have several categories.

We can do this by adding all of our categories within `c()`, separated by a comma between each category.

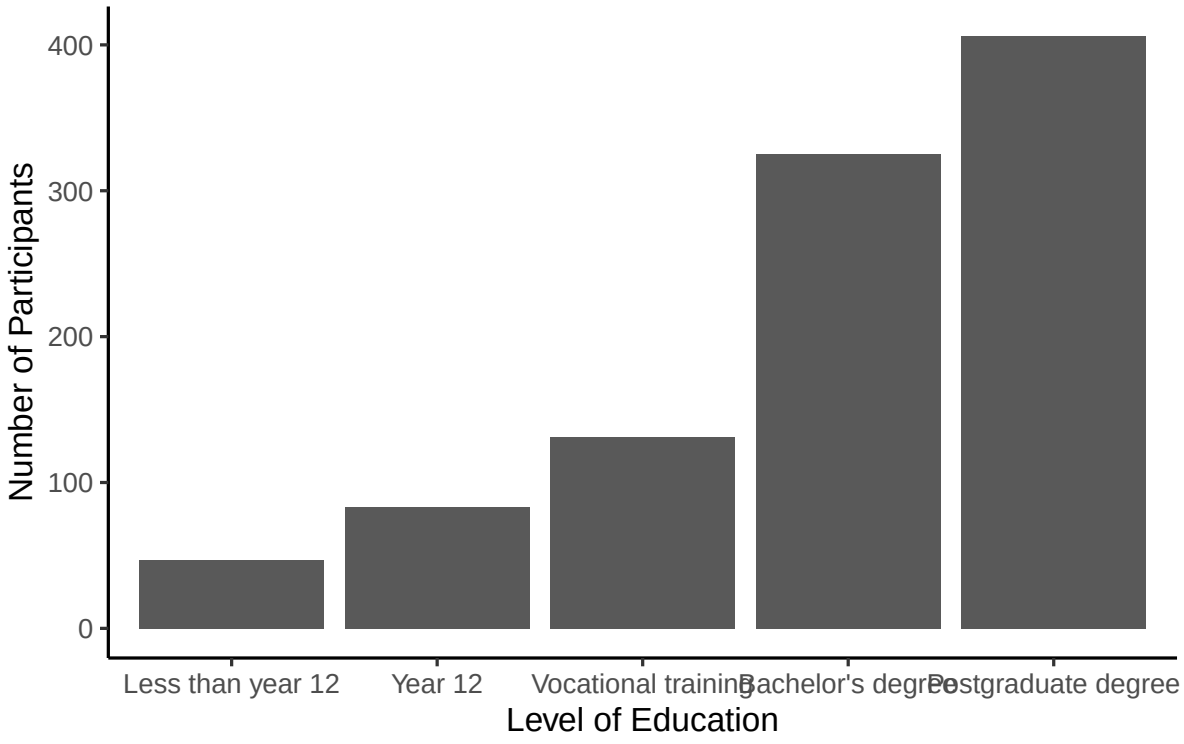
! Error mode

When you edit "labels", it is crucial the values you give it are in the right order. There would be nothing stopping us from writing `c("Male", "Female")` and R will gladly listen to you and add those labels. However, that would be inaccurate as 1s mean Female and 2s mean Male. We are only editing the labels and not the underlying values in the data. These errors are the most sneaky as it will not cause an error to fix, but they are still incorrect.

3.5.4 Activity 9 - Apply your plotting skills to a new variable

An important learning step is being able to apply or transfer what you learnt in one scenario to something new.

In the data set, there is a variable for the level of education: `educ`. Plot the new variable and try to recreate the customisation layers before checking the solution below.



Show me the solution code

To recreate the plot, this is the code:

```
# Plot the variable educ from summarydata
ggplot(summarydata, aes(x = educ)) +
  geom_bar() +
  theme_classic() +
  scale_x_discrete(name = "Level of Education",
                   labels = c("Less than year 12", # 1
                              "Year 12", # 2
                              "Vocational training", # 3
                              "Bachelor's degree", # 4
                              "Postgraduate degree")) + # 5
  scale_y_continuous(name = "Number of Participants")
```

3.6 Saving your Figures

The final step today will be to demonstrate how to save plots you create in `ggplot2`. It is so useful to be able to save a copy of your plots as an image file so that you can use them in a presentation or report. One approach we can use is the function `ggsave()`.

3.6.1 Activity 10 - Saving your last plot

There are two ways you can use `ggsave()`. If you do not tell `ggsave()` which plot you want to save, by default it will save **the last plot you created**.

To demonstrate this, let us run the code again from Activity 8 to produce the final version of our barplot. You do not need to write the code again if you already have it available in a code chunk, but make sure you run the code:

```
# Plot the variable sex from summarydata
ggplot(summarydata, aes(x = sex)) +
  geom_bar() +
  scale_x_discrete(name = "Participant Sex",
                   labels = c("Female", # 1 = Female
                              "Male")) + # 2 = Male
  scale_y_continuous(name = "Number of Participants")
```

Now that we have the plot we want to save as our last produced plot, all that `ggsave()` requires is for you to tell it the file path / name that it should save the plot to and the type of image file you want to create. The example below uses .png but you could also use .jpeg or another image type.

Type and run the following code into a new code chunk and then check your `figures` folder. If you have performed this correctly, then you should see the saved image. This is why we include a `figures` folder as part of the chapter structure, so you know exactly where your figures will be if you want to find them again.

```
ggsave("figures/participant_sex_barplot.png")
```

The image tends to save at a default size, or the size that the image is displayed in your viewer, but you can change this manually if you think that the dimensions of the plot are not correct or if you need a particular size or file type. Sometimes the dimensions look a little off when you save them, so you might need to play around with the size.

Type and run the following code to overwrite the image file with new dimensions. Try different dimensions and units to see the difference. You might want to create `participant_sex_barplot-v1.png`, `participant_sex_barplot-v2.png` etc. and compare them.

One final tip, by default, the plot has a transparent background which you do not notice on a white document, but looks odd on anything else. So, you can set a specific background colour through the argument `bg`.

```
ggsave("figures/participant_sex_barplot.png",
       width = 10, # 10 inches wide
       height = 8, # 8 inches high
       units = "in",
       bg = "white") # Make sure the background is white
```

Remember, you can use `?ggsave()` in the console window to bring up the help file for this function if you want to look at what other arguments are available.

3.6.2 Saving a specific plot

Alternatively, the second way of using `ggsave()` is to save your plot as an object, and then tell it which object you want to save.

Type and run the code below and then check your folder for the image file. Resize the plot if you think it needs it.

> **Warning**
>
> We do not add on `ggsave()` as a plot layer. Instead it is a separate line of code and we tell it which object to save. So, do not add `+ ggsave()` as a layer to your plot.

```
sex_barplot <- ggplot(summarydata, aes(x = sex)) +
  geom_bar() +
  scale_x_discrete(name = "Participant Sex",
                   labels = c("Female", # 1 = Female
                              "Male")) + # 2 = Male
  scale_y_continuous(name = "Number of Participants")


ggsave("figures/participant-sex-barplot.png",
       plot = sex_barplot)
```

Note that when you save a plot to an object, you will not see the plot displayed anywhere. To get the figure to display, you need to type the object name in the console (i.e., `sex_barplot`). The benefit of saving figures this way is that if you are making several plots, you cannot accidentally save the wrong one because you are explicitly specifying which plot to save rather than just saving the last one.

3.7 Test Yourself

To end the chapter, we have some knowledge check questions to test your understanding of the concepts we covered in the chapter. We then have some error mode tasks to see if you can find the solution to some common errors in the concepts we covered in this chapter.

3.7.1 Knowledge check

Question 1. Which of these is the appropriate order of functions to create a barplot?

- (A) geom_bar() + ggplot()
- (B) ggplot() + geom_bar()
- (C) geom_plot() + geom_boxplot()
- (D) ggplot() %>% geom_bar()

Question 2. Why would this line of code not create a barplot, assuming you already loaded all data and libraries and you spelt the data and column names correctly?

```
ggplot(summarydata, aes(x = sex)) +
  geom_barplot()
```

- (A) because this would create a histogram
- (B) because you have piped the barplot and not added it
- (C) because you have not included a y axis
- (D) because there is no geom_barplot() and it should be geom_bar()

Question 3. If I wanted precisely 5 bars in my histogram, what argument would I use?

- (A) ggplot() + geom_histogram(binwidth = 5)
- (B) ggplot() + geom_histogram()
- (C) ggplot() + geom_histogram(bins = 5)
- (D) ggplot() + geom_histogram(bars = 5)

Explain this answer

- `ggplot() + geom_histogram(bins = 5)`. This is the **correct** answer as you are asking ggplot2 to give you the plot organised into 5 bins.
- `ggplot() + geom_histogram(bars = 5)`. This is incorrect as you bars is not the right argument name. You want 5 bars, but the argument is bins.
- `ggplot() + geom_histogram(binwidth = 5)`. This is incorrect as binwidth controls the x-axis range to include per bar, rather than the number of bars.
- `ggplot() + geom_histogram()`. This is incorrect as you did not control the number of bins, so it will default to 30.

3.7.2 Error mode

The following questions are designed to introduce you to making and fixing errors. For this topic, we focus on reading data and using ggplot2. Remember to keep a note of what kind of

error messages you receive and how you fixed them, so you have a bank of solutions when you tackle errors independently.

Create and save a new R Markdown file for these activities by following the instructions in Chapter 2. You should have a blank R Markdown file below line 10. Below, we have several variations of a code chunk and inline code errors. Copy and paste them into your R Markdown file, click knit, and look at the error message you receive. See if you can fix the error and get it working before checking the answer.

Question 4. Copy the following code chunk into your R Markdown file and press knit. You should receive an error like `Error in read_csv(): ! could not find function "read_csv"`.

````
```{r}
pinfo <- read_csv("data/participant-info.csv")
```
````

Explain the solution

If you only added this code chunk in, you have not loaded tidyverse yet. Remember R Markdown knits from start to finish in a fresh session, so it will not work even if you have loaded already tidyverse outside the R Markdown document. So, you would need to add `library(tidyverse)` first.

Question 5. Copy the following code chunk into your R Markdown file and press knit. You should receive an error like `! participant-info.csv does not exist in current working directory`.

````
```{r}
library(tidyverse)

pinfo <- read_csv("participant-info.csv")
```
````

Explain the solution

You had tidyverse loaded this time, but it is not pointing to the right folder. Your working directory should be the main chapter folder, where `participant-info.csv` does not exist. You will need to edit it to `data/participant-info.csv` to work.

Question 6. Copy the following code chunk into your R Markdown file and press knit. You should receive a long error where the problem is buried in the first five lines:

```
Error in geom_histogram()
```

```
! Problem while computing stat.

i Error occurred in the 1st layer.

Caused by error in setup_params():

! stat_bin() requires an x or y aesthetic.
```

````
```{r}
library(tidyverse)

pinfo <- read_csv("data/participant-info.csv")

# Plot the variable age from pinfo
ggplot(pinfo, x = age) +   # Plot age on the x axis
  geom_histogram()
```
````

> Explain the solution
>
> This is potentially a sneaky one where we missed the `aes()` argument and it is only line 5 of the error which gives it away: `! stat_bin() requires an x or y aesthetic`. The first ggplot2 layer has two key components: the data object you want to use, and the aesthetics to set. You need to add "aes()" around where you specify the x-axis: `ggplot(pinfo, aes(x = age))`.

Question 7. Copy the following code chunk into your R Markdown file and press knit. This…works, but does not look quite right?

````
```{r}
library(tidyverse)

pinfo <- read_csv("data/participant-info.csv")

# Plot the variable age from pinfo
ggplot(pinfo, aes(x = age)) # Plot age on the x axis
  geom_histogram()
```
````

> Explain the solution
>
> There is a missing `+` between the two ggplot2 layers. The code should be:

```
# Plot the variable age from pinfo
ggplot(pinfo, aes(x = age)) +  # Plot age on the x axis
  geom_histogram()
```

At the moment, it runs the first layer to create an empty plot, then prints the information contained within geom_histogram.

Question 8. Copy the following code chunk into your R Markdown file and press knit. You should receive a long error again with lines 5-7 key:

```
! stat_bin() requires a continuous x aesthetic.

x the x aesthetic is discrete.

i Perhaps you want stat="count"?
```

````
```{r}
library(tidyverse)

pinfo <- read_csv("data/participant-info.csv")

# Plot the variable age from pinfo
ggplot(pinfo, aes(x = age)) +   # Plot age on the x axis
  geom_histogram() +
  scale_x_discrete(name = "Participant Age")
```
````

Explain the solution

The error message here is a little more useful and points to how we tried to edit the x-axis name. In a histogram, the x-axis is continuous for the range of a numeric variable. We tried using the discrete version of the layer to control the axis (`scale_x_discrete(name = "Participant Age")`) which we had to use for the bar plot. To fix the error, you would need to correct the layer to `scale_x_continuous(name = "Participant Age")`.

3.8 Words from this Chapter

Below you will find a list of words that were used in this chapter that might be new to you in case it helps to have somewhere to refer back to what they mean. The links in this table take you to the entry for the words in the PsyTeachR Glossary. Note that the Glossary is written

by numerous members of the team and as such may use slightly different terminology from that shown in the chapter.

term	definition
assignment-operator	The symbol <-, which functions like = and assigns the value on the right to the object on the left
barplot	also known as a bar chart, barplots represent the frequency or count of a variable through the height of one or more bars.
comment	Comments are text that R will not run as code. You can annotate .R files or chunks in R Markdown files with comments by prefacing each line of the comment with one or more hash symbols (#).
console	The pane in RStudio where you can type in commands and view output messages.
csv	Comma-separated variable: a file type for representing data where each variable is separated from the next by a comma.
data-visualisation	A graphical representation of your data set.
data-wrangling	The process of preparing data for visualisation and statistical analysis.
descriptive	Statistics that describe an aspect of data (e.g., mean, median, mode, variance, range)
double	A data type representing a real decimal number
environment	A data structure that contains R objects such as variables and functions
factor-data-type	A data type where a specific set of values are stored with labels
geom	The geometric style in which data are displayed, such as boxplot, density, or histogram.
histogram	A type of plot showing the frequency of each observation organised into bins. Bins control the width of each bar and how many observations it represents.
numeric	A data type representing a real decimal number or integer.
object	A word that identifies and stores the value of some data for later use.
tidyverse	A set of R packages that help you create and work with tidy data

3.9 End of chapter

Well done! It takes a while to get used to the layering system in ggplot2, particularly if you are used to making graphs a different way. But once it clicks, you will be able to make informative and professional visualisations with ease. Remember, data visualisation is useful for yourself to quickly plot your data, and it's useful for your reader in communicating your key findings.

4 Data wrangling 1: Join, select, and mutate

In this chapter, we start our exploration of data wrangling. Some of you might have experience painstakingly copying and pasting values into new columns or trying to match up values from multiple spreadsheets. As well as taking a long time, there is so much room for error as you might repeat or miss values.

We have mentioned a few times now the benefits of working with R/RStudio to develop reproducible research practices over the first few chapters. But, if you take nothing else away from these materials, developing your data wrangling skills is one of the primary benefits that will benefit you in many assessments and careers. Researchers actually spend far more of their time cleaning and preparing their data than they spend analysing it. Dasu & Johnson (2003) estimated that up to 80% of time spent on data analysis involves data preparation tasks! Although every data set presents unique challenges, there are some systematic principles that you will constantly use to make your analyses less error-prone and more efficient. Our mantra is: the data changes but the skills stay the same.

Over the next three chapters, we are going to introduce you to a range of functions within the tidyverse for wrangling data. In this chapter, we will cover joining two data sets by a common identifier, selecting columns to simplify your data, arranging values within a data set, and mutating data to create new variables.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Join two data sets by matching one or more identifying columns in common.
- Select a range and reorder variables in your data set.
- Arrange values in numerical or alphabetical order.
- Modify or create variables, such as recoding values or creating new groups.

4.1 Chapter preparation

4.1.1 Introduction to the data set

For this chapter, we are using open data from Woodworth et al. (2018) one more time. In the last two chapters, we asked you to trust us and copy some code until we reached data wrangling, and now is the time to fill in those gaps. If you need a reminder, the abstract of their article is:

> We present two datasets. The first dataset comprises 992 point-in-time records of self-reported happiness and depression in 295 participants, each assigned to one of four intervention groups, in a study of the effect of web-based positive-psychology interventions. Each point-in-time measurement consists of a participant's responses to the 24 items of the Authentic Happiness Inventory and to the 20 items of the Center for Epidemiological Studies Depression (CES-D) scale. Measurements were sought at the time of each participant's enrolment in the study and on five subsequent occasions, the last being approximately 189 days after enrolment. The second dataset contains basic demographic information about each participant.

In summary, we have one data set containing demographic information about participants and a second data set containing measurements of two scales on happiness and depression.

4.1.2 Organising your files and project for the chapter

Before we can get started, you need to organise your files and project for the chapter, so your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, create a new folder called `Chapter_04_06_datawrangling`. As we are spending three chapters on data wrangling, we will work within one folder. Within `Chapter_04_06_datawrangling`, create two new folders called `data` and `figures`.
2. Create an R Project for `Chapter_04_06_datawrangling` as an existing directory for your chapter folder. This should now be your working directory.
3. We will work within one folder, but create a new R Markdown for each chapter. Create a new R Markdown document and give it a sensible title describing the chapter, such as `04 Data Wrangling 1`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Chapter_04_06_datawrangling` folder.
4. If you already have the two files from chapter 3, copy and paste them into the `data/` folder. If you need to download them again, the links are data file one (ahi-cesd.csv) and data file two (participant-info.csv). Right click the links and select "save link as", or clicking

the links will save the files to your Downloads. Make sure that both files are saved as ".csv". Save or copy the file to your `data/` folder within `Chapter_04_06_datawrangling`.

You are now ready to start working on the chapter!

> **Reminder of file management if you use the online server**
>
> If we support you to use the online University of Glasgow R Server, working with files is a little different. If you downloaded R / RStudio to your own computer or you are using one of the library/lab computers, please ignore this section.
>
> 1. Log on to the **R server** using the link we provided to you.
> 2. In the file pane, click `New folder` and create the same structure we demonstrated above.
> 3. Download these two data files which we used in Chapter 3. Data file one: ahi-cesd.csv. Data file two: participant-info.csv. Save the two files into the `data` folder you created for chapter 3. To download a file from this book, right click the link and select "save link as". Make sure that both files are saved as ".csv". Do not open them on your machine as often other software like Excel can change setting and ruin the files.
> 4. Now that the files are stored on your computer, go to RStudio on the server and click `Upload` then `Browse` and choose the folder for the chapter you are working on.
> 5. Click `Choose file` and go and find the data you want to upload.

4.1.3 Activity 1 - Load tidyverse and read the data files

As the first activity, try and test yourself by loading tidyverse and reading the two data files. As a prompt, save the data files to these two object names to be consistent with the activities below, but you can check your answer below if you are stuck.

```
# Load the tidyverse package below
?

# Load the two data files
# This should be the ahi-cesd.csv file
dat <- ?

# This should be the participant-info.csv file
pinfo <- ?
```

Show me the solution

You should have the following in a code chunk:

```
# Load the tidyverse package below
library(tidyverse)

# Load the two data files
# This should be the ahi-cesd.csv file
dat <- read_csv("data/ahi-cesd.csv")

# This should be the participant-info.csv file
pinfo <- read_csv("data/participant-info.csv")
```

4.2 Tidyverse and the dplyr package

So far, we have loaded a package called tidyverse in every chapter and it is going to be at the core of all the data skills you develop. The tidyverse (https://www.tidyverse.org/, Wickham (2017) is an ecosystem containing six core packages: dplyr, tidyr, readr, purrr, ggplot2, and tibble. Within these six core packages, you have access to functions that will pretty much cover everything you need to wrangle and visualise your data.

In chapter 3, we introduced you to the package ggplot2 for data visualisation. In this chapter, we focus on functions from the dplyr package, which the authors describe as a grammar of data manipulation (in the wrangling sense, not deviously making up data).

The dplyr package contains several key functions based on common English verbs to help you understand what the code is doing. For an overview, we will introduce you to the following functions:

Function	Description
`*_join()`	Add columns from two data sets by matching observations
`select()`	Include or exclude certain variables (columns)
`mutate()`	Create new variables (columns)
`arrange()`	Change the order of observations (rows)
`filter()`	Include or exclude certain observations (rows)
`group_by()`	Organize the observations (rows) into groups
`summarise()`	Create summary variables for groups of observations

Just looking at the names gives you some idea of what the functions do. For example, `select()` selects columns and `arrange()` orders observations. You will be surprised by how far you can

get with data wrangling using just these functions. There will always be unique problems to solve, but these functions cover the most common that apply to almost every data set.

In this chapter, we focus on the `*_join()` series of functions, `select()`, `arrange()`, and `mutate()`.

4.3 Joining two data frames with `*_join()` functions

The first thing we will do is combine data files. We have two files, `dat` and `pinfo`, but what we really want is a single file that has both the happiness and depression scores and the demographic information about the participants as it makes it easier to work with the combined data.

To do this, we are going to use the function `inner_join()`. So far, we have described these types of functions as `*_join()`. This is because there are a series of functions that join two data sets in slightly different ways. You do not need to memorise these, but it might be useful to refer back to later.

Join function	Description
`inner_join()`	Keep observations in data set x that has a matching key in data set y
`left_join()`	Keep all observations in data set x
`right_join()`	Keep all observations in data set y
`full_join()`	Keep all observations in both data set x and y

> **!** Important
>
> As these functions join data sets in different ways, they will produce different sample sizes depending on the presence of missing data in one or both data sets. For example, `inner_join()` will be the strictest as you must have matching observations in each data set. On the other hand, `full_join()` will be the least strict, as you retain observations that may not exist in one data set or the other.

4.3.1 Activity 2 - Join the files together

We are going to join `dat` and `pinfo` by common identifiers. When we use `inner_join()`, this means we want to keep all the observations in `dat` that also has a corresponding identifier in `pinfo`. This is known as an **inner-join**, where you would exclude participants if they did not have a matching observation in one of the data sets.

The code below will create a new object, called `all_dat`, that combines the data from both `dat` and `pinfo` using the columns `id` and `intervention` to match the participants' data across the two sets of data. `id` is a code or number for each unique participant and will be the most common approach you see for creating an identifier. `intervention` is the group the participant was placed in for the study by Woodworth et al. (2018).

Type and run the code in a new code chunk to inner join the two sets of data.

```
all_dat <- inner_join(x = dat,
                      y = pinfo,
                      by = c("id", "intervention"))
```

To break down what this code is doing:

- `all_dat` is the new object you created with the joined data.
- `x` is the first argument and it should be the first data set / object you want to combine.
- `y` is the second argument and it should be the second data set / object you want to combine.
- `by` is the third argument and it lists the identifier as the name(s) of the column(s) you want to combine the data by in quote marks. In this scenario, there are two identifiers common to each data set. They both contain columns called "id" and "intervention". We have to wrap them in `c()` to say that there is more than one column to combine by. If there was only one common identifier, you would write `by = "id"`.

! Why does my data include .x and .y columns?

If your data sets have more than one common column, you must enter them all in the `by` argument. This tells R there are matching columns and values across the data sets. If you do not enter all the common columns, then R will add on a .x and .y when it adds them together, to label which come from each data set.
For example, try and run this code and look at the columns in `all_dat2`. You will see it has an extra column compared to `all_dat` as there is both "intervention.x" and "intervention.y".

```
all_dat2 <- inner_join(x = dat,
                       y = pinfo,
                       by = "id")
```

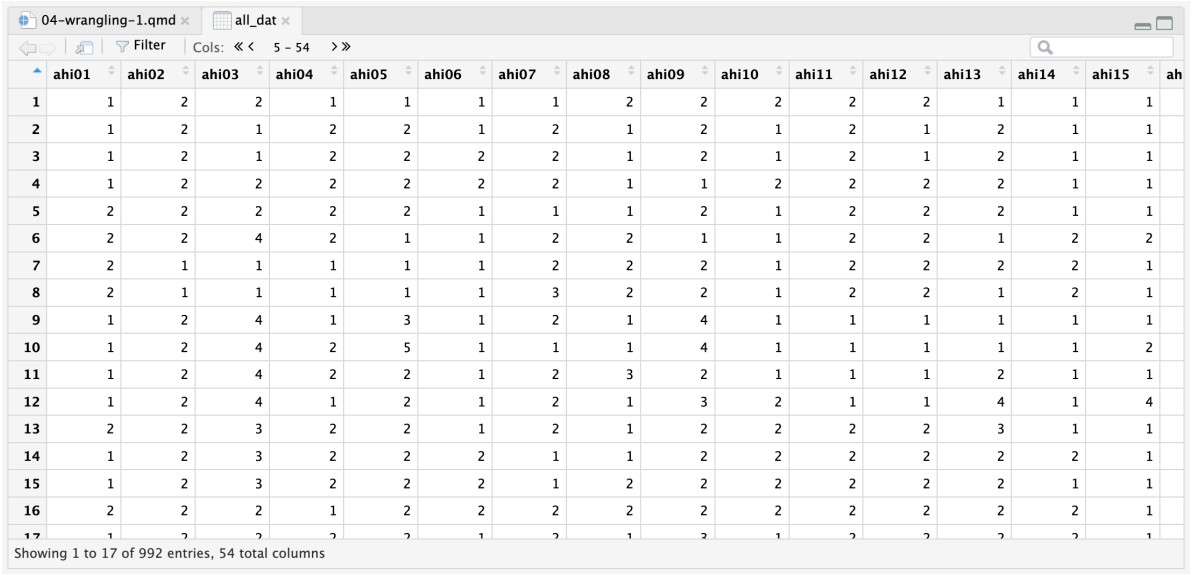
4.3.2 Activity 3 - Explore your data objects

Once you have run this code, you should now see the new `all_dat` object in the environment pane. Remember to get into the habit of exploring your data and objects as you make changes, to check your wrangling is working as intended.

There are two main ways you can do this:

1. Click on the data object in the Environment pane. This will open it up as a tab in RStudio, and you will be able to scroll through the rows and columns (Figure 4.1).

> **!** Why do I not see all my columns?
>
> One common source of confusion is not seeing all your columns when you open up a data object as a tab. This is because RStudio shows you a maximum of 50 columns at a time. If you have more than 50 columns, to see more, you must use the arrows at the top of the tab where it says "Cols:". For example in `all_dat`, it will say 1-50, if you click the right arrow, it will then say 5-54 so you can see the final 4 columns.



	ahi01	ahi02	ahi03	ahi04	ahi05	ahi06	ahi07	ahi08	ahi09	ahi10	ahi11	ahi12	ahi13	ahi14	ahi15	ah
1	1	2	2	1	1	1	1	2	2	2	2	2	1	1	1	
2	1	2	1	2	2	1	2	1	2	1	2	1	2	1	1	
3	1	2	1	2	2	2	2	1	2	1	2	1	2	1	1	
4	1	2	2	2	2	2	2	1	1	2	2	2	2	1	1	
5	2	2	2	2	2	1	1	1	2	1	2	2	2	1	1	
6	2	2	4	2	1	1	2	2	1	1	2	2	1	2	2	
7	2	1	1	1	1	1	2	2	2	1	2	2	2	2	1	
8	2	1	1	1	1	1	3	2	2	1	2	2	1	2	1	
9	1	2	4	1	3	1	2	1	4	1	1	1	1	1	1	
10	1	2	4	2	5	1	1	1	4	1	1	1	1	1	2	
11	1	2	4	2	2	1	2	3	2	1	1	1	2	1	1	
12	1	2	4	1	2	1	2	1	3	2	1	1	4	1	4	
13	2	2	3	2	2	1	2	1	2	2	2	2	3	1	1	
14	1	2	3	2	2	2	1	1	2	2	2	2	2	2	1	
15	1	2	3	2	2	2	1	2	2	2	2	2	2	1	1	
16	2	2	2	1	2	2	2	2	2	2	2	2	2	2	1	
17	1	2	2	2	2	1	2	1	3	1	2	2	2	2	1	

Figure 4.1: Exploring a data object in RStudio by opening it as a tab. You can navigate around the columns and rows without opening it up in something like Excel. If there are more than 50 columns, you can click the arrows next to Cols.

2. Use the `glimpse()` function to see an overview of the data objects.

We explored this in chapter 3, but `glimpse()` tells you how many rows and columns your data have, plus an overview of responses per column. Note: you will see a preview of all 54 columns,

but we have shortened the preview to 10 columns to take up less space in the book.

```
glimpse(all_dat)
```

```
Rows: 992
Columns: 10
$ id           <dbl> 12, 162, 162, 267, 126, 289, 113, 8, 185, 185, 246, 185, ~
$ occasion     <dbl> 5, 2, 3, 0, 5, 0, 2, 2, 2, 4, 4, 0, 4, 0, 1, 4, 0, 5, 4, ~
$ elapsed.days <dbl> 182.025139, 14.191806, 33.033831, 0.000000, 202.096887, 0~
$ intervention <dbl> 2, 3, 3, 4, 2, 1, 1, 2, 3, 3, 3, 3, 1, 2, 2, 2, 3, 2, 2, ~
$ ahi01        <dbl> 1, 1, 1, 1, 2, 2, 2, 2, 1, 1, 1, 1, 2, 1, 1, 2, 1, 1, 2, ~
$ ahi02        <dbl> 2, 2, 2, 2, 2, 2, 1, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 3, ~
$ ahi03        <dbl> 2, 1, 1, 2, 2, 4, 1, 1, 4, 4, 4, 4, 3, 3, 3, 2, 2, 2, 3, ~
$ ahi04        <dbl> 1, 2, 2, 2, 2, 2, 1, 1, 1, 2, 2, 1, 2, 2, 2, 1, 2, 2, 1, ~
$ ahi05        <dbl> 1, 2, 2, 2, 2, 1, 1, 1, 3, 5, 2, 2, 2, 2, 2, 2, 2, 2, 2, ~
$ ahi06        <dbl> 1, 1, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 1, 1, 1, ~
```

> Try this
>
> Now you have explored `all_dat`, try and use one or both of these methods to explore the original `dat` and `pinfo` objects to see how they changed. Notice how the number of rows/observations and columns change from the original objects to when you join them.

4.4 Selecting variables of interest with `select()`

Data sets often have a lot of variables we do not need and it can be easier to focus on just the columns we do need. In `all_dat`, we have 54 variables which takes ages to scroll through and it can be harder to find what you are looking for.

For the two scales on happiness and depression, we have all their items, as well as their total scores. We can create a data set that only includes the key variables and ignores all the individual items using the select() function. There are two ways you can use select: by selecting the variables you want to include, or by selecting the variables you want to ignore.

4.4.1 Activity 4 - Selecting variables you want to include

If there are a smaller number of variables you want to include, then it will be more efficient to specify which variables you want to **include**. Returning to the data wrangling from chapter 3, we can select the columns from `all_dat` that we want to keep.

```
summarydata <- select(.data = all_dat, # First argument as the data object
                      id, # Stating variables we want to include
                      occasion,
                      elapsed.days,
                      intervention,
                      ahiTotal,
                      cesdTotal,
                      sex,
                      age,
                      educ,
                      income)
```

To break down this code:

- We are creating a new object called `summarydata`.
- From `all_dat`, we are selecting 10 columns we want to keep, which we list one by one.

> **Note**
>
> In this example, the variables are in the same order as they were `all_dat`, but they do not need to be. You can use `select()` to create a new variable order if that helps you see all the important variables first. You can also rename variables as you select or reorder them, using the form `new_name = old_name`.

Keep in mind it is important you select variables and assign them to a new object, or overwrite the old object. Both work, but think about if you need the original object later in your analysis and you do not want to go back and rerun code to recreate it. If you just use the select function on it's own, it does not do anything to the object, R just shows you the variables you selected:

```
select(.data = all_dat, # First argument as the data object
       id, # Stating variables we want to include
       occasion,
       elapsed.days,
       intervention,
       ahiTotal,
       cesdTotal,
       sex,
       age,
       educ,
       income)
```

If you have several variables in order that you want to select, you can use a shortcut to avoid typing out every single name. When you select variables, you can use the format `firstcolumn:lastcolumn` to select all the variables from the first column you specify until the last column.

For example, if we wanted to isolate the individual items, we could use the following code:

```
scaleitems <- select(.data = all_dat, # First argument as the data object
                     ahi01:cesd20) # Range of variables to select
```

You can also pair this with individual variable selection:

```
scaleitems <- select(.data = all_dat, # First argument as the data object
                     id, # Individual variable to include
                     ahi01:cesd20) # Range of variables to select
```

Try this

If you wanted to select all the variables from `id` to `intervention`, plus all the variables from `ahiTotal` to `income`, how could you use this shortcut format? Try and complete the following code to recreate `summarydata`. Check your answer below when you have tried on your own.

```
summarydata2 <- ?
```

Solution

Instead of typing all 10 variables, you can select them using two ranges to ignore the scale items in the middle:

```
summarydata2 <- select(.data = all_dat, # First argument as the data object
                       id:intervention, # variable range 1
                       ahiTotal:income) # variable range 2
```

4.4.2 Activity 5 - Selecting variables you want to ignore

Alternatively, you can also state which variables you do not want to keep. This is really handy if you want to keep many columns and only remove one or two.

For example, if we wanted to remove two variables, you add a dash (-) before the variable name:

```
all_dat_reduced2 <- select(.data = all_dat,
                           -occasion, # Remove occasion
                           -elapsed.days) # Remove elapsed.days
```

This also works using the range method, but you must add the dash before the first and last column in the range you want to remove. For example, we can recreate `summarydata` one more time by removing the scale items in the middle:

```
summarydata3 <- select(.data = all_dat, # data object
                       -ahi01:-cesd20) # Remove range of variables
```

> Tip
>
> You can see there were at least three different ways of creating `summarydata` to keep the 10 variables we want to focus on. This is an important lesson as there is often not just one unique way of completing a task in R.
> When you first start coding, you might begin with the long way that makes sense to you. As you practice more, you recognise ways to simplify your code.

4.5 Arranging variables of interest with `arrange()`

Another handy skill is being able to change the order of observations within columns in your data set. The function arrange() will sort the rows/observations by one or more columns. This can be useful for exploring your data set and answering basic questions, such as: who was the youngest or oldest participant?

4.5.1 Activity 6 - Arranging in ascending order

Using `summarydata`, we can order the participants' ages in ascending order:

```
age_ascend <- arrange(summarydata,
                      age)
```

To break down the code,

- We create a new object called `age_ascend`.
- We apply the function `arrange()` to the `summarydata` object. Note we have not typed `.data =` to start reinforcing how you can omit the argument name providing the arguments are in the correct order.

- We order the observations by `age`, which is by default in ascending order from smallest to largest.

If you look in `age_ascend`, we organised the data in ascending order based on age and can see the youngest participant was 18 years old.

4.5.2 Activity 7 - Arranging in descending order

By default, `arrange()` sorts observations in ascending order from the smallest to largest value, or alphabetical order from A to Z. If you want to arrange observations in descending order, you can wrap the name of the variable in the `desc()` function.

For example, we can order participants from oldest to youngest:

```
age_descend <- arrange(summarydata,
                       desc(age)) # descending order of age
```

This time, we can see the oldest participant was 83 years old.

4.5.3 Activity 8 - Sorting by multiple columns

Finally, you can also sort by more than one column and a combination of ascending and descending columns. Unlike `select()`, you might not need to save your sorted observations as a new object, you could use `arrange()` more as a tool to explore your data.

For example, we could look for the oldest female participant. Note: your code will show all 992 observations you could scroll through, but we show the first 10 to save space.

```
arrange(summarydata,
        sex, # order by sex first
        desc(age)) # then descending age
```

```
# A tibble: 10 x 10
      id occasion elapsed.days intervention ahiTotal cesdTotal   sex   age  educ
   <dbl>    <dbl>        <dbl>        <dbl>    <dbl>     <dbl> <dbl> <dbl> <dbl>
 1    51        4         94.9            2       86        15     1    83     2
 2    51        3         32.6            2       87         7     1    83     2
 3    51        0          0              2       90         5     1    83     2
 4    51        2         15.8            2       90         4     1    83     2
 5    51        5        186.             2       91        10     1    83     2
 6   244        0          0              2       64        33     1    77     3
```

```
 7   244        1         7.24              2       70        37     1    77     3
 8   244        2        16.9               2       71        16     1    77     3
 9   244        3        31.3               2       75        22     1    77     3
10   215        0         0                 4       76         1     1    75     3
# i 1 more variable: income <dbl>
```

Try this

Using `summarydata` and `arrange()`, sort the data to answer the following questions:

1. How old is the participant with the highest total happiness score (`ahiTotal`)? ___
2. What is the highest total depression score (`cesdTotal`) in a female participant (remember 1 = female, 2 = male)? ___

Solution

1. We only need to arrange by `ahiTotal` in descending order to find the highest value, then look at the age column.

```
arrange(summarydata,
        desc(ahiTotal)) # descending ahiTotal
```

2. We first order by `sex` in ascending order so 1s are first, then descending order of `cesdTotal` for the highest value.

```
arrange(summarydata,
        sex, # order by sex first
        desc(cesdTotal)) # Descending depression total
```

4.6 Modifying or creating variables with `mutate()`

In the final data wrangling function for this chapter, we can use the function mutate() to modify existing variables or create new variables. This is an extremely powerful and flexible function. We will not be able to cover everything you can do with it in this chapter but we will introduce you to some common tasks you might want to apply.

4.6.1 Activity 9 - Modifying existing variables

If you remember back to chapter 3, we had a problem where R interpreted variables like `sex`, `educ`, and `income` as numeric, but ideally we wanted to treat them as distinct categories or factors. We used `mutate()` to convert the three columns to factors:

```
# Overwrite summary data
summarydata <- mutate(summarydata, # mutate to change columns in summarydata
         sex = as.factor(sex), # save sex as a factor
         educ = as.factor(educ),
         income = as.factor(income))
```

To break down the code:

- We overwrite `summarydata` by assigning the function to an existing object name.
- We use the `mutate()` function on the old `summarydata` data by using it as the first argument.
- We can add one or more arguments to modify or create variables. Here, we modify an existing variable `sex`, use an equals sign (=), then how we want to modify the variable. In this example, we convert sex to a factor by using the function `as.factor(sex)`.

You might not just want to turn a variable into a factor, you might want to completely recode what it's values represent. For this, there is a function called case_match() which you can use within `mutate()`. For example, if we wanted to make `sex` easier to interpret, we could overwrite it's values from 1 and 2:

```
sex_recode <- mutate(summarydata,
                     sex = case_match(sex, # overwrite existing
                                      "1" ~ "Female", # old to new
                                      "2" ~ "Male")) # old to new
```

To break down this code,

- We create a new object `sex_recode` by mutating the `summarydata` object.
- We modify an existing variable `sex` by applying `case_match()` to `sex`.
- Within `case_match()`, the value on the left is the existing value in the data you want to recode. The value on the right is the new value you want to overwrite it to. So, we want to change all the 1s in the data to Female. We then add a new line for every old value we want to change.

Error mode

In the previous exercise, we already converted sex to a factor. So, we had to add quote marks around the old values (`"1"`) as they are no longer considered numeric. If you do not add the quote marks, you will get an error like `Can't convert "..1 (left)" <double> to <factor>`.
If you applied this step *before* converting `sex` to a factor, then `1 ~ "Female"` would work. This shows why it is important to keep data types in mind as R might not know what you mean if you state one data type when it is expecting another.

Try this

Using what you just learnt about using `mutate` and `case_match()`, recode the variable `income` and complete the code below. These are what the numeric values mean as labels:
1 = Below average
2 = Average
3 = Above average

```
income_recode <- mutate(summarydata,
                        income = ?
                          )
```

Check your code against the solution when you have attempted yourself first.

Solution

Following the same format as `sex`, we add a new label for each of the three levels of income.

```
income_recode <- mutate(summarydata,
                        income = case_match(income, # overwrite existing
                                            "1" ~ "Below average", # old to new
                                            "2" ~ "Average", # old to new
                                            "3" ~ "Above average")) # old to new
```

4.6.2 Activity 10 - Creating new variables

You can also create new variables using `mutate()`. There are many possibilities here, so we will demonstrate a few key principles for inspiration and you will learn how to tackle unique problems as you come to them.

In it's simplest application, you can use `mutate()` to add a single value to all rows. For example, you might want to label a data set before joining with another data set so you can identify their origin. Instead of overwriting an existing variable, we specify a new variable name and the value we want to assign:

```
summarydata <- mutate(summarydata,
                      study = "Woodworth et al. (2018)")
```

Using a similar kind of logic to `case_match()` we introduced you to earlier, there is an extremely flexible function called case_when() to help create new variables. Before we explain how it works, we will jump straight into an example to give you something concrete to work with.

Woodworth et al. (2018) includes scores from the Center for Epidemiological Studies Depression (CES-D) scale. Scores range from 0 to 60, with scores of 16 or more considered a cut-off for being at risk of clinical depression. We have the scores, so we can use `case_when()` to label whether participants are at risk or not.

```
summarydata <- mutate(summarydata,
                      depression_risk = case_when(
                        cesdTotal < 16 ~ "Not at risk",
                        cesdTotal > 15 ~ "At risk"))
```

To break down the code:

- We overwrite `summarydata` by mutating the existing `summarydata` object.
- We create a new variable called `depression_risk` by applying the `case_when()` function to the variable `cesdTotal`.
- We apply two comparisons to label responses as either "Not at risk" or "At risk". If `cesdTotal` is less than 16 (i.e., 15 or smaller), then it receives the value "Not at risk". If `cesdTotal` is more than 15 (i.e., 16 or higher), then it receives the value "At risk".

The function `case_when()` applies these criteria **line by line** as it works through your rows. Depending on which criteria your observation meet, it receives the label "Not at risk" or "At risk". You can also set the argument `.default` to assign one value for anything that does not pass any criteria you give it.

The comparisons use something called a Boolean expression. These are logical expressions which can return the values of TRUE or FALSE. To demonstrate the idea, imagine we were applying the logic manually to scores in the data. The first value is 50, so we could apply our criteria to see which one it meets:

```
50 < 16
50 > 15
```

```
[1] FALSE
[1] TRUE
```

R evaluates the first comparison as FALSE as 50 is not smaller than 16, but it evaluates the second comparison as TRUE as 50 is larger than 15. So, `case_when()` would apply the label "At risk" as the second statement evaluates to TRUE.

> **Try this**
>
> Try and pick a few more `cesdTotal` scores from the data and apply the criteria to see if they are evaluated as TRUE OR FALSE. It can be tricky moving from imagining what you want to do to being able to express it in code, so the more practice the better.

We have only used less than or greater than, but there are several options for expressing Boolean logic, the most common of which are:

Operator	Name	is TRUE if and only if
A < B	less than	A is less than B
A <= B	less than or equal	A is less than or equal to B
A > B	greater than	A is greater than B
A >= B	greater than or equal	A is greater than or equal to B
A == B	equivalence	A exactly equals B
A != B	not equal	A does not exactly equal B
A %in% B	in	A is an element of vector B

> **What is a vector?**
>
> Vectors are essentially a group or list of elements of the same data type (you will learn more about data types in Chapter 5). For example, `c(1, 2, 3, 4)` or `c("James", "Jude", "Phil", "Gaby")`.

Boolean expressions will come up again in chapter 5 when it comes to `filter()`, so there will be plenty more practice as you apply your understanding to different data sets and use cases.

Try this

Using what you just learnt about using `mutate` and `case_when()`, create a new variable called `happy` using the `ahiTotal` variable and complete the code below.
The Authentic Happiness Inventory (AHI) does not have official cutoffs, but let us pretend scores of **65 or more** are "happy" and scores of **less than 65** are "unhappy".

```
summarydata <- mutate(summarydata,
                      happy = ?
                        )
```

Check your code against the solution when you have attempted it yourself first.

Solution

Following the same format as `depression_risk` and `cesdTotal`, we add a new comparison for each criterion we want to use as a Boolean expression:

```
summarydata <- mutate(summarydata,
                      happy = case_when(
                        ahiTotal < 65 ~ "Unhappy",
                        ahiTotal > 64 ~ "Happy"))
```

If you looked at the table of Boolean operators, you could also express 65 or more as:

```
summarydata <- mutate(summarydata,
                      happy = case_when(
                        ahiTotal < 65 ~ "Unhappy",
                        ahiTotal >= 65 ~ "Happy"))
```

4.7 Test yourself

To end the chapter, we have some knowledge check questions to test your understanding of the concepts we covered in the chapter. We then have some error mode tasks to see if you can find the solution to some common errors in the concepts we covered in this chapter.

4.7.1 Knowledge check

Question 1. Which of the following functions would you use if you wanted to keep only certain columns?

- (A) select()
- (B) arrange()
- (C) mutate()
- (D) inner_join()

Question 2. Which of the following functions would you use if you wanted to join two data sets by their shared identifier?

- (A) select()
- (B) arrange()
- (C) mutate()
- (D) inner_join()

Question 3. Which of the following functions would you use if you wanted to add or modify a column?

- (A) select()
- (B) arrange()
- (C) mutate()
- (D) inner_join()

Question 4. When you use mutate(), which additional function could you use to recode an existing variable?

- (A) arrange()
- (B) case_when()
- (C) case_match()
- (D) filter()

Question 5. When you use mutate(), which additional function could you use to create a new variable depending on specific criteria you set?

- (A) arrange()
- (B) case_when()
- (C) case_match()
- (D) filter()

4.7.2 Error mode

The following questions are designed to introduce you to making and fixing errors. For this topic, we focus on data wrangling using the functions `inner_join()`, `select()`, and `mutate()`. Remember to keep a note of what kind of error messages you receive and how you fixed them, so you have a bank of solutions when you tackle errors independently.

Create and save a new R Markdown file for these activities. Delete the example code, so your file is blank from line 10. Create a new code chunk to load `tidyverse` and the two data files:

```
# Load the tidyverse package
library(tidyverse)

# Load the two data files
dat <- read_csv("data/ahi-cesd.csv")
pinfo <- read_csv("data/participant-info.csv")
```

Below, we have several variations of a code chunk error or misspecification. Copy and paste them into your R Markdown file below the code chunk to load `tidyverse` and the data. Once you have copied the activities, click knit and look at the error message you receive. See if you can fix the error and get it working before checking the answer.

Question 6. Copy the following code chunk into your R Markdown file and press knit. This…works, but we want 54 columns rather than 55 columns. Some of the columns do not look quite right?

````
```{r}
all_dat <- inner_join(x = dat,
                      y = pinfo,
                      by = c("id"))
```
````

Explain the solution

This was a prompt to look out for duplicate columns when we do not specify all the common columns between the data sets you want to join. You join by "id" which works, but because you did not also add "intervention", you get .x and .y appended to two "intervention" columns.

```
all_dat <- inner_join(x = dat,
                      y = pinfo,
                      by = c("id", "intervention"))
```

Question 7. Copy the following code chunk into your R Markdown file and press knit. You should receive an error like `! Can't subset columns that don't exist. x Column "interventnion" doesnt exist.`

````
```{r}
select_data <- select(.data = pinfo,
                      id,
                      intervetnion,
                      sex,
                      age,
                      educ,
                      income)
```
````

Explain the solution

This is an example of a sneaky typo causing an error. R is case and spelling sensitive, so it does not know what you mean when you asked it to select the column "intervetnion" rather than "intervention". To fix the error, you just need to fix the typo:

```
select_data <- select(.data = pinfo,
                      id,
                      intervention,
                      sex,
                      age,
                      educ,
                      income)
```

Question 8. Copy the following code chunk into your R Markdown file and press knit. You should receive an error like `! Cant convert "..1 (left)" <character> to <double>.`

```{r}
recode_variable <- mutate(pinfo,
                          sex = case_match(sex,
                                           "1" ~ "Female",
                                           "2" ~ "Male"))
```

Explain the solution

This is the opposite problem to what we warned about in the `case_match` section. You need to honour data types and we have not converted sex to a factor or character in this example. So, R does not know how to match the character "1" against the number/double 1 in the data. To fix the error, you need to remove the double quotes to give R a number/double like it can see in the data:

```{r}
recode_variable <- mutate(pinfo,
                          sex = case_match(sex,
                                           1 ~ "Female",
                                           2 ~ "Male"))
```

Question 9. Copy the following code chunk into your R Markdown file and press knit. We want to create two groups depending on if we consider a participant a teenager if they are younger than 20, or not a teenger if they are 20 years or older. The code below…works? This is a sneaky one, so think about the criteria we want vs the criteria we set.

```{r}
age_groups <- mutate(pinfo,
                     age_groups = case_when(
                       age < 20 ~ "Teenager",
                       age > 20 ~ "Not a teenager"))
```

Explain the solution

This is a really sneaky one as it does not actually affect a participant in the data, but there is a small mismatch between the criteria we want and the criteria we set.
In our "teenager" group, this is accurate as we want to classify them if they are younger than 20. However, in the "not a teenager" group we currently set the criterion if they are older than 20, i.e., 21 or older. This would mean 20 year old participants are stuck in the middle with no group.
We see this kind of mistake a lot, so think carefully about your Boolean expression and check examples in the console if you are unsure. To fix, you could use:

```r
age_groups <- mutate(pinfo,
                     age_groups = case_when(
                       age < 20 ~ "Teenager",
                       age > 19 ~ "Not a teenager"))
```

or

```r
age_groups <- mutate(pinfo,
                     age_groups = case_when(
                       age < 20 ~ "Teenager",
                       age >= 20 ~ "Not a teenager"))
```

4.8 Words from this Chapter

Below you will find a list of words that were used in this chapter that might be new to you in case it helps to have somewhere to refer back to what they mean. The links in this table take you to the entry for the words in the PsyTeachR Glossary. Note that the Glossary is written by numerous members of the team and as such may use slightly different terminology from that shown in the chapter.

term	definition
arrange()	Order the rows of a data set by the values of one or more columns.
boolean-expression	A logical statement in programming to evaluate a condition and return a Boolean value, which can be TRUE or FALSE.
case_match()	You can switch values from old to new. Statements are evaluated sequentially, meaning the old value is replaced with the first new value it matches.
case_when()	An if else statement to check old values against a set of criteria. Statements are evaluated sequentially, meaning each observation is checked against the criteria, and it receives the first match it passes.
data-wrangling	The process of preparing data for visualisation and statistical analysis.
function	A named section of code that can be reused.
inner-join	A mutating join that returns all the rows that have a match in the other table.
mutate()	You can create new columns that are functions of existing variables. You can also modify variables if the name is the same as an existing column.
package	A group of R functions.
select()	Select, reorder, or rename variables in your data set.

4.9 End of Chapter

Excellent work so far! Data wrangling is a critical skill and being able to clean and prepare your data using code will save you time in the long run. Manually tidying data might seem quicker now when you are unfamilar with these functions, but it is open to errors which may not have a paper trail as you edit files. By reproducibly wrangling your data, you can still make mistakes, but they are reproducible mistakes you can fix.

In the next chapter, we start by recapping the key functions from this chapter on a new data set, then introduce you to more data wrangling functions from dplyr to expand your toolkit.

5 Data wrangling 2: Filter and summarise

One of the key aspects in a researcher's toolbox is the knowledge and skill to work with data regardless of how it comes to you. When you run a study, you might get lots of different data types in various different files. For instance, some experimental software creates a new file for every participant, and each participant's file might contain columns and rows of different data types, only some of which are important. Being able to wrangle that data, manipulate it into different layouts, extract the parts you need, and summarise it, is one of the most important skills we will help you learn throughout this book.

In the last chapter, we introduced you to several one-table functions from dplyr which we use to wrangle data. Over the course of this book, we will reinforce these functions and skills across different data sets to give you a wide range of exposure to what psychology is about, and to reiterate that the same skills apply across different data sets. Always remember: **while the data changes, the skills stay the same!**

In this chapter, we are going to continue developing our understanding of data, and build on the knowledge and skills you have developed so far. We start with a recap of data wrangling functions from Chapter 4 and ask you to apply them to a new data set. Feel free through to refer back to Chapter 4 for help - this is not a test - but try and complete the activities independently to judge how well you can transfer your skills to a new scenario. We then introduce you to new data wrangling functions to filter and summarise.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Apply your data wrangling skills to a new unseen data set.
- Filter observations to retain a subset of your data, such as keeping only postgraduate students.
- Summarise your data to calculate summary statistics, either across all of your observations, or by subsetting across one or more additional variables.

5.1 Chapter preparation

5.1.1 Introduction to the data set

For this chapter, we are using open data from Witt et al. (2018). The abstract of their article is:

> Can one's ability to perform an action, such as hitting a softball, influence one's perception? According to the action-specific account, perception of spatial layout is influenced by the perceiver's abilities to perform an intended action. Alternative accounts posit that purported effects are instead due to nonperceptual processes, such as response bias. Despite much confirmatory research on both sides of the debate, researchers who promote a response-bias account have never used the Pong task, which has yielded one of the most robust action-specific effects. Conversely, researchers who promote a perceptual account have rarely used the opposition's preferred test for response bias, namely, the postexperiment survey. The current experiments rectified this. We found that even for people naive to the experiment's hypothesis, the ability to block a moving ball affected the ball's perceived speed. Moreover, when participants were explicitly told the hypothesis and instructed to resist the influence of their ability to block the ball, their ability still affected their perception of the ball's speed.

To summarise, their research question was: **does your ability to perform an action influence your perception?** For instance, does your ability to hit a tennis ball influence how fast you perceive the ball to be moving? Or to phrase another way, do expert tennis players perceive the ball moving slower than novice tennis players?

This experiment does not use tennis players, instead they used the Pong task like the classic retro arcade game. Participants aimed to block moving balls with various sizes of paddles. Participants tend to estimate the balls as moving faster when they have to block it with a smaller paddle as opposed to when they have a bigger paddle. In this chapter, we will wrangle their data to reinforce skills from Chapter 4, and add more dplyr functions to your toolkit.

5.1.2 Organising your files and project for the chapter

Before we can get started, you need to organise your files and project for the chapter, so your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, you should have a folder from chapter 4 called `Chapter_04_06_datawrangling` where you created an R Project.

2. Create a new R Markdown document and give it a sensible title describing the chapter, such as `05 Data Wrangling 2`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Chapter_04_06_datawrangling` folder.
3. We are working with a new data set, so please save the following data file: witt_2018.csv. Right click the link and select "save link as", or clicking the link will save the files to your Downloads. Make sure that you save the file as ".csv". Save or copy the file to your `data/` folder within `Chapter_04_06_datawrangling`.

You are now ready to start working on the chapter!

5.2 Select, arrange, and mutate recap

Before we introduce you to new functions, we will recap data wrangling functions from Chapter 4 to select, arrange, and mutate. Following along is one thing but being able to transfer your understanding to a new data set is a key sign of your skill development. Feel free to use Chapter 4 to help you, but try and complete the recap activities independently before checking the solutions. This will help prepare you as we move from the chapters, to the data analysis journeys, to the assessments, and to your future career.

5.2.1 Activity 1 - Load tidyverse and read the data file

As the first activity, try and test yourself by loading tidyverse and reading the data file. As a prompt, save the data file to this object name to be consistent with the activities below, but you can check your answer below if you are stuck.

```
# Load the tidyverse package below
?

# Load the data file
# This should be the witt_2018.csv file
pong_data <- ?
```

Show me the solution

You should have the following in a code chunk:

```
# Load the tidyverse package below
library(tidyverse)

# Load the data file
# This should be the witt_2018.csv file
pong_data <- read_csv("data/witt_2018.csv")
```

5.2.2 Activity 2 - Explore `pong_data`

Remember the first critical step when you come across any new data is exploring to see how many columns you are working with, how many rows/observations there are, and what the values look like. For example, you can click on `pong_data` in the environment and scroll around it as a tab. You can also get a preview of your data by using the `glimpse()` function.

```
glimpse(pong_data)
```

```
Rows: 4,608
Columns: 8
$ Participant     <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ~
$ JudgedSpeed     <dbl> 1, 0, 1, 0, 1, 0, 1, 0, 0, 0, 1, 1, 0, 1, 0, 1, 0, ~
$ PaddleLength    <dbl> 50, 250, 50, 250, 250, 50, 250, 50, 250, 50, 50, 250, ~
$ BallSpeed       <dbl> 5, 3, 4, 3, 7, 5, 6, 2, 4, 4, 7, 7, 3, 6, 5, 7, 2, 5, ~
$ TrialNumber     <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16,~
$ BackgroundColor <chr> "red", "blue", "red", "red", "blue", "blue", "red", "r~
$ HitOrMiss       <dbl> 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 0, 1, 1, ~
$ BlockNumber     <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ~
```

If you look at that table, you can see there are 8 columns and 4608 rows. Seven of the column names are `<dbl>`, short for double, and one is `<chr>`, short for character. We will need to keep the data types in mind as we wrangle the data.

5.2.3 Data types in R

We try and balance developing your data skills in a practical way while slowly introducing some of the underlying technical points. In the last chapter, we warned about honoring data types so R knew how to handle numbers/doubles vs factors. Now we have explored a few data sets, it is time to clarify some key differences between data types in R.

We often store data in two-dimensional tables, either called data frames, tables, or tibbles. There are other ways of storing data that you will discover in time but in this book, we will

be using data frame or tibbles (a special type of data frame in the tidyverse). A data frame is really just a table of data with columns and rows of information. Within the cells of the data frame - a cell being where a row and a column meet - you get different types of data, including double, integer, character and factor. To summarise:

Type of Data	Description
Double	Numbers that can take decimals
Integer	Numbers that cannot take decimals
Character	Tends to contain letters or be words
Factor	Nominal (categorical). Can be words or numbers (e.g., animal or human, 1 or 2)

Double and integer can both be referred to as numeric data, and you will see this word from time to time. For clarity, we will use double as a term for any number that can take a decimal (e.g. 3.14) and integer as a term for any whole number (no decimal, e.g. 3).

Somewhat confusingly, double data might not have decimal places in it. For instance, the value of 1 could be double as well as integer. However, the value of 1.1 could only be double and never integer. Integers cannot have decimal places. The more you work with data the more this will make sense, but it highlights the importance of looking at your data and checking what type it is as the type determines what you can do with the data.

Functions to convert variables

Until now, we have used the function `as.factor()` which takes an existing variable and converts it to a factor where possible. There are functions which convert variables to each data type, such as `as.character()`, `as.numeric()`, and `as.Date()`. In a data frame, each variable can only be one data type. For example, a variable like age would only be numeric/double for age in years, while a variable like occupation would be character or a factor for distinct groups. You can use these conversion functions to convert a whole variable to another data type where possible. If there is an errant data entry and it is not possible to convert it to the desired data type, it will replace it with an NA and give you a warning.

In `pong_data`, each row (observation) represents one trial per participant and there are 288 trials for each of the 16 participants. Most of the data is a double (i.e., numbers) and one column is a character (i.e., text). The columns (variables) we have in the data set are:

Variable	Type	Description
Participant	double	participant number
JudgedSpeed	double	speed judgement (1 = fast, 0 = slow)

Variable	Type	Description
PaddleLength	double	paddle length (pixels)
BallSpeed	double	ball speed (2 pixels/4ms)
TrialNumber	double	trial number
BackgroundColor	character	background display colour
HitOrMiss	double	hit ball = 1, missed ball = 0
BlockNumber	double	block number (out of 12 blocks)

5.2.4 Activity 3 - `select()` a range of columns

Either by inclusion (stating all the variables you want to keep) or exclusion (stating all the variables you want to drop), create a new object named `select_dat` and select the following columns from `pong_data`:

- `Participant`
- `PaddleLength`
- `TrialNumber`
- `BackgroundColor`
- `HitOrMiss`

```
# select 5 variables from pong_data
select_dat <- ?
```

Show me the solution

You should have the following in a code chunk:

```
# select 5 variables from pong_data
select_dat <- select(pong_data,
                     Participant,
                     PaddleLength,
                     TrialNumber,
                     BackgroundColor,
                     HitOrMiss)
```

or

```
# remove 3 variables from pong_data
select_dat <- select(pong_data,
                     -JudgedSpeed,
                     -BallSpeed,
                     -BlockNumber)
```

5.2.5 Activity 4 - Reorder the variables using `select()`

We can also use `select()` to reorder your columns, as the new data object will display the variables in the order that you entered them.

Use `select()` to keep only the columns `Participant`, `JudgedSpeed`, `BallSpeed`, `TrialNumber`, and `HitOrMiss` from `pong_data` but this time, display them in ascending alphabetical order. Save this tibble in a new object named `reorder_dat`.

```
# reorder the 5 variables from pong_data
reorder_dat <- ?
```

Show me the solution

You should have the following in a code chunk:

```
# reorder the 5 variables from pong_data
reorder_dat <- select(pong_data, # original data
                      BallSpeed,
                      HitOrMiss,
                      JudgedSpeed,
                      Participant,
                      TrialNumber)
```

5.2.6 Activity 5 - Reorder observations using `arrange()`

Reorder observations in the data using the following two variables: `HitOrMiss` (putting hits (1) first) and `JudgedSpeed` (putting fast judgement (1) first). Store this in an object named `arrange_dat`.

```
# arrange pong_data by HitOrMiss and JudgedSpeed
arrange_dat <- ?
```

Now try and answer the following questions about the data.

1. What is the trial number (`TrialNumber`) in the 1st row? _
2. What is the background colour (`BackgroundColor`) in the 10th row? _____

Show me the solution

You needed to include `desc()` to change it from running smallest-to-largest to largest-to-smallest as the values are 0 and 1. You should have the following in a code chunk:

```
# arrange pong_data by HitOrMiss and JudgedSpeed
arrange_dat <- arrange(pong_data, # original data
                       desc(HitOrMiss),
                       desc(JudgedSpeed))
```

5.2.7 Activity 6 - Modifying or creating variables using `mutate()`

Some of these values could be a little easier to understand. They are represented in the data by 0s and 1s, but it might not be immediately obvious what they mean.

Create a new variable called `JudgedSpeedLabel` by mutating the original `pong_data` object. Change the values in `JudgedSpeed` using the following labels:

0 = Slow

1 = Fast

```
# mutate pong_data and recode values into a new variable
pong_data <- ?
```

Show me the solution

You should have the following in a code chunk:

```
# mutate pong_data and recode values into a new variable
pong_data <- mutate(pong_data,
                    JudgedSpeedLabel = case_match(JudgedSpeed,
                                                  0 ~ "Slow",
                                                  1 ~ "Fast"))
```

5.3 Removing or retaining observations using `filter()`

Now we have revisited key data wrangling functions from Chapter 4 to select, arrange, and mutate, it is time to add some new functions from dplyr to your toolkit.

Using select, we could remove columns, but there are many situations where you want to include or exclude certain observations/rows. The function filter() will possibly be one of your most used for data wrangling. For example, imagine you want to only analyse participants who provided informed consent and exclude participants who did not. Similarly, you might want to focus your analyses only on participants who are under the age of 21.

5.3.1 Activity 7 - Filter using one criterion

We will jump straight into an example. Imagine that you realised you made a mistake creating your experiment and all your trial numbers are wrong. The first trial (trial number 1) was a practice, so you should exclude it and your experiment actually started on trial 2.

```
pong_data_filter <- filter(pong_data,
                           TrialNumber > 1)
```

To break down the code:

- We create a new object called `pong_data_filter` by applying the filter function to `pong_data`.
- We add the Boolean expression `TrialNumber > 1` to keep all responses higher than 1 (i.e., 2 or higher).

The `filter()` function uses our old friends the Boolean expressions we introduced you to in Chapter 4. You can add one or more logical expressions to filter observations. The function retains observations when they are evaluated to TRUE and ignores observations when they are evaluated to FALSE. Remember, when you are working out how to express your ideas in code, test them out. For example, we can see what the expression would do to different trial numbers:

```
1 > 1
2 > 1
```

```
[1] FALSE
[1] TRUE
```

1 is not larger than 1, so it's evaluated to FALSE and would be ignored. 2 is larger than 2, so it's evaluated to TRUE and would be retained. Explore the two data sets `pong_data` and `pong_data_filter` and the number of rows they have to see the effects of applying the function.

As a reminder from Chapter 4, the most common Boolean expressions are:

Operator	Name	is TRUE if and only if
A < B	less than	A is less than B
A <= B	less than or equal	A is less than or equal to B
A > B	greater than	A is greater than B
A >= B	greater than or equal	A is greater than or equal to B
A == B	equivalence	A exactly equals B
A != B	not equal	A does not exactly equal B
A %in% B	in	A is an element of vector B

Try this

Using the `filter()` example and the table above, imagine we wanted to only keep trials where participants judged the speed to be "Fast". Use the `pong_data_filter` after removing trial number 1 and assign it to a new object `pong_data_fast`. You could use the `JudgedSpeed` or `JudgedSpeedLabel` variable to do this.
For a hint, you want to keep responses when they are equivalent to "Fast" or 1 depending on the variable you use.

```
# Retain fast judged speed trials
pong_data_fast <- filter(pong_data_filter,
                         ?)
```

Solution

You were looking for the equivalence Boolean operator (==) to retain responses which were equal to "Fast" or 1. If you used `JudgedSpeedLabel`, you should have:

```
# Retain fast judged speed trials
pong_data_fast <- filter(pong_data_filter,
                         JudgedSpeedLabel == "Fast")
```

If you used `JudgedSpeed`, you should have:

```
# Retain fast judged speed trials
pong_data_fast <- filter(pong_data_filter,
                         JudgedSpeed == 1)
```

Note we use a double equals == and not a single equals = for the Boolean operator. We also must honour the data type for the expression we set.

5.3.2 Activity 8 - Filter using two or more criteria

You explored using one criterion to filter out or retain observations/rows, but you can make the expressions arbitrarily more complicated by adding two or more criteria to evaluate against. Just note the more criteria you add, the more selective you are being. You are probably going to be excluding more and more observations, so think about what you want to achieve.

Focusing on one variable, you can specify multiple values to compare against. For example, you might want to only keep responses which had a ball speed of 2 or 4:

```
pong_data_BallSpeed <- filter(pong_data_filter,
                              BallSpeed == 2 | BallSpeed == 4)
```

To break down the code:

- We create a new object called `pong_data_BallSpeed` by applying the filter function to `pong_data_filter`.
- We add the Boolean expression `BallSpeed == 2`, the vertical line symbol (`|`), then a second expression `BallSpeed == 4`. The vertical line symbol (`|`) means "or", so our expression is retain `BallSpeed` responses which equal 2 OR 4, and ignore all the others.

For two values, this is pretty straightforward, but it could get out of hand when you have four or five values to evaluate against. There is a super handy shortcut from the Boolean expressions table for "in" which we can apply if we wanted to keep ball speeds of 2, 4, 5, and 7:

```
pong_data_BallSpeed <- filter(pong_data_filter,
                              BallSpeed %in% c(2, 4, 5, 7))
```

You can read the expression here as: for each observation/row, check whether the value of `BallSpeed` is in the vector of numbers 2, 4, 5, 7. Remember `filter()` works by whether the expression is evaluted to TRUE or FALSE, so you can see how it works by testing some numbers:

```
1 %in% c(2, 4, 5, 7)
2 %in% c(2, 4, 5, 7)
```

```
[1] FALSE
[1] TRUE
```

1 is not present in `c(2, 4, 5, 7)`, so it is evaluated to FALSE and would be ignored. 2 is presented in `c(2, 4, 5, 7)`, so it is evaluated to TRUE and would be retained.

You can also add two or more expressions including multiple variables by adding them to the function separated by commas. For example, imagine we wanted to retain observations/rows which had a "Fast" speed judgement with ball speeds of 2, 4, 5, and 7:

```
pong_fast_BallSpeed <- filter(pong_data_filter,
                              JudgedSpeedLabel == "Fast",
                              BallSpeed %in% c(2, 4, 5, 7))
```

In the first expression, we only want to keep observations/rows which have a `JudgedSpeedLabel` of "Fast". In the second expression, we only want to keep observations/rows which have a BallSpeed of 2, 4, 5, or 7. In other words, retain "Fast" observations AND those with a ball speed of 2, 4, 5, or 7. Adding more expressions makes your criteria more selective as rows must pass both conditions to be retained in the data.

Try this

Using the examples above, imagine we wanted to only keep trials where:

1. The `PaddleLength` is 50.
2. The `BackgroundColor` is red.
3. The `HitOrMiss` is 1.

Use the `pong_data_filter` object and assign it to a new object `pong_data_three_criteria`.

```
# apply three criteria to filter pong_data_filter
pong_data_three_criteria <- filter(pong_data_filter,
                                   ?)
```

Solution

You should have the following in a code chunk:

```
# apply three criteria to filter pong_data_filter
pong_data_three_criteria <- filter(pong_data_filter,
                                   PaddleLength == 50,
                                   BackgroundColor == "red",
                                   HitOrMiss == 1)
```

5.4 Counting observations using `count()`

As we work from wrangling data towards analysing your data to produce numerical summaries, we can start introducing different ways of summarising your data set.

In it's simplest sense, we can look at different ways of counting your observations. Often, it is helpful to know how many observations you have, either in total, or broken down by groups. This can help you spot if something has gone wrong in a calculation, e.g., if you have done something with the code and your mean or median is only being calculated using a subset of the values you intended. Alternatively, it can be useful for reporting descriptive statistics, such as how many participants were in your study or how many people were in each group.

5.4.1 Activity 9 - Counting observations

To count observations, you have the function count(). Without any additional arguments, you can use the function to report how many observations are in your data set:

```
count(pong_data_filter)
```

```
# A tibble: 1 x 1
      n
  <int>
1  4592
```

This corresponds nicely with the number of observations you can see in the data environment window and from when we have used `glimpse()` for a summary of the object.

You can then add one or more variables to the function to count the number of observations within each variable and across the combination of variables when you supply two or more. For example, we could count the number of observations within `BackgroundColor`:

```
count(pong_data_filter,
      BackgroundColor) # count observations within variable 1
```

And it would give the answer of:

```
# A tibble: 2 x 2
  BackgroundColor     n
  <chr>           <int>
1 blue             2304
2 red              2304
```

We can see there are an equal number of blue and red backgrounds across all the observations.

Try this

One way of sense checking your data and making sure there is not a sneaky error is checking how many observations there are per unique participant and ensuring that matches up with what you understand about the study.
Use the `count()` function on the `pong_data_filter` object to answer the following questions about the data:

1. How many observations do we have for each unique `Participant` in the data? _____
2. `HitOrMiss` codes for whether the `Participant` hit or missed the ball in the trial. If you count the number of `HitOrMiss` per `Participant`, participant number 3 made _____ hits and ___ misses.

```
# count observations per Participant
count(pong_data_filter,
      ?)

# count observations of HitOrMiss per Participant
# Hint: you can add multiple variables with a comma.
count(pong_data_filter,
      ?)
```

Solution

To answer question 1, we only need to add `Participant` as an argument after the data `pong_data_filter`.

```
# count observations per Participant
count(pong_data_filter,
      Participant)
```

To answer question 2, we need both `Participant` and `HitOrMiss` as arguments after the data `pong_data_filter`, as we want the number of hits and misses per participant.

```
# count observations of HitOrMiss per Participant
count(pong_data_filter,
      Participant,
      HitOrMiss)
```

5.5 Summarising data using `summarise()` and `group_by()`

Counting data is useful, but it might not be the only way of summarising data that you want. A more flexible function is summarise() which you can use to calculate summary statistics across your whole data frame, or grouped by additional variables.

5.5.1 Activity 10 - Summarising all the observations

To start with something familiar, we can use `summarise()` to count observations. The function works in a similar format to `mutate()` where you enter a variable name and tell R what function you want applying to the data frame or variable. For example, we can use the `n()` function to calculate the number of observations in `pong_data_filter`:

```
N_observations <- summarise(pong_data_filter,
                            N_observations = n())
```

To break down the code:

- We create a new object `N_observations` by applying the `summarise()` function to `pong_data_filter`.
- We create a new variable name called `N_observations`, add an equals for what that new variable represents, and add our desired function `n()`. You do not need to add any further arguments, it calculates the number of observations in the object you give it.

This creates a new object as a data frame with 1 observation and 1 column to produce a single number:

```
# A tibble: 1 x 1
  N_observations
           <int>
1           4592
```

Reassuringly, this is exactly the same as we received for `count()`. If you only want the number of observations, then `count()` will be more efficient. However, if you want to produce the number of observations in addition to other summary statistics, then `summarise()` is going to be more useful.

To demonstrate the flexibility of `summarise()`, we can add another summary statistic for the mean hit rate. When binary outcomes like a hit or a miss are coded as 0 and 1, taking the mean provides the proportion of hits (or whatever is coded as 1).

```
summarise(pong_data_filter,
          N_observations = n(),
          hit_proportion = mean(HitOrMiss,
                                na.rm = TRUE))
```

```
# A tibble: 1 x 2
  N_observations hit_proportion
           <int>          <dbl>
1           4592          0.688
```

In this example, we have not saved the `summarise()` output to a new object, just printed it's result. We can see we get the number of observations as before, but we also get the mean value for the hit rate. The proportion of hits across all observations was 0.688 or 68.8%.

! Why is my mean NA?

When you use the `mean()` function, you might find the result is `NA`. This is likely due to the presence of an NA or missing value in your variable. NAs are contagious as if you try and calculate the mean of a set of numbers containing one or more NA values, the overall mean will also be an NA.
So, the `mean()` function has an additional argument `na.rm = TRUE` which tells R what to do if there are missing values. The job of `na.rm` is to say whether to remove (rm) the NAs (`na.rm = TRUE`) or not (`na.rm = FALSE`).
This data set has no missing values but we showed you how to use it here so you can try to remember it exists in future. You do not need to use it all the time and you should think carefully about whether you should ignore NAs, but the option is there if you need it.

Try this

Using what you learnt above, apply the `summarise()` function to calculate the mean value of `JudgedSpeed` using the `pong_data_filter` object and fill in the blanks below. Remember, calculating the mean of a binary outcome of 0s and 1s tells you the proportion, so the mean here would be the proportion of responses judged to be fast.
Rounded to 3 decimal places, the mean proportion of fast responses is _____ or rounded to 1 decimal place _____%.

```
# mean value of JudgedSpeed for the proportion
summarise(pong_data_filter,
          ?)
```

Solution

You only needed to add one argument to calculate the mean of the `JudgedSpeed` variable. We called the new variable `fast_proportion`, but this was not important for the answer. Just make sure you call your variables something sensible, so you could understand what it means later.

```
# mean value of JudgedSpeed for the proportion
summarise(pong_data_filter,
          fast_proportion = mean(JudgedSpeed))
```

5.5.2 Activity 11 - Grouping your summary statistics

Summarising your whole data set is great, but there will often be times you want separate summary statistics for different groups in your data. The group_by() function takes an existing data frame or tibble and creates a grouped data frame. As a data frame, this does not look much different, but it adds a kind of hidden property which functions like `summarise()` detects and uses.

As an example, let us see how the summary statistics compare between each level of judged speed. For the initial step, we need to apply the `group_by()` function:

```
# Group pong_data_filter by JudgedSpeedLabel
pong_data_grouped <- group_by(pong_data_filter,
                              JudgedSpeedLabel)
```

To break down the code:

- We create a new object `pong_data_grouped` by applying the `group_by()` function to `pong_data_filter`.
- We add one or more variables we want to group any summary statistics by. In this case, we group by `JudgedSpeedLabel` so we will get separate values for fast and slow.

If you open `pong_data_grouped` as a tab, it does not look any different. Remember, `group_by()` adds a kind of hidden property. To check this, we can run the `str()` function on the data object which will show us the structure of an object:

```
# Show the structure of the data object pong_data_grouped
str(pong_data_grouped)
```

```
gropd_df [4,592 x 9] (S3: grouped_df/tbl_df/tbl/data.frame)
 $ Participant     : num [1:4592] 1 1 1 1 1 1 1 1 1 ...
 $ JudgedSpeed     : num [1:4592] 0 1 0 1 0 1 0 0 0 1 ...
 $ PaddleLength    : num [1:4592] 250 50 250 250 50 250 50 250 50 50 ...
 $ BallSpeed       : num [1:4592] 3 4 3 7 5 6 2 4 4 7 ...
 $ TrialNumber     : num [1:4592] 2 3 4 5 6 7 8 9 10 11 ...
 $ BackgroundColor : chr [1:4592] "blue" "red" "red" "blue" ...
 $ HitOrMiss       : num [1:4592] 1 0 1 1 1 1 1 1 0 ...
 $ BlockNumber     : num [1:4592] 1 1 1 1 1 1 1 1 1 ...
 $ JudgedSpeedLabel: chr [1:4592] "Slow" "Fast" "Slow" "Fast" ...
 - attr(*, "groups")= tibble [2 x 2] (S3: tbl_df/tbl/data.frame)
  ..$ JudgedSpeedLabel: chr [1:2] "Fast" "Slow"
  ..$ .rows           : list<int> [1:2]
  .. ..$ : int [1:2512] 2 4 6 10 11 13 15 17 19 22 ...
  .. ..$ : int [1:2080] 1 3 5 7 8 9 12 14 16 18 ...
  .. ..@ ptype: int(0)
  ..- attr(*, ".drop")= logi TRUE
```

The two key elements here are in the first line (`gropd_df [4,592 × 9] (S3: grouped_df/tbl_df/tbl/data.fr` and below the variables (`- attr(*, "groups")... ..$ JudgedSpeedLabel: chr [1:2] "Fast" "Slow"`). The first line confirms we now have a grouped data frame and the two lines below the variables show the values we group by.

The next step is applying the `summarise()` function as before. Here, we will calculate the total and mean number of hits by whether the participants judged the speed to be fast or slow:

```
# Sum hits for the number of hits
# Mean hits for the proportion of hits
hits_by_judgedspeed <- summarise(pong_data_grouped,
                                 sum_hits = sum(HitOrMiss),
                                 prop_hits = mean(HitOrMiss))
```

Calling the object shows we now get two rows per summary statistic:

```
hits_by_judgedspeed
```

```
# A tibble: 2 x 3
  JudgedSpeedLabel sum_hits prop_hits
  <chr>               <dbl>     <dbl>
1 Fast                 1651     0.657
2 Slow                 1508     0.725
```

Although there were more hits in the fast judged speed, the proportion of hits to misses was lower. Participants hit .657 (65.7%) of trials they judged to be fast but .725 (72.5%) of trials they judged to be slow.

Try this

Using what you learnt above, apply the `group_by()` and `summarise()` functions to calculate the sum and mean value of `HitOrMiss` depending on whether `BackgroundColor` was blue or red. In your `group_by()` object, make sure you use the `pong_data_filter` object. After writing the code and checking the new object, answer the following questions:

1. Rounded to 2 decimal places, the mean proportion of hits to the **blue** background was _____ or rounded to 0 decimal places ___%.
2. Rounded to 3 decimal places, the mean proportion of hits to the **red** background was _____ or rounded to 1 decimal place _____%.

```
# Group pong_data_filter by BackgroundColor
pong_data_background <- ?

# Sum hits for the number of hits
# Mean hits for the proportion of hits
hits_by_background <- ?
```

Solution

There are two steps here to follow the previous example. The main difference is using `BackgroundColor` in `group_by()`, and then the `summarise()` element is largely the same.

```r
# Group pong_data_filter by BackgroundColor
pong_data_background <- group_by(pong_data_filter,
                                 BackgroundColor)

# Sum hits for the number of hits
# Mean hits for the proportion of hits
hits_by_background <- summarise(pong_data_background,
                                sum_hits = sum(HitOrMiss),
                                prop_hits = mean(HitOrMiss))
```

R Markdown tip of the chapter: Create pretty tables

After we introduced you to R Markdown to create reproducible documents in Chapter 2, we are going to add a tip in every chapter to demonstrate extra functionality.
R Markdown is great for embedding plots and statistics in reproducible documents, but tables can be a little tricky. If you only call objects like `hits_by_background`, the output does not look super professional and it is not consistent with APA formatting guidelines. There are a few options available to you. One of the packages that helps create R Markdown - knitr - can create tables from objects you create. There is a function called `kable()` which can create tables with no further arguments, but you will need to edit the object to make sure it has headers and labels consistent with APA. The following code creates a simple table if you have knitr installed:

```r
knitr::kable(hits_by_judgedspeed)
```

You will need to knit your document to see what it looks like, but it should look similar to Figure 5.1. The row labels are fine, but you would need to tidy up the headers and round `prop_hits` to three decimals (see the function `round()`).

JudgedSpeedLabel	sum_hits	prop_hits
Fast	1651	0.6572452
Slow	1508	0.7250000

Figure 5.1: Example of using kable() to create tables in R Markdown.

See The R Markdown Cookbook for a guide on creating tables using `kable()`.
Alternatively, there is a package called gt which can also create tables with plenty of formatting options. See their documentation https://gt.rstudio.com/ online for further information.

5.5.3 Ungrouping data

For a final word of warning, there is an additional function which removes a group from a data frame. For example, if you wanted to use objects like `pong_data_grouped` for additional wrangling, visualisation, or analysis, it can create problems if you leave the group property. If you only use these objects to create summary tables like `hits_by_judgedspeed`, then there is no issue.

It is good practice to ungroup the data before performing another function using the ungroup() function:

```
pong_data_grouped <- ungroup(pong_data_grouped)
```

If you run `str(pong_data_grouped)` again, you will see we removed the grouping property. Remember, you only need to apply this if you are using the object in further steps. We will demonstrate in the next chapter how you can add this in a more streamlined way.

5.6 Test yourself

To end the chapter, we have some knowledge check questions to test your understanding of the concepts we covered in the chapter. We then have some error mode tasks to see if you can find the solution to some common errors in the concepts we covered in this chapter.

5.6.1 Knowledge check

Question 1. What type of data would these most likely be:

- Male =
- (A) Double
- (B) Integer
- (C) Character
- 7.15 =
- (A) Character
- (B) Double

- (C) Integer
- 137 =
- (A) Double
- (B) Integer
- (C) Character

Explain this answer

There are several different types of data as well as different levels of measurement and it takes a while to recognise the nuanced differences. It is important to try to remember which is which because you can only do certain types of analyses on certain types of data and certain types of measurements. For instance, you cannot take the average of characters or categorical data. Likewise, you can do any maths on double data, just like you can on interval and ratio data. Integer data is funny in that sometimes it is ordinal and sometimes it is interval, sometimes you should take the median, sometimes you should take the mean. The main point is to always know what type of data you are using and to think about what you can and cannot do with them.
Note: in the last answer, 137 could also be double as it is not clear if it could take a decimal or not.

Question 2. Which of the dplyr functions would you use to count the number of observations in your data set or variables?

- (A) mutate
- (B) count
- (C) group_by
- (D) select
- (E) filter

Question 3. Which of the dplyr functions would you use to calculate the mean of a column?

- (A) select
- (B) mutate

- (C) group_by
- (D) filter
- (E) summarise

Question 4. Which of the dplyr functions would you use to remove certain observations (e.g., remove all males)?

- (A) select
- (B) count
- (C) group_by
- (D) mutate
- (E) filter
- (F) summarise

Question 5. Which of the dplyr functions would you use to subset summary statistics by?

- (A) mutate
- (B) group_by
- (C) count
- (D) select
- (E) filter
- (F) summarise

5.6.2 Error mode

The following questions are designed to introduce you to making and fixing errors. For this topic, we focus on data wrangling using the functions `filter()`, `count()`, and `group_by()` and `summarise()`. Remember to keep a note of what kind of error messages you receive and how you fixed them, so you have a bank of solutions when you tackle errors independently.

Create and save a new R Markdown file for these activities. Delete the example code, so your file is blank from line 10. Create a new code chunk to load `tidyverse` and the data file:

```
# Load the tidyverse package below
library(tidyverse)

# Load the data file
pong_data <- read_csv("data/witt_2018.csv")
```

Below, we have several variations of a code chunk error or misspecification. Copy and paste them into your R Markdown file below the code chunk to load `tidyverse` and the data. Once you have copied the activities, click knit and look at the error message you receive. See if you can fix the error and get it working before checking the answer.

Question 6. Copy the following code chunk into your R Markdown file and press knit. We want to filter data to only include a paddle length of 50. You should receive the error starting with `Error in "filter()" ! We detected a named input`.

````
```{r}
# filter pong_data to retain PaddleLength of 50
pong_data_filter <- filter(pong_data,
                           PaddleLength = 50)
```
````

Explain the solution

In the code, we use a single equals sign (`=`) rather than the Boolean operator a double equals sign (`==`). With a single equals, R is interpreting this as "PaddleLength is equal to 50" like you were saving an object or setting an argument. The error message below line two tries to help and suggests you might need to include `==` instead.

```
# filter pong_data to retain PaddleLength of 50
pong_data_filter <- filter(pong_data,
                           PaddleLength == 50)
```

Question 7. Copy the following code chunk into your R Markdown file and press knit. We want to count the number of trials per block (`BlockNumber`). This…works, but if you look at the output, have we counted the number of trials?

````
```{r}
# Count block numbers from pong_data
count_blocknumbers <- summarise(pong_data,
                                N_blocks = sum(BlockNumber))
```
````

Explain the solution

The mistake is using `sum()` to count the number of trials per block. `sum()` would only work when you have 0s and 1s. Here, it just adds up all the numbers, totalling 29952. There are two options here. In every other scenario, you need to either `count()`:

```
# Count block numbers from pong_data
count_blocknumbers <- count(pong_data,
                            BlockNumber)
```

or `group_by()` and 'n():

```
# Group by block number
group_blocks <- group_by(pong_data,
                         BlockNumber)
# Then calculate the number of trials per block
count_blocknumbers <- summarise(group_blocks,
                                N_blocks = n())
```

Question 8. Copy the following code chunk into your R Markdown file and press knit. Here, we want the proportion of fast judgements per paddle length by taking the mean of `JudgedSpeed`. This code… works, but do we have a proportion of fast judgements per paddle length?

````
```{r}
# Mean judged speed for the proportion of fast judgements
hits_by_background <- summarise(pong_data,
                                prop_fast = mean(JudgedSpeed))
```
````

Explain the solution

We wanted the mean proportion of fast judgements, but we forgot to add a group by! We only got one value, so we need to add an initial step to group the responses by `PaddleLength` first, before we then calculate the mean proportion.

```r
# Group pong_data by paddle length
pong_data_paddle <- group_by(pong_data,
                             PaddleLength)

# Mean judged speed for the proportion of fast judgements
hits_by_background <- summarise(pong_data_paddle,
                             prop_fast = mean(JudgedSpeed))
```

5.7 Words from this Chapter

Below you will find a list of words that were used in this chapter that might be new to you in case it helps to have somewhere to refer back to what they mean. The links in this table take you to the entry for the words in the PsyTeachR Glossary. Note that the Glossary is written by numerous members of the team and as such may use slightly different terminology from that shown in the chapter.

term	definition
character	A data type representing strings of text.
count()	Count the observations in your data set, or the number of observations in one or more variables.
data-frame	A container data type for storing tabular data.
double	A data type representing a real decimal number
factor	A data type where a specific set of values are stored with labels; An explanatory variable manipulated by the experimenter
filter()	The ability to subset a data frame to keep all observations/rows that satisfy one or more conditions.
function	A named section of code that can be reused.
group_by()	Take an existing data frame or tibble and convert it to a grouped data frame.
integer	A data type representing whole numbers.
numeric	A data type representing a real decimal number or integer.
summarise()	Creates a new data frame to summarise all the observations you provide. You can also group by an additional variable to create separate summary statistics.
tibble	A container for tabular data with some different properties to a data frame
ungroup()	Remove a grouping property from a grouped data frame or tibble.

5.8 End of chapter

Brilliant work again! You have another handful of functions added to your data wrangling toolkit and we are almost ready to tackle more advanced plotting techniques and inferential statistics.

In the next chapter, we finish the key data wrangling functions. For example, showing you how you can pipe together multiple functions to streamline your code. We will also demonstrate how to pivot your data wider from long form where there are multiple observations per participant to wide form where there is one row per participant, and vice versa.

6 Data Wrangling 3: Pivots and Pipes

In the last chapter, we added two more functions to your data wrangling toolkit. You learnt how to filter data to retain or remove observations and summarise data to calculate different summary statistics.

In this chapter, we start with another recap of all your data wrangling skills so far on a new data set. There is no substitute for practice when it comes to data skills. By applying your skills to new data, you can transfer your knowledge to novel scenarios and develop independence. We then add two more sets of data wrangling functions. First, we demonstrate pivots to restructure your data from wide format into long format, and vice versa. Second, we show how you can string together multiple functions from the tidyverse using pipes. These help streamline your code to avoid creating lots of intermediary objects.

After this chapter, you will be ready for the first data analysis journey chapter: Analysis Journey 1: Data Wrangling. This is where you can test the skills you have developed so far on a more independent task as a bridge between the core chapters and your assessments.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Apply all your data wrangling skills to a new data set.
- Restructure data into different formats, such as long and wide form.
- Understand the tidy data structure for how most of the tidyverse functions expect your data to look.
- String together multiple functions using pipes.

6.1 Chapter preparation

6.1.1 Introduction to the data set

For this chapter, we are using open data from Alter et al. (2024). The abstract of their article is:

> The biggest difference in statistical training from previous decades is the increased use of software. However, little research examines how software impacts learning statistics. Assessing the value of software to statistical learning demands appropriate, valid, and reliable measures. The present study expands the arsenal of tools by reporting on the psychometric properties of the Value of Software to Statistical Learning (VSSL) scale in an undergraduate student sample. We propose a brief measure with strong psychometric support to assess students' perceived value of software in an educational setting. We provide data from a course using SPSS, given its wide use and popularity in the social sciences. However, the VSSL is adaptable to any statistical software, and we provide instructions for customizing it to suit alternative packages. Recommendations for administering, scoring, and interpreting the VSSL are provided to aid statistics instructors and education researchers understand how software influences students' statistical learning.

To summarise, they developed a new scale to measure students' perceived value of software to learning statistics - Value of Software to Statistical Learning (VSSL). The authors wanted to develop this scale in a way that could be adapted to different software, from SPSS in their article (which some of you may have used in the past), to perhaps R in future. Alongside data from their new scale, they collected data from other scales measuring a similar kind of construct (e.g., Students' Attitudes toward Statistics and Technology) and related constructs (e.g., Quantitative Attitudes).

In this chapter, we will wrangle their data to reinforce skills from Chapter 4 and 5. Scale data is extremely common to work with in psychology and there is a high likelihood you will use one or more in your dissertation or future careers. After recapping skills from the past two chapters on this new data set, we will add more data wrangling functions to your toolkit.

6.1.2 Organising your files and project for the chapter

Before we can get started, you need to organise your files and project for the chapter, so your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, you should have a folder from chapter 4 called `Chapter_04_06_datawrangling` where you created an R Project.
2. Create a new R Markdown document and give it a sensible title describing the chapter, such as `06 Data Wrangling 3`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Chapter_04_06_datawrangling` folder.
3. We are working with a new data set separated into two files. The links are data file one (Alter_2024_demographics.csv) and data file two (Alter_2024_scales.csv). Right click the links and select "save link as", or clicking the links will save the files to your

Downloads. Make sure that both files are saved as ".csv". Save or copy the file to your `data/` folder within `Chapter_04_06_datawrangling`.

You are now ready to start working on the chapter!

6.2 Recapping all the previous dplyr functions

In this first section, we will prepare the data for some analysis later by practicing the data wrangling skills you learnt in Chapters 4 and 5 on this new data set.

6.2.1 Activity 1 - Load tidyverse and read the data files

As the first activity, load tidyverse and read the two data files. As a prompt, save the data files to these object names to be consistent with the activities below, but you can check your answer below if you are stuck.

```
# Load the tidyverse package below
?

# Load the data files
# This should be the Alter_2024_demographics.csv file
demog <- ?

# This should be the Alter_2024_scales.csv file
scales <- ?
```

Show me the solution

You should have the following in a code chunk:

```
# Load the tidyverse package below
library(tidyverse)

# Load the data files
# This should be the Alter_2024_demographics.csv file
demog <- read_csv("data/Alter_2024_demographics.csv")

# This should be the Alter_2024_scales.csv file
scales <- read_csv("data/Alter_2024_scales.csv")
```

6.2.2 Activity 2 - Explore `demog` and `scales`

The data from Alter et al. (2024) is split into two data files. In `demog`, we have the participant ID (`StudentIDE`) and several demographic variables. The columns (variables) we have in the data set are:

Variable	Type	Description
StudentIDE	double	Participant number
GenderE	double	Gender: 1 = Female, 2 = Male, 3 = Non-Binary
RaceEthE	double	Race: 1 = Black/African American, 2 = Hispanic/Other Latinx, 3 = White, 4 = Multiracial, 5 = Asian/Pacific Islander, 6 = Native American/Alaska Native, 7 = South/Central American
GradeE	character	Expected grade: 1 = A, 2 = B, 3 = C, 4 = D, 5 = F
StuStaE	character	Student status: 1 = Freshman, 2 = Sophomore, 3 = Junior, 4 = Senior or Higher
GPAE	character	Expected Grade Point Average (GPA)
MajorE	character	Degree major
AgeE	double	Age in years

In `scales`, we then have the participant ID (`StudentIDE`) and all the individual scale items. The columns (variables) we have in the data set are:

Variable	Type	Description
StudentIDE	double	Participant number
MA1E to MA8E	double	**Enjoyment of Mathematics and statistics**, not analysed in this study.
QANX1E to QANX4E	double	**Quantitative anxiety**: four items scored on a 5-point Likert scale ranging from 1 (Not at all Anxious) to 5 (Extremely Anxious)

Variable	Type	Description
QINFL1E to QINFL7E	double	**Quantitative attitudes**: seven items scored on a 5-point Likert scale ranging from 1 (Strongly Disagree) to 5 (Strongly Agree)
QSF1E to QSF4E	double	**Study motivation**, not analysed in this study.
QHIND1E to QHIND5E	double	**Quantitative hindrances**: five items scored on a 5-point Likert scale ranging from 1 (Strongly Disagree) to 5 (Strongly Agree)
QSC1E to QSC4E	double	**Mathematical self-efficacy**, not analysed in this study.
QSE1E to QSE6E	double	**Mathematical ability**, not analysed in this study.
SPSS1E to SPSS10E	double	**VSSL scale on SPSS**: 10 items scored on a 5-point Likert scale ranging from 1 (Never True) to 5 (Always True)

Try this

Now we have introduced the two data sets, explore them using different methods we introduced. For example, opening the data objects as a tab to scroll around, explore with `glimpse()`, or even try plotting some of the variables to see what they look like using visualisation skills from Chapter 3.

6.2.3 Activity 3 - Joining the two data sets using `inner_join()`

At the moment, we have two separate data sets, but it will make things easier to join them together so we have both demographic information and the participants' responses to the scales.

We did not recap joining data sets in the last chapter, so you might need to revisit Chapter 4 - Joining two data frames - for a recap.

Create a new data object called `full_data` and see if you can spot a common variable between both data sets that you can use an identifier.

```
# join demog and scales by a common identifier
full_data <- ?
```

Show me the solution

You should have the following in a code chunk:

```
# join demog and scales by a common identifier
full_data <- inner_join(x = demog,
                        y = scales,
                        by = "StudentIDE")
```

6.2.4 Activity 4 - Selecting a range of columns using `select()`

There are some scales in the data that Alter et al. (2024) did not analyse, so we can get rid of them to declutter. Furthermore, the purpose of their study was to validate the new VSSL scale and they found some items did not make the cut. Create a new object called `full_data_select` and retain the following variables from your new `full_data` object:

- `StudentIDE`
- `GenderE`
- `RaceEthE`
- `AgeE`
- `QANX1E` to `QINFL7E`
- `QHIND1E` to `QHIND5E`
- `SPSS1E`, `SPSS4E`, `SPSS5E`, `SPSS6E`, `SPSS7E`, `SPSS8E`, `SPSS9E`.

Remember: you can select variables either by **retaining** the variables you want to keep, or **removing** the variables you want to remove. You should have **27** columns remaining.

```
# select the key variables listed above
full_data_select <- ?
```

Show me the solution

You should have the following in a code chunk if you chose to retain:

```
# select the key variables listed above
full_data_select <- select(full_data,
                           StudentIDE,
                           GenderE,
                           RaceEthE,
                           AgeE,
                           QANX1E:QINFL7E,
                           QHIND1E:QHIND5E,
                           SPSS1E, SPSS4E, SPSS5E, SPSS6E, SPSS7E, SPSS8E, SPSS9E)
```

or the following if you chose to remove:

```
# select the key variables listed above
full_data_select <- select(full_data,
                           -GradeE,
                           -StuStaE,
                           -GPAE,
                           -MajorE,
                           -MA1E:-MA8E,
                           -QSF1E:-QSF4E,
                           -QSC1E:-QSE6E,
                           -SPSS2E, -SPSS3E, -SPSS10E)
```

There are a similar number to retain or remove, so there is no real time saving one way or the other.

6.2.5 Activity 5 - Reorder observations using `arrange()`

For a quick check of the data, order the values of `AgeE` using the object `full_data_select` and answer the following questions:

1. The youngest participant is ___ years old.
2. The old participant is ___ years old.

```
# youngest participants
?

# oldest participants
?
```

Show me the solution

You should have the following in a code chunk:

```
# youngest participants
arrange(full_data_select,
        AgeE)

# oldest participants
arrange(full_data_select,
        desc(AgeE))
```

6.2.6 Activity 6 - Modifying or creating variables using `mutate()`

At the moment, we have categorical variables such gender (`GenderE`) and race (`RaceEthE`) which have numerical codes. When it comes to summarising or plotting later, this would not be the easiest to understand.

Using the `full_data_select` object, use `mutate()` to recode these two existing variables and replace the numbers with labels and create a new object `full_data_mutate`. As a reminder of what each number refers to:

`GenderE`

- 1 = Female
- 2 = Male
- 3 = Non-binary

`RaceEthE`

- 1 = Black/African American
- 2 = Hispanic/Other Latinx
- 3 = White
- 4 = Multiracial
- 5 = Asian/Pacific Islander
- 6 = Native American/Alaska Native
- 7 = South/Central American

```
# recode gender and race to labels
full_data_mutate <- ?
```

Show me the solution

You should have the following in a code chunk (some lines wrap due to being quite long, but it will look right if you copy and paste it to your RStudio):

```
# recode gender and race to labels
full_data_mutate <- mutate(full_data_select,
                           GenderE = case_match(GenderE,
                                                1 ~ "Female",
                                                2 ~ "Male",
                                                3 ~ "Non-binary"),
                           RaceEthE = case_match(RaceEthE,
                                                 1 ~ "Black/African American",
                                                 2 ~ "Hispanic/Other Latinx",
                                                 3 ~ "White",
                                                 4 ~ "Multiracial",
                                                 5 ~ "Asian/Pacific Islander",
                                                 6 ~ "Native American/Alaska Native",
                                                 7 ~ "South/Central American"))
```

6.2.6.1 Bonus activity - reverse coding scales

For a bonus activity, we want to demonstrate a super common task when working with scale data. Often, scales will **reverse code** some items to express the same idea in opposite ways: one positive and one negative. If the scale is measuring a consistent construct, the responses should be more positive in one and more negative in the other. If you analysed this immediately, you would get two opposing answers, so a key data wrangling step is reverse coding some items so all the numbers mean a similar thing.

In Alter et al. (2024), the three VSSL items we removed were the ones which needed to be reverse coded, but it is a good excuse to practice. Using the `scales` object, what function could you use to recode existing responses? Hint: we want to recode 1 to 5, 2 to 4, etc.

```
# recode items 2, 3, and 10
scales_reverse <- mutate(scales,
                         SPSS2_R = ?,
                         SPSS3_R = ?,
                         SPSS10_R = ?)
```

Show me the solution

Based on what we covered before, we expect you will have completed a perfectly accurate but long process of recoding each item one by one:

```
# recode items 2, 3, and 10
scales_reverse <- mutate(scales,
                         SPSS2_R = case_match(SPSS2E,
                                              1 ~ 5,
                                              2 ~ 4,
                                              3 ~ 3,
                                              4 ~ 2,
                                              5 ~ 1),
                         SPSS3_R = case_match(SPSS3E,
                                              1 ~ 5,
                                              2 ~ 4,
                                              3 ~ 3,
                                              4 ~ 2,
                                              5 ~ 1),
                         SPSS10_R = case_match(SPSS10E,
                                              1 ~ 5,
                                              2 ~ 4,
                                              3 ~ 3,
                                              4 ~ 2,
                                              5 ~ 1))
```

However, there is a neat shortcut where you can subtract the response from the biggest scale unit plus 1. For example, if you have a 5-point scale, you would subtract the response from 6, if you have a 7-point scale, from 8 etc.

```
# Reverse code by subtracting responses from 6
scales_reverse <- mutate(scales,
                         SPSS2_R = 6 - SPSS2E,
                         SPSS3_R = 6 - SPSS3E,
                         SPSS10_R = 6 - SPSS10E)
```

Explore your new data object to see what the new reverse coded variables look like.

6.2.7 Activity 7 - Removing or retaining observations using `filter()`

To practice filtering data to retain specific participants, imagine we wanted to focus on two specific groups of people.

First, we just want to explore the data of "Non-binary" participants. Second, we want to explore the data of "Female", "Asian/Pacific Islander" participants. Use `filter()` on the `full_data_mutate` object to create two objects: `NB_participants` and `F_asian_participants`.

```
# non-binary participants
NB_participants <- ?

# female, Asian/Pacific Islander participants
F_asian_participants <- ?
```

After creating the objects, answer the following questions:

1. We have _ non-binary participant(s) in the data set.
2. We have _ female, Asian/Pacific Islander participant(s) in the data set.

Show me the solution

You should have the following in a code chunk:

```
# non-binary participants
NB_participants <- filter(full_data_mutate,
                          GenderE == "Non-binary")

# female, Asian/Pacific Islander participants
F_asian_participants <- filter(full_data_mutate,
                          GenderE == "Female",
                          RaceEthE == "Asian/Pacific Islander")
```

6.2.7.1 Bonus activity - Removing NAs with `drop_na()`

One concept we will spend more time on in Chapter 11 - Screening Data - is removing participants who do not provide an answer. We delve more into the decision making in the course materials, but there is a handy function in tidyr called `drop_na()`. You could do this using filter, but the standalone function streamlines things. If you run the function on your whole data set, it will remove observations with one or more NAs in all their variables:

```
# remove observations with any NAs
no_NAs <- drop_na(full_data_mutate)
```

However, often you do not want to remove all variables with an NA as there might be valuable information elsewhere. You can add one or more variables to ask `drop_na()` to only remove NAs present in those specific variables:

```
# remove observations with any NAs
age_NAs <- drop_na(full_data_mutate,
                   AgeE)
```

This impacts the number of participants we remove as we had **171** when we removed all NAs, but **179** when we only removed NAs in age.

6.2.8 Activity 8 - Summarising data using `count()` and `summarise()`

6.2.8.1 Counting observations

As the final recap activity, it is time to calculate some summary statistics to understand our data set. First, use `count()` on the `full_data_mutate` object to answer the following questions:

1. How many observations do we have of each gender? ___ males, _____ females, and _ non-binary.
2. How many observations do we have of each race? _____ white, ___ Black/African American, and _ NA with missing data.

```
# count each group in GenderE
?

# count each group in RaceE
?
```

Show me the solution

You should have the following in a code chunk:

```
# count each group in GenderE
count(full_data_mutate,
      GenderE)

# count each group in RaceE
count(full_data_mutate,
      RaceEthE)
```

6.2.8.2 Summarising observations

One useful demographic summary is the mean and standard deviation (*SD*) of participant ages. We have covered the function for the mean (`mean()`) several times, but a key part of coding is knowing what you want, but not the function to do it. So, in the process of the next answer, try and find the function for the standard deviation on your own. If you are really stuck though, you can see the hint below.

Give me a hint for the SD function

```
# Function for the standard deviation
sd()
```

```
# Mean and SD age
mean_age <- summarise(full_data_mutate,
                      mean_age = ?,
                      SD_age = ?)
```

Show me the solution

You should have the following in a code chunk:

```
# Mean and SD age
mean_age <- summarise(full_data_mutate,
                      mean_age = mean(AgeE, na.rm = TRUE),
                      SD_age = sd(AgeE, na.rm = TRUE))
```

Remember, if there are NAs present in the data like this, you need to add `na.rm = TRUE` or handle NAs prior to applying the function.

❗ Error mode

As a transition point to restructuring data, imagine we wanted to calculate the sum score of the items to calculate a number for the whole scale per participant. Based on how we have used `mutate()` or `summarise()` before, you might try:

```
sum_VSSL <- mutate(full_data_mutate,
                        VSSL = sum(c(SPSS1E, SPSS4E, SPSS5E, SPSS6E, SPSS7E, SPSS8E, SPSS9E)
```

However, if you look at the object, the VSSL column is the same for every participant (4413) which does not look right? This is due to how functions work within `mutate()`. It is essentially applying the `sum()` function to all the columns first and adding them together, rather than summing the values of each column within each participant.
We can fix this problem by restructuring the data.

6.3 Restructuring data using `pivot_longer()` and `pivot_wider()`

Apart from joining two data sets, we have pretty much just worked with the data files as they come to us where each row represents one observation/participant and each column represents one variable. That is great but there are scenarios where you get data sets in messier formats that do not follow this pattern. Furthermore, you might need to restructure your data to perform certain functions, like taking the mean/sum of many columns per participant or visualising multiple elements. Before we work on the data wrangling side, we need a brief explanation of data formats.

6.3.1 Tidy data

For most of this book, we use a type of data organisation known as tidy data. Any data in this format is easily processed through the tidyverse family of packages. However, the data you work with will not always be formatted in the most efficient way possible. If that happens, then our first step is to put it into a tidy data format. There are two fundamental principles defining tidy data:

1. Each variable must have its own column.
2. Each observation must have its own row.

Wickham (2014) adds the following principle:

3. Each type of observation unit forms a table.

Grolemund and Wickham (2023) restate this third principle as: "Each value must have its own cell (i.e. no grouping two variables together, e.g. time/date in one cell)" where a cell is where any specific row and column meet. A single data point in a data frame / tibble is a cell for example. The Grolemund and Wickham (2023) book is a very useful source for further reading and it is free, but browsing the chapter on tidy data will help you visualise how you want to arrange data.

> **Note**
>
> If you have worked with any kind of data before, particularly if you have used Excel, it is likely that you will have used **wide format** or **long format** data. In wide format, each participant's data is all in one row with multiple columns for different data points. This means that the data set tends to be very wide and you will have as many rows as you have participants.
> Long format is where each **row** is a single observation, typically a single trial in an experiment or a response to a single item on a questionnaire. When you have multiple trials per participant, you will have multiple rows for the same participant. To identify participants, you would need a variable with some kind of participant id, which can be as simple as a distinct integer value for each participant. In addition to the participant identifier, you would have any measurements taken during each observation (e.g., response time) and what experimental condition the observation was taken under.
> In wide format data, each **row** corresponds to a single participant, with multiple observations for that participant spread across columns. So for instance, with survey data, you would have a separate column for each survey question.
> Tidy data is a mix of both of these approaches and most functions in the tidyverse assume the tidy format, so typically the first thing you need to do when you get data is think about what format you need your data to perform the functions and analyses you want. For some functions, you need your data in wide format, and in others you need your data in long format. This means being able to quickly restructure your data is a key skill.

6.3.2 Activity 9: Gathering with `pivot_longer()`

In it's current format, we have wide data where each row is a separate participant and each column is a separate variable. We can use the function pivot_longer() from the tidyr package within tidyverse.

The pivot functions can be easier to show than explain first, so type and run the following code using the `full_data_mutate` object:

```
full_data_long <- pivot_longer(data = full_data_mutate,
                        cols = SPSS1E:SPSS9E,
```

```
                        names_to = "Question",
                        values_to = "Response")
```

To break down the code:

- We create a new data object called `full_data_long` by applying the `pivot_longer()` function to `full_data_mutate`.
- In the `cols` argument, we specify the columns we want to gather. We use the colon method here like `select()` to choose the 7 columns for the VSSL items. If the columns are not in order, you could use the `c()` method instead (e.g., `cols = c(SPSS1E, SPSS9E)`).
- The `names_to` argument is what your first new column will be called. All the column names you selected in `cols` will be pivoted into this new column, so call it something sensible you will remember later. Here, we call the new column "Question".
- The `values_to` argument is what your second new column will be called. For all the columns you gather, the response of each participant will be in one column stacked on top of each other next to its label in "Question". You also need to call this something memorable, like "Response" here.

Now, explore the new `full_data_long` object you just created and compare it to `full_data_mutate`. Instead of **181** rows, we now have **1267** rows. Instead of 27 variables, we now have 22 variables. We have 181 participants who responded to 7 VSSL items, so we pivot the data into long format to get 181 * 7 = **1267** rows.

Visually, you can see the difference with a preview of just the participant ID and VSSL items here:

6.3.2.1 Original wide format

```
# A tibble: 10 x 8
   StudentIDE SPSS1E SPSS4E SPSS5E SPSS6E SPSS7E SPSS8E SPSS9E
        <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
 1          1      4      3      3      3      4      4      4
 2          2      4      4      4      4      4      4      4
 3          3      3      2      3      2      2      3      3
 4          4      2      2      2      2      2      2      2
 5          5      4      3      4      4      3      4      3
 6          6      2      3      2      1      3      3      3
 7          7      4      2      4      4      2      3      2
 8          8      2      3      3      3      3      3      2
 9          9      3      3      3      1      4      3      2
```

```
10         10      4      4      3      5      4      2      4
```

6.3.2.2 New long format

```
# A tibble: 10 x 3
   StudentIDE Question Response
        <dbl> <chr>       <dbl>
 1          1 SPSS1E          4
 2          1 SPSS4E          3
 3          1 SPSS5E          3
 4          1 SPSS6E          3
 5          1 SPSS7E          4
 6          1 SPSS8E          4
 7          1 SPSS9E          4
 8          2 SPSS1E          4
 9          2 SPSS4E          4
10          2 SPSS5E          4
```

Now we have our data in long form, we can calculate summary statistics for participants using `group_by()` and `summarise()`. First, we group the data by the participant ID, as we want one value per participant:

```
# group full_data_long by StudentIDE
longdata_grouped <- group_by(full_data_long,
                             StudentIDE)
```

Second, we create a new variable using `summarise()` to take the sum of all the items. This will create the VSSL scale score consistent with Alter et al. (2024):

```
# Calculate the sum of VSSL items by taking the sum of Response
VSSL_sum <- summarise(longdata_grouped,
                      VSSL_sum = sum(Response))
```

Our new object goes from 1267 rows back to 181 as we grouped by the participant ID and took the sum of `Response`. This means we apply the function we provide `summarise()` to all the rows we want to group by, in this case across all 7 VSSL items. Your new object has just two columns: `StudentIDE` and `VSSL_sum` and should look like the following extract:

```
# A tibble: 6 x 2
  StudentIDE VSSL_sum
       <dbl>    <dbl>
```

```
1           1       25
2           2       28
3           3       18
4           4       14
5           5       25
6           6       17
```

At this point, you could join the object to `full_data_mutate` to add the scale score to all the other variables.

Try this

We calculated the VSSL scale score by pivoting longer, grouping the data, and taking the sum of the 7 items. To test your understanding, complete the same steps to calculate the scale score of **Quantitative anxiety** using the four columns `QANX1E` to `QANX4E`. The scale score here also involves taking the sum of the columns. Use the `full_data_mutate` object as your starting point for the data.
Check your attempt with the solution below when you have tried on your own.

```
# gather the four quant anxiety items to long form
quant_anxiety_long <- ?

# group the long data by participant ID
quant_anxiety_group <- ?

# calculate the sum quant anxiety per participant
sum_quant_anxiety <- ?
```

To check your answers:

1. Participant 1 has a sum quantitative anxiety score of _
2. Participant 5 has a sum quantitative anxiety score of ___

Solution

We complete the task in three steps. First, we pivot longer using the four columns QANX1E to QANX4E to create the new `quant_anxiety_long` object. Second, we group that new long data object by the participant ID. Third, we calculate the sum quantitative anxiety score by taking the sum of the responses per participant ID.

```r
# gather the four quant anxiety items to long form
quant_anxiety_long <- pivot_longer(data = full_data_mutate,
                                   cols = QANX1E:QANX4E,
                                   names_to = "Question",
                                   values_to = "Response")

# group the long data by participant ID
quant_anxiety_group <- group_by(quant_anxiety_long,
                                StudentIDE)

# calculate the sum quant anxiety per participant
sum_quant_anxiety <- summarise(quant_anxiety_group,
                               sum_quant_anxiety = sum(Response))
```

6.3.3 Spreading with `pivot_wider()`

You might also find yourself in situations where you must restructure data in the opposite direction: from long to wide. There is a complementary function called pivot_wider() where you can spread values from one column to multiple columns. You need two columns in your long form data set, one for the variable names which will be your new column names, then one for the responses which will be the values in each cell.

To demonstrate this function, we will transform `full_data_long` back to wide format so we have 7 columns of VSSL items:

```r
full_data_wide <- pivot_wider(data = full_data_long,
                              names_from = "Question",
                              values_from = "Response")
```

To break down the code:

- We create a new object `full_data_wide` by applying the function `pivot_wider()` to `full_data_long`.
- In the `names_from` argument, we add the column name "Question" which contains the names of the variables you want as your new column names.
- In the `values_from` argument, we add the column name "Response" which contains the values of the variables which will be the cells of your data frame.

The new object `full_data_wide` should now look exactly the same as the `full_data_mutate` object we started with.

Do I need to add quotes to the column names?

You might have noticed we added quotes around the column names to specify the `names_from` and `values_from` arguments. When we specify columns in tidyverse functions, we do not need to add the quotes, we can just type the name and it will work (`names_from = "Question"` and `names_from = Question` would both work here). However, in other functions outside the tidyverse, you normally need to add the quotes around column names. When to add quotes or not can take a while to get used to, so this is just a note to highlight you might try one method and it does not work, but you can try the other method if you get an error.

Try this

In the `pivot_longer()` section, you should have created a new object `quant_anxiety_long` if you completed the "Try this" activity. To test your understanding of `pivot_wider()`, spread the four items and responses of **Quantitative anxiety** back to wide format. Use the `quant_anxiety_long` object as your starting point and create a new object called `quant_anxiety_wide`.
Check your attempt with the solution below when you have tried on your own.

```
# spread the quant anxiety items back to wide form
quant_anxiety_wide <- ?
```

Solution

This task follows the exact format as `full_data_wide` if you named your variables the same as ours. It is just important the `names_from` and `values_from` columns are the same as those you used in `quant_anxiety_long`.

```
# spread the quant anxiety items back to wide form
quant_anxiety_wide <- pivot_wider(quant_anxiety_long,
                                  names_from = "Question",
                                  values_from = "Response")
```

6.4 Combining several functions with pipes

In this final section on data wrangling, we are not covering new functions, but a new way of working. So far, we have created lots of new objects by applying individual tidyverse functions, but there is a way to string together several functions and streamline your code. We wanted to introduce you to the individual functions first to develop your fundamentals skills and

understanding of what the functions do, but now we can be a little more efficient.

Instead of creating several objects, you can use pipes. We write pipes as **%>%** and you can read them as "and then". Pipes allow you to string together 'sentences' of code into 'paragraphs' so that you do not need to create intermediary objects.

This is another one of those concepts that is initially easier to show than tell:

```
# Create an object starting with demog
full_data_pipe <-  demog %>%
  # Join with scales
  inner_join(y = scales,
             by = "StudentIDE") %>%
  # Select key columns
  select(StudentIDE,
         GenderE,
         RaceEthE,
         AgeE,
         QANX1E:QINFL7E,
         QHIND1E:QHIND5E,
         SPSS1E, SPSS4E, SPSS5E, SPSS6E, SPSS7E, SPSS8E, SPSS9E) %>%
  # Recode variables with labels
  mutate(GenderE = case_match(GenderE,
                              1 ~ "Female",
                              2 ~ "Male",
                              3 ~ "Non-binary"),
         RaceEthE = case_match(RaceEthE,
                               1 ~ "Black/African American",
                               2 ~ "Hispanic/Other Latinx",
                               3 ~ "White",
                               4 ~ "Multiracial",
                               5 ~ "Asian/Pacific Islander",
                               6 ~ "Native American/Alaska Native",
                               7 ~ "South/Central American"))
```

Instead of creating all the intermediary objects, we go straight from joining the two data sets to recoding the variables in mutate, all in one object. Side by side, you can see the difference in the process we had to go through:

6.4.0.1 Creating separate objects

```
# join demog and scales by a common identifier
full_data <- inner_join(x = demog,
                        y = scales,
                        by = "StudentIDE")

# select the key variables listed above
full_data_select <- select(full_data,
                           StudentIDE,
                           GenderE,
                           RaceEthE,
                           AgeE,
                           QANX1E:QINFL7E,
                           QHIND1E:QHIND5E,
                           SPSS1E, SPSS4E:SPSS9E)

# recode gender and race to labels
full_data_mutate <- mutate(full_data_select,
                           GenderE = case_match(GenderE,
                                                1 ~ "Female",
                                                2 ~ "Male",
                                                3 ~ "Non-binary"),
                           RaceEthE = case_match(RaceEthE,
                                                 1 ~ "Black...",
                                                 2 ~ "Hispanic...",
                                                 3 ~ "White",
                                                 4 ~ "Multiracial",
                                                 5 ~ "Asian...",
                                                 6 ~ "Native American...",
                                                 7 ~ "South..."))
```

6.4.0.2 Combining functions using pipes

```
# Create an object starting with demog
full_data_pipe <-  demog %>%
  # Join with scales
  inner_join(y = scales,
             by = "StudentIDE") %>%
  # Select key columns
  select(StudentIDE,
         GenderE,
```

```
        RaceEthE,
        AgeE,
        QANX1E:QINFL7E,
        QHIND1E:QHIND5E,
        SPSS1E, SPSS4E:SPSS9E) %>%
  # Recode variables with labels
  mutate(GenderE = case_match(GenderE,
                              1 ~ "Female",
                              2 ~ "Male",
                              3 ~ "Non-binary"),
         RaceEthE = case_match(RaceEthE,
                               1 ~ "Black...",
                               2 ~ "Hispanic...",
                               3 ~ "White",
                               4 ~ "Multiracial",
                               5 ~ "Asian...",
                               6 ~ "Native American...",
                               7 ~ "South..."))
```

As you get used to using pipes, remember you can interpret them as "and then". So, we could explain the function of the code to ourselves as:

- Create `full_data_pipe` by starting with `demog` data, **and then**
- Join with the `scales` data using `StudentIDE` as an identifier, **and then**,
- Select our key columns, **and then**
- Mutate to recode gender and race.

It can be tricky at first to understand what pipes are doing from a conceptual point of view, but it is well worth learning to use them. When your code starts getting longer, they are much more efficient and you write less code which is always a good thing to debug and find errors. You also have fewer objects in your environment as we created one object instead of three, tidying your workspace.

> **!** Error mode
>
> One key difference that can trip people up is we no longer specify the data object as the first argument in each function. The reason that this function - the `%>%` - is called a pipe is because it 'pipes' the data through to the next function. When you wrote the code previously, the first argument of each function was the dataset you wanted to work on. When you use pipes, it will automatically take the data from the previous line of code so you do not need to specify it again.

For example, if we tried to specify `demog` again in `select()`, we would just receive an error.

```
# Create an object starting with demog
full_data_pipe <-  demog %>%
  # Join with scales
  inner_join(y = scales,
             by = "StudentIDE") %>%
  # Select key columns
  select(.data = demog,
         StudentIDE,
         GenderE,
         RaceEthE,
         AgeE,
         QANX1E:QINFL7E,
         QHIND1E:QHIND5E,
         SPSS1E, SPSS4E:SPSS9E)
```

Try this

Pipes also work with other functions like `filter()`, `group_by()` and `summarise()`. If you start with the object `full_data_mutate`, try and express the following instructions in code:

1. Create a new object `age_groups` using `full_data_mutate` as your starting point, **and then**
2. Filter to only include "White" and "Black/African American" participants using `RaceEthE`, **and then**,
3. Group the observations by `RaceEthE`, **and then**,
4. Summarise the data to calculate the mean and standard deviation `AgeE`.

Check your attempt with the solution below when you have tried on your own.

```
# create age_groups by filtering, grouping, and summarising
age_groups <- full_data_mutate %>%
  ?
```

Solution

We complete this task in three steps. First, we filter `full_data_mutate` to just focus on White and Black/African American participants. Second, we group the data by `RaceEthE` so our summary statistics are split into two groups. Third, we calculate the mean and SD age.

```
# create age_groups by filtering, grouping, and summarising
age_groups <- full_data_mutate %>%
  filter(RaceEthE %in% c("White", "Black/African American")) %>%
  group_by(RaceEthE) %>%
  summarise(mean_age = mean(AgeE, na.rm = TRUE),
            SD_age = sd(AgeE, na.rm = TRUE))
```

6.5 Test yourself

To end the chapter, we have some knowledge check questions to test your understanding of the concepts we covered in the chapter. We then have some error mode tasks to see if you can find the solution to some common errors in the concepts we covered in this chapter.

6.5.1 Knowledge check

Which function(s) would you use to approach each of the following problems?

Question 1. We have a data set of 400 adults but we want to remove anyone with an age of 50 years or more. To do this, we could use:

- (A) filter()
- (B) select()
- (C) summarise()
- (D) arrange()
- (E) group_by()
- (F) mutate()

Question 2. We are interested in overall summary statistics for our data, such as the mean and total number of observations for a variable. To do this, we could use:

- (A) select()
- (B) arrange()
- (C) filter()
- (D) mutate()
- (E) group_by()
- (F) summarise()

Question 3. Our data set has a column with the number of cats a person has and a column with the number of dogs. We want to calculate a new column which contains the total number of pets each participant has. To do this, we could use:

- (A) select()
- (B) arrange()
- (C) filter()
- (D) group_by()
- (E) summarise()
- (F) mutate()

Question 4. We want to calculate the mean value of a column for several groups in our data set. To do this, we could use:

- (A) arrange() and mutate()
- (B) filter() and select()
- (C) group_by() and arrange()
- (D) group_by() and summarise()

Question 5. If we wanted to apply the following wrangling steps with pipes, which series of functions would work? With the object `wide_data`, select several columns **and then**, pivot three columns longer **and then**, group by a participant ID **and then**, calculate the sum of responses.

- (A) wide_data %>% select() %>% pivot_longer() %>% group_by() %>% summarise()
- (B) select() %>% pivot_longer() %>% group_by() %>% summarise() %>% wide_data
- (C) long_data %>% select() %>% pivot___longer_wider() %>% group_by() %>% summarise()
- (D) wide_data %>% pivot_longer() %>% select() %>% summarise() %>% group_by()

6.5.2 Error mode

The following questions are designed to introduce you to making and fixing errors. For this topic, we focus on data wrangling using past functions, `pivot_longer()`, and pipes (`%>%`). Remember to keep a note of what kind of error messages you receive and how you fixed them, so you have a bank of solutions when you tackle errors independently.

Create and save a new R Markdown file for these activities. Delete the example code, so your file is blank from line 10. Create a new code chunk to load tidyverse and the data files:

```
# Load the tidyverse package below
library(tidyverse)

# Load the data files
# This should be the Alter_2024_demographics.csv file
demog <- read_csv("data/Alter_2024_demographics.csv")

# This should be the Alter_2024_scales.csv file
scales <- read_csv("data/Alter_2024_scales.csv")
```

Below, we have several variations of a code chunk error or misspecification. Copy and paste them into your R Markdown file below the code chunk to load tidyverse and the data files. Once you have copied the activities, click knit and look at the error message you receive. See if you can fix the error and get it working before checking the answer.

Question 6. Copy the following code chunk into your R Markdown file and press knit. In this code chunk, we want to calculate the mean and SD age of all participants using `demog`. There are two errors/omissions here to try and fix:

1. One causes the document not to knit. You should receive an error like `Caused by error in "SD()": ! could not find function "SD"`.

2. The other looks like we just get NA values?

```
```{r}
# calculate the mean and SD age
demog %>%
  summarise(mean_age = mean(AgeE),
            SD_age = SD(AgeE))
```
```

Explain the solution

The first error is using the wrong function name for SD. Because we always abbreviate standard deviation to SD, it is tempting to try and use that as the function name. However, the function is lowercase: `sd()`.
The second error is not including the `na.rm = TRUE` argument. There are NAs in the data, so you either need to address them before running the function, or ignoring the NAs with `na.rm = TRUE`.

```
# calculate the mean and SD age
demog %>%
  summarise(mean_age = mean(AgeE, na.rm = TRUE),
            SD_age = sd(AgeE, na.rm = TRUE))
```

Question 7. Copy the following code chunk into your R Markdown file and press knit. We want to calculate the sum of the five quantitative hindrances items per participant. This code... works, but does it look like it fits in the possible 5-25 range?

```
```{r}
# sum quant hindrances items per participant
sum_quant_hindrance <- scales %>%
  mutate(sum_quant_hindrance = sum(c(QHIND1E, QHIND2E, QHIND3E, QHIND4E, QHIND5E), na.rm = TR
```
```

Explain the solution

This is the main of warning we flagged in the opening section to `pivot_longer()`. Intuitively, it is the right idea to try and calculate the sum in a new column. However, in `mutate()`, it sums all the columns, not the observations for each participant.
Instead, we can pivot longer focusing on the quantitative hindrance items, group by participant ID, and summarise.

```r
# sum quant hindrances items per participant
sum_quant_hindrance <- scales %>%
  # pivot longer on 5 quant hindrances items
  pivot_longer(cols = QHIND1E:QHIND5E,
               names_to = "Question",
               values_to = "Response") %>%
  # group by student ID
  group_by(StudentIDE) %>%
  # summarise for sum of new long column
  summarise(sum_quant_hindrance = sum(Response, na.rm = TRUE))
```

Question 8. Copy the following code chunk into your R Markdown file and press knit. We want to filter `demog` to focus on female participant and calculate the mean age of the female participants. You should receive an error containing `Caused by error:! "..1$StudentIDE" must be a logical vector, not a double vector` which is not the most helpful error for diagnosing the problem.

````
```{r}
# filter for females then calculate mean age
demog %>%
  filter(.data = demog,
         GenderE == 2) %>%
  summarise(.data = demog,
            mean_age = mean(AgeE, na.rm = TRUE))
```
````

Explain the solution

We are using pipes but we tried adding in the `.data` argument in each line. Remember `%>%` "pipes" the previous line into the next line, so you do not need to specify an object for it to work with. If you try and specify the .data argument with pipes, it thinks you are trying to set the next argument in the list.

```r
# filter for females then calculate mean age
demog %>%
  filter(GenderE == 2) %>%
  summarise(mean_age = mean(AgeE, na.rm = TRUE))
```

6.6 Words from this Chapter

Below you will find a list of words that were used in this chapter that might be new to you in case it helps to have somewhere to refer back to what they mean. The links in this table take you to the entry for the words in the PsyTeachR Glossary. Note that the Glossary is written by numerous members of the team and as such may use slightly different terminology from that shown in the chapter.

term	definition
pipe	A way to order your code in a more readable format using the symbol %>%
pivot_longer()	Gather data by increasing the number of rows and decreasing the number of columns.
pivot_wider()	Spread data by decreasing the number of rows and increasing the number of columns.
reverse-code	Having two similar questions, one expressed in a positive way, and another expressed in a negative way.
tidy-data	A format for data that maps the meaning onto the structure.

6.7 End of chapter

Brilliant work again! You recapped data wrangling functions from the past two chapters to a new data set, and added two more concepts to your arsenal: pivots and pipes. There really is no substitute for practicing on new data to transfer your knowledge and understanding. As you work with more and more data, you will see how far these data wrangling functions take you. They will your foundational skills for any new data set and give you the confidence to search for new functions when there is a new problem to solve.

This is a key milestone, so remember to go over anything you are unsure of. If you have any questions about data wrangling, please post them on Teams, visit the GTA support sessions, or pop into office hours.

At this point, we direct you to the first data analysis journey chapter: Analysis Journey 1: Data Wrangling. This is a bridge between the structured learning in these chapters and your assessments. We present you with a new data set, show you what the end product should look like, and see if you can apply your data wrangling skills to get there. If you get stuck, we have a range of hints and steps you can unhide, then the solution to check your attempts against.

In the next core chapter though, we turn to more advanced data visualisation to demonstrate how to create scatterplots, boxplots, and violin-boxplots.

7 Scatterplots, boxplots, and violin-boxplots

Back in Chapter 3, we introduced you to data visualisation in R/RStudio using the package ggplot2. You developed foundational skills in using the layering system and customising your plots, but we only covered visualising one variable at a time in a histogram or barplot. This gets you a long way, but you typically want to visualise the relationship or difference between variables.

In this chapter, we develop your data visualisation skills to cover scatterplots, boxplots, and violin-boxplots. This will give you the skills to visualise your data in the next few chapters on inferential statistics. This is the final data visualisation specific chapter in the book, but by learning these core concepts, you will be able to find out how to create additional types of data visualisation independently.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Create and edit a scatterplot to visualise the relationship between two continuous variables.
- Create and edit a boxplot to visualise summary statistics for a continuous outcome.
- Create and edit a violin-boxplot to visualise the density of data points in a continuous outcome.
- Customise your plots to include colourblind-friendly colour palettes and facet your data to visualise multiple independent variables.

7.1 Chapter preparation

7.1.1 Introduction to the data set

For this chapter, we are using open data from Zhang et al. (2014). The abstract of their article is:

> Although documenting everyday activities may seem trivial, four studies reveal that creating records of the present generates unexpected benefits by allowing future rediscoveries. In Study 1, we used a time-capsule paradigm to show that individuals underestimate the extent to which rediscovering experiences from the past will be curiosity provoking and interesting in the future. In Studies 2 and 3, we found that people are particularly likely to underestimate the pleasure of rediscovering ordinary, mundane experiences, as opposed to extraordinary experiences. Finally, Study 4 demonstrates that underestimating the pleasure of rediscovery leads to time-inconsistent choices: Individuals forgo opportunities to document the present but then prefer rediscovering those moments in the future to engaging in an alternative fun activity. Underestimating the value of rediscovery is linked to people's erroneous faith in their memory of everyday events. By documenting the present, people provide themselves with the opportunity to rediscover mundane moments that may otherwise have been forgotten.

In summary, they were interested in whether people could predict how interested they would be in rediscovering past experiences. They call it a "time capsule" effect, where people store photos or messages to remind themselves of past events in the future.

At the start of the study (time 1), participants in a romantic relationship wrote about two kinds of experiences. An "extraordinary" experience with their partner on Valentine's day and an "ordinary" experience one week before. They were then asked how enjoyable, interesting, and meaningful they predict they will find these recollections in three months time (time 2). Three months later, Zhang et al. randomised participants into one of two groups. In the "extraordinary" group, they reread the extraordinary recollection. In the "ordinary" group, they reread the ordinary recollection. All the participants completed measures on how enjoyable, interesting, and meaningful they found the experience, but this time what they actually felt, rather than what they predict they will feel.

They predicted participants in the ordinary group would underestimate their future feelings (i.e., there would be a bigger difference between time 1 and time 2 measures) compared to participants in the extraordinary group. In this chapter, we focus on a composite measure which took the mean of items on interest, meaningfulness, and enjoyment.

7.1.2 Organising your files and project for the chapter

Before we can get started, you need to organise your files and project for the chapter, so your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, create a new folder called `Chapter_07_dataviz`. Within `Chapter_07_dataviz`, create two new folders called `data` and `figures`.

2. Create an R Project for `Chapter_07_dataviz` as an existing directory for your chapter folder. This should now be your working directory.
3. Create a new R Markdown document and give it a sensible title describing the chapter, such as `07 Scatterplots Boxplots Violins`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Chapter_07_dataviz` folder.
4. We are working with a new data set, so please save the following data file: Zhang_2014.csv. Right click the link and select "save link as", or clicking the link will save the files to your Downloads. Make sure that you save the file as ".csv". Save or copy the file to your `data/` folder within `Chapter_07_dataviz`.

You are now ready to start working on the chapter!

7.1.3 Activity 1 - Read and wrangle the data

As the first activity, try and test yourself by completing the following task list to practice your data wrangling skills. Create an object called `zhang_data` to be consistent with the tasks below. If you want to focus on data visualisation, then you can just type the code in the solution.

Try this

To wrangle the data, complete the following tasks:

1. Load the tidyverse package.
2. Read the data file `data/Zhang_2014.csv`.
3. Select the following columns:
   - `Gender`
   - `Age`
   - `Condition`
   - `T1_Predicted_Interest_Composite` renamed to `time1_interest`
   - `T2_Actual_Interest_Composite` renamed to `time2_interest`.
4. There is currently no identifier, so create a new variable called `participant_ID`. Hint: try `participant_ID = row_number()`.
5. Recode two variables to be easier to understand and visualise:
   - Gender: 1 = "Male", 2 = "Female".
   - Condition: 1 = "Ordinary", 2 = "Extraordinary".

Your data should now be in wide format and ready to create a scatterplot.

Show me the solution

You should have the following in a code chunk:

```
# Load the tidyverse package below
library(tidyverse)

# Load the data file
# This should be the Zhang_2014.csv file
zhang_data <- read_csv("data/Zhang_2014.csv")

# Wrangle the data for plotting.
# select and rename key variables
# mutate to add participant ID and recode
zhang_data <- zhang_data %>%
  select(Gender,
         Age,
         Condition,
         time1_interest = T1_Predicted_Interest_Composite,
         time2_interest = T2_Actual_Interest_Composite) %>%
  mutate(participant_ID = row_number(),
         Condition = case_match(Condition,
                                1 ~ "Ordinary",
                                2 ~ "Extraordinary"),
         Gender = case_match(Gender,
                             1 ~ "Male",
                             2 ~ "Female"))
```

7.1.4 Activity 2 - Explore the data

Try this

After the wrangling steps, try and explore `zhang_data` to see what variables you are working with. For example, opening the data object as a tab to scroll around, explore with `glimpse()`, or try plotting some of the individual variables to see what they look like using visualisation skills from Chapter 3.

In `zhang_data`, we have the following variables:

Variable	Type	Description
Gender	character	Participant gender: Male (1) or Female (2)
Age	double	Participant age in years.
Condition	character	Condition participant was randomly allocated into: Ordinary (1) or Extraordinary (2).
time1_interest	double	How interested they predict they will find the recollection on a 1 (not at all) to 7 (extremely) scale. This measure is the mean of enjoyment, interest, and meaningfulness.
time2_interest	double	How interested they actually found the recollection on a 1 (not at all) to 7 (extremely) scale. This measure is the mean of enjoyment, interest, and meaningfulness.
participant_ID	integer	Our new participant ID as an integer from 1 to 130.

We will use this data set to demonstrate different ways of visualising continuous variables, either combining multiple continuous variables in a scatterplot or splitting continuous variables into categories in a boxplot or violin-boxplot.

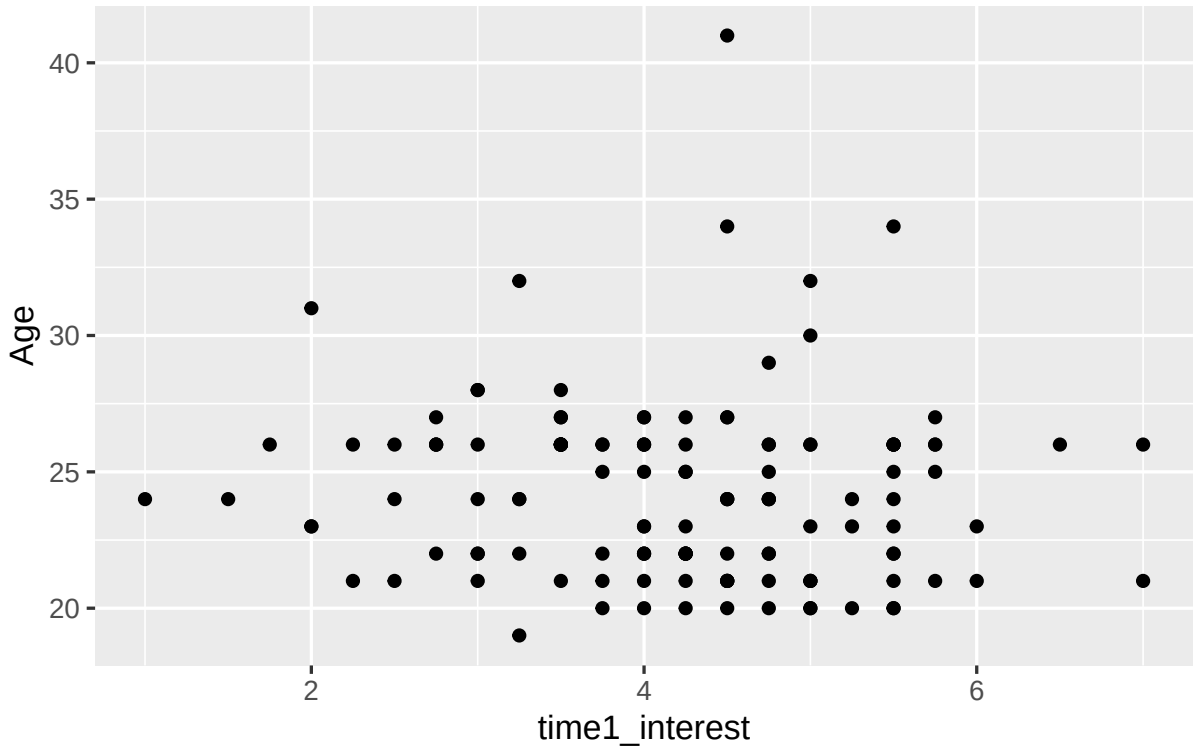
7.2 Scatterplots

The first visualisation is a scatterplot to show the relationship between two continuous variables. One variable goes on the x-axis and the other variables goes on the y-axis. Each dot then represents the intersection of those two variables per observation/participant. You will use these plots often when reporting a correlation or regression.

7.2.1 Activity 3 - Creating a basic scatterplot

Let us start by making a scatterplot of `Age` and `time1_interest` to see if there is any relationship between the two. We need to specify both the x- and y-axis variables, but the only difference to what we created in Chapter 3 is using a new layer `geom_point`.

```
zhang_data %>%
  ggplot(aes(x = time1_interest, y = Age)) +
       geom_point()
```

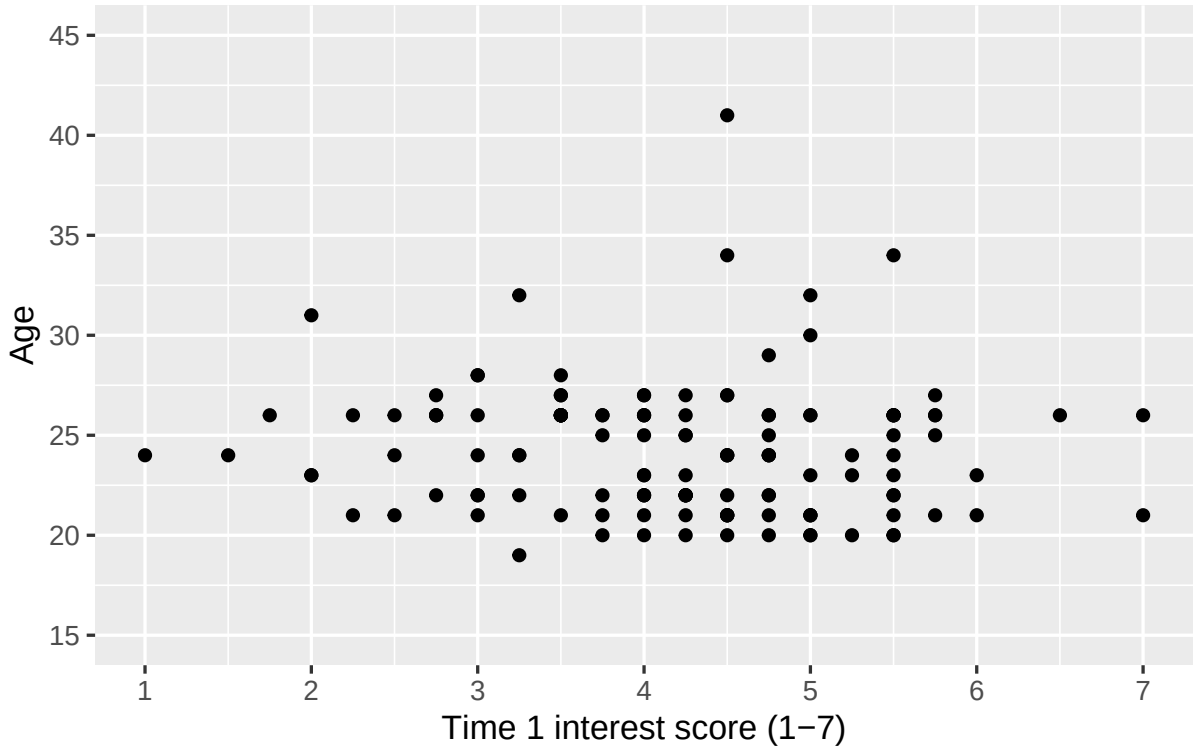


7.2.2 Activity 4 - Editing axis labels

This plot is great for some exploratory data analysis, but it looks a little untidy to put into a report. We can use the `scale_x_continuous` and `scale_y_continuous` layers to control the tick marks, as well as the axis name.

```
zhang_data %>%
  ggplot(aes(x = time1_interest,y = Age)) +
  geom_point() +
  scale_x_continuous(name = "Time 1 interest score (1-7)",
                     breaks = c(1:7)) + # tick marks from 1 to 7
  scale_y_continuous(name = "Age",
                     limits = c(15, 45), # change limits to 15 to 45
                     breaks = seq(from = 15, # sequence from 15
```

```
                                to = 45, # to 45
                                by = 5)) # in steps of 5
```



To break down these new arguments/functions in the layers:

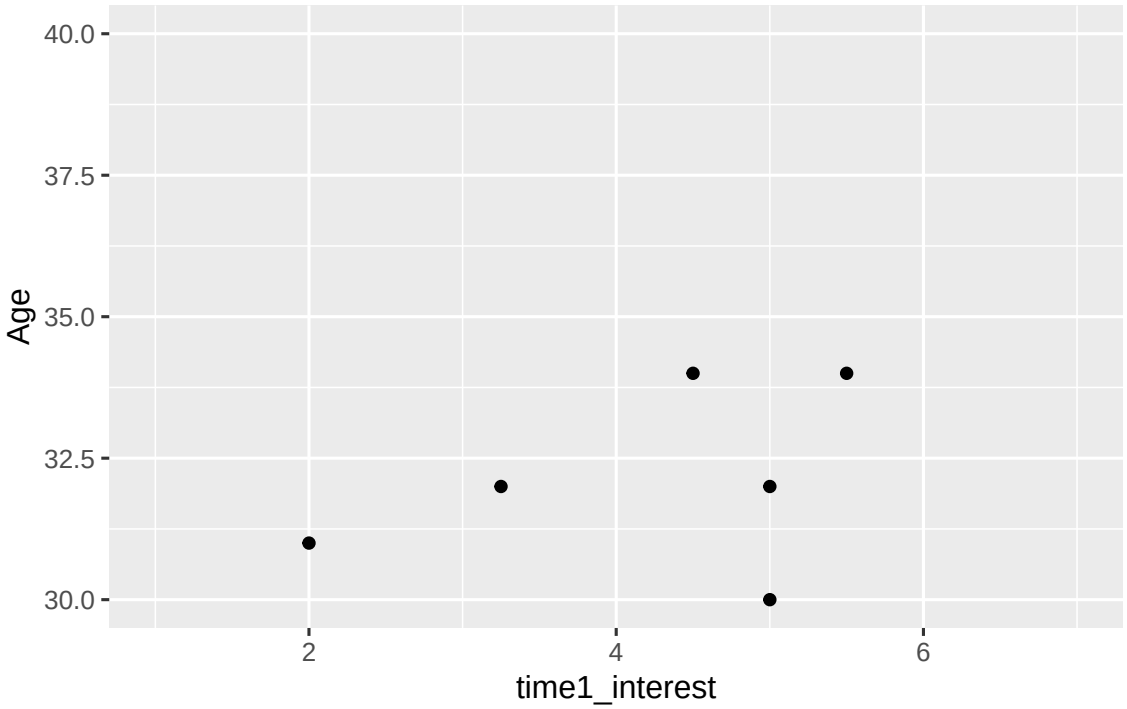
- `breaks` set the tick marks on the plot. We demonstrate two ways of setting this. On the x-axis, we just manually set values for 1 to 7. On the y-axis, we use a second function to set the breaks.
- `seq()` creates a sequence of numbers and can save a lot of time when you need to add lots of values. We set three arguments, `from` for the starting point, `to` for the end point, and `by` for the steps the sequence goes up in.
- `limits` controls the start and end point of the graph scale. In the original graph, we can see there are points below 20 and above 40, so we might want to increase the `limits` of the graph to include a wider range.

❗ Error mode

When controlling the limits of the graph, sometimes you want to decrease the `limits` range to zoom in on an element of the data. If you decrease the range which cuts off some data points, you must be very careful as it actually cuts off data which you would receive a warning about:

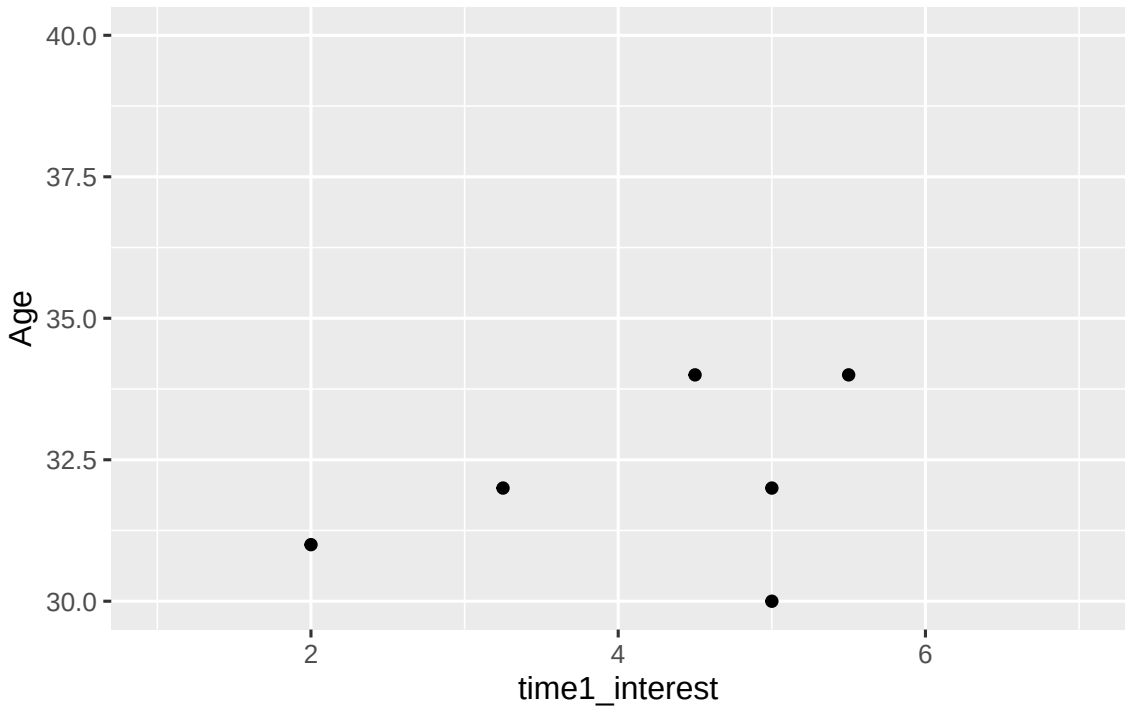
```
zhang_data %>%
  ggplot(aes(x = time1_interest,y = Age)) +
  geom_point() +
  scale_y_continuous(name = "Age",
                     limits = c(30, 40)) # in steps of 5
```

```
Warning: Removed 124 rows containing missing values or values outside the scale range
(`geom_point()`).
```



You must be very careful when truncating axes, but if you *do* need to do it, there is a different function layer to use:

```
zhang_data %>%
  ggplot(aes(x = time1_interest,y = Age)) +
  geom_point() +
  coord_cartesian(ylim = c(30, 40))
```

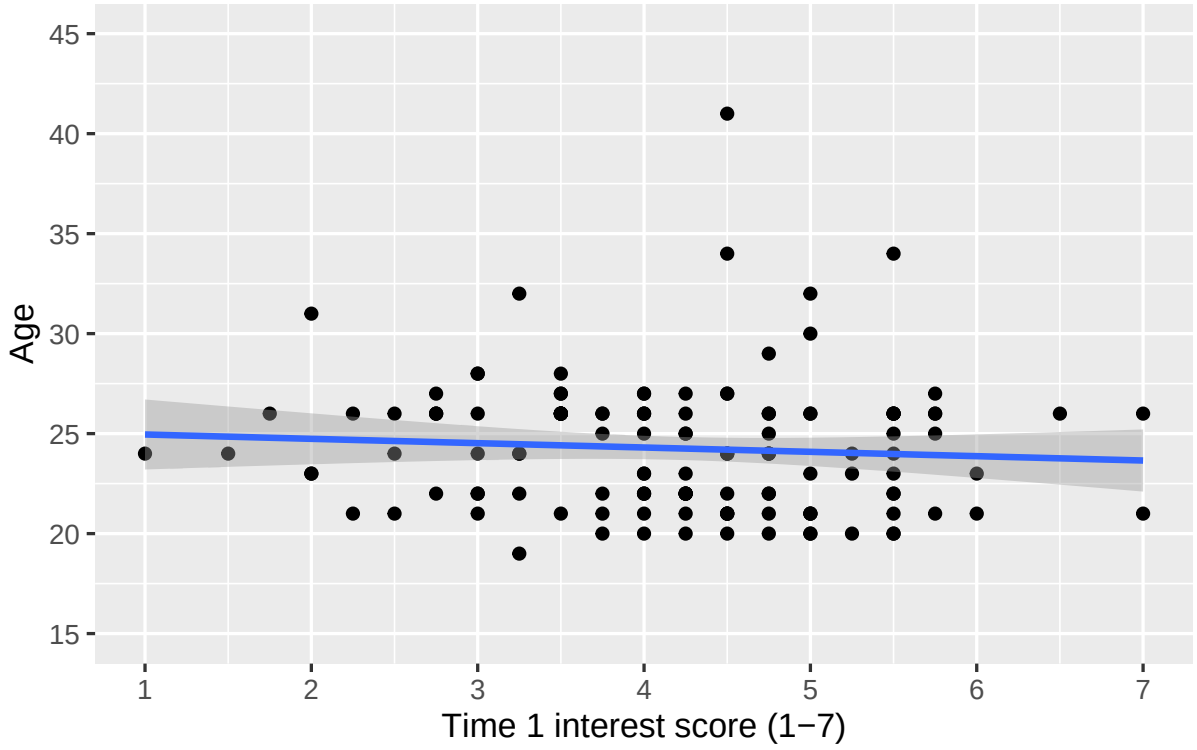


7.2.3 Activity 5 - Adding a regression line

It is often useful to add a regression line or line of best fit to a scatterplot. You can add a regression line with the `geom_smooth()` layer and by default will also provide a 95% confidence interval ribbon. You can specify what type of line you want to draw, most often you will need `method = "lm"` for a linear model or a straight line.

```
zhang_data %>%
  ggplot(aes(x = time1_interest,y = Age)) +
  geom_point() +
  scale_x_continuous(name = "Time 1 interest score (1-7)",
                     breaks = c(1:7)) + # tick marks from 1 to 7
  scale_y_continuous(name = "Age",
                     limits = c(15, 45), # change limits to 15 to 45
```

```
                    breaks = seq(from = 15, # sequence from 15
                                 to = 45, # to 45
                                 by = 5)) +  # in steps of 5
  geom_smooth(method = "lm")
```



With the regression line, we can see there is very little relationship between age and interest score at time 1.

> **!** Important
>
> Remember, you can save your plots using the function `ggsave()`. You can use the function after creating the last plot, or saving your plot as an object and using the `plot` argument. You have a `Figures/` directory for the chapter, so try and save the plots you make to remind yourself later.

Try this

So far, we made a scatterplot of age against interest at time 1. Now, create a scatterplot on your own using the two interest rating variables: `time1_interest` and `time2_interest`. After you made the scatterplot, it looks like there is a

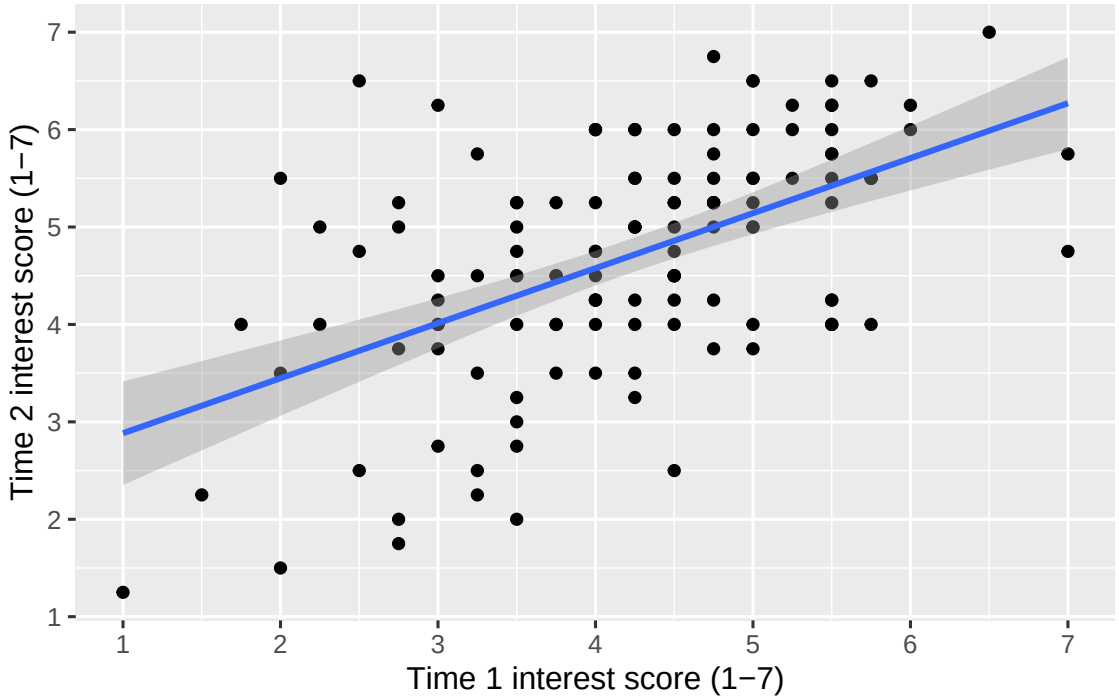
- (A) positive
- (B) negative

relationship between interest ratings at time 1 and time 2.

Show me the solution

You should have the following in a code chunk:

```
zhang_data %>%
  ggplot(aes(x = time1_interest, y = time2_interest)) +
  geom_point() +
  scale_x_continuous(name = "Time 1 interest score (1-7)",
                     breaks = c(1:7)) + # tick marks from 1 to 7
  scale_y_continuous(name = "Time 2 interest score (1-7)",
                     breaks = c(1:7)) + # tick marks from 1 to 7
  geom_smooth(method = "lm")
```



7.2.4 Activity 6 - Creating a grouped scatterplot

Before we move on, we can add a third variable to show how the relationship might differ for different groups within our data. We can do this by adding the `colour` argument to `aes()` and setting it as whatever variable we would like to distinguish between. In this case, we will see how the relationship between age and interest at time 1 differs for the male and female participants. There are a few participants with missing gender, so we will first filter them out.

```
zhang_data %>%
  drop_na(Gender) %>%
  ggplot(aes(x = time1_interest, y = Age, colour = Gender)) +
  geom_point() +
  scale_x_continuous(name = "Mean interest score (1-7)",
                     breaks = c(1:7)) +
  scale_y_continuous(name = "Age") +
  geom_smooth(method = "lm")
```

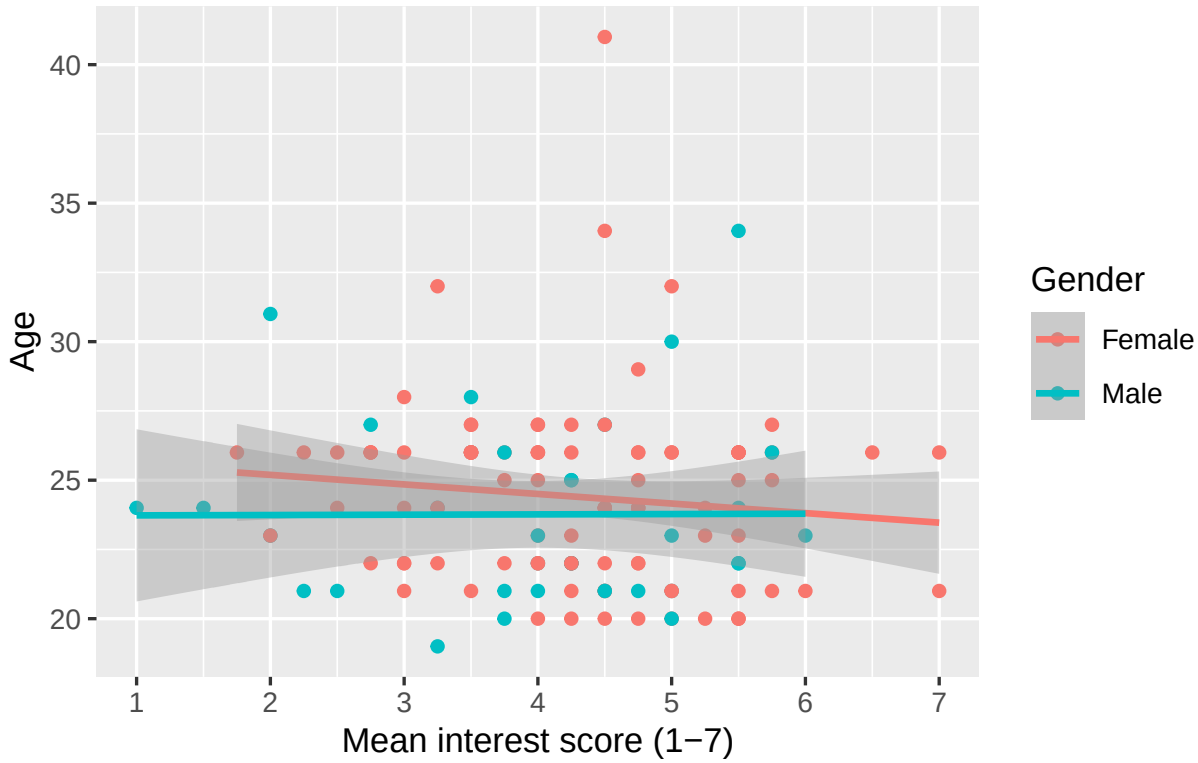


Figure 7.1: Grouped scatterplot

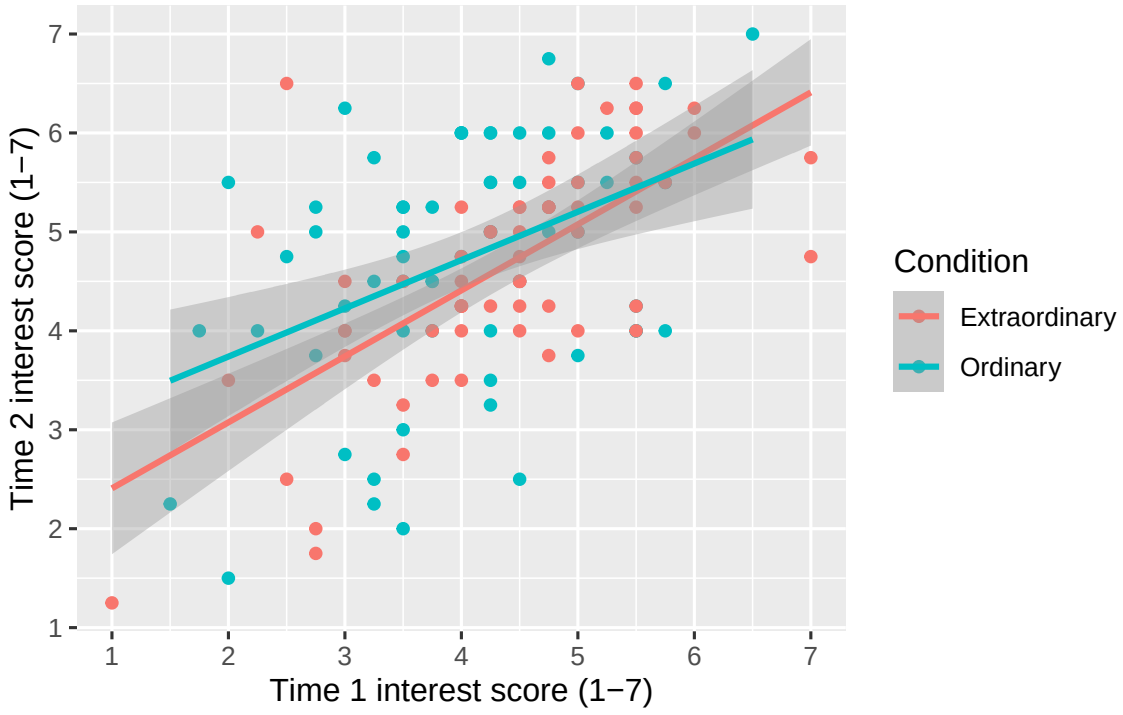
Try this

For your independent scatterplot of the two interest rating variables: `time1_interest` and `time2_interest`, add a `colour` argument using the `Condition` variable. This will show the relationship between time 1 and time 2 interest separately for participants in the ordinary and extraordinary groups.

Show me the solution

You should have the following in a code chunk:

```
zhang_data %>%
  ggplot(aes(x = time1_interest, y = time2_interest, colour = Condition)) +
  geom_point() +
  scale_x_continuous(name = "Time 1 interest score (1-7)",
                     breaks = c(1:7)) + # tick marks from 1 to 7
  scale_y_continuous(name = "Time 2 interest score (1-7)",
                     breaks = c(1:7)) + # tick marks from 1 to 7
  geom_smooth(method = "lm")
```



7.3 Boxplots

The next visualisation is the boxplot which presents a range of summary statistics for your outcome, which you can split between different groups on the x-axis, or add further variables to divide by. For the boxplot element, you get five summary statistics: the median centre line, the first and third quartile as the box (essentially, the interquartile range), and 1.5 times the first and third quartiles as the whiskers extending from the box. If there are any values beyond the whiskers, you see the individual data points and this is one definition of an outlier (more on that in Chapter 11)

7.3.1 Activity 7 - Creating a basic boxplot

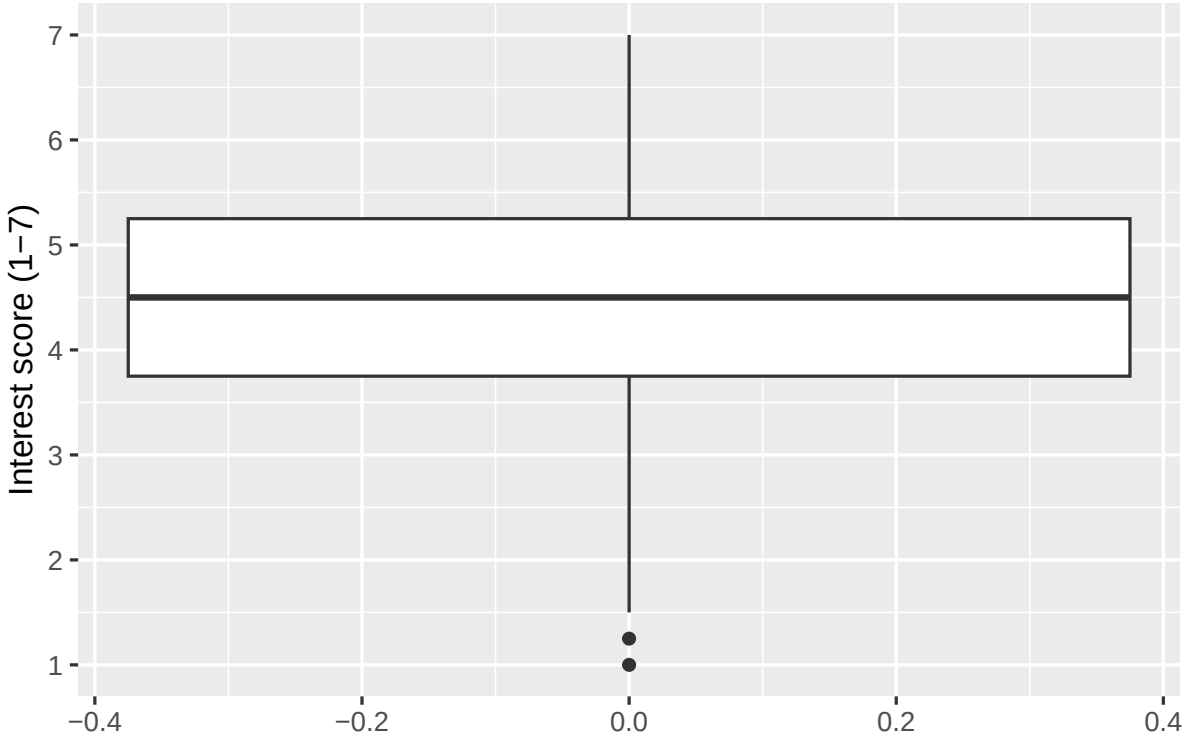
Before we create the boxplot, we need a final data wrangling step. At the moment, we have `time1_interest` and `time2_interest` in wide format, but to plot together, we need to express it as a single variable. For that, we must restructure the data. This is why we spent so much time on data wrangling, as you might need to quickly restructure your data to plot certain elements.

> Try this
>
> To wrangle the data, gather the variables `time1_interest` and `time2_interest`. Create a new object called `zhang_data_long` and use the names `Time` and `Interest` for your column names to be consistent with the demonstrations below.

> Show me the solution
>
> You should have the following in a code chunk:
>
> ```
> # gather the data to convert to long format
> zhang_data_long <- zhang_data %>%
>   pivot_longer(cols = time1_interest:time2_interest,
>                names_to = "Time",
>                values_to = "Interest")
> ```

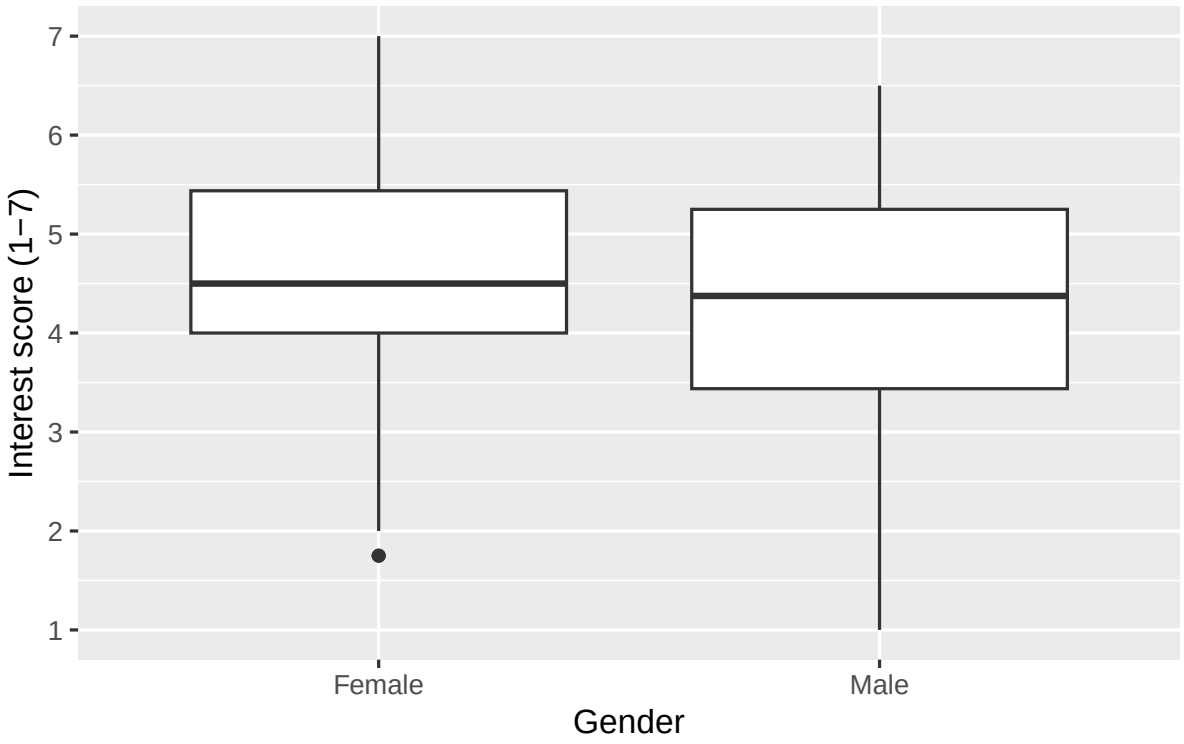
If you only want to visualise one continuous variable, we need one variable on the y-axis and a new function layer `geom_boxplot()`.

```
zhang_data_long %>%
  ggplot(aes(y = Interest)) +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7))
```



Typically, you want to compare the outcome between one or more categories, so we can add a categorical variable like gender to the x-axis, removing the missing values first.

```
zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender)) +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7))
```

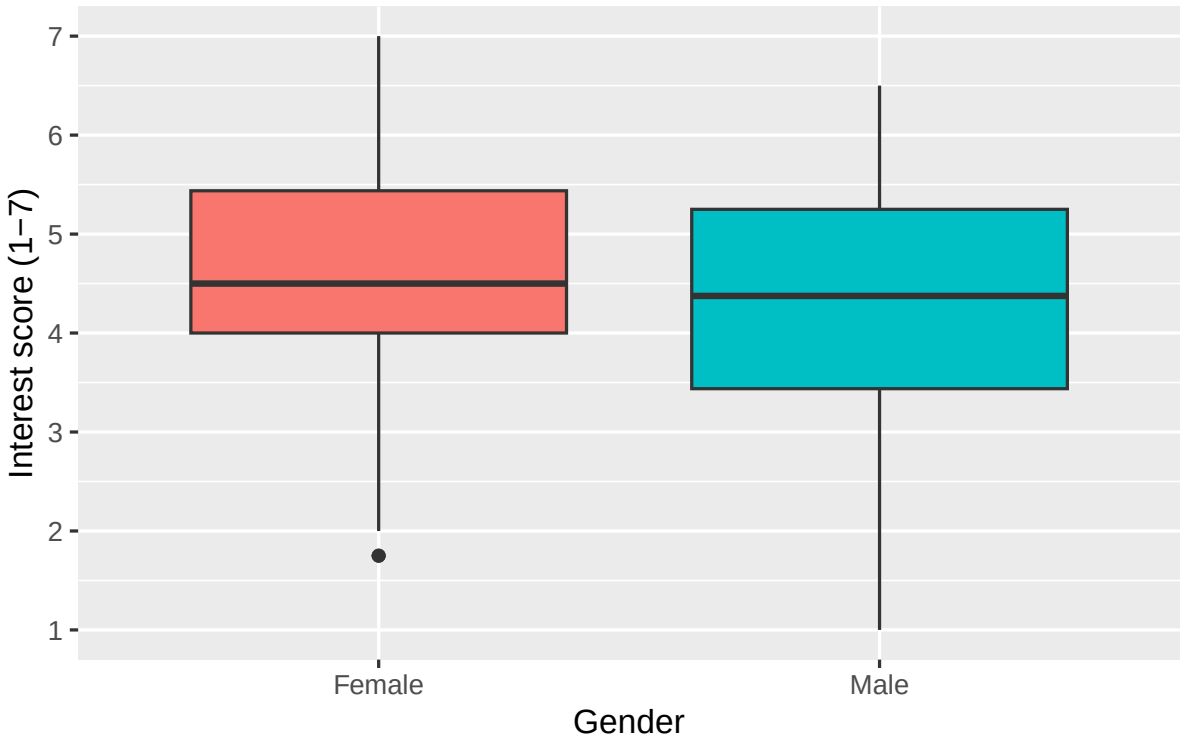


7.3.2 Activity 8 - Adding colour to variables

It is not as important when you only have one variable on the x-axis, but one useful feature is adding colour to distinguish between categories. You can control this by adding a variable to the `fill` argument within `aes()`.

By default, we get a legend which is redundant when we only have different colours on the x-axis, so we can turn it off by adding `guides(fill = FALSE)` as a layer.

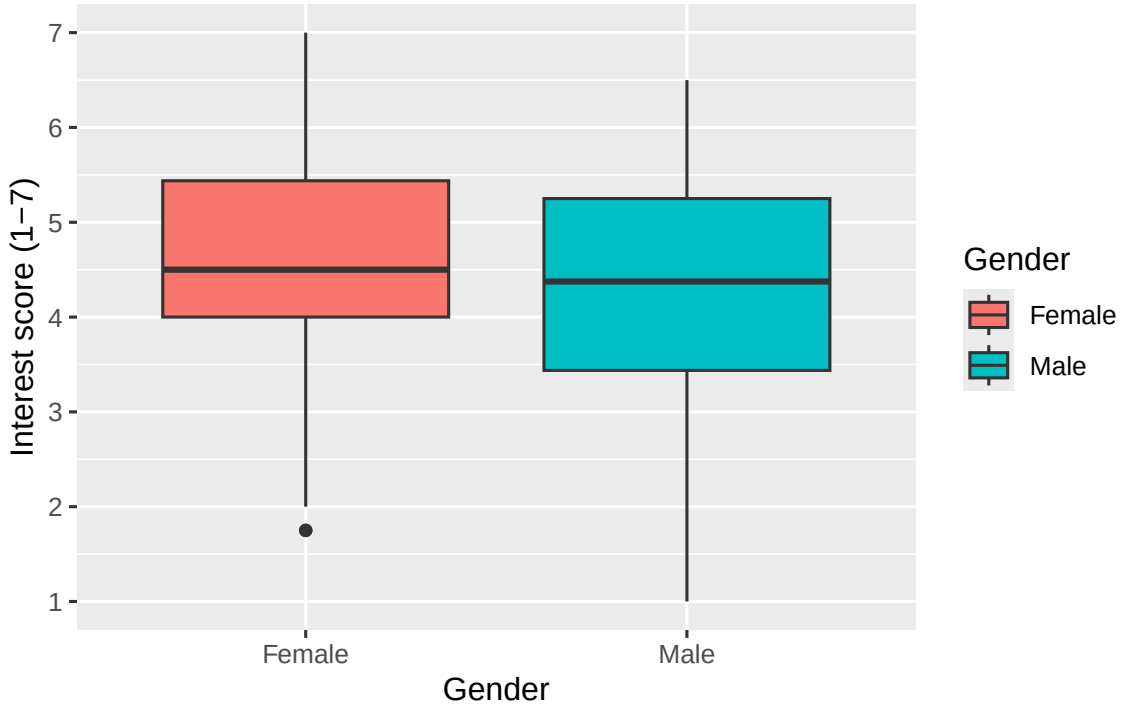
```
zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender, fill = Gender)) +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  guides(fill = FALSE) # remove the legend
```



! Error mode

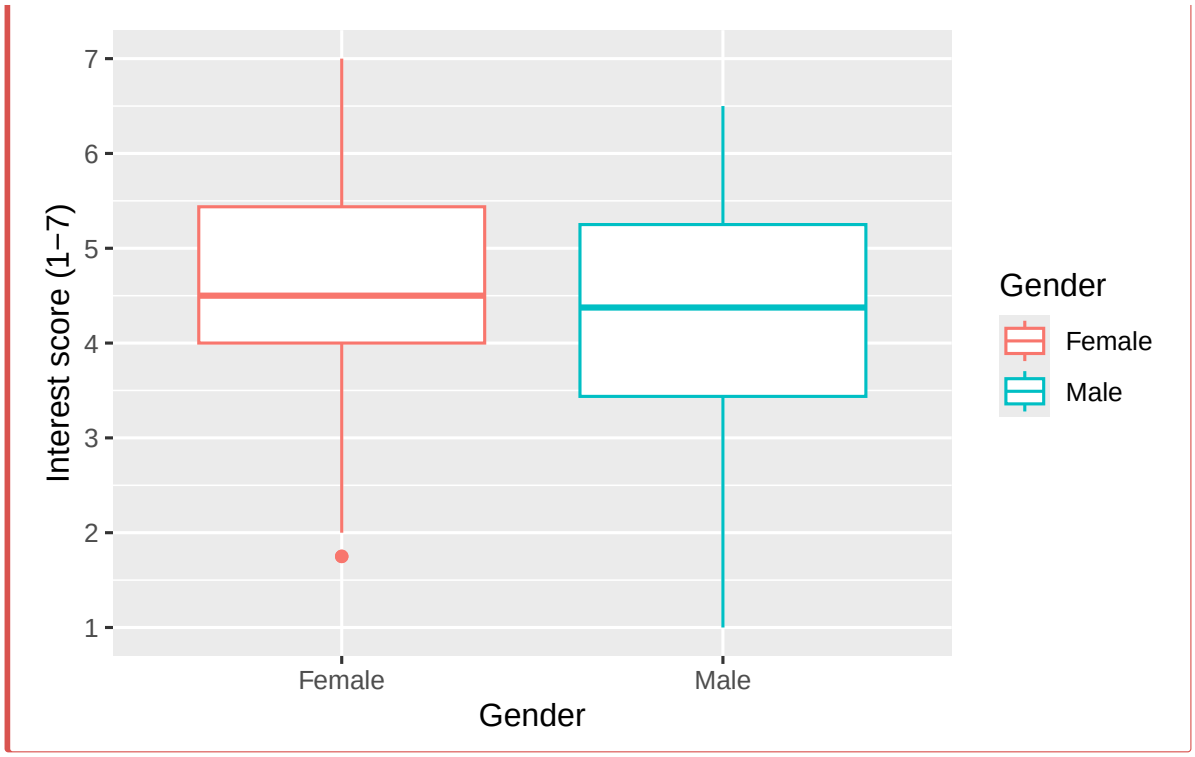
You might have noticed we have now used two different arguments to control the colour. In scatterplots, we used `colour`. In boxplots, we used `fill`. It is one of those concepts that takes time to recognise which you need, depending on the type of geom you are using. Roughly, `colour` is when you want to control the outline or symbol, like the points. Whereas `fill` is when you want the inside of a geom coloured. You can see the difference here by controlling `fill` first:

```
zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender, fill = Gender)) +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7))
```



Then `colour`:

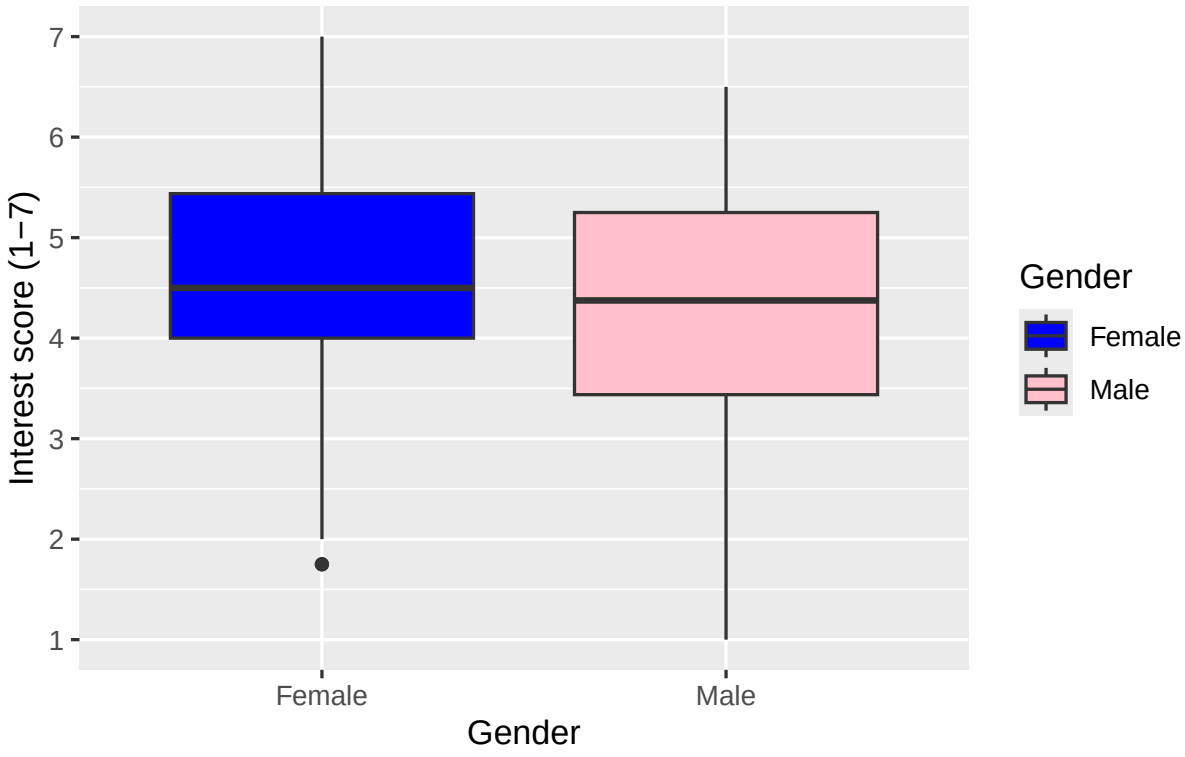
```
zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender, colour = Gender)) +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7))
```



7.3.3 Activity 9 - Controlling colours

ggplot2 has a default colour scheme which is fine for quick plots, but it is useful to control the colour scheme. You can do this manually by editing `scale_fill_discrete()` and choosing colours through the `type` argument (you can do this through character names or choosing a HEX code: https://r-charts.com/colors/).

```
zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender, fill = Gender)) +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  scale_fill_discrete(type = c("blue", "pink"))
```



Alternatively (and what we recommend), you can use `scale_fill_viridis_d()`. This function does exactly the same thing but it uses a colour-blind friendly palette (which also prints in black and white). There are 5 different options for colours and you can see them by changing `option` to A, B, C, D or E. We like option E with `alpha = 0.6` (to control transparency and soften the tone) but play around with the options to see what you prefer.

```
zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender, fill = Gender)) +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  scale_fill_viridis_d(option = "E",
                       alpha = 0.6) +
  guides(fill = "none")
```

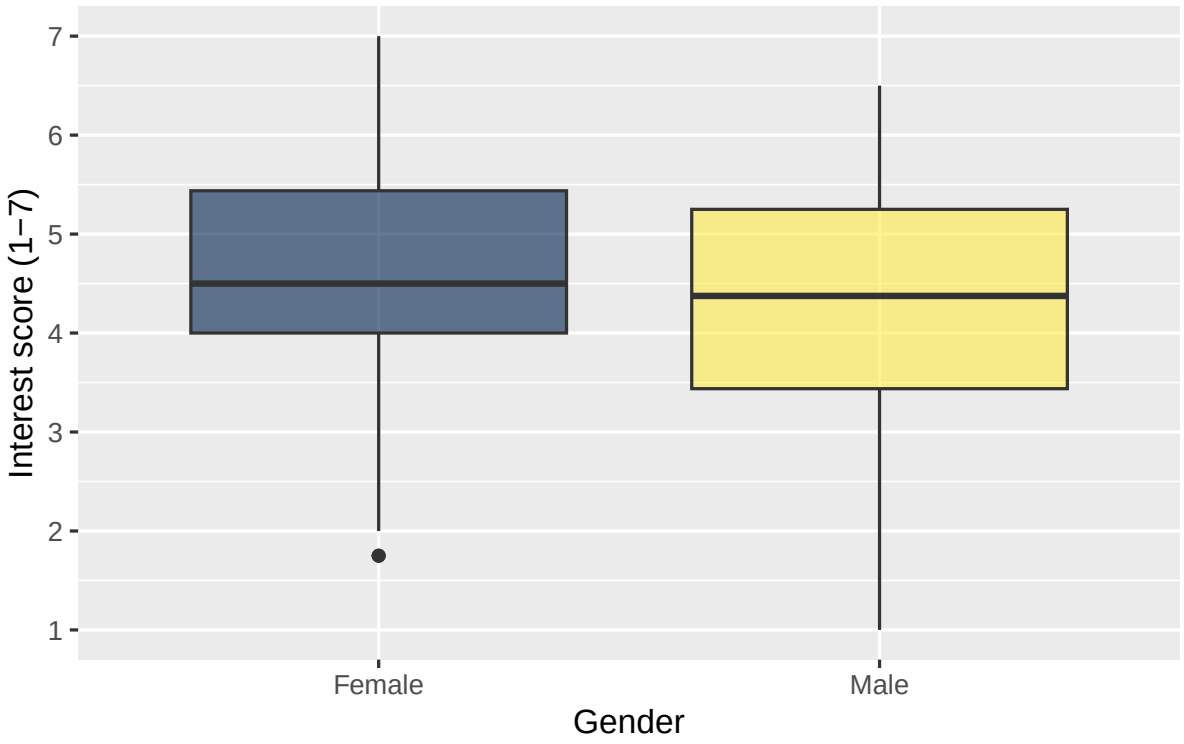


Figure 7.2: Boxplots with friendly colours

Try this

For your independent boxplot, use `zhang_data_long` to visualise `Interest` as your continuous variable and `Condition` for different categories. This will show the difference in interest rating between those in the ordinary and extraordinary groups.
Comparing the ordinary and extraordinary groups, it looks like

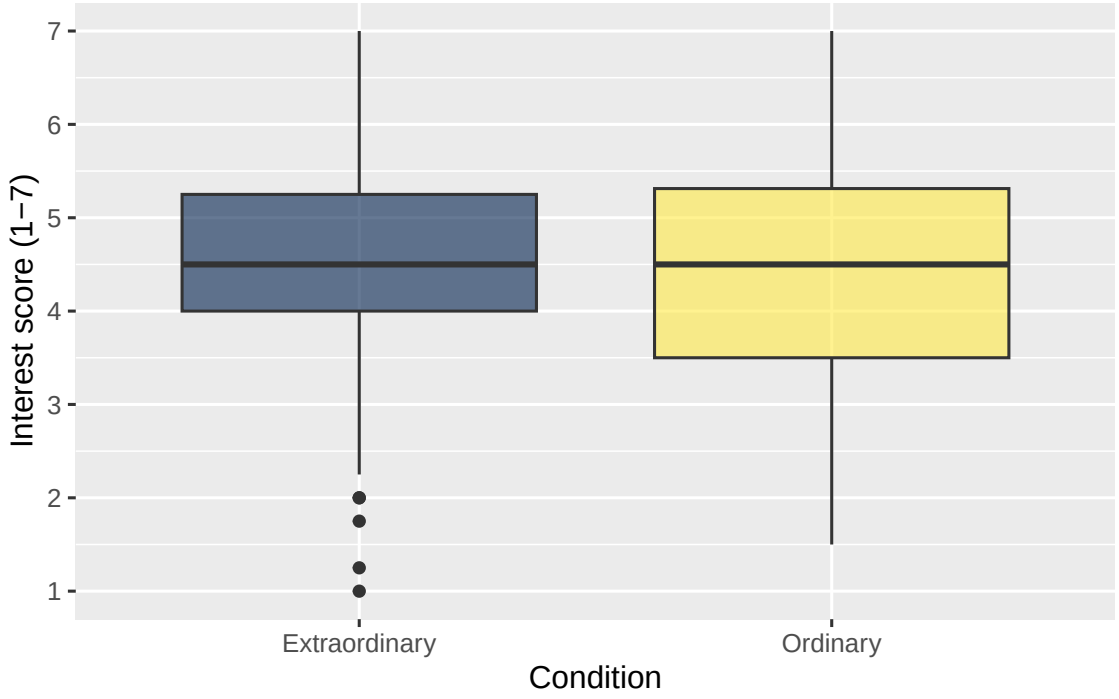
- (A) ordinary score higher on average
- (B) very little difference on average
- (C) extraordinary score higher on average

.

Show me the solution

You should have the following in a code chunk:

```
zhang_data_long %>%
  ggplot(aes(y = Interest, x = Condition, fill = Condition)) +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  scale_fill_viridis_d(option = "E",
                       alpha = 0.6) +
  guides(fill = "none")
```



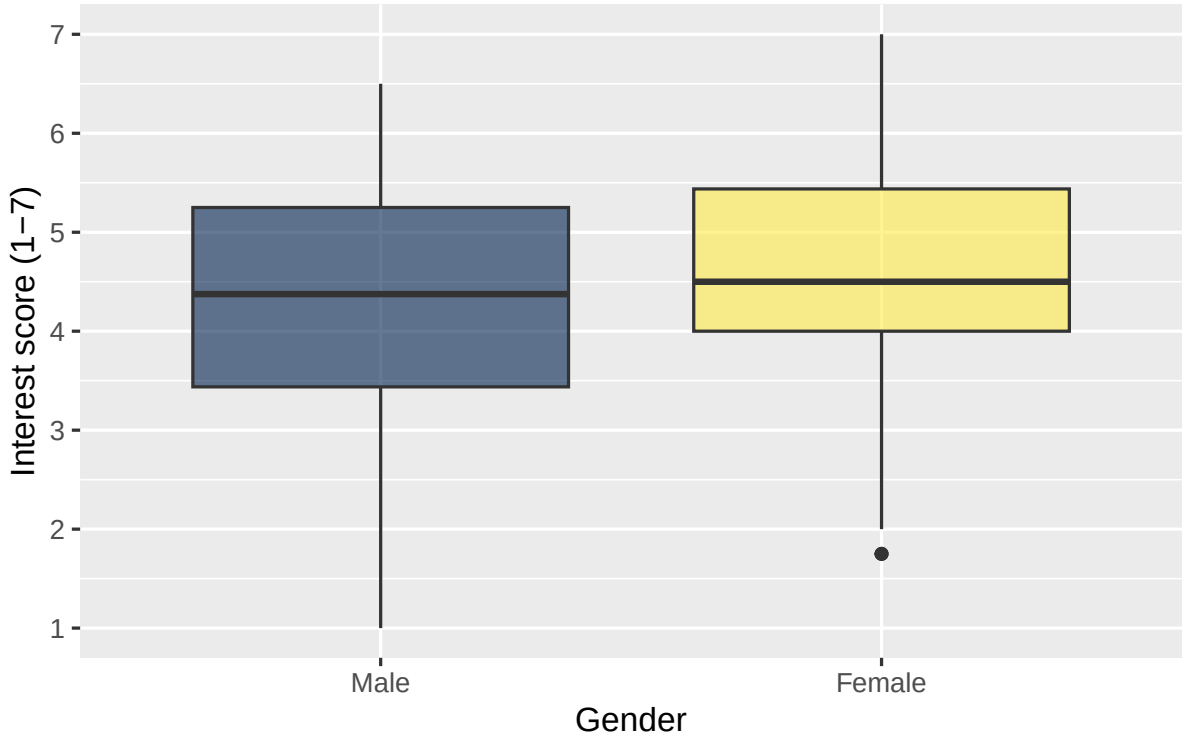
7.3.4 Activity 10 - Ordering categories

When we plot variables like `Gender` on the x-axis, R has an internal order it sets unless you create a factor. The default is alphabetical or numerical. In previous plots, it displayed Female then Male, as F comes before M.

Controlling the order of categories is an important design choice to communicate your message, and the most direct way is controlling the factor order before plotting. Here, we add `mutate()`

in a pipe and manually set the factor levels, just be careful as it is case sensitive to the values in your data.

```
zhang_data_long %>%
  drop_na(Gender) %>%
  mutate(Gender = factor(Gender,
                         levels = c("Male", "Female"))) %>%
  ggplot(aes(y = Interest, x = Gender, fill = Gender)) +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  scale_fill_viridis_d(option = "E",
                       alpha = 0.6) +
  guides(fill = "none")
```

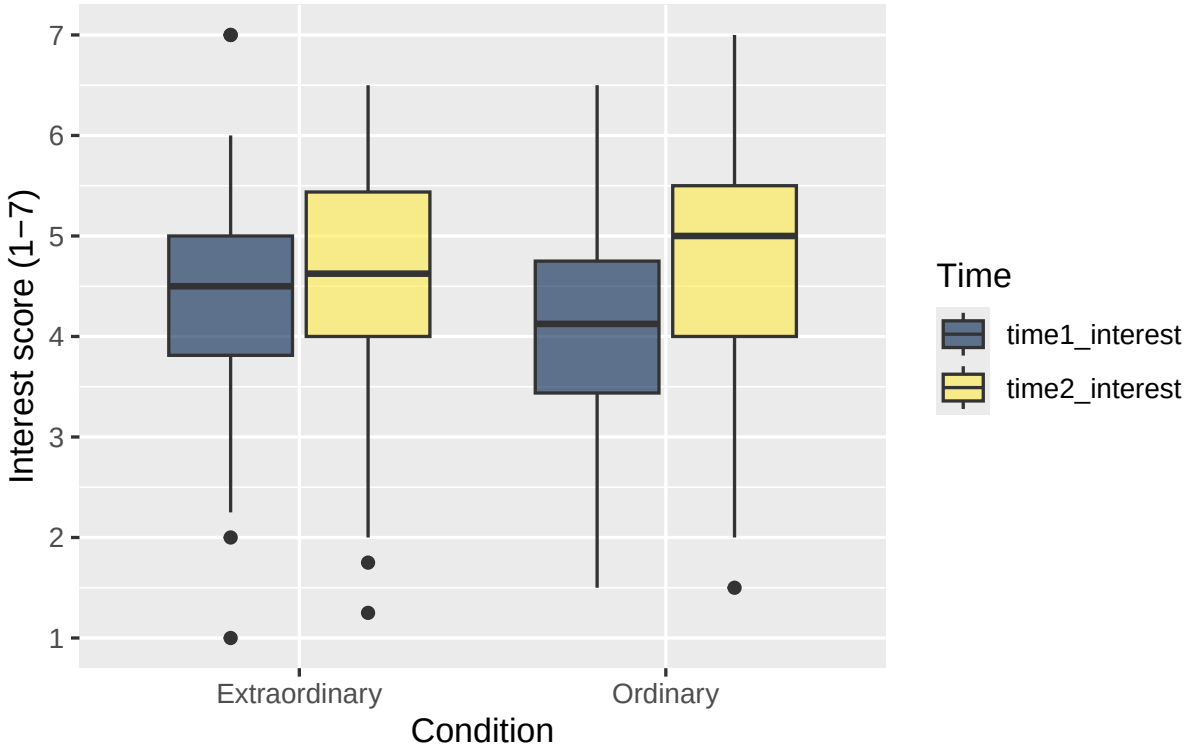


7.3.5 Activity 11- Boxplots for multiple factors

When you only have one independent variable, using the `fill` argument to change the colour can be a little redundant as the colours do not add any additional information. It makes more sense to use colour to represent a second variable.

For this example, we will use `Condition` and `Time` as variables. `fill()` now specifies a second independent variable, rather than repeating the variable on the x-axis as in the previous plot, so we do not want to deactivate the legend.

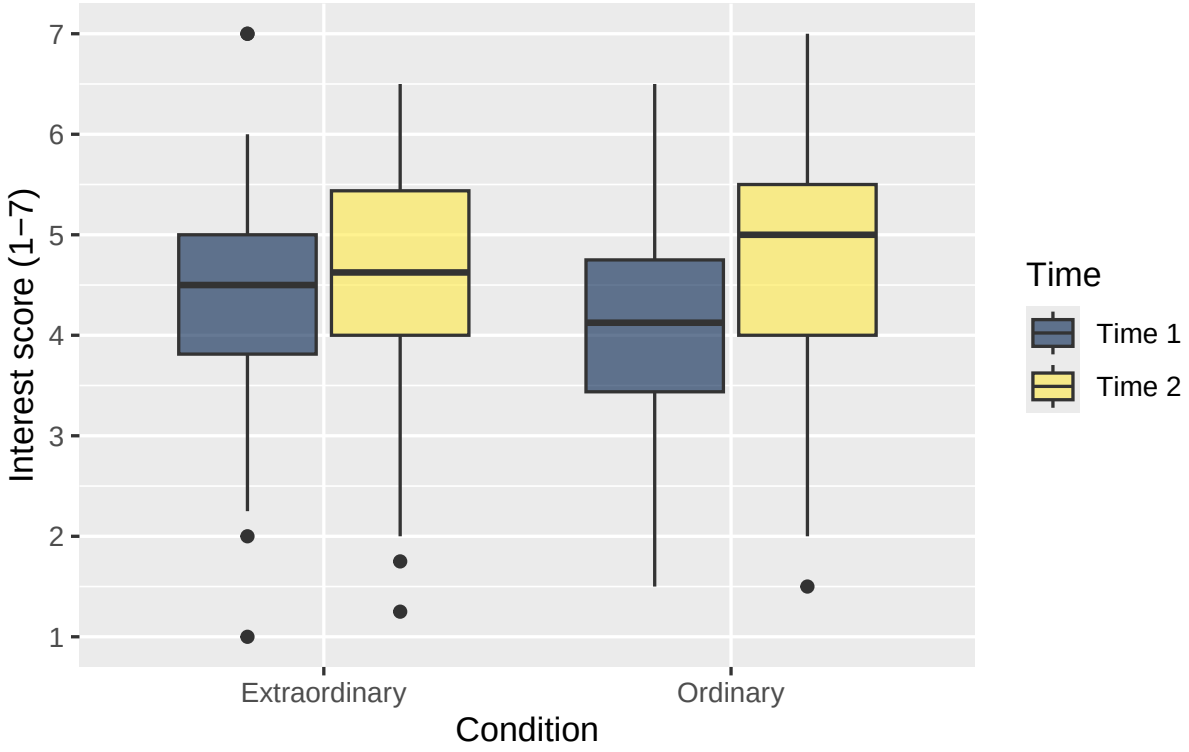
```
zhang_data_long %>%
  ggplot(aes(y = Interest, x = Condition, fill = Time)) +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  scale_fill_viridis_d(option = "E",
                       alpha = 0.6)
```



As a final point here, the `fill` values on the legend are not the most professional looking. Like reordering factors, the easiest way of addressing this is editing the underlying data before piping to ggplot2.

```
zhang_data_long %>%
  mutate(Time = case_match(Time,
                           "time1_interest" ~ "Time 1",
                           "time2_interest" ~ "Time 2")) %>%
```

```
ggplot(aes(y = Interest, x = Condition, fill = Time)) +
geom_boxplot() +
scale_y_continuous(name = "Interest score (1-7)",
                   breaks = c(1:7)) +
scale_fill_viridis_d(option = "E",
                     alpha = 0.6)
```



7.4 Violin-boxplots

Boxplots are great for your own exploratory data analysis but you do not often see them reported in isolation. They visualise summary statistics, but you do not get much sense of the underlying distribution of values. When you want to communicate continuous outcomes, researchers in psychology are using violin-boxplots more often. This combines both elements: a violin plot to show the distribution of the data, and a boxplot to add summary statistics. This is where ggplot2 comes into it's own as we can add and customise several layers.

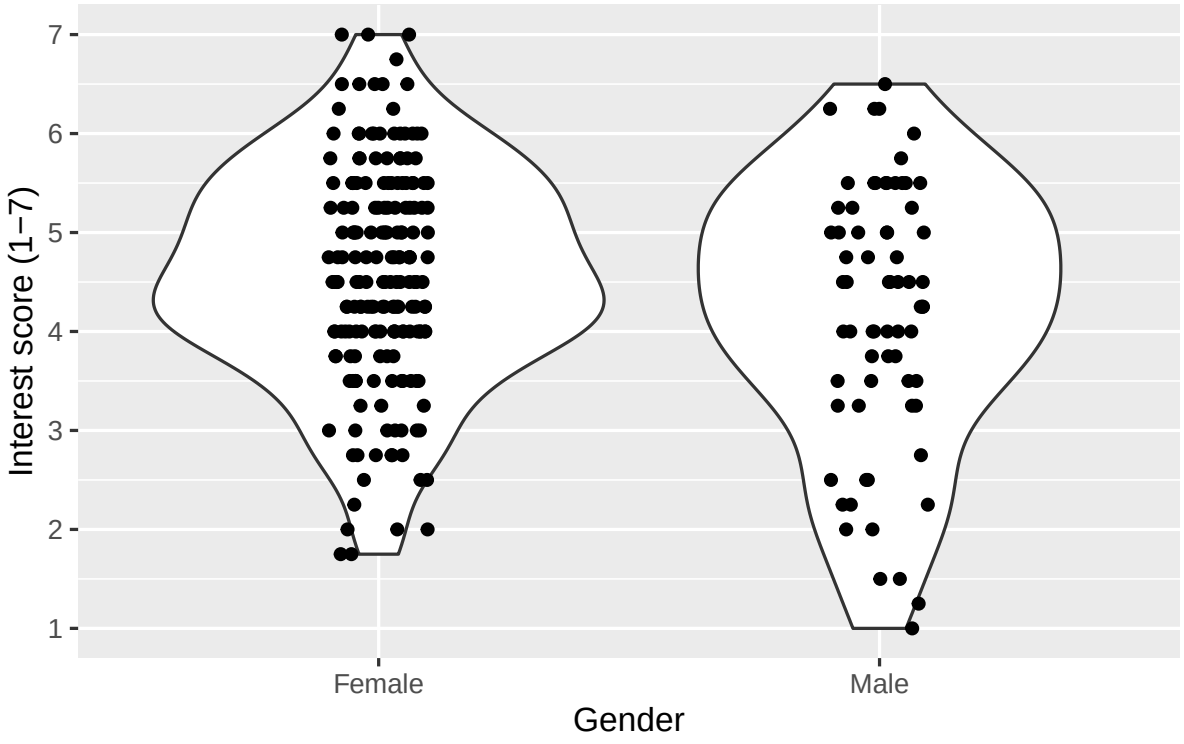
7.4.1 Activity 12 - Creating a basic violin plot

Violin plots get their name as they look something like a violin when the data are roughly normally distributed. They show density, so the fatter the violin element, the more data points there are for that value. Compared to the boxplot, the only difference is changing the layer to `geom_violin()`.

```
zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender)) +
  geom_violin() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7))
```

The distribution of values is great, but sometimes it might be useful to also add the underlying data points. These are all important design choices as it can be useful when you have smaller amounts of data, but overwhelming when you have thousands of data points. So, keep in mind what you want to communicate. Here, we use the layer `geom_jitter()` to jitter the points slightly, so they are not all in a vertical line and we get a better sense of the density.

```r
zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender)) +
  geom_violin() +
  geom_jitter(height = 0, # do not jitter height
              width = .1) + # jitter width of points
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7))
```

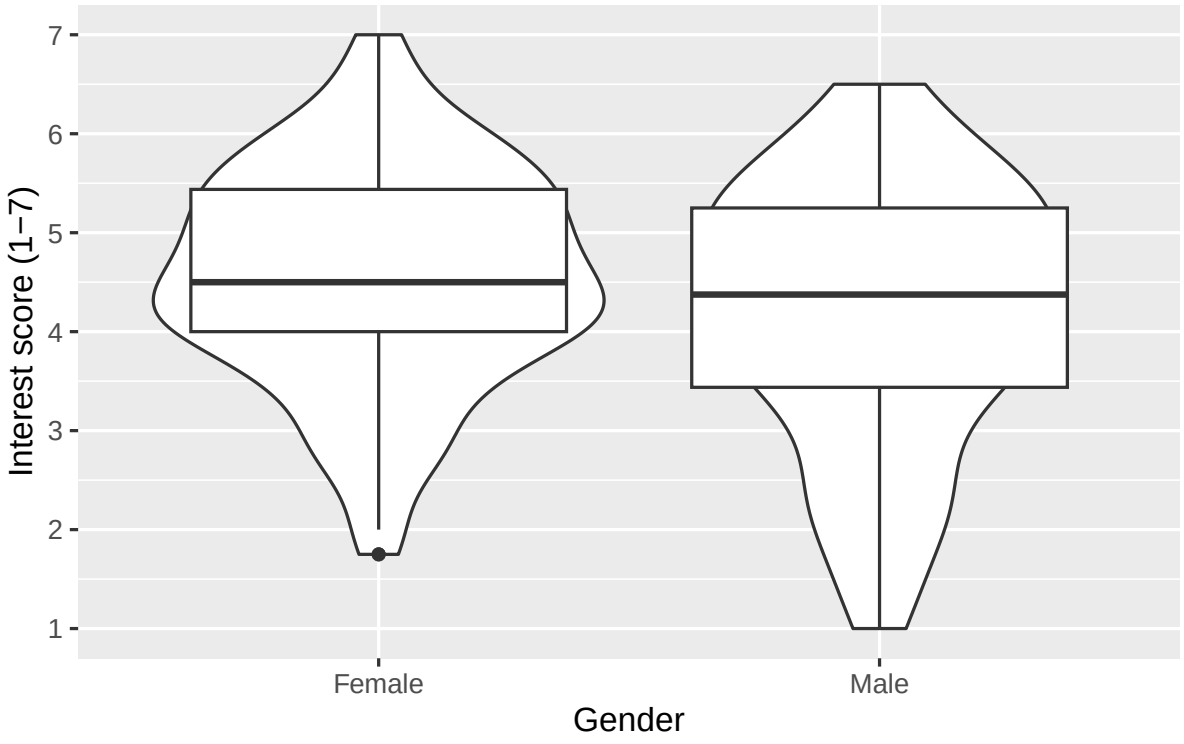


> **!** Important
>
> It is important to remember that R is very literal. ggplot2 works on a system of layers. It will add new geoms on top of existing ones and it will not stop to think whether this is a good idea. Try running the code above but put `geom_jitter()` first and then add `geom_violin()`. The order of your layers matters.

7.4.2 Activity 13 - Creating a violin-boxplot

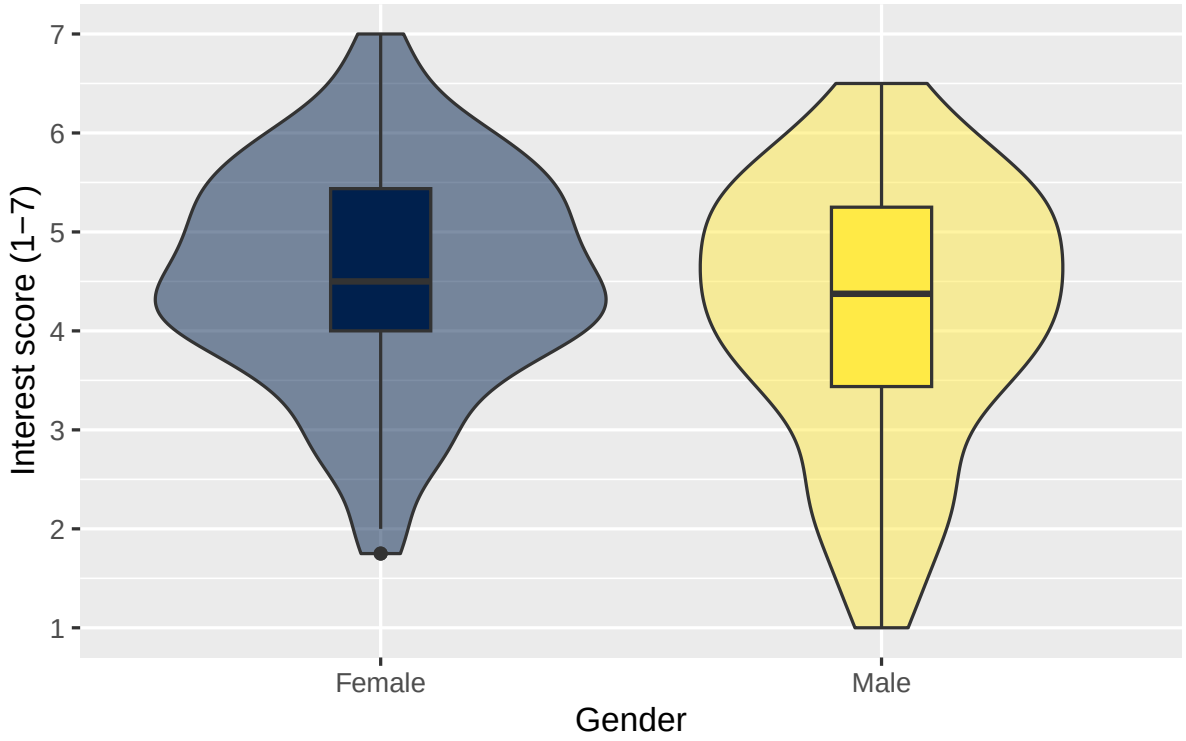
Instead of adding the data points in a layer, we can add a boxplot to create the violin-boxplot. This way, we get distribution information from the violin layer and summary statistics from the boxplot layer.

```
zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender)) +
  geom_violin() +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7))
```



On it's own, this does not look great. We can edit the settings to reduce the width of the boxplots, add a colour scheme, and add transparency to the violin layer to make it easier to see the boxplot.

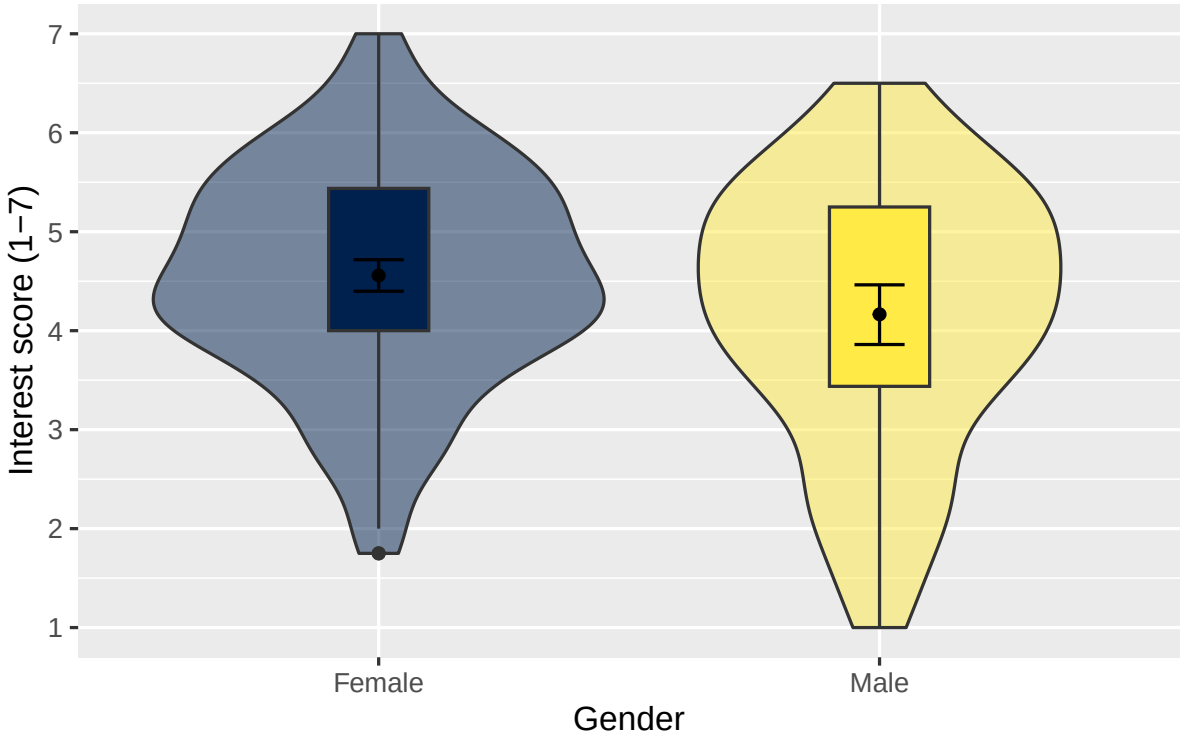
```
zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender, fill = Gender)) +
  geom_violin(alpha = 0.5) +
  geom_boxplot(width = 0.2) +
  scale_fill_viridis_d(option = "E") +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  guides(fill = "none")
```



The boxplot uses the median for the centre line, but in your report you might be presenting means per category which will be slightly different. One further variation is removing the centre median line, and replacing it with the mean and 95% confidence interval (more on that in the lectures and Chapter 8). This way, you get three layers: the violin plot for the density, the boxplot for distribution summary statistics, and the mean and 95% confidence interval.

This code uses two calls to `stat_summary()` which is a layer to add summary statistics. The first layer draws a `point` to represent the mean, and the second draws an `errorbar` that represents the 95% confidence interval around the mean.

```r
zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender, fill = Gender)) +
  geom_violin(alpha = 0.5) +
  geom_boxplot(width = 0.2,
               fatten = NULL) +
  stat_summary(fun = "mean",
               geom = "point") +
  stat_summary(fun.data = "mean_cl_boot", # confidence interval
               geom = "errorbar",
               width = 0.1) +
  scale_fill_viridis_d(option = "E") +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  guides(fill = "none")
```

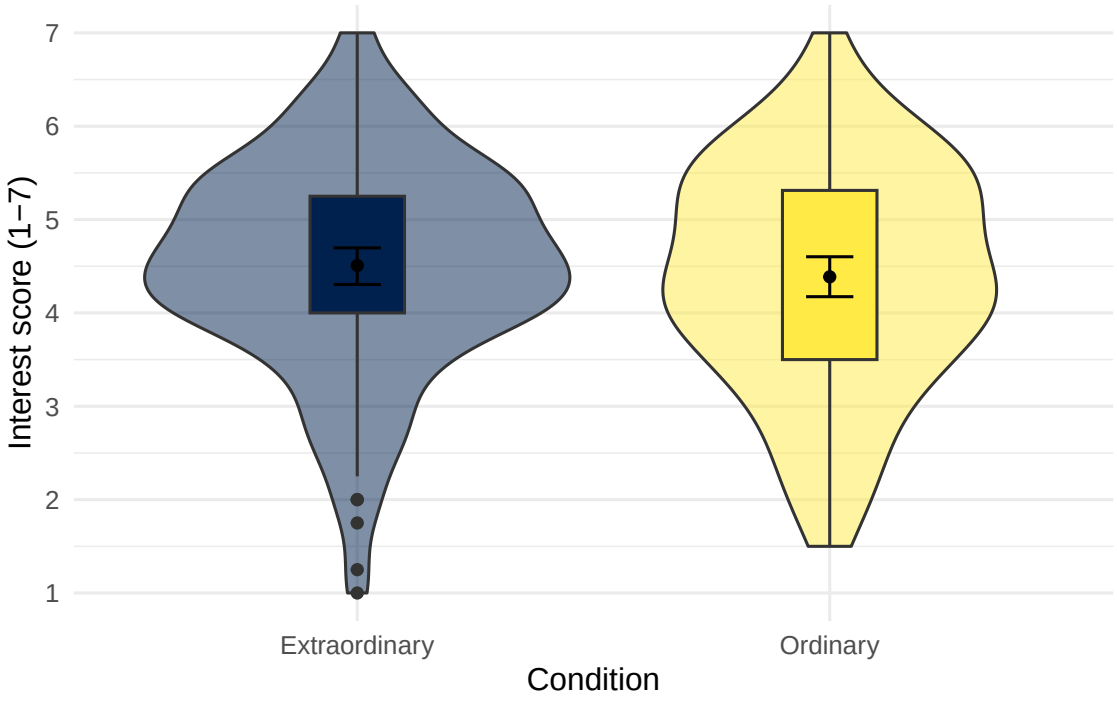


Warning

When you run the line `stat_summary(fun.data = "mean_cl_boot", geom = "errorbar", width = .1)` for the first time, you might be prompted to install the R package Hmisc. If you are on your own computer, follow the instructions in the Console to install the package. If you are on a university computer, this should already be installed.

Try this

For your independent violin-boxplot, use `zhang_data_long` to visualise `Interest` as your continuous variable and `Condition` for different categories on the x-axis. Try and create the plot to look like this, so you might need to play around with different themes:



Show me the solution

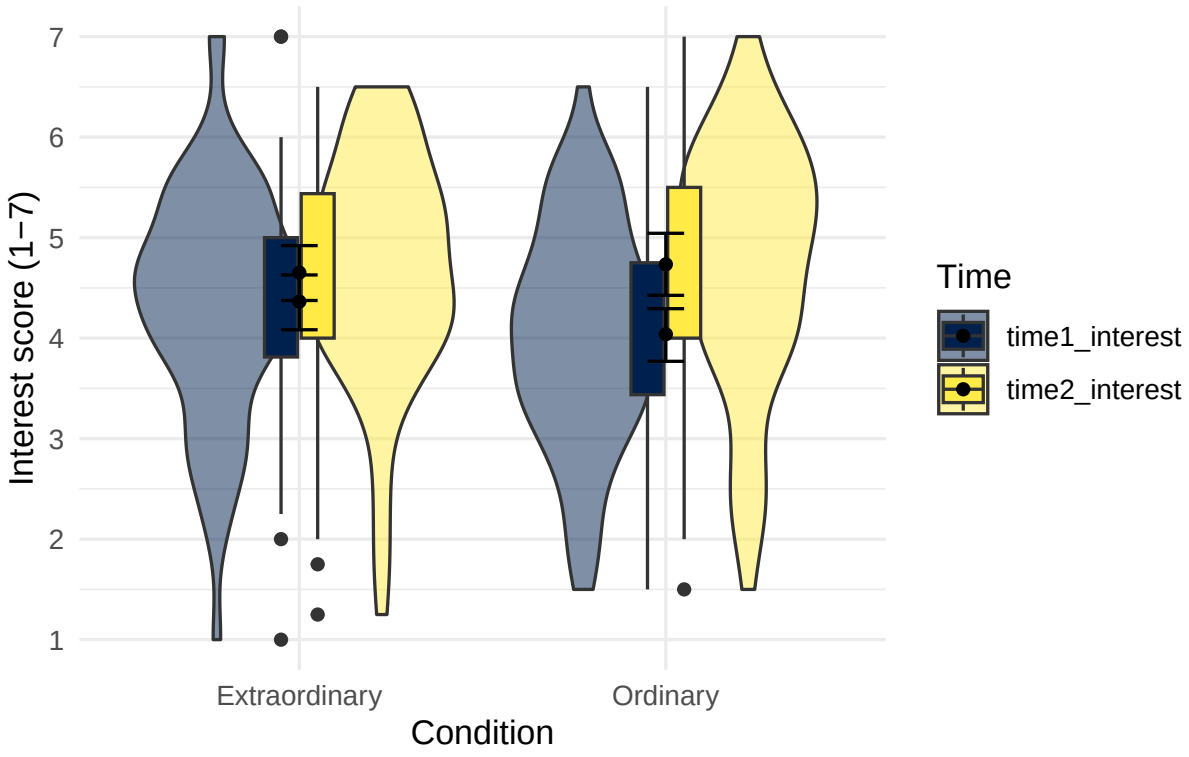
You should have the following in a code chunk:

```
zhang_data_long %>%
  ggplot(aes(y = Interest, x = Condition, fill = Condition)) +
  geom_violin(alpha = 0.5) +
  geom_boxplot(width = 0.2,
               fatten = NULL) +
  stat_summary(fun = "mean",
               geom = "point") +
  stat_summary(fun.data = "mean_cl_boot",
               geom = "errorbar",
               width = .1) +
  scale_fill_viridis_d(option = "E") +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  theme_minimal() +
  guides(fill = "none")
```

7.4.3 Activity 14 - Adding additional variables

Like boxplots, we can add a second grouping variable to `fill` instead of just using it for colour.

```
zhang_data_long %>%
  ggplot(aes(y = Interest, x = Condition, fill = Time)) +
  geom_violin(alpha = 0.5) +
  geom_boxplot(width = 0.2,
               fatten = NULL) +
  stat_summary(fun = "mean",
               geom = "point") +
  stat_summary(fun.data = "mean_cl_boot",
               geom = "errorbar",
               width = .1) +
  scale_fill_viridis_d(option = "E") +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  theme_minimal()
```

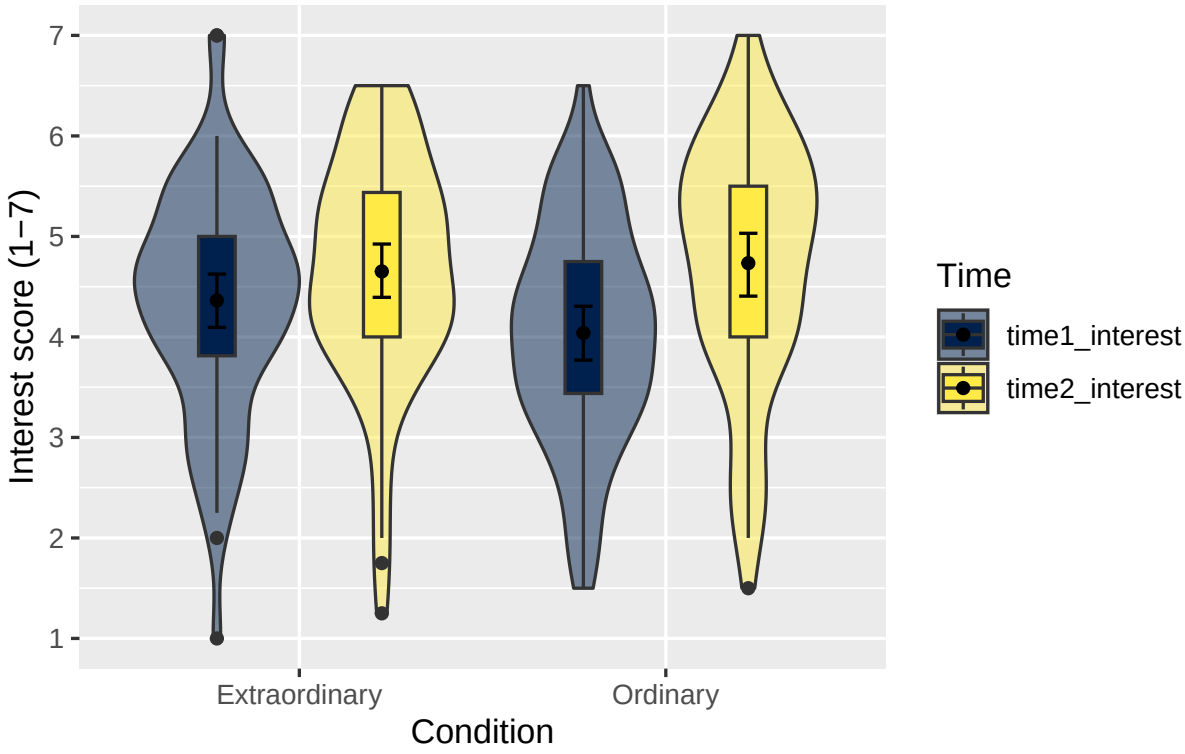


However, unless you are trying to recreate a Kandinsky painting in ggplot2, that does not look quite right. This is because we have multiple layers that each plot separate groups in different ways. To make it all fall into line, we need to add a constant value to offset the elements. We start off by defining a position dodge value as an object. This way, we can use the object name later, and we only need to edit it in one place if we wanted to change the value.

```
# specify as an object, so we only change it in one place
dodge_value <- 0.9

zhang_data_long %>%
  ggplot(aes(y = Interest, x = Condition, fill = Time)) +
  geom_violin(alpha = 0.5) +
  geom_boxplot(width = 0.2,
               fatten = NULL,
               position = position_dodge(dodge_value)) +
  stat_summary(fun = "mean",
               geom = "point",
               position = position_dodge(dodge_value)) +
  stat_summary(fun.data = "mean_cl_boot",
               geom = "errorbar",
               width = .1,
```

```
              position = position_dodge(dodge_value)) +
  scale_fill_viridis_d(option = "E") +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7))
```



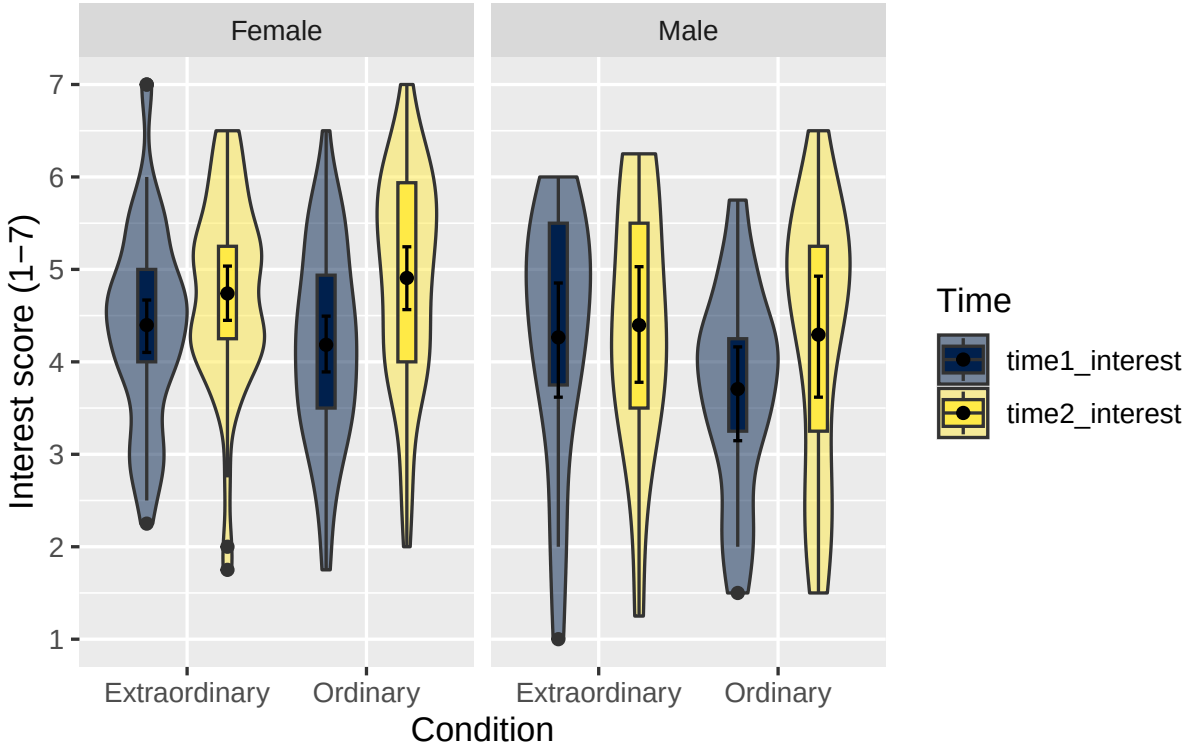
This looks much better! Remember, if you want to change the legend labels, the easiest way is recoding the data before piping to ggplot2.

Finally, we might want to add a third variable to group the data by. There is a facet function that produces different plots for each level of a grouping variable which can be very useful when you have more than two factors. The following code shows interest ratings for all three variables we have worked with: Condition, Time, and Gender.

```
# specify as an object, so we only change it in one place
dodge_value <- 0.9

zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Condition, fill = Time)) +
  geom_violin(alpha = 0.5) +
```

```
  geom_boxplot(width = 0.2,
               fatten = NULL,
               position = position_dodge(dodge_value)) +
  stat_summary(fun = "mean",
               geom = "point",
               position = position_dodge(dodge_value)) +
  stat_summary(fun.data = "mean_cl_boot",
               geom = "errorbar",
               width = .1,
               position = position_dodge(dodge_value)) +
  facet_wrap(~ Gender) + # facet by Gender
  scale_fill_viridis_d(option = "E") +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7))
```



Facets work in the same way as adding a variable to `fill`. It is not easy to change the labels within ggplot2, you are better off editing the values in your data first.

7.5 Test yourself

To end the chapter, we have some knowledge check questions to test your understanding of the concepts we covered in the chapter. We then have some error mode tasks to see if you can find the solution to some common errors in the concepts we covered in this chapter.

7.5.1 Knowledge check

Question 1. You want to plot several summary statistics including the median for your outcome, which ggplot2 layer could you use?

- (A) geom_boxplot()
- (B) geom_point()
- (C) geom_violin()

Question 2. You want to create a scatterplot to show the correlation between two continuous variables, which ggplot2 layer could you use?

- (A) geom_violin()
- (B) geom_point()
- (C) geom_boxplot()

Question 3. You want to show the density of values in your outcome, which ggplot2 layer could you use?

- (A) geom_point()
- (B) geom_violin()
- (C) geom_boxplot()

Question 4. To separate a scatterplot into different groups, you could specify a grouping variable using the `fill` argument to change the colour of the points? TRUE / FALSE

Explain this answer

This was a sneaky one, but relates to the error mode warning within the chapter. There are two ways to add a grouping variable for separate colours: `colour` and `fill`. In this scenario, `colour` would change the colour of the points, whereas `fill` would only change

the colour of the regression line and its 95% confidence interval ribbon. Sometimes you need to play around with the settings to produce the effects you want.

Question 5. The order of layers is important in ggplot2. Which order of layers would show individual data points on top of a boxplot?

- (A) data %>% ggplot() + geom_boxplot() + geom_jitter()
- (B) data + ggplot() + geom_jitter() + geom_boxplot()
- (C) data %>% ggplot() + geom_jitter() + geom_boxplot()
- (D) data + ggplot() + geom_boxplot() + geom_jitter()

Explain this answer

In addition to the layer order, we also added an error mode feature to recognise when you need to use the pipe `%>%` vs the `+`.

- `data %>% ggplot() + geom_boxplot() + geom_jitter()` was the correct answer as we add data point after the boxplot.
- `data + ggplot() + geom_boxplot() + geom_jitter()` had the right order, but we used `+` instead of the pipe between the data and the initial `ggplot()` function.
- `data + ggplot() + geom_jitter() + geom_boxplot()` and `data %>% ggplot() + geom_jitter() + geom_boxplot()` both had the wrong layer order as the boxplot would overlay the points.

7.5.2 Error mode

The following questions are designed to introduce you to making and fixing errors. For this topic, we focus on the new types of data visualisation. Remember to keep a note of what kind of error messages you receive and how you fixed them, so you have a bank of solutions when you tackle errors independently.

Create and save a new R Markdown file for these activities. Delete the example code, so your file is blank from line 10. Create a new code chunk to load tidyverse and wrangle the data files:

```
# Load the tidyverse package below
library(tidyverse)
```

```r
# Load the data file
# This should be the Zhang_2014.csv file
zhang_data <- read_csv("data/Zhang_2014.csv")

# Wrangle the data for plotting.
# select and rename key variables
# mutate to add participant ID and recode
zhang_data <- zhang_data %>%
  select(Gender,
         Age,
         Condition,
         time1_interest = T1_Predicted_Interest_Composite,
         time2_interest = T2_Actual_Interest_Composite) %>%
  mutate(participant_ID = row_number(),
         Condition = case_match(Condition,
                                1 ~ "Ordinary",
                                2 ~ "Extraordinary"),
         Gender = case_match(Gender,
                             1 ~ "Male",
                             2 ~ "Female"))

# gather the data to convert to long format
zhang_data_long <- zhang_data %>%
  pivot_longer(cols = time1_interest:time2_interest,
               names_to = "Time",
               values_to = "Interest")
```

Below, we have several variations of a code chunk error or misspecification. Copy and paste them into your R Markdown file below the code chunk to load tidyverse and the data files. Once you have copied the activities, click knit and look at the error message you receive. See if you can fix the error and get it working before checking the answer.

Question 6. Copy the following code chunk into your R Markdown file and press knit. This code… works, but it does not look quite right? Why are the tick marks not displaying properly?

````
```{r}
zhang_data %>%
  ggplot(aes(x = time1_interest, y = time2_interest)) +
  geom_point() +
  theme_classic() +
  scale_x_discrete(name = "Time 1 interest score (1-7)",
````
````

```
                     breaks = c(1:7)) + # tick marks from 1 to 7
  scale_y_discrete(name = "Time 2 interest score (1-7)",
                     breaks = c(1:7)) + # tick marks from 1 to 7
  geom_smooth(method = "lm")
```

Explain the solution

In this example, we used the wrong function for continuous variables. We used `scale_x_discrete` and `scale_y_discrete`, instead of `scale_x_continuous` and `scale_y_continuous`. We must honour the variable type when we customise the plot, so think about what type of variable is on each axis and which function lets you edit it.

```
zhang_data %>%
  ggplot(aes(x = time1_interest, y = time2_interest)) +
  geom_point() +
  theme_classic() +
  scale_x_continuous(name = "Time 1 interest score (1-7)",
                     breaks = c(1:7)) + # tick marks from 1 to 7
  scale_y_continuous(name = "Time 2 interest score (1-7)",
                     breaks = c(1:7)) + # tick marks from 1 to 7
  geom_smooth(method = "lm")
```

Question 7. Copy the following code chunk into your R Markdown file and press knit. You should receive an error like `Error in "fortify()":! "data" must be a <data.frame>, or an object coercible by "fortify()"` which is a little cryptic.

```
```{r}
zhang_data_long +
  ggplot(aes(y = Interest, x = Condition, fill = Condition)) +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  scale_fill_viridis_d(option = "E",
                       alpha = 0.6) +
  guides(fill = FALSE)
```
```

Explain the solution

Once we start using a mixture of tidyverse functions, it is important to remember which uses a pipe `%>%` between layers, and which uses `+`. Here, we tried using the `+` between the data object and the initial `ggplot()` layer. We need a pipe here or it thinks you are trying to set the data argument using `aes()`.

```
zhang_data_long %>%
  ggplot(aes(y = Interest, x = Condition, fill = Condition)) +
  geom_boxplot() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  scale_fill_viridis_d(option = "E",
                       alpha = 0.6) +
  guides(fill = FALSE)
```

Question 8. Copy the following code chunk into your R Markdown file and press knit. We want to change the order of the categories to present males then female. This code…works, but is it doing what we think it is doing?

````
```{r}
zhang_data_long %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender)) +
  geom_violin() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  scale_x_discrete(labels = c("Male", "Female"))
```
````

Explain the solution

We have introduced this error several times, but we see it so often it is worth reinforcing. When we change the labels, this is really just to tidy things up. The underlying data does not change, we are just trying to communicate it clearer. If we want to change the order of categories, we must change the underlying order of the data as a factor or R will default to alphabetical/numerical. So, we mutate Gender as a factorm, then pipe to ggplot2.

```r
zhang_data_long %>%
  mutate(Gender = factor(Gender,
                         levels = (c("Male", "Female")))) %>%
  drop_na(Gender) %>%
  ggplot(aes(y = Interest, x = Gender)) +
  geom_violin() +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7))
```

7.6 Words from this Chapter

Below you will find a list of words that were used in this chapter that might be new to you in case it helps to have somewhere to refer back to what they mean. The links in this table take you to the entry for the words in the PsyTeachR Glossary. Note that the Glossary is written by numerous members of the team and as such may use slightly different terminology from that shown in the chapter.

term	definition
boxplot	Visualising a continuous variable by five summary statistics: the median centre line, the first and third quartile, and 1.5 times the first and third quartiles.
scatterplot	Plotting two variables on the x- and y-axis to show the correlation/relationship between the variables.
violin-boxplots	A combination of a violin plot to show the density of data points and a boxplot to show summary statistics of distribution.

7.7 End of chapter

Well done, you have completed the second chapter dedicated to data visualisation! This is a key area for psychology research and helping to communicate your findings to your audience. Data visualisation also comes with a lot of responsibility. There are lots of design choices to make and help communicate your findings as effectively and transparently as possible. We could dedicate a whole book to data visualisation possibilities in R and ggplot2, so we have added a range of further reading sources in the Additional Resources appendix.

In the next chapter, we start on inferential statistics introducing you to the concept of regression by focusing on one continuous predictor variable.

8 Regression with one continuous predictor

So far in this book, we have been building your data wrangling and visualisation skills and you now have the basis for a lot of the work you will do in research. Most of the work in data analysis is invested in getting your data into an appropriate form for analysis. Once you get there, the functions for inferential statistics are pretty short, but the challenge now comes to expressing your design as a statistical model and interpreting the output.

In this chapter, we focus on simple linear regression for testing research questions and hypotheses for the relationship between two continuous predictors. We will also explore the concepts of correlation and checking the statistical assumptions of your regression model.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Visualise the relationship between two continuous variables using a scatterplot.
- Apply and interpret a Pearson's and Spearman's correlation.
- Apply and interpret linear regression with one continuous predictor variable.
- Check the assumptions of linear regression through diagnostic plots.

8.1 Chapter preparation

8.1.1 Introduction to the data set

For this chapter, we are using open data from Dawtry et al. (2015). The abstract of their article is:

> The present studies provide evidence that social-sampling processes lead wealthier people to oppose redistribution policies. In samples of American Internet users, wealthier participants reported higher levels of wealth in their social circles (Studies 1a and 1b). This was associated, in turn, with estimates of higher mean wealth in the wider U.S. population, greater perceived fairness of the economic status quo, and opposition to redistribution policies. Furthermore, results from a large-scale, nationally representative New Zealand survey revealed that low levels of neighborhood-level socioeconomic deprivation?an objective index of wealth within

> participants' social circles mediated the relation between income and satisfaction with the economic status quo (Study 2). These findings held controlling for relevant variables, including political orientation and perceived self-interest. Social-structural inequalities appear to combine with social-sampling processes to shape the different political attitudes of wealthier and poorer people.

In summary, the authors investigated why people with more money tend to oppose wealth redistribution policies like higher taxes for higher incomes to decrease inequality in society. We are using data from Study 1A where 305 people completed measures on household income, predicted population income, their predicted social circle income, in addition to measures on support for wealth redistribution and fairness and satisfaction with the current system.

They predicted people with higher incomes have social circles with higher incomes, so they are more satisfied with the current system of wealth redistribution and less interested in changing it. In essence, poorer people and richer people have different experiences of how rich and equal their country is. In this chapter, we will explore the relationship between a range of these variables.

8.1.2 Organising your files and project for the chapter

Before we can get started, you need to organise your files and project for the chapter, so your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, create a new folder called `Chapter_08_regression_continuous`. Within `Chapter_08_regression_conti` create two new folders called `data` and `figures`.
2. Create an R Project for `Chapter_08_regression_continuous` as an existing directory for your chapter folder. This should now be your working directory.
3. Create a new R Markdown document and give it a sensible title describing the chapter, such as `08 Correlations and Regression`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Chapter_08_regression_continuous` folder.
4. We are working with a new data set, so please save the following data file: Dawtry_2015.csv. Right click the link and select "save link as", or clicking the link will save the files to your Downloads. Make sure that you save the file as ".csv". Save or copy the file to your `data/` folder within `Chapter_08_regression_continuous`.

You are now ready to start working on the chapter!

8.1.3 Activity 1 - Read and wrangle the data

As the first activity, try and test yourself by completing the following task list to practice your data wrangling skills. Create a final object called `dawtry_clean` to be consistent with the tasks below. If you want to focus on correlations and regression, then you can just type the code in the solution.

Try this

To wrangle the data, complete the following tasks:

1. Load the following packages (three of these are new, so revisit Chapter 1 if you need a refresher of installing R packages, but remember not to install packages on the university computers / online server):
    - tidyverse
    - effectsize
    - correlation
    - performance
2. Read the data file `data/Dawtry_2015.csv` to the object name `dawtry_data`.
3. Reverse code two items: `redist2` and `redist4` to create two new variables `redist2_R` and `redist4_R`. See the codebook below, but they are on a 1-6 scale.
4. Summarise the data to calculate the mean `fairness_satisfaction` score, by taking the mean of two items: `fairness` and `satisfaction`.
5. Summarise the data to calculate the mean `redistribution` score, by taking the mean of four items: `redist1`, `redist2_R`, `redist3`, and `redist4_R`.
6. Create a new object called `dawtry_clean` by joining `dawtry_data` with your two new variables `fairness_satisfaction` and `redistribution`.
7. Decrease the number of columns in `dawtry_clean` by selecting `PS`, all the columns between `Household_Income` and `redistribution`, but removing the two reverse coded items `redist2_R` and `redist4_R`.

Your data should look like this to be ready to analyse:

```
Rows: 305
Columns: 11
$ PS                                <dbl> 233, 157, 275, 111, 52, 11, 76, 90~
$ Household_Income                  <dbl> NA, 20.00, 100.00, 150.00, 500.00,~
```

```
$ Political_Preference                <dbl> 5, 5, 5, 8, 5, 3, 4, 3, 2, 3, NA, ~
$ age                                 <dbl> 40, 59, 41, 59, 35, 34, 36, 39, 40~
$ gender                              <dbl> 2, 2, 2, 2, 1, 2, 2, 2, 2, 1, NA, ~
$ Population_Inequality_Gini_Index    <dbl> 38.78294, 37.21451, 20.75000, 35.3~
$ Population_Mean_Income              <dbl> 29715, 123630, 60000, 59355, 15360~
$ Social_Circle_Inequality_Gini_Index <dbl> 28.056738, 24.323388, 14.442577, 2~
$ Social_Circle_Mean_Income           <dbl> 21150, 65355, 107100, 86640, 56850~
$ fairness_satisfaction               <dbl> 1.0, 3.5, 5.0, 7.0, 4.5, 2.5, 3.0,~
$ redistribution                      <dbl> 5.50, 3.25, 3.75, 2.75, 3.00, 3.75~
```

Show me the solution

You should have the following in a code chunk:

```r
# Load the packages below
library(tidyverse)
library(effectsize)
library(correlation)
library(performance)

# Load the data file
# This should be the Dawtry_2015.csv file
dawtry_data <- read_csv("data/Dawtry_2015.csv")

# Reverse code redist2 and redist4
dawtry_data <- dawtry_data %>%
  mutate(redist2_R = 7 - redist2,
         redist4_R = 7 - redist4)

# calculate mean fairness and satisfaction score
fairness_satisfaction <- dawtry_data %>%
  pivot_longer(cols = fairness:satisfaction,
               names_to = "Items",
               values_to = "Response") %>%
  group_by(PS) %>%
  summarise(fairness_satisfaction = mean(Response)) %>%
  ungroup()

# calculate mean wealth redistribution score
redistribution <- dawtry_data %>%
  pivot_longer(cols = c(redist1, redist2_R, redist3, redist4_R),
               names_to = "Items",
               values_to = "Response") %>%
  group_by(PS) %>%
  summarise(redistribution = mean(Response)) %>%
  ungroup()

# join data and select columns for focus
dawtry_clean <- dawtry_data %>%
  inner_join(fairness_satisfaction, by = "PS") %>%
  inner_join(redistribution, by = "PS") %>%
  select(PS, Household_Income:redistribution, -redist2_R, -redist4_R)
```

8.1.4 Activity 2 - Explore the data

> Try this
>
> After the wrangling steps, try and explore `dawtry_clean` to see what variables you are working with. For example, opening the data object as a tab to scroll around, explore with `glimpse()`, or try plotting some of the individual variables using a histogram.

In `dawtry_clean`, we have the following variables:

Variable	Type	Description
PS	double	Participant ID number.
Household_Income	double	Household income in US Dollars ($).
Political_Preference	double	Political attitudes: 1 = very liberal/very left-wing/strong Democrat to 7 = very conservative/very right-wing/strong Republican.
age	double	Age in years.
gender	double	1 = "Male", 2 = "Female.
Population_Inequality_Gini_Index	double	Measure of income inequality from 0 (perfect equality) to 100 (perfect inequality), here where participants estimated population in equality.
Population_Mean_Income	double	Participant estimate of the mean household income in the population ($).
Social_Circle_Inequality_Gini_Index	double	Measure of income inequality from 0 (perfect equality) to 100 (perfect inequality), here where participants estimated inequality in their social circle.
Social_Circle_Mean_Income	double	Participant estimate of the mean household income in their social circle ($).
fairness_satisfaction	double	Perceived fairness and satisfaction about the current system of wealth redistribution: Mean of two items (1 extremely fair – 9 extremely unfair)

Variable	Type	Description
redistribution	double	Support for wealth distribution: Mean of four items (1 strongly disagree – 6 strongly agree).

We will use this data set to demonstrate correlations and regression when you have one continuous predictor.

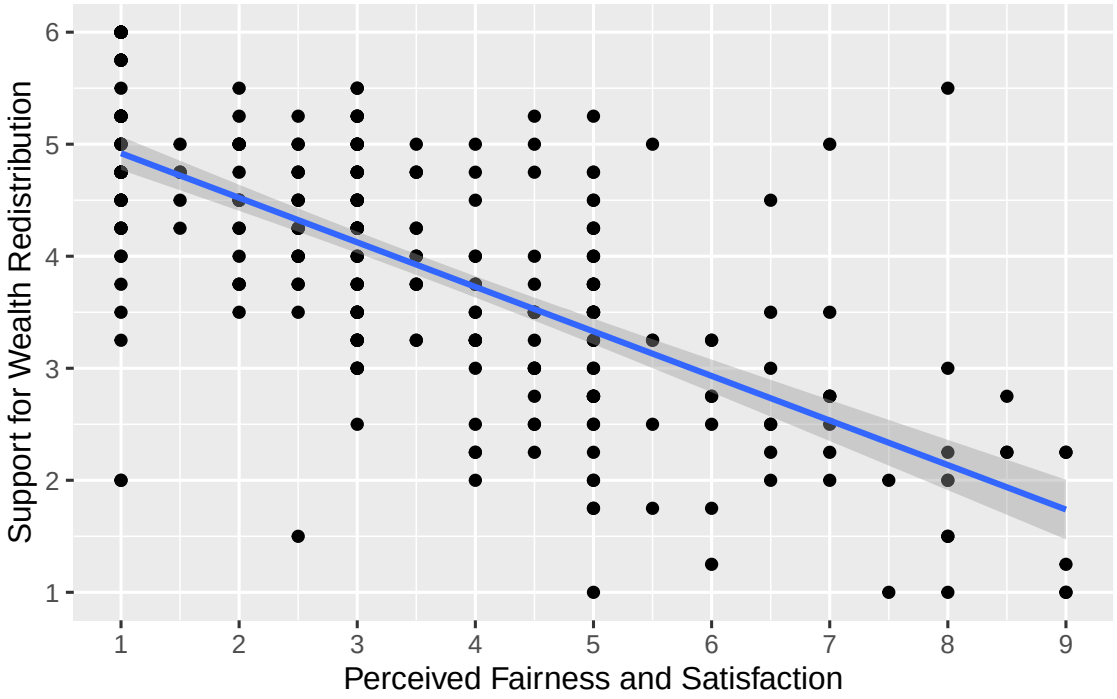
8.2 Correlation

Before we cover regression as a more flexible framework for inferential statistics, we think it is useful to start with correlation to get a feel for how we can capture the relationship between two variables. As a reminder from the course materials, correlations are standardised to range from -1 (a perfect negative correlation) to 1 (a perfect positive correlation). A value of 0 would mean there is no correlation between your variables.

8.2.1 Activity 3 - Visualise the relationship

To explore the relationship between two variables, it is useful to create a scatterplot early for yourself, then provide a more professional looking version to help communicate your results. For most of the demonstrations in this chapter, we will try and answer the research question: "Is there a relationship between support for wealth redistribution and fairness and satisfaction with the current system?"

> Try this
>
> Using your data visualisation skills from Chapter 7, recreate the scatterplot below using the variables `fairness_satisfaction` and `redistribution` from `dawtry_clean`.



Looking at the graph, we can describe the relationship as

- (A) positive
- (B) little to no correlation
- (C) negative

.

Show me the solution

The scatterplot shows a negative correlation between the two variables. You need to be careful interpreting fairness and satisfaction as it is coded a little counterintuitive. Higher values mean great *dissatisfaction*.
As support for wealth redistribution increases to be more positive, perceived fairness and satisfaction tends to decrease. This makes sense as people who are more dissatisfied with the current system think there should be more wealth redistribution strategies.
You should have the following in a code chunk:

```
dawtry_clean %>%
  ggplot(aes(x = fairness_satisfaction, y = redistribution)) +
  geom_point() +
  geom_smooth(method = "lm") +
  scale_x_continuous(name = "Perceived Fairness and Satisfaction",
                     breaks = c(1:9)) +
  scale_y_continuous(name = "Support for Wealth Redistribution",
                     breaks = c(1:6))
```

8.2.2 Activity 4 - Calculate the correlation coefficient

Visualising the relationship between two variables is great for our understanding, but it does not tell us anything about the inferential statistics for what we can learn from our sample in hypothesis testing and measures of effect size.

A correlation is a specific application of the general linear model. We want to capture the covariation between two variables. If you are interested, see the Handy Workbook (McAleer, 2023) for the calculations behind different types of correlation and how it represents the covariance of two variables compared to their total variability. They are not the only methods, but the two most common versions of a correlation are:

- Pearson's product-moment correlation (often shortened to the Pearson correlation) and symbolised by **r**.
- Spearman's rank correlation coefficient (often shortened to the Spearman correlation) and symbolised by r_s or sometimes the Greek letter **rho** ρ.

There is a function built into R (`cor.test()`) to calculate the correlation between two variables, but we tend to use the `correlation()` function from the correlation package as it has more consistent reporting features. The `correlation()` function requires:

- The name of the data set you are using.
- The name of the first variable you want to select for the correlation.
- The name of the second variable you want to select for the correlation.
- The type of correlation you want to run: e.g. `pearson`, `spearman`.

For our `dawtry_clean` data, we would run the following code for a two-tailed Pearson correlation:

```r
correlation(data = dawtry_clean,
            select = "fairness_satisfaction",
            select2 = "redistribution",
            method = "pearson",
            alternative = "two.sided")
```

```
Parameter1            |     Parameter2 |     r |         95% CI | t(303) |      p
-------------------------------------------------------------------------------
fairness_satisfaction | redistribution | -0.70 | [-0.75, -0.64] | -17.08 | < .001

Observations: 305
```

Your output will look a little different due to how our book renders tables, but you should get the same information. For the three key concepts of inferential statistics, we get

- **Hypothesis testing**: $p < .001$, suggesting we can reject the null hypothesis assuming $\alpha = .05$.
- **Effect size**: r = -.70, suggesting a strong negative correlation.
- **Confidence interval**: [-0.75, -0.64], showing the precision around the effect size estimate.

To summarise: a Pearson correlation showed there was a strong, negative, statistically significant relationship between attitudes on wealth redistribution and perceived fairness and satisfaction, r (303) = -0.70, $p < .001$, 95% CI = [-0.75, -0.64].

If we had reason to use a Spearman correlation instead, all we need to do is change the `method` argument.

```r
correlation(data = dawtry_clean,
            select = "fairness_satisfaction",
            select2 = "redistribution",
            method = "spearman",
            alternative = "two.sided")
```

```
Parameter1            |     Parameter2 |   rho |         95% CI |        S |      p
-----------------------------------------------------------------------------------
fairness_satisfaction | redistribution | -0.68 | [-0.74, -0.61] | 7.95e+06 | < .001

Observations: 305
```

Similarly, we could report the results as: a Spearman correlation showed there was a strong, negative, statistically significant relationship between attitudes on wealth redistribution and perceived fairness and satisfaction, r_s (303) = -0.68, $p < .001$, 95% CI = [-0.74, -0.61].

Try this

Great work following along so far, but now it is time to test your understanding on a new set of variables. Use the variables `age` and `redistribution` from `dawtry_clean`. We can ask the question: "What is the relationship between age and attitudes on wealth redistribution?"

1. Create a scatterplot to visualise the relationship between `age` and `redistribution` from `dawtry_clean`.
2. Apply the Pearson correlation to get your inferential statistics and answer the following questions:
    - **Hypothesis testing**: Assuming $\alpha = .05$, the relationship between age and wealth redistribution is

- (A) statistically significant
- (B) not statistically significant

.

```
- **Effect size**: Rounded to 2 decimals, the value for Pearson's correlation coefficient i
```

- (A) -0.14
- (B) -0.03
- (C) 0.08
- (D) -0.49

.

```
- **Confidence interval**: Rounded to 2 decimals, the lower bound is
```

- (A) -0.14
- (B) -0.03

- (C) 0.08
- (D) -0.49

and the upper bound is

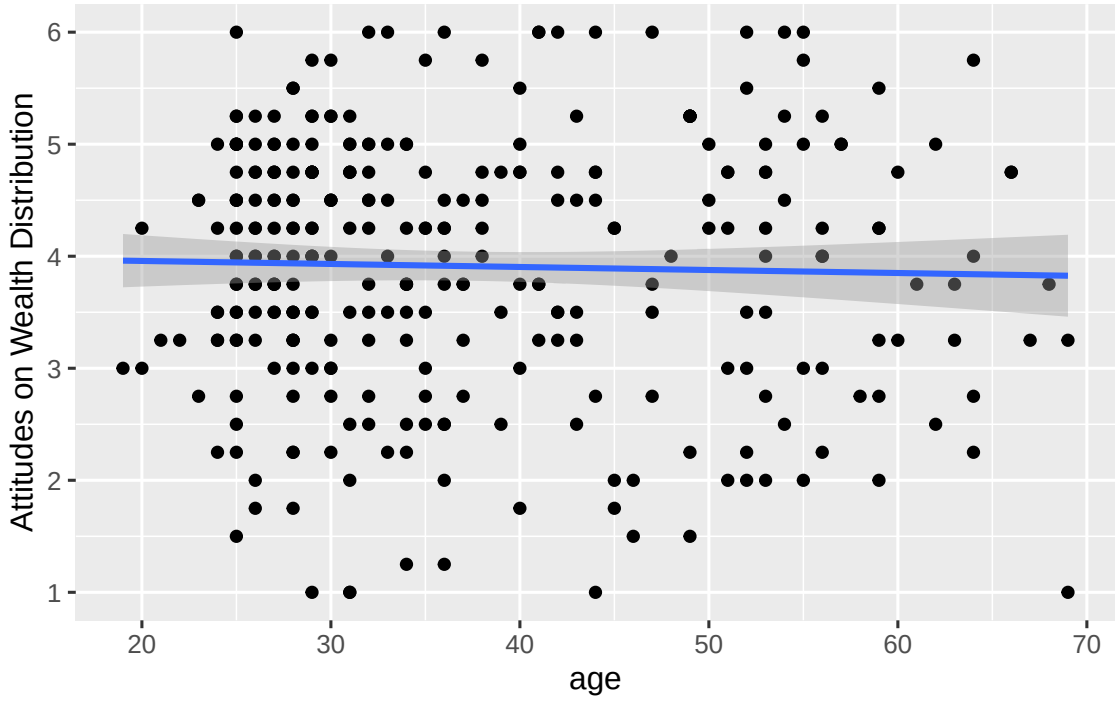
- (A) -0.14
- (B) -0.03
- (C) 0.08
- (D) -0.49

.

Show me the solution

The scatterplot shows very little correlation between the two variables. The regression line is almost flat and there does not appear to be a clear pattern to the data points.

```
dawtry_clean %>%
  ggplot(aes(x = age, y = redistribution)) +
  geom_point() +
  geom_smooth(method = "lm") +
  scale_y_continuous(name = "Attitudes on Wealth Distribution",
                     breaks = c(1:6))
```



For our inferential statistics, the relationship is not statistically significant and the Pearson correlation coefficient is very weak, r (302) = -0.03, p = .625, 95% CI = [-0.14, 0.08]. Note there is a missing value for age, so we have one few participant / degrees of freedom.

```
correlation(data = dawtry_clean,
            select = "age",
            select2 = "redistribution",
            method = "pearson",
            alternative = "two.sided")
```

```
# Correlation Matrix (pearson-method)

Parameter1 |     Parameter2 |     r |        95% CI | t(302) |     p
-------------------------------------------------------------------
age        | redistribution | -0.03 | [-0.14, 0.08] |  -0.49 | 0.625

p-value adjustment method: Holm (1979)
Observations: 304
```

8.2.3 Reporting your correlation reproducibly

When you write reports, you can take the numbers from your output and type them out but it is easy to make typos or forget to update your numbers. By writing reproducible reports in R, you can avoid this by adding a little code to format the numbers into APA format.

For correlations, the first step is saving your `correlation()` function as an object.

```
fairness_redist_object <- correlation(data = dawtry_clean,
                                      select = "fairness_satisfaction",
                                      select2 = "redistribution",
                                      method = "pearson",
                                      alternative = "two.sided")
```

If you look in the Environment, the correlation package helpfully saves the output as a data frame which makes it easy to work with. For the following code, this is a function we have created, so we do not expect you to understand everything at this point. You just need to copy and paste it into your .Rmd file before you want to reference the correlation. Click show the correlation formatting function as we initially hide it to avoid taking up lots of space.

```
report_correlation <- function(correlation_object){
  # This function will only work for correlation package objects
  # Step 1 = save all the numbers with formatting
  r_type <- ifelse(correlation_object$Method == "Pearson correlation",
                   "*r* ", # if true, report as Pearson correlation
                   "*r_s* ") # if false, report as Spearman correlation
  # save degrees of freedom
  df <- correlation_object$df_error
  # save r rounded to 3 decimals with any trailing zeros
  r <- sprintf("%.3f", round(correlation_object$r, 3))
  # save p value with formatting if less than .001
  pval <- correlation_object$p
  if (pval >= 0.001){
    pval <- str_sub(as.character(pval), 2, 5)
    pval <-  paste0(", *p* = ", pval)
  # If p < .001, manually format as p < .001
  } else if (pval < 0.001){
    pval <- ", *p* < .001"
  }
  # save lower 95% CI
  lower_CI <- round(correlation_object$CI_low, 3)
  # save lower 95% CI
  upper_CI <- round(correlation_object$CI_high, 3)
```

```
  # Switch CIs depending on sign
  r_CI <- ifelse(r > 0,
                 paste0(lower_CI, ", ", upper_CI),
                 paste0(upper_CI, ", ", lower_CI))

  # Step 2 = add them together in APA format
  output <- paste0(r_type,
                   "(", df,") = ",
                   r,
                   pval,
                   ", 95% CI = [", r_CI, "]")

  return(output)
}
```

Once you have saved the object and added the formatting function, you can use the function to format your correlation:

```
report_correlation(fairness_redist_object)
```

```
[1] "*r* (303) = -0.700, *p* < .001, 95% CI = [-0.638, -0.753]"
```

You can add that as inline code to insert into your report to make your inferential statistics reproducible. Just note it's difficult to apply all the APA format details, so you might need to remove leading zeros, add italics to the math symbols etc.

8.3 Linear regression with one continuous predictor

Now you know how to calculate a correlation in R, we can turn to simple linear regression as a more flexible tool for modelling the relationship between variables.

In Research Methods 1, we focus on just two variables, before scaling up to more complicated models in Research Methods 2. In this chapter, we focus the relationship between a continuous outcome and one continuous predictor, before extending the framework to one categorical predictor in Chapter 9. There is also a chapter in the Handy Workbook (McAleer, 2023) dedicated to manually calculating simple linear regression.

8.3.1 Activity 5- Calculating descriptive statistics

For all the information we want to include in a report, calculating descriptive statistics is helpful for the reader to show the context behind the results you present. Here, we can report the mean and standard deviation of our two variables.

```
dawtry_clean %>%
  # pivot longer to avoid repeating yourself
  pivot_longer(cols = fairness_satisfaction:redistribution,
               names_to = "Variable",
               values_to = "Value") %>%
  # group by Variable to get one value per variable
  group_by(Variable) %>%
  # mean and SD, rounded to 2 decimals
  summarise(mean_variable = round(mean(Value), 2),
            sd_variable = round(sd(Value), 2))
```

```
# A tibble: 2 x 3
  Variable              mean_variable sd_variable
  <chr>                         <dbl>       <dbl>
1 fairness_satisfaction          3.54        2.02
2 redistribution                 3.91        1.15
```

> **Note**
>
> If you want some reinforcement of how these skills apply to published research, look at Table 1 in Dawtry et al. (2015). The means and standard deviations here (and the correlation in Activity 4) exactly reproduce the values they report.

If other types of descriptive statistic would be more suitable to your data, then you can just replace the functions you use within `summarise()`.

8.3.2 Activity 6 - Using the `lm()` function

For our research question of "is there a relationship between support for wealth redistribution and fairness and satisfaction", we can address it with simple linear regression.

Instead of a standardised correlation coefficient, we can frame it as whether knowing fairness and satisfaction can predict values of support for wealth redistribution. The design is still correlational, so it does not tell us anything about a causal relationship in isolation. We use the word predict in the statistical sense, where we can ask whether knowing values of one variable help us predict values of another variable with a degree of error.

The first step is to create an object (`lm_redistribution`) for the linear model.

```
lm_redistribution <- lm(redistribution ~ fairness_satisfaction,
                        data = dawtry_clean)
```

The function `lm()` is built into R and is incredibly flexible for creating linear regression models.

- The first argument is to specify a formula which defines our model. The first component (`redistribution`) is our outcome variable for what we are interested in modelling.
- The tilde (`~`) separates the equation, where everything on the right is your predictor variable(s). In simple linear regression, we just have one predictor, which is `fairness_satisfaction` in our model here. This is saying we want to predict `redistribution` as our outcome from `fairness_satisfaction` as our predictor.
- We then specify the data frame we want to use.

> **Note**
>
> In some resources, you might see people enter the same model as `redistribution ~ 1 + fairness_satisfaction`. The `1 +` component explicitly tells R to fit an intercept, plus a slope from `fairness_satisfaction`. R includes an intercept by default, so you do not need to add it, but some people like to include it for clarity.

When you create this object, it stores a bunch of information, but does not really tell us all the statistics we expect. If you simply print the object in the console, it will tell you the intercept and coefficient(s), but none of the model fitting nor hypothesis testing values. If you look at the object in the R environment, you will see it is a list containing several elements. It stores things like the model, the residuals, and other information you can use.

```
lm_redistribution
```

```

Call:
lm(formula = redistribution ~ fairness_satisfaction, data = dawtry_clean)

Coefficients:
          (Intercept)  fairness_satisfaction
               5.3169                -0.3975
```

To get that extra information, we need to call the `summary()` function around the linear model object to explore it's properties like estimates and model fit.

```r
summary(lm_redistribution)
```

```
Call:
lm(formula = redistribution ~ fairness_satisfaction, data = dawtry_clean)

Residuals:
    Min      1Q  Median      3Q     Max
-2.9193 -0.5279  0.0233  0.4782  3.3634

Coefficients:
                      Estimate Std. Error t value Pr(>|t|)
(Intercept)            5.31686    0.09488   56.04   <2e-16 ***
fairness_satisfaction -0.39754    0.02328  -17.08   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8218 on 303 degrees of freedom
Multiple R-squared:  0.4905,    Adjusted R-squared:  0.4888
F-statistic: 291.7 on 1 and 303 DF,  p-value: < 2.2e-16
```

To walk through the output, `Call:` summarises the model you specified. `Residuals:` provides a summary of the model residuals which we will come back to later. `Coefficients:` provides our model output, this time with inferential statistics. The two key lines are:

1. `(Intercept)` - This is the value of the outcome when our predictor is set to 0. For a fairness and satisfaction value of 0, we would expect a value of 5.32 for redistribution. You get a p-value for this, but in isolation it is not too useful. It just compares the intercept estimate to 0 which typically you are not interested in.

- `fairness_satisfaction` - This is the regression slope or coefficient. This is the change in the outcome for every 1 unit change in the predictor. So, for every 1 unit increase in fairness and satisfaction, we expect support for wealth redistribution to decrease (as we have a negative value) by 0.40 units. This is consistent with the correlation as we have a negative relationship between the two variables. Looking at the p-value, this is statistically significant ($p < .001$), suggesting we can reject the null hypothesis and conclude there is an effect here.

> **i** Does it matter if the slope is positive or negative?
>
> When you have a continuous predictor, the sign is important to keep in mind. A positive slope would mean an increase in the predictor is associated with increased values of your

outcome. A negative slope would mean an increase in the predictor is associated with decreased values of your outcome. This is crucial for interpreting the coefficient.

At the bottom of the model output, you then get the fit statistics. Multiple R^2 tells you how much variance in your outcome your predictor(s) explain. Adjusted R^2 tends to be more conservative as it adjusts for the number of predictors in the model (something we will not cover until Chapter 14), but they will be very similar when you have one predictor. Adjusted R^2 is .49, suggesting fairness and satisfaction explains 49% of the variance in support for wealth redistribution.

Finally, we have the model fit statistics to tell us whether the model explains a significant amount of variance in the outcome. With one predictor, the p-value next to the coefficient and next to the model fit will be identical, as one predictor is the whole model. The F-statistic is 291.7, the model degrees of freedom is 1, the residual degrees of freedom is 303, and the p-value is $p < .001$.

! What does 2e-16 mean?

For the p-value here, the output looks a little weird. R reports very small or very large numbers using scientific notation to save space. We normally report p-values to three decimals, so we report anything smaller as $p < .001$ to say it is smaller than this.
If you want to see the real number, you can use the following function which shows just how small the p-value is:

```
format(2e-16, scientific = FALSE)
```

```
[1] "0.0000000000000002"
```

i How are correlation and regression the same?

If you are interested in the relationship between the two concepts, we said correlation was a specific application of the general linear model. It describes the - standardised - covariation between two variables compared to their total variability. For values of -1 and 1, knowing the value of one variable perfectly correlates to the value of your other variable. As you approach 0, the relationship between the variables is less perfect, meaning there is more variability left over compared to the covariance.
In regression, we frame it as how much variance you explain compared to the total amount of variance. The more variance your predictor explains, the less unexplained variance there is left over. We no longer calculate r, we calculate R^2 as the proportion of variance in your outcome explained by your model. A value of 0 would be you explain no variance and a value of 1 means you explain all the variance.
You can see the connection between the two by comparing the value of Pearson's r

from Activity 4 (-.70) to the value of R^2 = .4905. If you take the square root to get r (`sqrt(.4905)`), you get .70, which is exactly the same absolute value since R^2 can only be positive.
So, when you have a single continuous predictor, it is the exact same process as correlation, just expressed slightly different.

8.3.3 Activity 7 - Calculating confidence intervals

In the standard `lm()` and `summary()` output, we get most of the key values we need for our inferential statistics, but the one thing missing is confidence intervals around our estimates. Fortunately, R has a built-in function called `confint()` for calculating confidence intervals using your linear model object.

```
confint(lm_redistribution)
```

```
                            2.5 %     97.5 %
(Intercept)             5.1301581  5.5035664
fairness_satisfaction -0.4433442 -0.3517332
```

Normally, you focus on the confidence interval around your slope estimate as the intercept is not usually super useful for interpreting your findings when you have a continuous predictor. Now, we can summarise the three key concepts of inferential statistics as:

- **Hypothesis testing**: $p < .001$, suggesting we can reject the null hypothesis assuming $\alpha = .05$. Fairness and satisfaction is a significant predictor of support for wealth redistribution.
- **Effect size**: b_1 = -0.40, suggesting fairness and satisfaction is a negative predictor.
- **Confidence interval**: [-0.44, -0.35], showing the precision around the slope estimate.

Try this

Great work following along so far, but now it is time to test your understanding on a new set of variables. This time, use `redistribution` as your outcome, `age` as your predictor, and use `dawtry_clean` as your data. We can ask the same question as before: "What is the relationship between age and attitudes on wealth redistribution?".
Apply simple linear regression to get your inferential statistics and answer the following questions:

- **Hypothesis testing**: Assuming $\alpha = .05$, age is a

- (A) statistically significant
- (B) non-significant

predictor of support for wealth redistribution.

- **Effect size**: Rounded to 2 decimals, the age coefficient is
- (A) 4.01
- (B) -0.003
- (C) 0.005
- (D) 0.22

.

- **Confidence interval**: Rounded to 2 decimals, the lower bound of the age coefficient is
- (A) 3.59
- (B) -0.01
- (C) 4.44
- (D) 0.01

and the upper bound is

- (A) 3.59
- (B) -0.01
- (C) 4.44
- (D) 0.01

.

Show me the solution

The conclusions are the same as when we calculated the correlation where age is not a statistically significant predictor of support for wealth redistribution. As a regression model, we get the same conclusions expressed in a slightly different way. Age is negative, but the size of the slope is very small (-0.003) and non-significant ($p = .625$). We explain pretty much no variance in support for wealth redistribution ($R^2 = .0008$), so age is not very informative as a predictor.

```
# Create lm object for age as a predictor
lm_age <- lm(redistribution ~ age,
             data = dawtry_clean)

# summary of the model object
summary(lm_age)

# confidence intervals around estimates
confint(lm_age)
```

```
Call:
lm(formula = redistribution ~ age, data = dawtry_clean)

Residuals:
     Min       1Q   Median       3Q      Max
-2.93382 -0.69527  0.08099  0.84379  2.13621

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  4.011931   0.216042   18.57   <2e-16 ***
age         -0.002693   0.005499   -0.49    0.625
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.153 on 302 degrees of freedom
  (1 observation deleted due to missingness)
Multiple R-squared:  0.0007938, Adjusted R-squared:  -0.002515
F-statistic: 0.2399 on 1 and 302 DF,  p-value: 0.6246

                 2.5 %     97.5 %
(Intercept)  3.58679351 4.43706821
age         -0.01351424 0.00812738
```

8.3.4 Activity 8 - Centering and standardising predictors

So far, we have covered specifying your outcome and predictor variables as their raw values in the data. However, there are two variations that are useful to understand: centering and standardising predictors. These do not change the model fitting or p-values, but change how you interpret the intercept and/or slope.

8.3.4.1 Centering predictors

Centering predictors is where you change the values of your predictor, but not their scale. Typically, this means substracting the mean of your predictor from each observation. This changes how you interpret the intercept of your regression model.

Remember the interpretation of the intercept is the predicted value of your outcome when your predictor is set to 0. If 0 is not present in your data or a value of 0 would be uninformative, the intercept can be difficult to interpret. When you center your predictor, 0 becomes the mean value of your predictor. So, the intercept is now the predicted value of your outcome for the mean value of your predictor, but the slope itself does not change. You can see the impact of this by plotting the data side by side in Figure 8.1.

```
dawtry_clean <- dawtry_clean %>%
  # subtract fairness values from mean of fairness
  mutate(fairness_center = fairness_satisfaction - mean(fairness_satisfaction))
```

The relationship between the two variables is exactly the same, but the values of fairness and satisfaction shifted so the mean is 0. If you create a new linear model object, you can see the difference this makes to the output.

```
lm_center <- lm(redistribution ~ fairness_center,
                data = dawtry_clean)

summary(lm_center)
```

```
Call:
lm(formula = redistribution ~ fairness_center, data = dawtry_clean)

Residuals:
    Min      1Q  Median      3Q     Max
-2.9193 -0.5279  0.0233  0.4782  3.3634
```

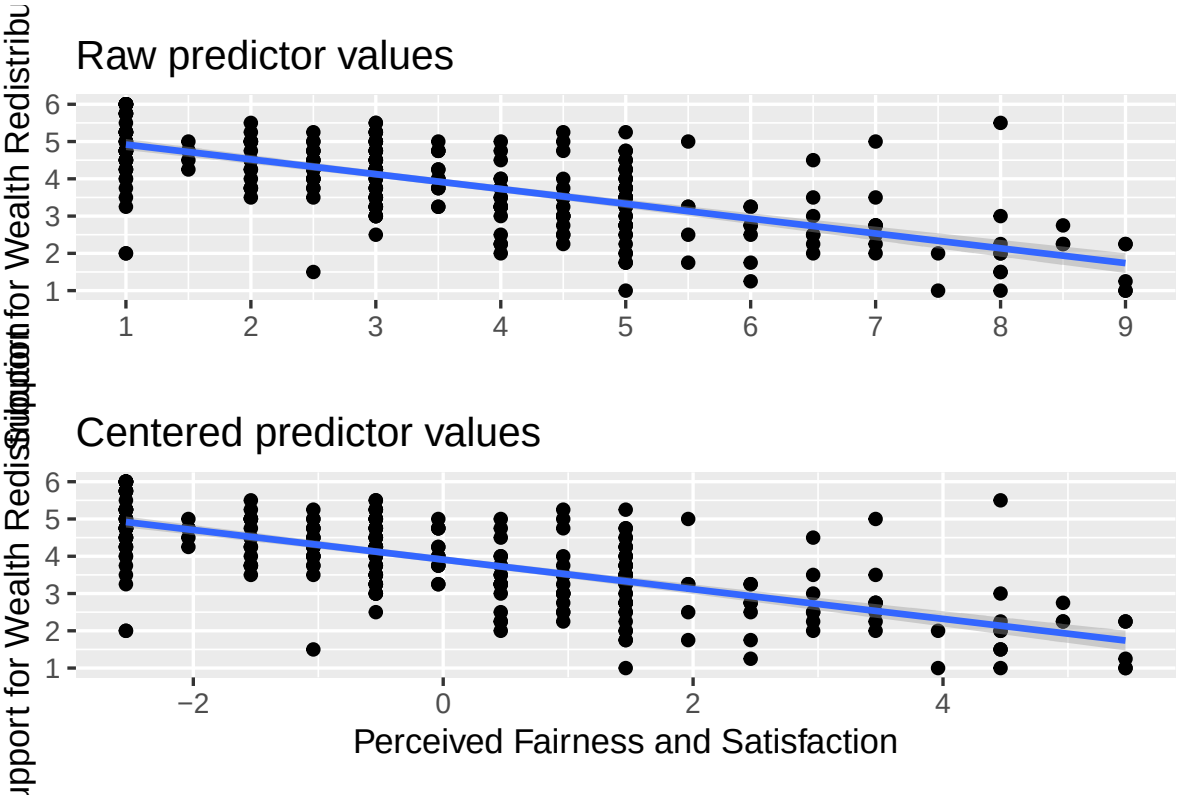


Figure 8.1: Top: The relationship between wealth redistribution and perceived fairness and satisfaction using raw values. Bottom: The relationship after centering perceived fairness and satisfaction values.

```
Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)      3.90984    0.04706   83.09   <2e-16 ***
fairness_center -0.39754    0.02328  -17.08   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8218 on 303 degrees of freedom
Multiple R-squared:  0.4905,    Adjusted R-squared:  0.4888
F-statistic: 291.7 on 1 and 303 DF,  p-value: < 2.2e-16
```

Every single one of the values remains the same apart from the intercept. Now, we can interpret it as the predicted value of redistribution when fairness and satisfaction is set to 0, i.e., the mean value. So, for the mean value of fairness and satisfaction, we would predict a value of 3.91 for redistribution.

8.3.4.2 Standardising predictors

Standardising predictors is where you first convert your values to z-scores. This means you interpret the values as standard deviations rather than your original units. This is more useful in multiple regression (Chapter 14) to compare the magnitude of predictors, but it is useful to get used to now when you only have one predictor to focus on.

The first step is to standardise **all** your variables, not just the predictor this time. This involves subtracting the mean of your variable from each value, and dividing by the standard deviation of the variable. They now have a mean of 0 and a standard deviation of 1.

```
# Be careful with the bracket placement to subtract the mean first
dawtry_clean <- dawtry_clean %>%
  mutate(redistribution_std = (redistribution - mean(redistribution)) / sd(redistribution),
         fairness_std = (fairness_satisfaction - mean(fairness_satisfaction)) / sd(fairness_s
```

Once we enter them into the model, we no longer have values in the original units of measurement, we now have them expressed as standard deviations.

```
lm_standardised <- lm(redistribution_std ~ fairness_std,
                      data = dawtry_clean)

summary(lm_standardised)
```

```
Call:
lm(formula = redistribution_std ~ fairness_std, data = dawtry_clean)

Residuals:
     Min       1Q   Median       3Q      Max
-2.53979 -0.45930  0.02026  0.41604  2.92617

Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)   7.387e-16  4.094e-02    0.00        1
fairness_std -7.003e-01  4.101e-02  -17.08   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.715 on 303 degrees of freedom
Multiple R-squared:  0.4905,    Adjusted R-squared:  0.4888
F-statistic: 291.7 on 1 and 303 DF,  p-value: < 2.2e-16
```

Like centering, the model fit and p-values do not change again, apart from the intercept. The relationship between the variables is exactly the same, but we changed their units. The intercept is tiny and close enough to zero that the p-value is 1.

More importantly, the slope is now expressed in standard deviations. Annoyingly, R prints the values in scientific notation, so this can be awkward to read (remember the `format()` function). Now, for every 1 standard deviation increase in our predictor, we predict the outcome to decrease by 0.70 standard deviations.

> **Tip**
>
> It is important to demonstrate the underlying concepts first but if you want a shortcut without needing to standardise all your variables, the effectsize package has a handy function called `standardize_parameters()` which you can apply to your initial `lm()` object.

```
standardize_parameters(lm_redistribution)

# Standardization method: refit

Parameter             | Std. Coef. |         95% CI
-------------------------------------------------
(Intercept)           |   7.39e-16 | [-0.08,  0.08]
fairness satisfaction |      -0.70 | [-0.78, -0.62]
```

8.4 Checking assumptions

For the inferential statistics to work as intended, the model makes certain assumptions about the data you are putting into it and the accuracy of the inferences depends on how sensible these assumption are. Remember these functions will always work even if the numbers you enter are nonsense, so it's important for you as the researcher to recognise when it's appropriate to use these techniques and when it is not.

8.4.1 Activity 9 - Diagnostic plots for linear regression

As a reminder, the assumptions for simple linear regression are:

1. The outcome is interval/ratio level data.
2. The predictor variable is interval/ratio or categorical (with two levels at a time).
3. All values of the outcome variable are independent (i.e., each score should come from a different participant/observation).
4. The predictors have non-zero variance.
5. The relationship between the outcome and predictor is linear.
6. The residuals should be normally distributed.
7. There should be homoscedasticity.

Assumptions 1-4 are pretty straight forward as they relate to your understanding of the design or a simple check on the data for non-zero variance (the responses are not all the exact same value).

Assumptions 5-7 require diagnostic checks on the residuals from the model. The residuals are the difference between your observed values in the data and the values your model predicts given it's assumptions. If you remember back, we highlighted the model output mentioned `Residuals:` and they are saved within the model object.

```
# head shows the first 6 values
head(lm_redistribution$residuals)
```

```
         1          2          3          4          5          6
 0.5806764 -0.6754769  0.4208311  0.2159084 -0.5279383 -0.5730156
```

What does the $ symbol mean?

We have not used this symbol in the book yet, but it is a base R operator for extracting information. You use it to access specific components within a data frame or object. Try the following in the console to see what it does:

- `dawtry_clean$age`
- `lm_redistribution$coefficients`

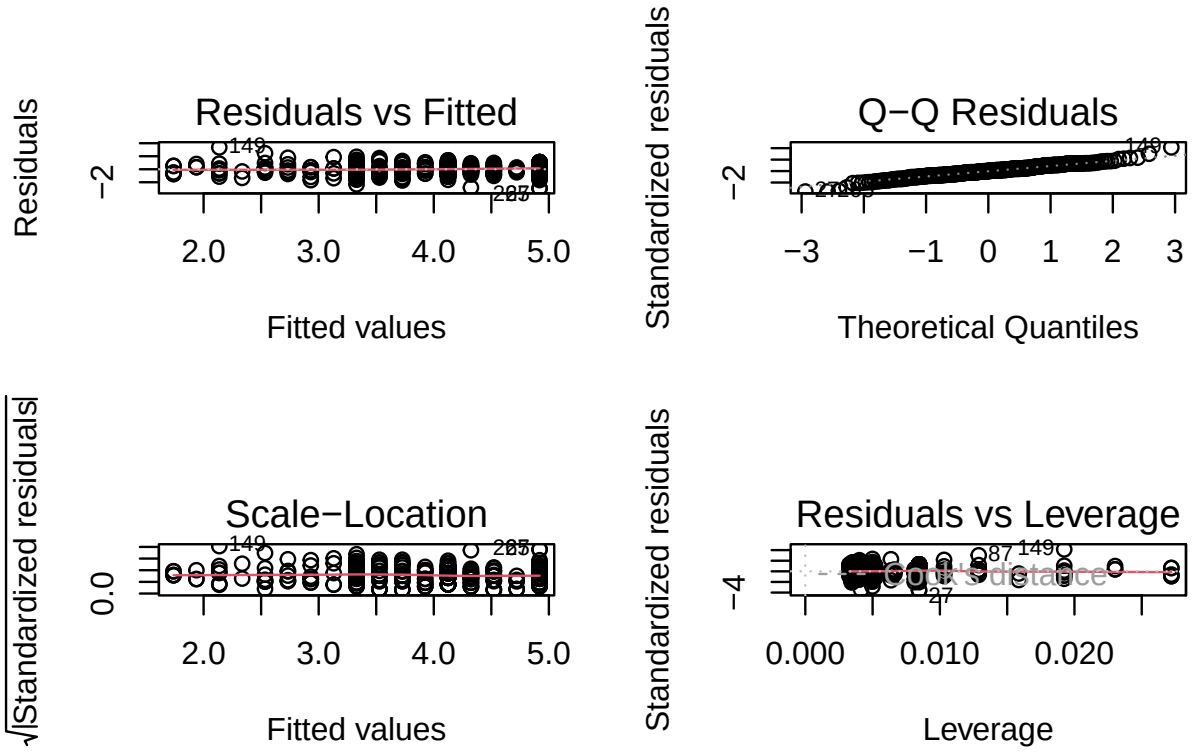
If you type an object name into the console and add the `$`, you will see all the components appear to auto complete.

In your reading, you might see individual statistical tests to check these assumptions, but they have more limitations than benefits. The best way to check the assumptions is through diagnostic plots which express the model residuals in different ways. We want to walk through this longer way of checking assumptions to develop a solid understanding before showing you a shortcut to see them all below.

In the code below, we use a format you will be less familiar with as all these functions come from base R. If you just run the code for the diagnostic plots `plot(lm_redistribution)`, each one gets individually printed to your Plots window. Here, we create a 2x2 panel to show them all together.

```
# Change the panel layout to 2 x 2
par(mfrow=c(2,2))

# plot the diagnostic plots
plot(lm_redistribution)
```

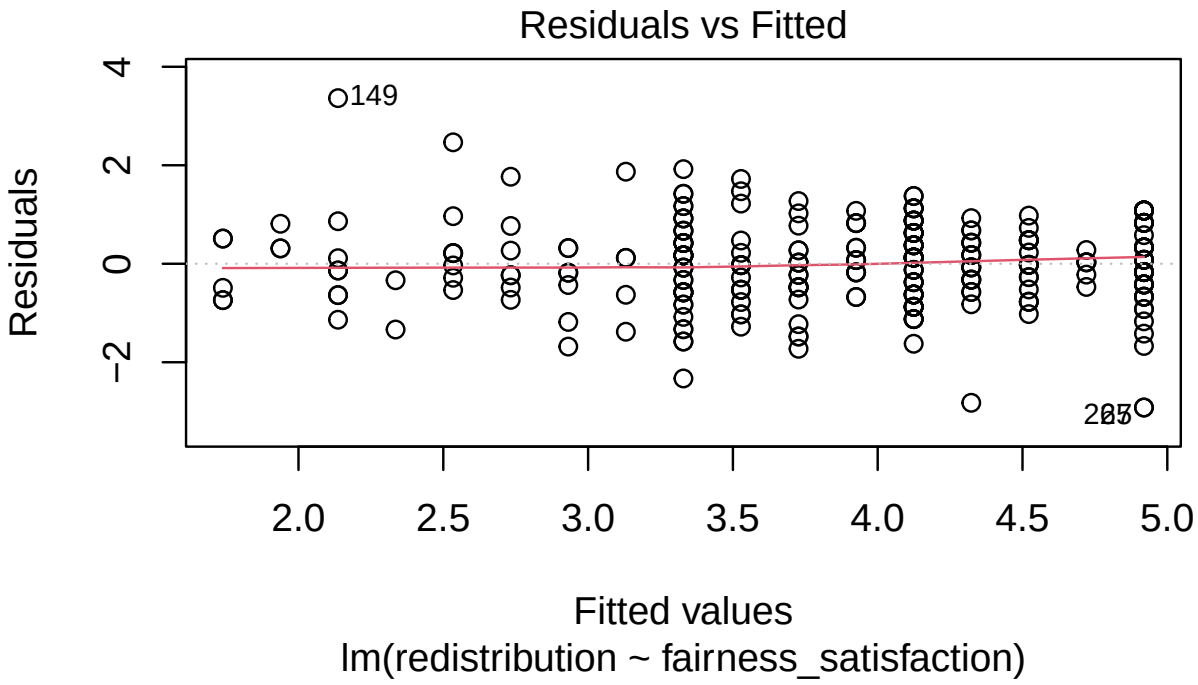


For more information on each of these plots, see this great resource by Kim (2015) via the University of Virginia, but we will break the key ones down below.

8.4.2 Checking linearity

To isolate each plot, we can use the `which` argument. Plot 1 is a residuals vs fitted plot and helps us check linearity by showing the residuals on the y-axis and the fitted (predicted) values on the x-axis.

```
plot(lm_redistribution,
     which = 1)
```



Here, you are looking out for a roughly flat horizontal red line. Common patterns to look out for if there is a problem are when the line has an obvious curve to look like a hump or several bends to look like an S.

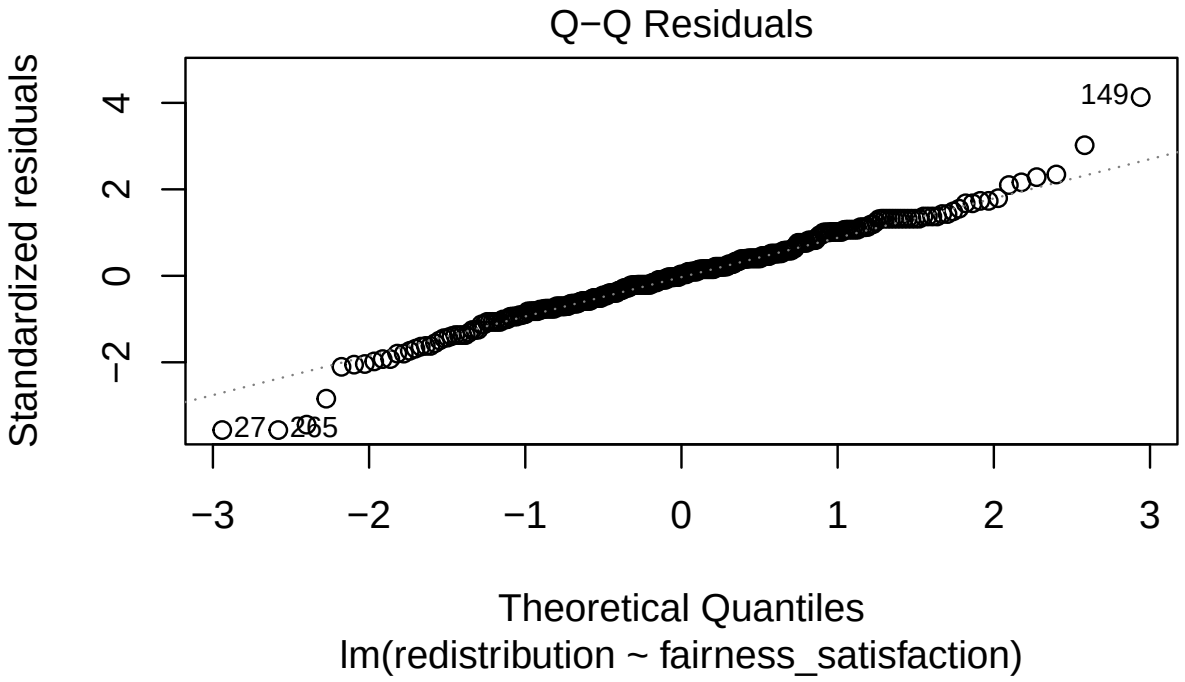
The only downside to using diagnostic plots is it takes experience to recognise when there is nothing wrong with a regression model compared to when it violates the assumptions. It is easy to see a little deviation and think there is some drastically wrong. Our advice is if you squint and it looks fine, it is probably fine. You are looking for clear and obvious deviations from what you expect and all the models we use in Chapters 8 and 9 are intentionally fine to develop foundational skills. In Chapter 11, we then introduce you to more problematic cases and what your options are.

> ! Error mode
>
> If you want to save these plots to add into a report, you might try using `ggsave()` like we have covered in the data visualisation chapters. However, it will not work as these plots have not been created by ggplot2.
> To save these plots, you can either right click and choose save as to save on your computer. Alternatively, if they open in the Plots window, you can click on Export and save them as an image or PDF to insert into your documents.

8.4.3 Checking normality

Plot 2 is a qq-plot (quantile-quantile plot) and helps us check the normality of the model residuals by showing the standardised residuals on the y-axis and the theoretical quantiles on the x-axis. A common misconception is your variables should all be normally distributed, but it is actually the model residuals which should be normal.

```
plot(lm_redistribution,
     which = 2)
```



In this plot, you are looking for the data points to roughly follow the dashed line. The idea is there should be a linear relationship between the residuals and the values we would expect under a normal distribution.

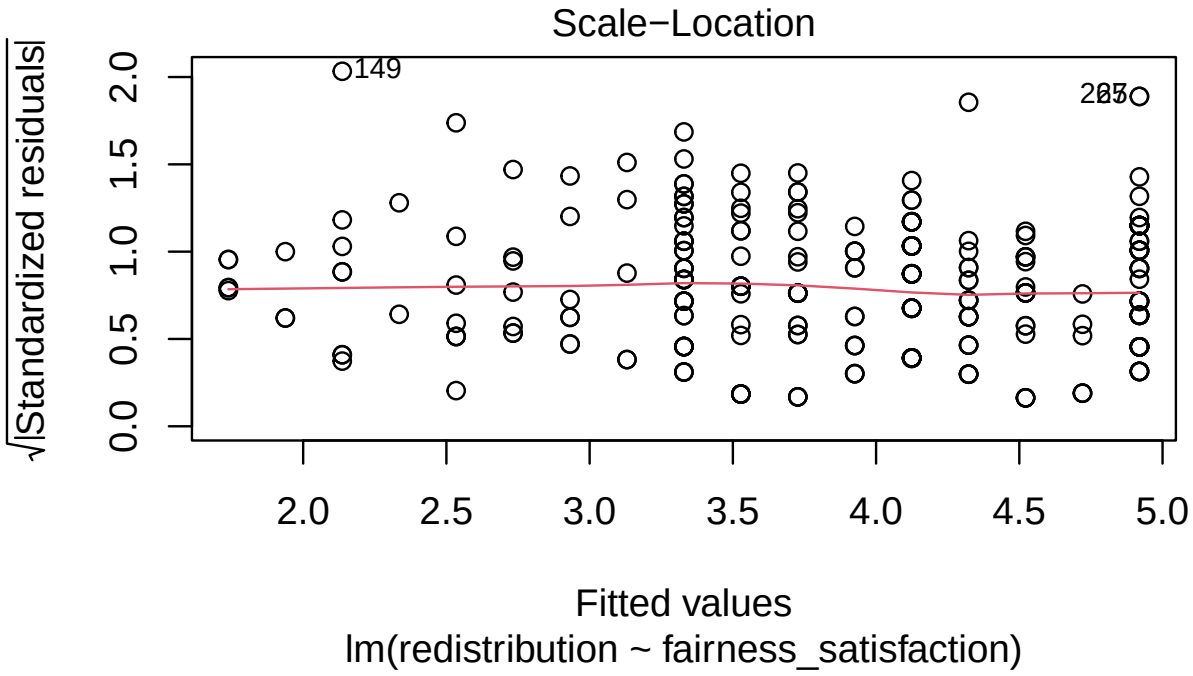
Like the other diagnostic plots, it is tempting to think there are problems where there are none. The vast majority of the points here follow the line nicely, but tail off a little at the extremes. It flags the points with the largest deviations but there do not appear to be any obvious problems.

When there are problems with normality, you are looking for obvious deviations, like the points curving around in a banana shape, or snaking around like an S.

8.4.4 Checking homoscedasticity

Plot 3 is a scale-location plot and helps us check homoscedasticity by showing the square root of the standardised residuals on the y-axis and the fitted values on the x-axis. Homoscedasticity is where the variance of the residuals is approximately equal across the range of your predictor(s).

```
plot(lm_redistribution,
     which = 3)
```



In this plot, you are looking out for a roughly random spread of points as you move from one end of the x-axis to the other. The red line should be roughly flat and horizontal.

When there is *heteroscedasticity*, the characteristic patterns to look out for are a kind of arrow shape where there is a wide spread of points at one end and decreases to a denser range at the other end, or a bow tie where there is a wide spread of points at each end and dense in the middle.

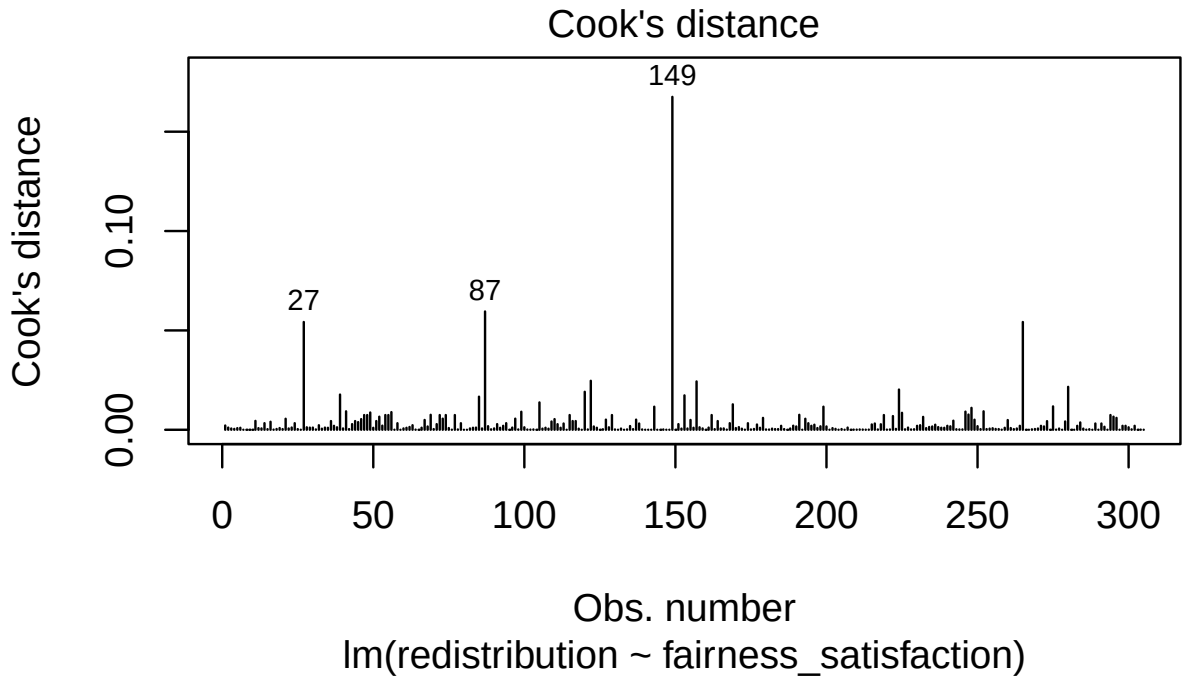
8.4.5 Checking influential cases

Finally, there are two main plots to help us identify influential cases. You might have heard of the term outlier before and this is one way of classifying data points that are different

enough to the rest of the data in a regression model. It is not strictly an assumption of linear regression, but it can affect the other assumptions. Identifying outliers is a complex decision and we will explore your options in the course materials and Chapter 11 on data screening.

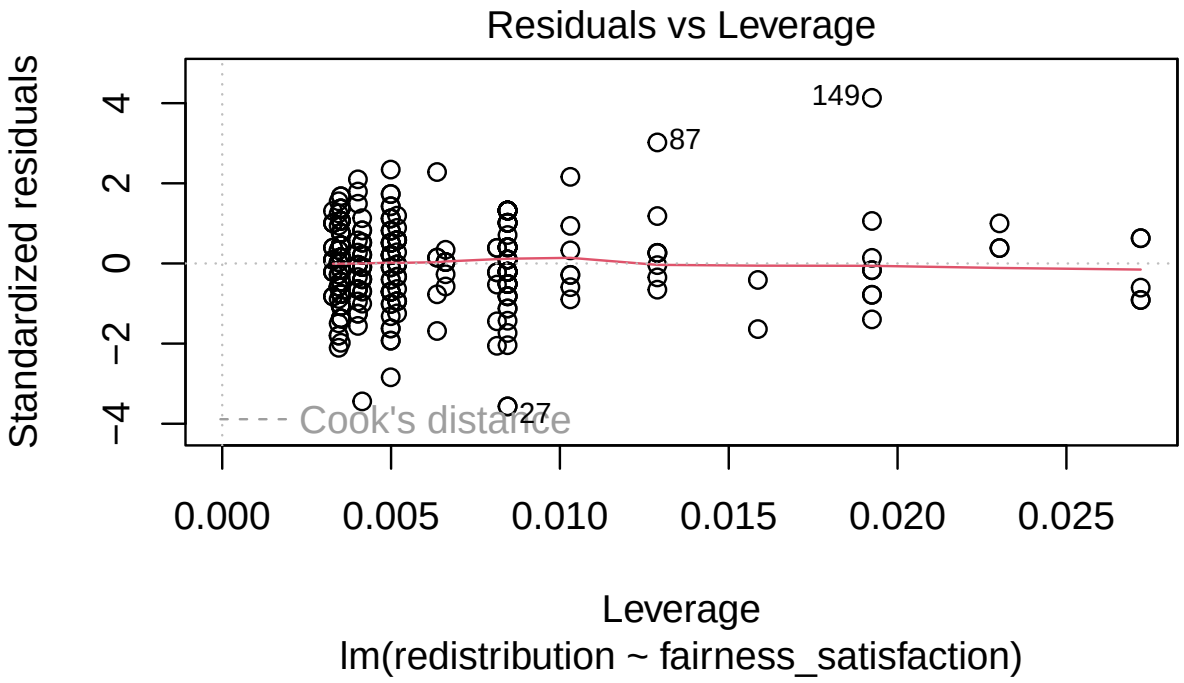
If you only run `plot(lm_redistribution)` and cycle through the plots, you do not see this version. This plot shows values of Cook's distance for each observation in your data along the x-axis. Cook's distance measures the influence of deleting a given observation, where higher values mean deleting that observation results in a larger change to the model estimates. There are different thresholds in the literature, but estimates range from 1, 0.5, to 4/n. We explore the decision making around this and your options in Chapter 11.

```
plot(lm_redistribution,
     which = 4)
```



Finally, we get a residuals vs leverage plot to show influential cases in a slightly different way. Instead of just the Cook's distance value of each observation, it plots the standardised residuals against leverage values.

```
plot(lm_redistribution,
     which = 5)
```

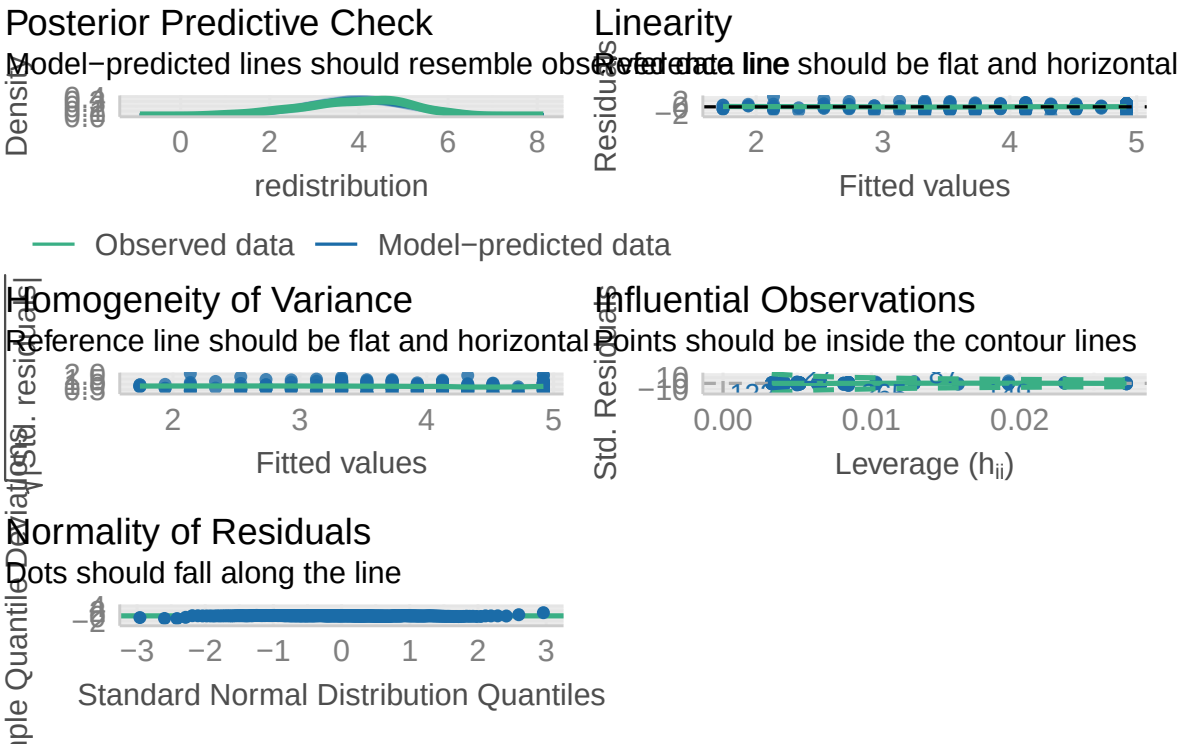


Influential points and potential outliers would have high leverage values and the plot will show a threshold of Cook's distance as red dashed lines. In this plot, they are not visible as there is no value with a big enough leverage value, but you would be looking for data points outside this threshold to identify influential values.

8.4.6 Checking all the assumptions

Now we have covered the individual diagnostic plots, there is a handy function called `check_model()` from the performance package. This function reports all the diagnostic checks from `plot()`, but tidies up the presentation and has some useful reminders of what you are looking for.

```
check_model(lm_redistribution)
```



The key difference is you get a posterior predictive check (essentially comparing values you observe compared to what your model predicts) and the qq-plot for normality of residuals looks a little different. Instead of a kind of angled line, the residuals are expressed as deviations instead, so the points should be close to a flat horizontal line. This version can make smaller deviations look worse, so keep in mind again you are looking for clear deviations in the overall pattern.

> **Note**
>
> The performance version of the diagnostic plots are actually created using ggplot2, so the function `ggsave()` would work here if you need to save the plot to add into your report.

> **Try this**
>
> In activity 7, you should have calculated the relationship between age and support for redistribution for your independent task. Using the model object `lm_age`, work through assumptions for simple linear regression and make a note of whether you think it meets the assumptions, or there might be any problems. Some of the assumptions you consider what you know about the design, while others you need the diagnostic plots.
>
> 1. The outcome is interval/ratio level data.

2. The predictor variable is interval/ratio or categorical (with two levels at a time).
3. All values of the outcome variable are independent (i.e., each score should come from a different participant/observation).
4. The predictors have non-zero variance.
5. The relationship between the outcome and predictor is linear.
6. The residuals should be normally distributed.
7. There should be homoscedasticity.

Show me the solution

1. The outcome is interval/ratio level data.

There is a debate here we cover in the course materials, but there is an argument you can treat the average of multiple Likert items as interval, but you need to be careful.

2. The predictor variable is interval/ratio or categorical (with two levels at a time).

Our predictor age is nicely ratio.

3. All values of the outcome variable are independent (i.e., each score should come from a different participant/observation).

You need to know this from the design / data collection, but it appears to be the case in this study.

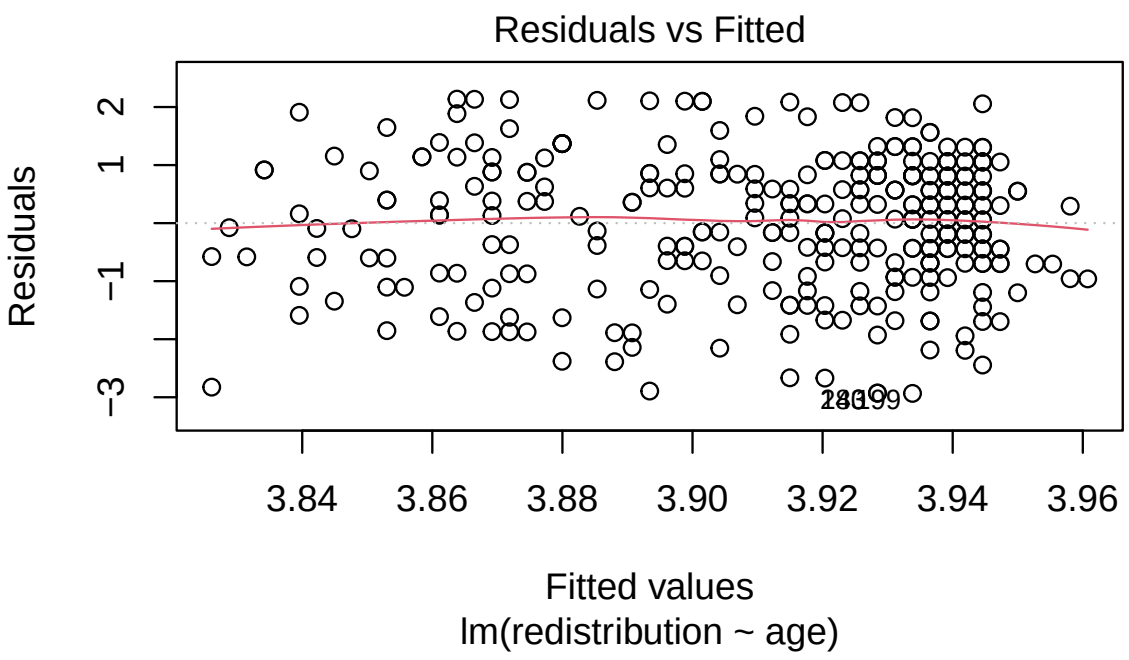
4. The predictors have non-zero variance.

There are a range of ages in the data.

5. The relationship between the outcome and predictor is linear.

Looking at the first plot, the red line is pretty flat and horizontal, so we are happy with this.

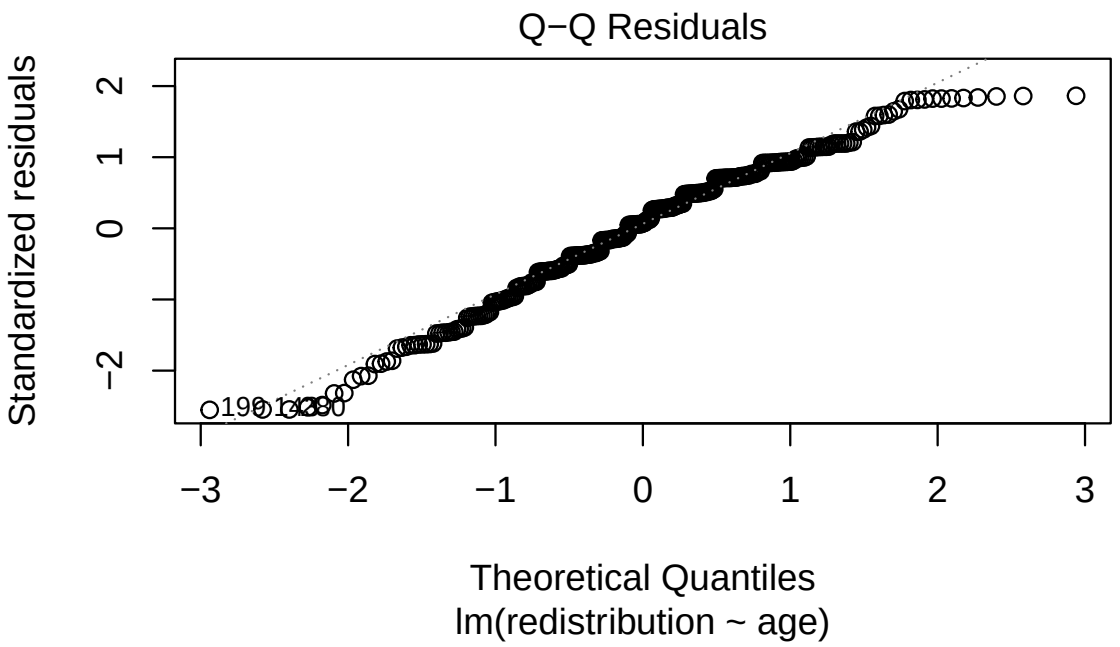
```
plot(lm_age, which = 1)
```



6. The residuals should be normally distributed.

The qq-plot is fine for the vast majority of the range. We just have a few deviations in the extreme ends of the x-axis, but this is a byproduct of using a scale score as our outcome as responses cannot go beyond 1-6.

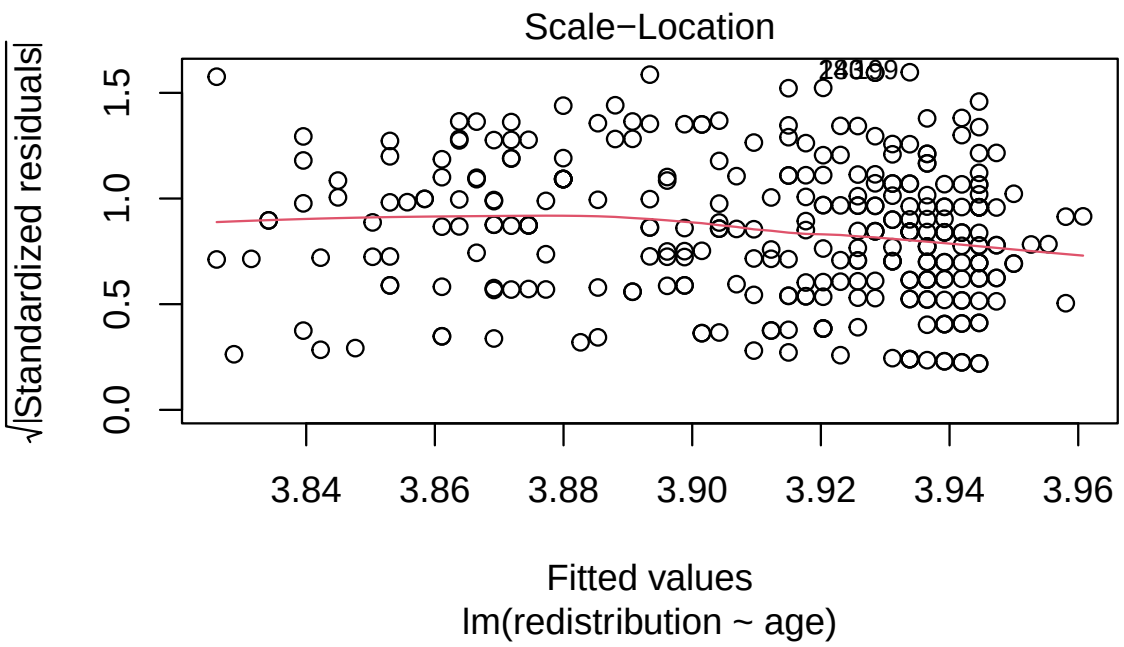
```
plot(lm_age, which = 2)
```



7. There should be homoscedasticity.

The red line is pretty flat and it looks like there is a fairly even range of values across the x-axis range.

```
plot(lm_age, which = 3)
```



All in all, there do not appear to be any issues with the assumptions here.

8.5 Reporting your results

Now we have some results to go with, there are a few recommendations on how to communicate that information. In psychology (and other disciplines), we tend to follow the American Psychological Association (APA) formatting guidelines as they provide a comprehensive standardised style to make sure information is being reported as easily digestible and consistent as possible. You can see this PDF online for a little cheat sheet for numbers and statistics, but we will outline some key principles to ensure you provide your reader with enough information.

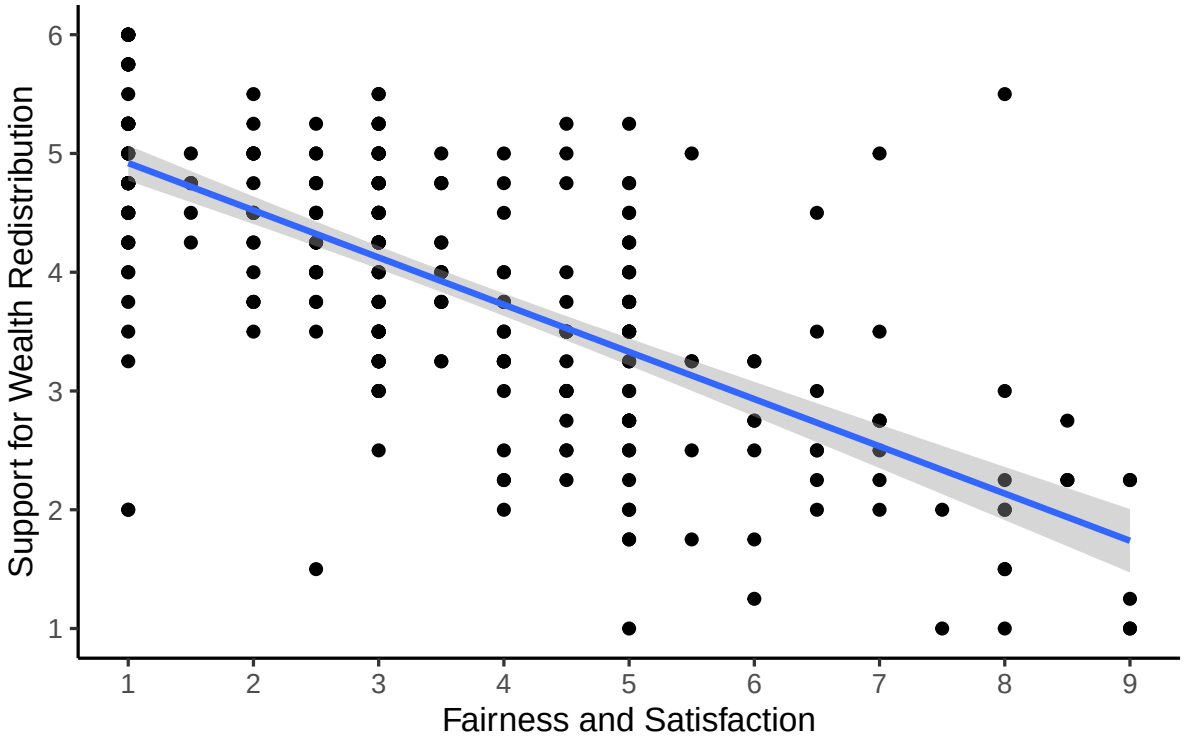
1. Explain to the reader what your linear regression model was. For example, what was your outcome and predictor variable?
2. Report descriptive statistics to help contextualise your findings. For example, the mean/standard deviation for your outcome and continuous predictor.
3. Provide an appropriate data visualisation to help communciate key patterns to the reader. For example, a scatterplot for the relationship between your outcome and predictor.
4. Report all three key inferential statistics concepts for the coefficient: the slope, the confidence interval around your slope, and the p-value for hypothesis testing. When you have one predictor in simple linear regression, you typically focus on the slope as your key

effect size that helps address your research question and hypothesis. APA style rounds numbers to 2 decimal places when numbers can be bigger than 1, and 3 decimals with no leading zero when it cannot be bigger than 1. When you report the unstandardised slope, you use the symbol b_1 but for the standardised slope, you use Beta instead β_1.

5. Provide an overview of the model fit statistics for whether your model explained a significant amount of variance in your outcome. Remember: the p-value for your model will be the same as for the slope in simple linear regression.

For our main example, we could summarise the findings as:

"Our research question was: is there a relationship between support for wealth redistribution and fairness and satisfaction with the current system? To test this, we applied simple linear regression using fairness and satisfaction as a predictor and support for wealth redistribution as our outcome. Figure 1 shows a scatterplot of the relationship.



Our model explained a statistically significant amount of variance in our outcome (adjusted R^2 = .489, F(1, 303) = 291.70, $p < .001$). Fairness and satisfaction was a negative predictor, where for every 1-unit increase we expect support for redistribution to decrease by 0.40 ($b_1 = -0.40$, 95% CI = [-0.44, -0.35], $p < .001$)."

Note: we have not included an APA formatted Figure title here as it is not easy to format in our book, so refer to the course materials for guidance.

8.5.1 Formatting your results reproducibly

After the correlation example, we can also make regression models reproducible to add into your reports. For regression models, the first step is saving your model as an object *before* you apply the `summary()` function. We created this in activity 6, but as a reminder:

```
lm_redistribution <- lm(redistribution ~ fairness_satisfaction,
                        data = dawtry_clean)
```

To make the reporting flexible, we then separate the model into two components: the overall model and the slope. For the overall model, you must save the reporting function first.

```
report_regression_model <- function(regression_object){
  # This function will only work for lm() objects
  # Step 1 = apply the summary function so we have both objects
  model_summary <- summary(regression_object)
  # Step 2 = save all the numbers with formatting
  # Save adjusted R2 with any trailing zeroes
  adj_r2 <- sprintf("%.3f", round(model_summary$adj.r.squared, 3))
  # save model degrees of freedom
  df1 <- model_summary$df[1]
  # save residual degrees of freedom
  df2 <- model_summary$df[2]
  # save F rounded to 2 decimals with any trailing zeroes
  Fval <- sprintf("%.2f", round(model_summary$fstatistic, 2))[1]
  # save p value with formatting if less than .001
  pval <- anova(regression_object)$`Pr(>F)`[1]
  if (pval >= 0.001){
    pval <- str_sub(as.character(pval), 2, 5)
    pval <-  paste0(", *p* = ", pval)
  # If p < .001, manually format as p < .001
  } else if (pval < 0.001){
    pval <- ", *p* < .001"
  }

  # Step 3 = add them together in APA format
  output <- paste0("adjusted $R^2$ = ",
                   adj_r2,
```

```
                    ", ",
                    "F(", df1, ", ", df2, ") = ", Fval,
                    pval)

  return(output)
}
```

Then you can run the function on your regression model.

```
report_regression_model(lm_redistribution)
```

```
[1] "adjusted $R^2$ = 0.489, F(2, 303) = 291.67, *p* < .001"
```

For the slope, there is a separate reporting function.

```
report_regression_slope <- function(regression_object){
  # This function will only work for lm() objects
  # Step 1 = apply the summary function so we have both objects
  model_summary <- summary(regression_object)
  # Step 2 = save all the numbers with formatting
  # $b_1 = -0.40$, 95% CI = [-0.44, -0.35], *p* < .001)
  # Save slope with any trailing zeroes
  b_1 <- sprintf("%.2f", round(model_summary$coefficients[2, 1], 2))
  # save p value with formatting if less than .001
  pval <- model_summary$coefficients[2, 4]
  if (pval >= 0.001){
    pval <- str_sub(as.character(pval), 2, 5)
    pval <-  paste0(", *p* = ", pval)
  # If p < .001, manually format as p < .001
  } else if (pval < 0.001){
    pval <- ", *p* < .001"
  }
  # save lower 95% CI
  lower_CI <- round(confint(regression_object)[2, 1], 2)
  # save lower 95% CI
  upper_CI <- round(confint(regression_object)[2, 2], 2)
  # Switch CIs depending on sign
  b1_CI <- ifelse(b_1 > 0,
                  paste0(lower_CI, ", ", upper_CI),
                  paste0(upper_CI, ", ", lower_CI))
```

```
  # Step 3 = add them together in APA format
  output <- paste0("$b_1$ = ",
                   b_1,
                   ", 95% CI = [", b1_CI, "]",
                   pval)

  return(output)
}
```

Then you can run the function on your regression model.

```
report_regression_slope(lm_redistribution)
```

```
[1] "$b_1$ = -0.40, 95% CI = [-0.35, -0.44], *p* < .001"
```

8.6 Test Yourself

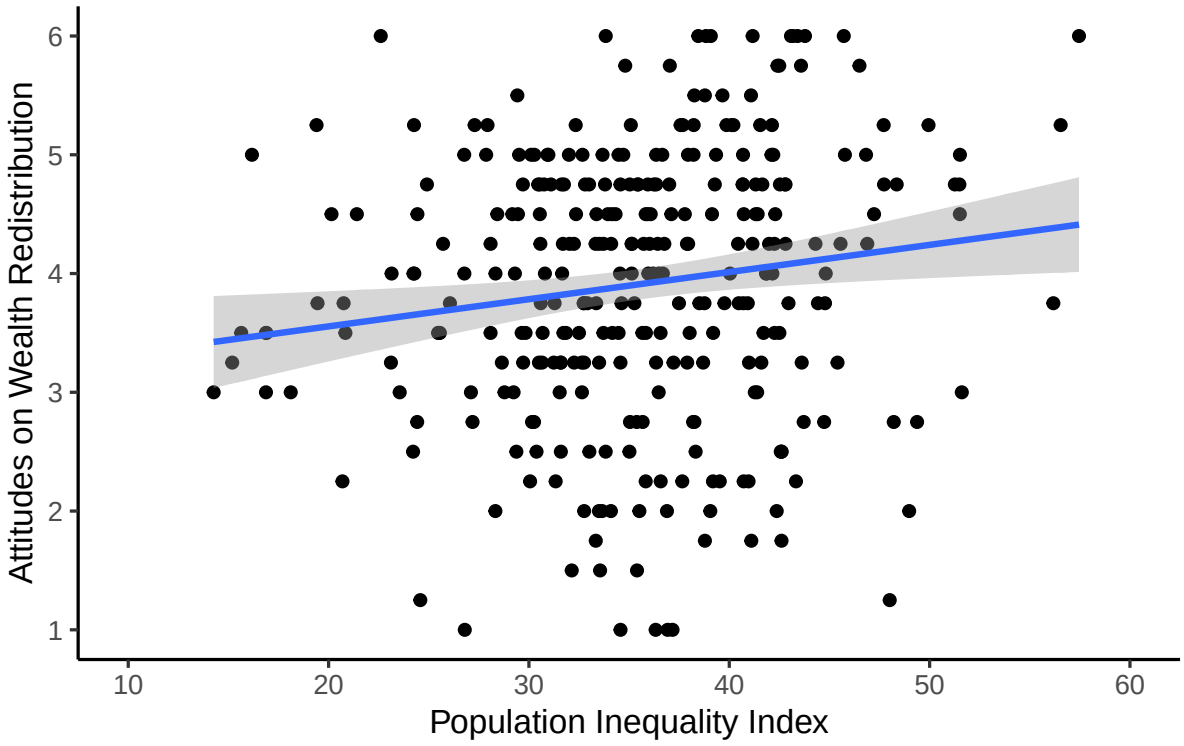
To end the chapter, we have some knowledge check questions to test your understanding of the concepts we covered in the chapter. We then have some error mode tasks to see if you can find the solution to some common errors in the concepts we covered in this chapter.

8.6.1 Knowledge check

For this chapter's knowledge check section, we have something a little different. Instead of purely conceptual questions about functions, we have another example of linear regression from Dawtry et al. (2015). Feel free to create this model yourself, but we will show you some output and ask you questions based on it.

For this model, we focus on the two variables estimated population inequality index (`Population_Inequality_Gini_Index`) and support for wealth redistribution (`redistribution`). Check back to the code book in Activity 2 if you need a reminder of what the variables mean.

Question 1. In the scatterplot of the relationship below, this shows a negative relationship between the inequality index and support for redistribution: TRUE / FALSE.



Question 2 For the next few questions, we have the output from a linear regression model and we would like you to interpret it.

```
Call:
lm(formula = redistribution ~ Population_Inequality_Gini_Index,
    data = dawtry_clean)

Residuals:
    Min      1Q  Median      3Q     Max
-2.9478 -0.6384  0.1389  0.8511  2.3854

Coefficients:
                                Estimate Std. Error t value Pr(>|t|)
(Intercept)                     3.097452   0.316914   9.774  < 2e-16 ***
Population_Inequality_Gini_Index 0.022879   0.008734   2.619  0.00925 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.139 on 303 degrees of freedom
```

```
Multiple R-squared:  0.02214,   Adjusted R-squared:  0.01892
F-statistic: 6.861 on 1 and 303 DF,  p-value: 0.009251
```

The outcome variable in this model is

- (A) Attitudes on Wealth Redistribution
- (B) Population Inequality Index

and the predictor variable is

- (A) Attitudes on Wealth Redistribution
- (B) Population Inequality Index

.

Question 3 Rounded to 2 decimals, when the predictor is 0, we predict a value of _____ for our outcome variable.

Question 4 The predictor is

- (A) significant
- (B) non-significant

with a p-value of _____.

Question 5 The predictor is

- (A) positive
- (B) negative

, where we expect for every 1-unit increase in the predictor a _____ -unit

- (A) increase
- (B) decrease

in the outcome.

8.6.2 Error mode

The following questions are designed to introduce you to making and fixing errors. For this topic, we focus on simple linear regression between two continuous variables. There are not many outright errors that people make here, more misspecifications that are not doing what you think they are doing.

Create and save a new R Markdown file for these activities. Delete the example code, so your file is blank from line 10. Create a new code chunk to load tidyverse and wrangle the data files:

```
# Load the packages below
library(tidyverse)
library(effectsize)
library(correlation)
library(performance)

# Load the data file
# This should be the Dawtry_2015.csv file
dawtry_data <- read_csv("data/Dawtry_2015.csv")

# Reverse code redist2 and redist4
dawtry_data <- dawtry_data %>%
  mutate(redist2_R = 7 - redist2,
         redist4_R = 7 - redist4)

# calculate mean fairness and satisfaction score
fairness_satisfaction <- dawtry_data %>%
  pivot_longer(cols = fairness:satisfaction,
               names_to = "Items",
               values_to = "Response") %>%
  group_by(PS) %>%
  summarise(fairness_satisfaction = mean(Response)) %>%
  ungroup()

# calculate mean wealth redistribution score
redistribution <- dawtry_data %>%
  pivot_longer(cols = c(redist1, redist2_R, redist3, redist4_R),
               names_to = "Items",
               values_to = "Response") %>%
  group_by(PS) %>%
  summarise(redistribution = mean(Response)) %>%
  ungroup()
```

```
# join data and select columns for focus
dawtry_clean <- dawtry_data %>%
  inner_join(fairness_satisfaction, by = "PS") %>%
  inner_join(redistribution, by = "PS") %>%
  select(PS, Household_Income:redistribution, -redist2_R, -redist4_R)
```

Below, we have several variations of a misspecification. Copy and paste them into your R Markdown file below the code chunk to wrangle the data. Once you have copied the activities, click knit and look at the output you receive. See if you can identify the mistake and fix it before checking the answer.

Question 6. Copy the following code chunk into your R Markdown file and press knit. We want to create a simple linear regression model to specify `fairness_satisfaction` as our outcome variable and `Political_Preference` as our predictor. Have we expressed that accurately?

````
```{r}
lm_fairness <- lm(Political_Preference ~ fairness_satisfaction,
                        data = dawtry_clean)

summary(lm_fairness)
```
````

Explain the solution

In this example, we mixed up the variables. The formula in `lm()` has the form `outcome ~ predictor`, so we mixed up the order. In simple linear regression, it makes no difference to the slope, but it is important to be able to express your model accurately and it would make a difference once you scale up to multiple linear regression.

```
lm_fairness <- lm(fairness_satisfaction ~ Political_Preference,
                        data = dawtry_clean)

summary(lm_fairness)
```

Question 7. Copy the following code chunk into your R Markdown file and press knit. We want to standardise the outcome and predictors, so that we get the intercept and slope estimates in standard deviations. Have we expressed that accurately?

````
```{r}
dawtry_clean <- dawtry_clean %>%
```
````

```
  mutate(fairness_std = (fairness_satisfaction - mean(fairness_satisfaction)) / sd(fairness_s

lm_fairness <- lm(fairness_std ~ Political_Preference,
                        data = dawtry_clean)

summary(lm_fairness)
```

Explain the solution

In this example, we only standardised the outcome. When we standardise predictors, we must standardise both the outcome and predictor so they are expressed in standard deviations. It is just when we center, we only center the predictor.

```
dawtry_clean <- dawtry_clean %>%
  mutate(fairness_std = (fairness_satisfaction - mean(fairness_satisfaction)) / sd(fairness
         Political_std = (Political_Preference - mean(Political_Preference, na.rm = TRUE))

lm_fairness <- lm(fairness_std ~ Political_std,
                        data = dawtry_clean)

summary(lm_fairness)
```

8.7 Words from this Chapter

Below you will find a list of words that were used in this chapter that might be new to you in case it helps to have somewhere to refer back to what they mean. The links in this table take you to the entry for the words in the PsyTeachR Glossary. Note that the Glossary is written by numerous members of the team and as such may use slightly different terminology from that shown in the chapter.

term	definition
centered-predictors	Usually, centering a predictor means subtracting the mean from each value, so the mean is 0. You can then interpret the intercept as the value of your outcome for the mean value of your predictor(s).
outcome	The outcome (also known as the dependent variable) is the variable you are interested in seeing a potential change in.
pearson	A standardised measure of the linear relationship between two variables that makes stringent assumptions about the population.

term	definition
predictor	The predictor (also known as an independent variable) is the variable you measure or manipulate to see how it is associated with changes in the outcome variable.
residuals	The difference between the observed value in the data and the predicted value from the model given its assumptions.
spearman	A standardised measure of the relationship between two variables that assumes a monotonic - but not necessarily a linear - relationship and makes less stringent assumptions about the population.
standardised-predictors	Standardising involves substracting the variable mean from each value and dividing it by the variable standard deviation. It then has the property of a mean of 0 and standard deviation of 1, so you interpret the units as standard deviations.

8.8 End of chapter

Great work, that was your first chapter working on inferential statistics!

We have spent so long developing your data wrangling and visualisation skills that the code for statistical models is pretty short. Hopefully, you now believe us when we said almost all the work goes into wrangling your data into a format you can analyse. Once it comes to inferential statistics, it shifts from wrangling the data being the most difficult to being able to express your research question/design and interpret the outcome being the most difficult.

In the next chapter, we reinforce most of the content by applying simple linear regression to a categorical predictor. This is when you want to test for differences between two groups on your outcome instead of testing the relationship between two continuous variables.

9 Regression with one categorical predictor

In Chapter 8, you finally started working on inferential statistics. We spent so long on data wrangling and visualisation that it now feels so much closer to being able to address your research questions. We covered linear regression and the concept of correlation for investigating the relationship between two continuous variables.

In this chapter, we focus on simple linear regression for testing research questions and hypotheses for the difference between two groups on one outcome. Like Chapter 8, we reinforce the idea that common statistical tests you come across are specific applications of the general linear model (Lindeløv, 2019). In this chapter, we explore the concepts of t-tests as those specific applications compared to recreating them using linear regression. We also have a bonus section on expressing a one-sample and paired-samples design as linear models.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Visualise the difference between two groups on an outcome.
- Apply and interpret a Student and Welch t-test.
- Apply and interpret linear regression with one categorical predictor variable.
- Apply and interpret linear regression adapted to one-sample and paired-samples designs.

9.1 Chapter preparation

9.1.1 Introduction to the data set

For most of this chapter, we are using open data from Lopez et al. (2023). The abstract of their article is:

> Imagine a bowl of soup that never emptied, no matter how many spoonfuls you ate—when and how would you know to stop eating? Satiation can play a role in regulating eating behavior, but research suggests visual cues may be just as important. In a seminal study by Wansink et al. (2005), researchers used self-refilling bowls to assess how visual cues of portion size would influence intake. The study found that participants who unknowingly ate from self-refilling bowls ate more soup than

> did participants eating from normal (not self-refilling) bowls. Despite consuming 73% more soup, however, participants in the self-refilling condition did not believe they had consumed more soup, nor did they perceive themselves as more satiated than did participants eating from normal bowls. Given recent concerns regarding the validity of research from the Wansink lab, we conducted a preregistered direct replication study of Wansink et al. (2005) with a more highly powered sample (N = 464 vs. 54 in the original study). We found that most results replicated, albeit with half the effect size (d = 0.45 instead of 0.84), with participants in the self-refilling bowl condition eating significantly more soup than those in the control condition. Like the original study, participants in the selfrefilling condition did not believe they had consumed any more soup than participants in the control condition. These results suggest that eating can be strongly controlled by visual cues, which can even override satiation.

In summary, they replicated an (in)famous experiment that won the Ig-Nobel prize. Participants engaged in a intricate setting (seriously, go and look at the diagrams in the article) where they ate soup from bowls on a table. In the control group, participants could eat as much soup as they wanted and could ask for a top-up from the researchers. In the experimental group, the soup bowls automatically topped up through a series of hidden tubes under the table. The idea behind the control group is they get an accurate visual cue by the soup bowl reducing, and the experimental group get an inaccurate visual cue by the soup bowl seemingly never reducing. So, the inaccurate visual cue would interfere with natural signs of getting full and lead to people eating more.

In the original article, participants in the experimental group ate more soup than participants in the control group, but the main author was involved in a series of research misconduct cases. Lopez et al. (2023) wanted to see if the result would replicate in an independent study, so they predicted they would find the same results. In this chapter, we will explore the difference between the control and experimental groups on several variables in their data set.

9.1.2 Organising your files and project for the chapter

Before we can get started, you need to organise your files and project for the chapter, so your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, create a new folder called `Chapter_09_regression_categorical`. Within `Chapter_09_regression_cate` create two new folders called `data` and `figures`.
2. Create an R Project for `Chapter_09_regression_categorical` as an existing directory for your chapter folder. This should now be your working directory.
3. Create a new R Markdown document and give it a sensible title describing the chapter, such as `09 t-tests and Regression`. Delete everything below line 10 so you have a

blank file to work with and save the file in your `Chapter_09_regression_categorical` folder.

4. We are working with a new data set, so please save the following data file: Lopez_2023.csv. Right click the link and select "save link as", or clicking the link will save the files to your Downloads. Make sure that you save the file as ".csv". Save or copy the file to your `data/` folder within `Chapter_09_regression_categorical`.

You are now ready to start working on the chapter!

9.1.3 Activity 1 - Read and wrangle the data

As the first activity, try and test yourself by completing the following task list to practice your data wrangling skills. In this example, there is not loads to do, you just need to tidy up some variables. Create a final object called `lopez_clean` to be consistent with the tasks below. If you want to focus on t-tests and regression, then you can just type the code in the solution.

Try this

To wrangle the data, complete the following tasks:

1. Load the following packages:
    - tidyverse
    - effectsize
    - performance
2. Read the data file `data/Lopez_2023.csv` to the object name `lopez_data`.
3. Create a new object called `lopez_clean` based on `lopez_data`:
    - Modify the variable `Condition` to turn it into a factor.
    - Create a new variable called `Condition_label` by recoding `Condition`. "0" is the "Control" group and "1" is the "Experimental" group.

Your data should look like this to be ready to analyse:

```
Rows: 464
Columns: 10
$ ParticipantID      <dbl> 1002, 1004, 1007, 1016, 1018, 1021, 1022, 1024, 102~
$ Sex                <dbl> 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 0, 0, 1, 1, 1, ~
$ Age                <dbl> 18, 19, 19, 21, 20, 20, 21, 21, 19, 20, 21, 20, 21,~
$ Ethnicity          <dbl> 7, 3, 3, 4, 1, 3, 1, 6, 4, 7, 1, 3, 3, 4, 7, 2, 3, ~
$ OzEstimate         <dbl> 3.0, 2.0, 1.0, 3.0, 5.0, 1.0, 1.0, 3.0, 4.0, 1.0, 4~
```

```
$ CalEstimate        <dbl> 65, 10, 20, 25, 50, 5, 20, 180, 470, 50, 130, 100, ~
$ M_postsoup         <dbl> 3.3, 3.1, 43.4, 5.5, 6.0, 0.8, 3.8, 4.5, 7.9, 8.1, ~
$ F_CaloriesConsumed <dbl> 73.19441, 68.75839, 962.61743, 121.99069, 133.08075~
$ Condition          <fct> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
$ Condition_label    <chr> "Control", "Control", "Control", "Control", "Contro~
```

Show me the solution

You should have the following in a code chunk:

```
# load the relevant packages
library(effectsize)
library(performance)
library(tidyverse)

# Read the Lopez_2023.csv file
lopez_data <- read_csv("data/Lopez_2023.csv")

# turn condition into a factor and recode
lopez_clean <- lopez_data %>%
  mutate(Condition = as.factor(Condition),
         Condition_label = case_match(Condition,
                                      "0" ~ "Control",
                                      "1" ~ "Experimental"))
```

9.1.4 Activity 2 - Explore the data

Try this

After the wrangling steps, try and explore `lopez_clean` to see what variables you are working with. For example, opening the data object as a tab to scroll around, explore with `glimpse()`, or try plotting some of the individual variables.

In `lopez_clean`, we have the following variables:

Variable	Type	Description
ParticipantID	double	Participant ID number.
Sex	double	Participant sex.
Age	double	Participant age in years.
Ethnicity	double	Participant ethnicity.

Variable	Type	Description
OzEstimate	double	Estimated soup consumption in ounces (Oz).
CalEstimate	double	Estimated soup consumption in calories (kcals).
M_postsoup	double	Actual soup consumption in ounces (Oz).
F_CaloriesConsumed	double	Actual soup consumption in calories (kcals).
Condition	integer	Condition labelled numerically as 0 (Control) and 1 (Experimental).
Condition_label	character	Condition as a direct label: Control and Experimental.

We will use this data set to demonstrate t-tests and regression when you have one categorical predictor.

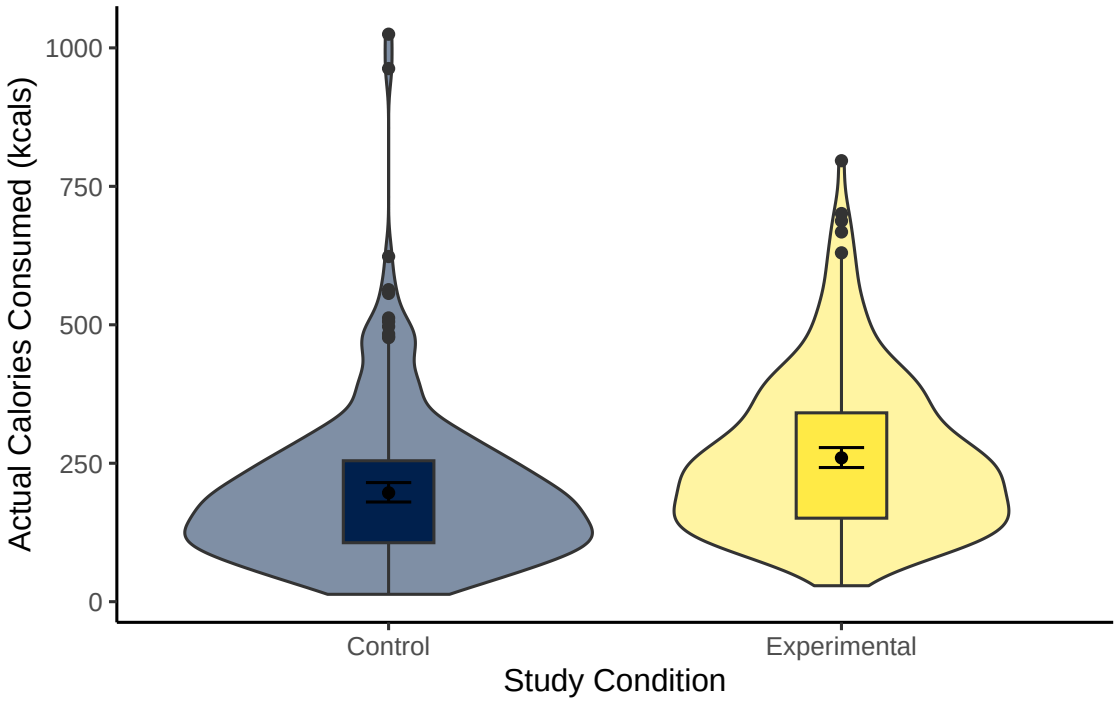
9.2 Comparing differences using the t-test

Like correlations are a specific application of the general linear model for the relationship between two continuous variables, t-tests are a specific application for the difference between two groups. Before we demonstrate how you can express this kind of design as a regression model, we cover t-tests so you know how to calculate and interpret them when you come across them in your research.

9.2.1 Activity 3 - Visualising the difference

To visualise the difference between two groups, it is useful to create something like a boxplot early for yourself, then provide a more professional looking violin-boxplot to help communicate your results. For most of the demonstrations in this chapter, we will try and answer the research question: "Is there a difference in actual calories consumed between the control and experimental groups?"

> Try this
>
> Using your data visualisation skills from Chapter 7, recreate the violin-boxplot below using the variables `F_CaloriesConsumed` and `Condition_label` from `lopez_clean`.



Looking at the graph, the

- (A) Control
- (B) Experimental

group consumed more calories on average.

Show me the solution

The violin-boxplot shows the experimental group who had the biased visual cues consumed more soup in calories than the control group who had the accurate visual cues. You should have the following in a code chunk:

```
lopez_clean %>%
  ggplot(aes(y = F_CaloriesConsumed, x = Condition_label, fill = Condition_label)) +
  geom_violin(alpha = 0.5) +
  geom_boxplot(width = 0.2,
               fatten = NULL) +
  stat_summary(fun = "mean",
               geom = "point") +
  stat_summary(fun.data = "mean_cl_boot", # confidence interval
               geom = "errorbar",
               width = 0.1) +
  scale_fill_viridis_d(option = "E") +
  scale_y_continuous(name = "Actual Calories Consumed (kcals)") +
  scale_x_discrete(name = "Study Condition") +
  guides(fill = FALSE) +
  theme_classic()
```

9.2.2 Activity 4 - Using the `t.test()` function

A t-test is a specific application of the general linear model. In this test, we express the difference in an outcome between two groups as a kind of standardised mean difference. If you are interested, see the Handy Workbook (McAleer, 2023) for the calculations behind the Student and Welch t-test. Conceptually, a t-test is the difference between two groups divided by the standard error of the difference. There are two main versions of a t-test:

- Student t-test
- Welch t-test

There is a function built into R to calculate the t-test: `t.test()`. The function requires:

- A formula like `lm()` where you specify the outcome/dependent variable and the predictor/independent variable in the form `outcome ~ predictor`.
- The data set you want to use.

For our `lopez_clean` data, we would run the following code for a two-tailed Welch t-test:

```
t.test(formula = F_CaloriesConsumed ~ Condition_label,
       data = lopez_clean)
```

```
    Welch Two Sample t-test
```

```
data:  F_CaloriesConsumed by Condition_label
t = -4.8578, df = 453.45, p-value = 1.638e-06
alternative hypothesis: true difference in means between group Control and group Experimental
95 percent confidence interval:
 -88.55610 -37.54289
sample estimates:
     mean in group Control mean in group Experimental
                  196.6818                   259.7313
```

For the three key concepts of inferential statistics, we get

- **Hypothesis testing**: $p < .001$, suggesting we can reject the null hypothesis assuming $\alpha = .05$.

> **!** What does 1.638e-06 mean?
>
> Remember: R reports very small or very large numbers using scientific notation to save space. We normally report p-values to three decimals, so we report anything smaller as $p < .001$ to say it is smaller than this.
> If you want to see the real number, you can use the following function which shows just how small the p-value is:
>
> ```
> format(1.638e-06, scientific = FALSE)
> ```
>
> ```
> [1] "0.000001638"
> ```

- **Effect size**: Somewhat annoyingly, we do not directly get the mean difference between groups as a raw/unstandardised mean difference. We must manually calculate it by subtracting the means of each group (196.6818 - 259.7313 = -63.05). So, those in the experimental group ate on average 63 more calories of soup than the control group.

> **!** Does it matter whether the difference is positive or negative?
>
> For effect sizes describing the difference between two groups, it is the absolute difference which is important, providing it is consistent with your predictions (if applicable). If you entered the groups the other way around, the mean difference would become 259.7313 - 196.6818 = 63.05. The same applies when we calculate a standardised mean difference like Cohen's d later.

- **Confidence interval**: [-88.56, -37.54], although we do not get the mean difference, we get the confidence interval around the mean difference.

To summarise: A Welch t-test showed participants in the experimental group ate significantly more calories of soup than participants in the control group, t (453.45) = -4.86, $p < .001$. On average, those in the experimental group ate 63.05 (95% CI = [37.54, 88.56]) more calories than those in the control group.

When you have statistics software like R to do the heavy lifting for you, there is not really a scenario where you would use the Student t-test anymore, but if you did, you can use the `var.equal` argument to say you assume there are equal variances in each group:

```
t.test(formula = F_CaloriesConsumed ~ Condition_label,
       data = lopez_clean,
       var.equal = TRUE)
```

```
    Two Sample t-test

data:  F_CaloriesConsumed by Condition_label
t = -4.8625, df = 462, p-value = 1.591e-06
alternative hypothesis: true difference in means between group Control and group Experimental
95 percent confidence interval:
 -88.52983 -37.56915
sample estimates:
     mean in group Control mean in group Experimental
                  196.6818                   259.7313
```

You can see the main difference between the two versions is the Welch t-test Student corrects the degrees of freedom, so they are a decimal. While the Student t-test does not correct the degrees of freedom, so they are predictably N - 2.

To summarise: A Student t-test showed participants in the experimental group ate significantly more calories of soup than participants in the control group, t (462) = -4.86, $p < .001$. On average, those in the experimental group ate 63.05 (95% CI = [37.57, 88.53]) more calories than those in the control group.

One further useful argument is specifying a one-tailed test if you have a specific prediction. The only downside to using linear models later is there is not a simple argument to apply a one-tailed test.

```
t.test(formula = F_CaloriesConsumed ~ Condition_label,
       data = lopez_clean,
       alternative = "less")
```

```
    Welch Two Sample t-test

data:  F_CaloriesConsumed by Condition_label
t = -4.8578, df = 453.45, p-value = 8.188e-07
alternative hypothesis: true difference in means between group Control and group Experimental
95 percent confidence interval:
     -Inf -41.6571
sample estimates:
     mean in group Control mean in group Experimental
                  196.6818                   259.7313
```

The difference here is specifying the `alternative` argument. You can use "less" or "greater" depending if you predict a negative (group A < group B) or positive difference (group A > group B).

9.2.3 Reporting your t-test reproducibly

Like correlations in Chapter 8, we can take objects like a t-test and add a little code to format the numbers into APA format. This means you can report your results reproducibly and avoid potential copy and paste errors.

For t-tests, the first step is saving your `t.test()` function as an object.

```
lopez_calories_object <- t.test(formula = F_CaloriesConsumed ~ Condition_label,
                                data = lopez_clean)
```

If you look in the Environment, you now have an object called `lopez_calories_object` which is a list of 10 items. For the following code, this is a function we have created, so we do not expect you to understand everything at this point as the objects are a little awkward to work with. You just need to copy and paste it into your .Rmd file before you want to reference the t-test. Click show the t-test formatting function as we initially hide it to avoid taking up lots of space.

```
report_ttest <- function(ttest_object){
  # This function will only work for t-test objects
  # Step 1 = save all the numbers with formatting
  tval <- sprintf("%.2f", round(ttest_object$statistic, 2))
  # save degrees of freedom
  df <- round(ttest_object$parameter, 2)
  # save p value with formatting if less than .001
```

```
  pval <- ttest_object$p.value
  if (pval >= 0.001){
    pval <- str_sub(as.character(pval), 2, 5)
    pval <-  paste0(", $p$ = ", pval)
  # If p < .001, manually format as p < .001
  } else if (pval < 0.001){
    pval <- ", $p$ < .001"
  }
  # save mean difference
  meandiff <- round(ttest_object$estimate[1] - ttest_object$estimate[2], 2)
  # save lower 95% CI
  lower_CI <- round(ttest_object$conf.int[1], 2)
  # save lower 95% CI
  upper_CI <- round(ttest_object$conf.int[2], 2)

  # Step 2 = add them together in APA format
  output <- paste0("*t* (", df,") = ",
                   tval,
                   pval,
                   ", mean difference = ", meandiff,
                   ", 95% CI = [", lower_CI, ", ", upper_CI, "]")

  return(output)
}
```

Once you have saved the object and added the formatting function, you can use the function to format your t-test:

```
report_ttest(lopez_calories_object)
```

```
[1] "*t* (453.45) = -4.86, $p$ < .001, mean difference = -63.05, 95% CI = [-88.56, -37.54]"
```

You can add that as inline code to insert into your report to make your inferential statistics reproducible. Just note it's difficult to apply all the APA format details, so you might need to remove leading zeros, add italics to the math symbols etc.

9.2.4 Activity 5 - Analysing ranks with the Mann-Whitney U test

As a final type of test variation here, like the Spearman is a non-parametric version of correlation, the Mann-Whitney U test is a non-parametric version of a t-test. Instead of using

the raw values, this test compares ranks between each group. You can use it when there are concerns with normality, outliers, or you are analysing a strictly ordinal outcome (more in Chapter 11).

The format is the same as for the t-test, but instead of the `t.test()` function, you have the `wilcox.test()` function (it also goes by the name Wilcoxon rank sum test).

```
wilcox.test(formula = F_CaloriesConsumed ~ Condition_label,
            data = lopez_clean,
            conf.int = TRUE)
```

```
    Wilcoxon rank sum test with continuity correction

data:  F_CaloriesConsumed by Condition_label
W = 18827, p-value = 3.021e-08
alternative hypothesis: true location shift is not equal to 0
95 percent confidence interval:
 -82.06643 -39.92418
sample estimates:
difference in location
             -59.88637
```

The output is similar to the t-test, but adapted to analysing ranks in a non-parametric test. By setting the argument `conf.int` to TRUE, you get the unstandardised effect size and it's confidence interval. Instead of the mean difference, you get the "difference in location". This represents - to quote the documentation as it is a little awkward - "the median of the difference between a sample from x and a sample from y". This means it is like a difference in medians, but the median difference in samples from each group rather than the median of the whole group.

To summarise: A Mann-Whitney U test showed participants in the experimental group ate significantly more calories of soup than participants in the control group, $W = 18827$, $p < .001$. For the difference in location, those in the experimental group ate 59.89 (95% CI = [39.92, 82.07]) more calories than those in the control group.

If you wanted to report this reproducibly, you first need to save the test as an object.

```
mannwhitney_cal <- wilcox.test(formula = F_CaloriesConsumed ~ Condition_label,
                               data = lopez_clean,
                               conf.int = TRUE)
```

We have then created a bespoke reporting function for the Mann-Whitney U test.

```
report_mannwhitney <- function(mannwhitney_object){
  # This function will only work for Wilcoxon.test objects
  # Step 1 = save all the numbers with formatting
  wval <- round(mannwhitney_object$statistic, 2)
  # save p value with formatting if less than .001
  pval <- mannwhitney_object$p.value
  if (pval >= 0.001){
    pval <- str_sub(as.character(pval), 2, 5)
    pval <-  paste0(", $p$ = ", pval)
  # If p < .001, manually format as p < .001
  } else if (pval < 0.001){
    pval <- ", $p$ < .001"
  }
  # save location difference
  locationdiff <- round(mannwhitney_object$estimate, 2)
  # save lower 95% CI
  lower_CI <- round(mannwhitney_object$conf.int[1], 2)
  # save lower 95% CI
  upper_CI <- round(mannwhitney_object$conf.int[2], 2)

  # Step 2 = add them together in APA format
  output <- paste0("*W* = ", wval,
                   pval,
                   ", location difference = ", locationdiff,
                   ", 95% CI = [", lower_CI, ", ", upper_CI, "]")

  return(output)
}
```

Once you have saved the object and added the formatting function, you can use the function to format your Mann-Whitney U test:

```
report_mannwhitney(mannwhitney_cal)
```

```
[1] "*W* = 18827, $p$ < .001, location difference = -59.89, 95% CI = [-82.07, -39.92]"
```

9.2.5 Activity 6 - Calculating Cohen's d

Raw/unstandardised effect sizes are great for putting results in context, particularly when the units are comparable across studies. For our outcome in this study, differences in calories are easy to put in context.

Alternatively, it can be useful to calculate standardised effect sizes. This helps for power analyses (more on that in Chapter 10) and when you want to compare across comparable studies with slightly different measurement scales.

There are different formulas for calculating Cohen's d, but if you know the t-value and degrees of freedom, you can calculate Cohen's d through:

$d = \frac{2t}{\sqrt{df}} = \frac{-9.725}{21.49} = -0.45$

It is important to know the concepts before you use shortcuts, but there is the `cohens_d()` function from the effectsize package which uses the same format as `t.test()`.

```
cohens_d(F_CaloriesConsumed ~ Condition_label,
         data = lopez_clean)
```

```
Cohen's d |         95% CI
--------------------------
-0.45     | [-0.64, -0.27]

- Estimated using pooled SD.
```

Try this

Great work following along so far, but now it is time to test your understanding on a new set of variables. Use the variables `CalEstimate` and `Condition_label` from `lopez_clean`. We can ask the question: "What is the difference in estimated calories consumed between the experimental and control groups?"

1. Create a violin-boxplot to visualise the difference between `CalEstimate` and `Condition_label` from `lopez_clean`.
2. Apply the Welch t-test to get your inferential statistics and answer the following questions:
    - **Hypothesis testing**: Assuming $\alpha = .05$, the difference between the experimental and control groups on estimated calories consumed was

- (A) statistically significant
- (B) not statistically significant

.

```
- **Effect size**: Rounded to 2 decimals, the raw effect size was an average difference of

- **Confidence interval**: Rounded to 2 decimals, the 95% confidence interval for the mean
```

- (A) -4.08
- (B) -0.03
- (C) 39.85
- (D) 0.33

to

- (A) -4.08
- (B) -0.03
- (C) 39.85
- (D) 0.33

. The 95% confidence interval for Cohen's d is

- (A) -4.08
- (B) -0.03
- (C) 39.85
- (D) 0.33

to

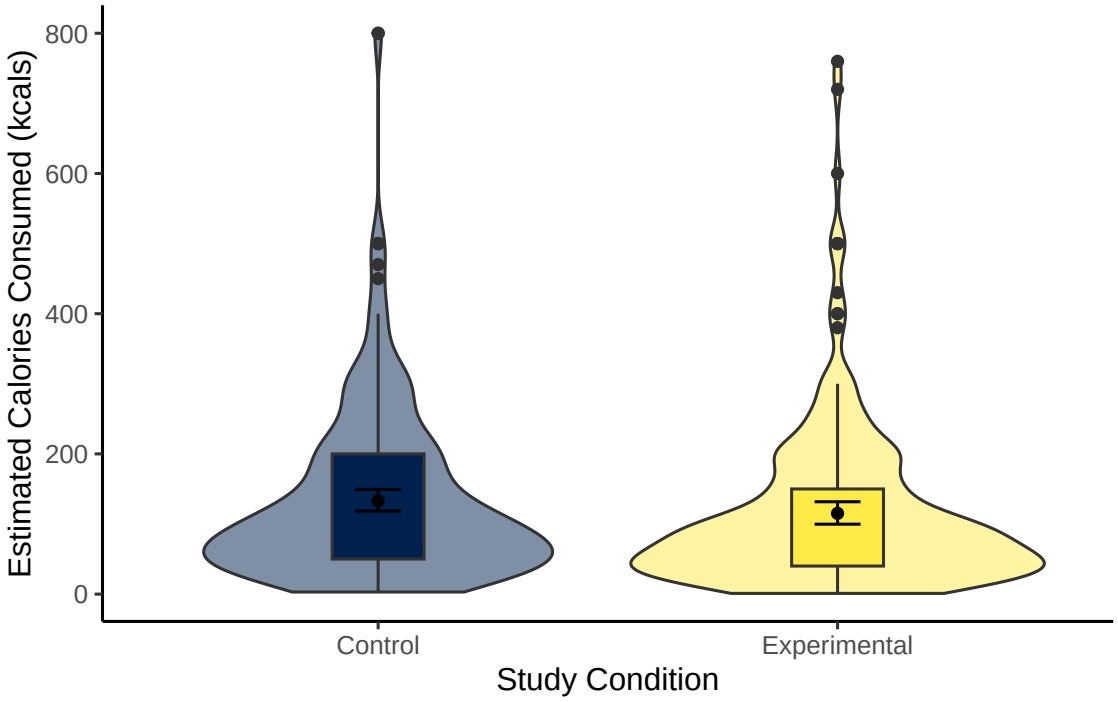
- (A) -4.08
- (B) -0.03
- (C) 39.85
- (D) 0.33

.

Show me the solution

The violin-boxplot shows little difference between the two groups on estimated calories consumed.

```
lopez_clean %>%
  ggplot(aes(y = CalEstimate, x = Condition_label, fill = Condition_label)) +
  geom_violin(alpha = 0.5) +
  geom_boxplot(width = 0.2,
               fatten = NULL) +
  stat_summary(fun = "mean",
               geom = "point") +
  stat_summary(fun.data = "mean_cl_boot", # confidence interval
               geom = "errorbar",
               width = 0.1) +
  scale_fill_viridis_d(option = "E") +
  scale_y_continuous(name = "Estimated Calories Consumed (kcals)") +
  scale_x_discrete(name = "Study Condition") +
  guides(fill = FALSE) +
  theme_classic()
```



For our inferential statistics, a Welch t-test showed the difference is not statistically significant, t (455.06) = 1.60, p = .110.

```
t.test(formula = CalEstimate ~ Condition_label,
       data = lopez_clean)
```

```
    Welch Two Sample t-test

data:  CalEstimate by Condition_label
t = 1.6001, df = 455.06, p-value = 0.1103
alternative hypothesis: true difference in means between group Control and group Experiment
95 percent confidence interval:
 -4.080399 39.846433
sample estimates:
     mean in group Control mean in group Experimental
                  133.0328                   115.1498
```

The control group estimated they consumed 17.88 (95% CI = [-4.08, 39.85]) more calories than the experimental group, but the difference was not significant. Expressed as a standardised effect size, this equates to Cohen's d = 0.15 (95% CI = [-0.03, 0.33]).

```
cohens_d(CalEstimate ~ Condition_label,
         data = lopez_clean)
```

```
Cohen's d |        95% CI
-------------------------
0.15      | [-0.03, 0.33]

- Estimated using pooled SD.
```

9.3 Linear regression with one categorical predictor

Now you know how to calculate a t-test in R, we can turn to simple linear regression as a more flexible tool for modelling the difference between two groups. As a reminder, there is a chapter in the Handy Workbook (McAleer, 2023) dedicated to manually calculating simple linear regression if you want to work through what the functions are doing behind the scenes.

9.3.1 Activity 7 - Descriptive statistics

For all the information we want to include in a report, calculating descriptive statistics is helpful for the reader to show the context behind the results you present. Here, we can report the mean and standard deviation of our outcome per group.

```
lopez_clean %>%
  group_by(Condition_label) %>%
  summarise(mean_cals = round(mean(F_CaloriesConsumed), 2),
            sd_cals = round(mean(F_CaloriesConsumed), 2))
```

```
# A tibble: 2 x 3
  Condition_label mean_cals sd_cals
  <chr>               <dbl>   <dbl>
1 Control              197.    197.
2 Experimental         260.    260.
```

> **Note**
>
> If you want some reinforcement of how these skills apply to published research, look at Table 1 in Lopez et al. (2023). The means and standard deviations here (and Cohen's d from Activity 5) exactly reproduce the values they report, apart from the *SD* for the control group (maybe there is a typo in their article).

9.3.2 Activity 8 - Using the `lm()` function

For our research question of "is there a difference in actual calories consumed between the control and experimental group?", we can address it with simple linear regression. In this study, we can make causal conclusions as it was an experiment to randomly allocate people into one of two groups, but you can also use regression to compare two self-selecting groups when you cannot make a causal conclusion in isolation. Think carefully about what you can conclude from your design.

Like Chapter 8, we start by defining our regression model with a formula in the pattern `outcome ~ predictor` and specify the data frame you want to use. We must then use the `summary()` function around your model object to get all the statistics you need.

There are two ways you can use a categorical predictor. First, we can code groups numerically which people called dummy coding. You code your first group 0 and you code your second group as 1, which maps on directly to how the regression model works. Let's look at the output.

```r
# Condition as a factor containing 0 and 1
lm_cals_numbers <- lm(formula = F_CaloriesConsumed ~ Condition,
                      data = lopez_clean)

summary(lm_cals_numbers)
```

```
Call:
lm(formula = F_CaloriesConsumed ~ Condition, data = lopez_clean)

Residuals:
    Min      1Q  Median      3Q     Max
-230.90  -99.09  -24.15   62.83  828.04

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  196.682      8.888  22.130  < 2e-16 ***
Condition1    63.049     12.966   4.863 1.59e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 139.4 on 462 degrees of freedom
Multiple R-squared:  0.04869,   Adjusted R-squared:  0.04663
F-statistic: 23.64 on 1 and 462 DF,  p-value: 1.591e-06
```

Compared to when we had a continuous predictor in Chapter 8, the output is identical. We just need to remember what the key numbers represent. The intercept is the predicted value of your outcome when your predictor is set to 0. When we have two groups coded as 0 and 1, this means the intercept is essentially the mean value of group 0 (here, the control group). We call this the reference group. You can confirm this by comparing the intercept estimate 196.68 to the mean value of the control group we calculated in Activity 6.

The slope estimate then represents how we predict the outcome to change for every 1-unit increase in the predictor. Since we coded the predictor 0 and 1, this just represents the shift from group 1 to group 2. We call the group we code as 1 the target group. You see the target group appended to the variable name, which is `Condition1` here. So, for a categorical predictor, the slope represents the mean difference between the reference group (0) and the target group (1): 63.05. In contrast to the t-test, this is our raw/unstandardised effect size for the mean difference we do not need to manually calculate.

> **Does it matter if the slope is positive or negative?**
>
> When you have a categorical predictor, the sign is only important for interpreting which group is bigger or smaller. The absolute size is relevant for the effect size where a larger absolute value indicates a larger effect. Whether the slope is positive or negative depends on the order of the groups and which has a larger mean. If the reference is larger than the target, you will get a negative slope. If the target is larger than the reference, you will get a positive slope.

Like the continuous predictor, we get values for R^2 and adjusted R^2, showing we explain .046 (in other words, 4.6%) variance in the outcome through our condition manipulation. We then get the model fit statistics, but with a single predictor, the p-value is identifical to the slope.

Alternatively, you can use character labels for your categorical predictor and it will still work. This time, we use `Condition_label`. By default, it will set the order of the reference and target groups alphabetically, but you can manually specify the order by setting factor levels.

```
# Condition_label as characters
lm_cals_labels <- lm(formula = F_CaloriesConsumed ~ Condition_label,
                     data = lopez_clean)

summary(lm_cals_labels)
```

```

Call:
lm(formula = F_CaloriesConsumed ~ Condition_label, data = lopez_clean)

Residuals:
    Min      1Q  Median      3Q     Max
-230.90  -99.09  -24.15   62.83  828.04

Coefficients:
                            Estimate Std. Error t value Pr(>|t|)
(Intercept)                  196.682      8.888  22.130  < 2e-16 ***
Condition_labelExperimental   63.049     12.966   4.863 1.59e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 139.4 on 462 degrees of freedom
Multiple R-squared:  0.04869,   Adjusted R-squared:  0.04663
F-statistic: 23.64 on 1 and 462 DF,  p-value: 1.591e-06
```

Note

If you want to test specifying the factor order to see how it affects the output, try running this code prior to the regression model:

```
# Specify group order of Experimental then Control
lopez_clean <- lopez_clean %>%
  mutate(Condition_label = factor(Condition_label,
                                  levels = c("Experimental", "Control")))
```

How are t-tests and regression the same?

If you are interested in the relationship between the two concepts, we said a t-test was a specific application of the general linear model. In the t-test calculations, it expresses the mean difference between groups by the standard error of the difference. In essence, it describes the difference in standard errors, which we can describe with a t-distribution to calculate p-values.
In regression, we frame the model as how much variance you explain compared to the total amount of variance. The more variance your predictor explains, the less unexplained variance there is left over. For the slope estimate though, this is identical to the t-test as we estimate the mean difference between groups plus the standard error around the mean difference. We calculate a p-value for the slope from a t-distribution, so you get a t-value in the output.
You can see the process is identical by comparing the key values from the regression output to the Student t-test. We can recreate the mean difference to compare to the slope, the t-value is the same, the p-value is the same, the degrees of freedom are the same, and the 95% confidence intervals below are the same.
So, when you have a single categorical predictor, it is the exact same process as the Student t-test, just expressed slightly different. The only downside to this procedure is it is much more difficult to recreate the Welch t-test.

9.3.3 Activity 9 - Calculating confidence intervals

The only thing we are missing is our confidence intervals around the estimates which we can calculate through the `confint()` function.

```
confint(lm_cals_numbers)
```

```
                2.5 %    97.5 %
(Intercept) 179.21657 214.14704
Condition1   37.56915  88.52983
```

Now, we can summarise the three key concepts of inferential statistics as:

- **Hypothesis testing**: $p < .001$, suggesting we can reject the null hypothesis assuming $\alpha = .05$. The experimental group ate significantly more calories of soup than the control group.
- **Effect size**: $b_1 = 63.05$, suggesting the experimental group ate on average 63 more calories than the control group.
- **Confidence interval**: [37.57, 88.53], showing the precision around the slope estimate.

Try this

Now it is time to test your understanding on a new set of variables. This time, use `CalEstimate` as your outcome, `Condition_label` as your predictor, and use `lopez_clean` as your data. We can ask the same question as Activity 5: "What is the difference in estimated calories consumed between the experimental and control groups?". Apply simple linear regression to get your inferential statistics and answer the following questions:

- **Hypothesis testing**: Assuming $\alpha = .05$, Condition is a
- (A) statistically significant
- (B) non-significant

predictor of estimates calories consumed.

- **Effect size**: Rounded to 2 decimals, the Condition slope coefficient means there was a mean difference of
- (A) 133.03
- (B) 7.68
- (C) -17.88
- (D) 11.19

.

- **Confidence interval**: Rounded to 2 decimals, the lower bound of the slope is

- (A) 117.94
- (B) -39.88
- (C) 148.12
- (D) 4.11

and the upper bound is

- (A) 117.94
- (B) -39.88
- (C) 148.12
- (D) 4.11

.

Show me the solution

The conclusions are the same as when we calculated the t-test, where condition is not a statistically significant predictor of estimated calories consumed. As a regression model, we get the same conclusions expressed in a slightly different way. Condition is a negative but non-significant predictor (p = .111). The control group ate 17.88 (b_1 = -17.88, 95% CI = [-39.88, 4.11]) more calories than the experimental group. We explain very little variance in estimated calories consumed (adjusted R^2 = .003), so the condition manipulation had little effect.

```
# Create lm object for condiiton label as a predictor
lm_cal_est <- lm(CalEstimate ~ Condition_label,
                 data = lopez_clean)

# summary of the model object
summary(lm_cal_est)

# confidence intervals around estimates
confint(lm_cal_est)
```

```
Call:
lm(formula = CalEstimate ~ Condition_label, data = lopez_clean)

Residuals:
    Min      1Q  Median      3Q     Max
-130.03  -83.03  -33.03   44.85  666.97

Coefficients:
                            Estimate Std. Error t value Pr(>|t|)
(Intercept)                  133.033      7.679  17.324   <2e-16 ***
Condition_labelExperimental  -17.883     11.192  -1.598    0.111
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 119.9 on 459 degrees of freedom
  (3 observations deleted due to missingness)
Multiple R-squared:  0.005531,  Adjusted R-squared:  0.003365
F-statistic: 2.553 on 1 and 459 DF,  p-value: 0.1108

                                2.5 %     97.5 %
(Intercept)                117.94256 148.123015
Condition_labelExperimental -39.87763   4.111599
```

9.3.4 Activity 10 - Standardising predictors

For simple linear regression with two levels of a categorical predictor, centering the variable does not help, but we can standardise our outcome to express the estimate in standard deviations rather than the raw units. This is analogous to calculating Cohen's d as we express the standardised mean difference. In contrast to continuous predictors, we only need to standardise the outcome, rather than both the outcome and predictor(s). We then use the standardised variable as our outcome.

```r
# Be careful with the bracket placement to subtract the mean first
lopez_clean <-lopez_clean %>%
  mutate(actual_calories_std = (F_CaloriesConsumed - mean(F_CaloriesConsumed)) / sd(F_Calorie

# Condition as a factor containing 0 and 1
lm_cals_std <- lm(formula = actual_calories_std ~ Condition,
                      data = lopez_clean)

summary(lm_cals_std)
```

```
Call:
lm(formula = actual_calories_std ~ Condition, data = lopez_clean)

Residuals:
    Min      1Q  Median      3Q     Max
-1.6173 -0.6941 -0.1692  0.4401  5.8000

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.20749    0.06225  -3.333 0.000928 ***
Condition1   0.44163    0.09082   4.863 1.59e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.9764 on 462 degrees of freedom
Multiple R-squared:  0.04869,   Adjusted R-squared:  0.04663
F-statistic: 23.64 on 1 and 462 DF,  p-value: 1.591e-06
```

Note, the estimate may be slightly different to directly calculating Cohen's d as there are a few formulas. If you compare to Activity 5, we got $d = 0.45$ there and 0.44 here. Between the estimate and 95% confidence intervals, they are off by .02, so it does not have a material impact on the results.

> **Tip**
>
> As before, once you know how it works conceptually, there is a shortcut where you do not need to standardise all your variables first. The effectsize package has a handy function called `standardize_parameters()` which you can apply to your initial `lm()` object.

```
standardize_parameters(lm_cals_numbers)
```

```
# Standardization method: refit

Parameter     | Std. Coef. |         95% CI
-----------------------------------------
(Intercept)   |      -0.21 | [-0.33, -0.09]
Condition [1] |       0.44 | [ 0.26,  0.62]
```

9.4 Checking assumptions

For the inferential statistics to work as intended, the model makes certain assumptions about the data you are putting into it and the accuracy of the inferences depends on how sensible these assumption are.

9.4.1 Activity 11 - Diagnostic plots for linear regression

We have the same assumptions for simple linear regression now we have a categorical predictor:

1. The outcome is interval/ratio level data.
2. The predictor variable is interval/ratio or categorical (with two levels at a time).
3. All values of the outcome variable are independent (i.e., each score should come from a different participant/observation).
4. The predictors have non-zero variance.
5. The relationship between the outcome and predictor is linear.
6. The residuals should be normally distributed.
7. There should be homoscedasticity.

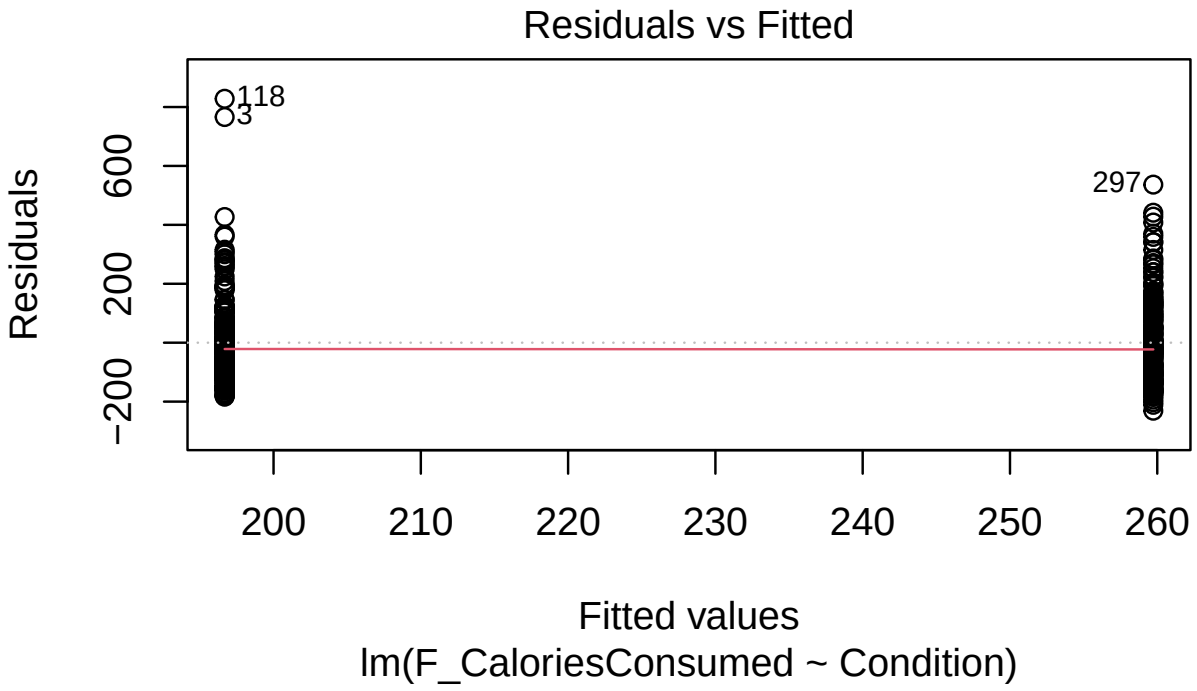
Assumptions 1-4 are pretty straight forward as they relate to your understanding of the design or a simple check on the data for non-zero variance (the responses are not all the exact same value).

Assumptions 5-7 require diagnostic checks on the residuals from the model. In contrast to continuous predictors, they are a little harder to identify patterns in. As we only have two values on the x-axis (0 and 1), all the residuals will be organised into vertical lines and the trend lines to help spot patterns do not look quite right.

9.4.2 Checking linearity

When you have a categorical predictor with two levels, you meet linearity by default, so you **do not** need to check this assumption directly. When you have two levels, you can only fit a straight line between the values.

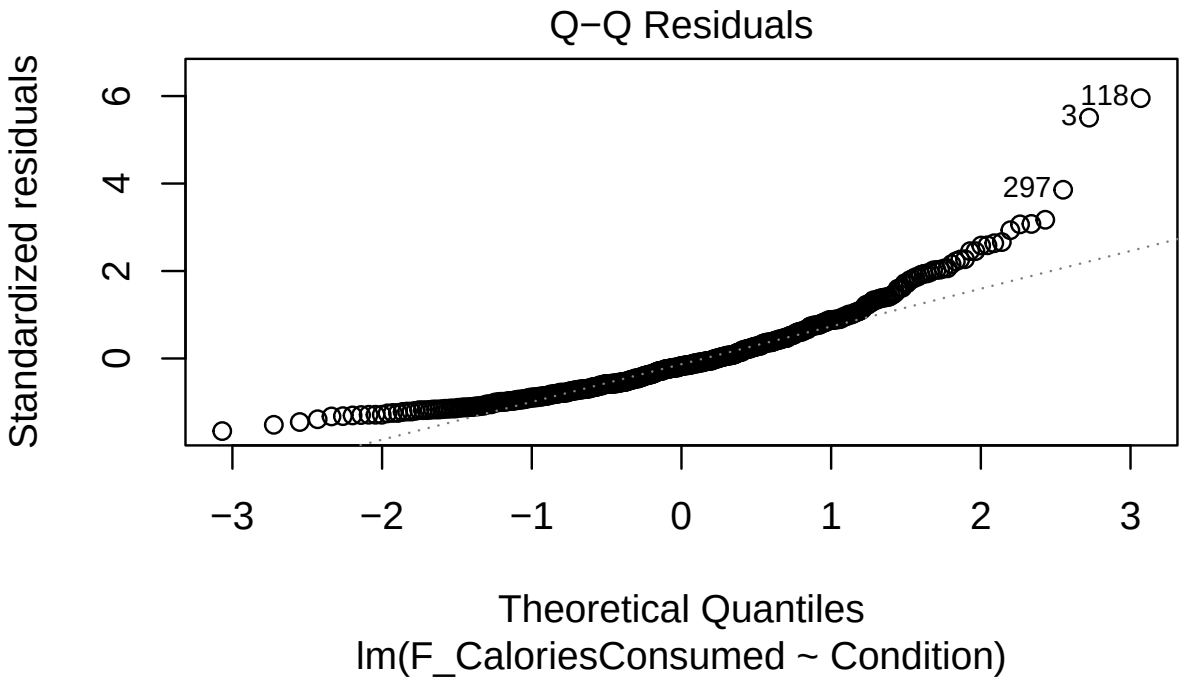
```
plot(lm_cals_numbers,
     which = 1)
```



9.4.3 Checking normality

The qq-plot is still the same to interpret. Now, this example presents a useful case of decision making in data analysis we explore more in Chapter 11. The plot here is approaching signs of violating normality as there is a clear curve to the data points with 3 and 118 the largest deviations (you can see these on the violin-boxplot as the two highest values in the control group). For this chapter, we are sticking with it and it would be consistent with how the original authors analysed the data, but note this would be a key decision to make and justify when reporting the analysis.

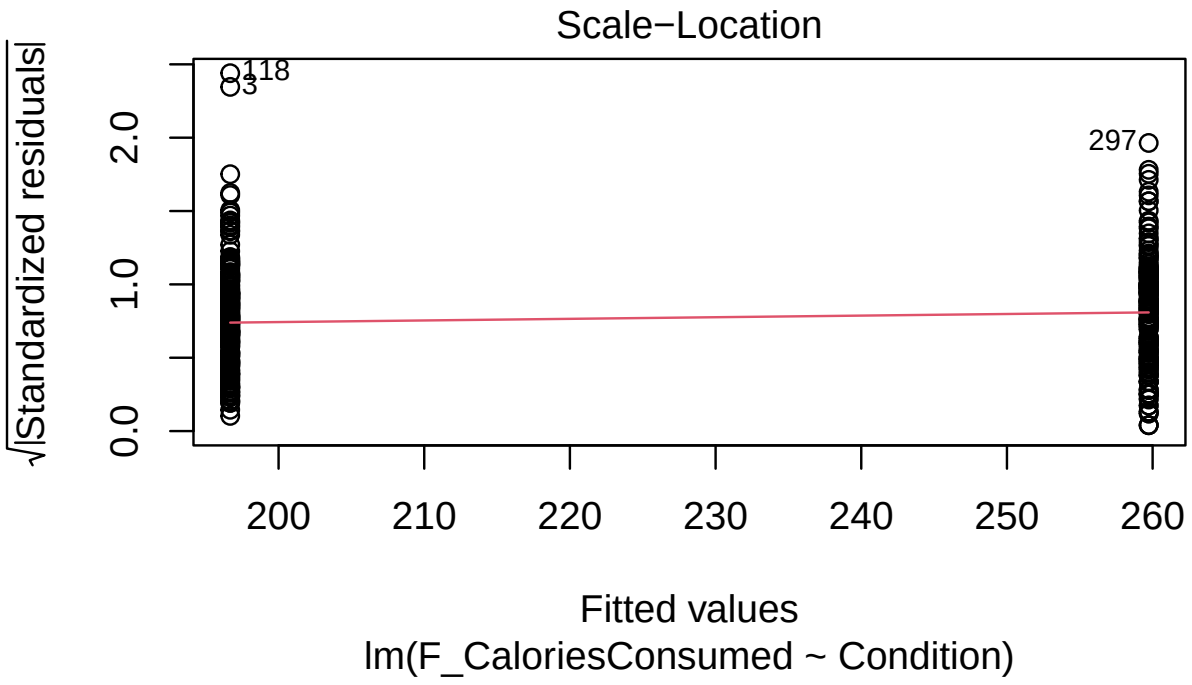
```
plot(lm_cals_numbers,
     which = 2)
```



9.4.4 Checking homoscedasticity

The scale-location plot is harder to interpret when you have a categorical predictor. Like linearity, the points are all arranged in two vertical lines as we only have two levels. You are looking out for the spread of the two lines to be roughly similar. They look fine here, just points 118 and 3 separated a little from the other points.

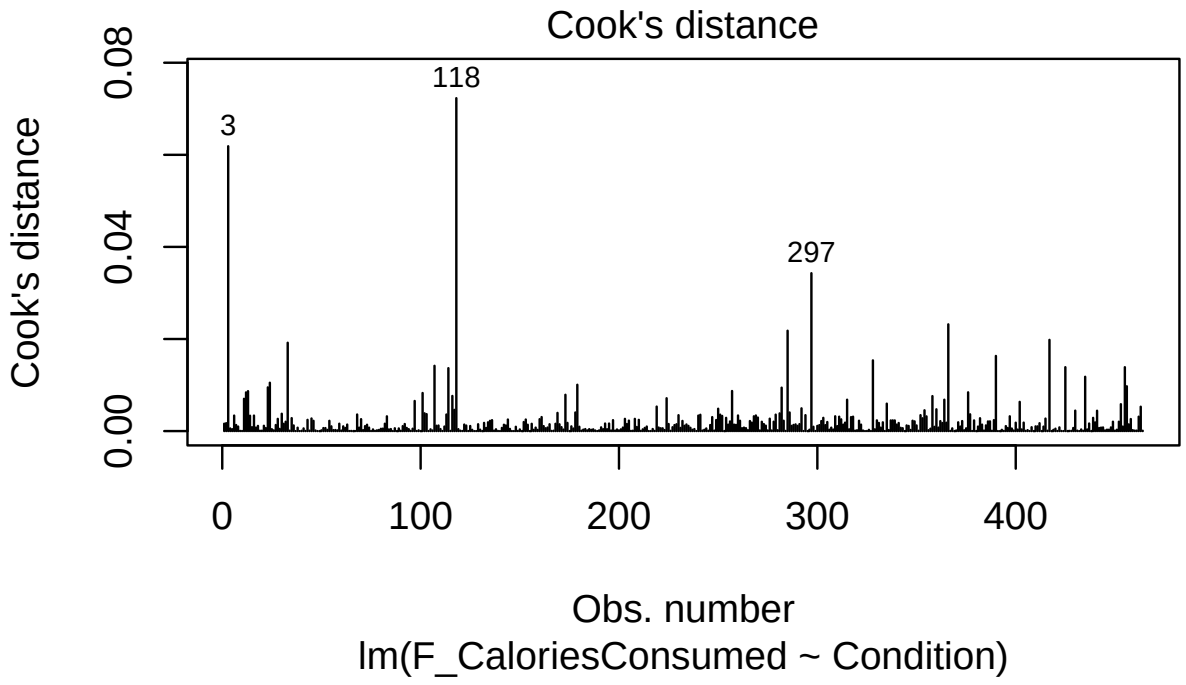
```
plot(lm_cals_numbers,
     which = 3)
```



9.4.5 Checking influential cases

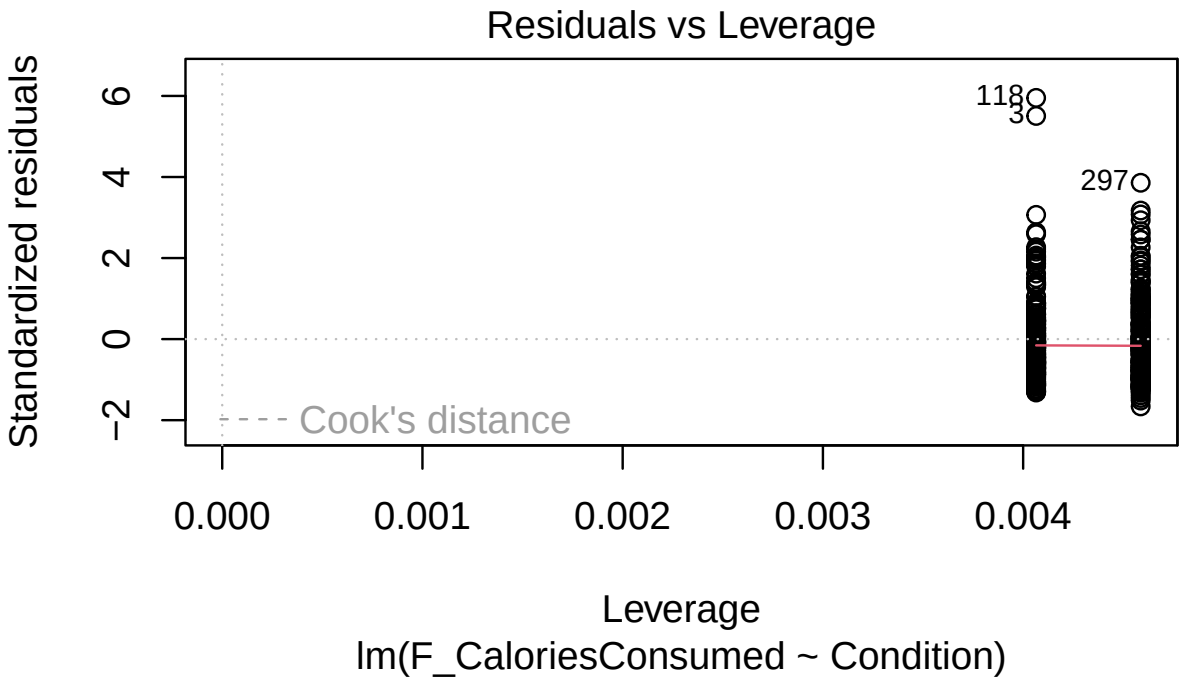
Finally, we have our plots for identifying influential cases. First, we get Cook's distance for all the observations in your data. We see points 3 and 118 come up yet again, but although they are the largest deviations, they do not necessarily have worrying Cook's distance values. There are different thresholds in the literature, but estimates range from 1, 0.5, to 4/n. It would only be under this final most conservative estimate (0.009) we would highlight several observations for further inspection.

```
plot(lm_cals_numbers,
     which = 4)
```



Finally, the fifth plot shows residual values against leverage. Like Chapter 8, we cannot see the Cook's distance threshold it uses in the plot as none of the points are a large enough deviation, despite 3 and 188 sticking out again.

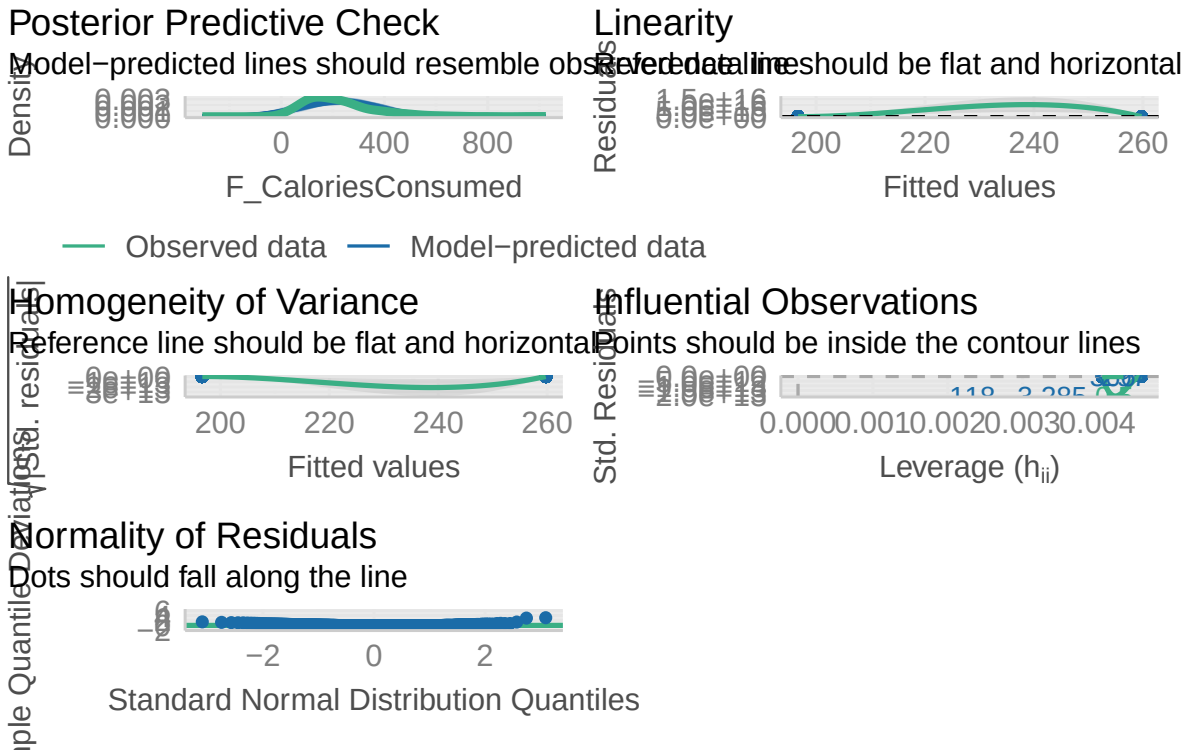
```
plot(lm_cals_numbers,
     which = 5)
```



9.4.6 Checking all the assumptions

Now we have covered the individual diagnostic plots, there is a handy function called `check_model()` from the performance package. Like the `plot()` function, the output for linearity, homoscedasticity, and influential observations does not plot right as we only have two values for the predictor and the plot lines do not really work. Do not worry, you have not done anything wrong.

```
check_model(lm_cals_numbers)
```



What might explain the funky normality?

If you are interested, the posterior predictive check here provides an insight into why we get potential problems with normality. The outcome is ratio but cannot be smaller than 0 as we cannot have negative calories. So, in the green line for the observed data, the data are a little skewed as it drops off prior to 0. However, the model does not know that and it happily predicts normally distributed values which go below 0, creating a mismatch between what the model predicts and the values we enter into it.
Remember the models will work regardless of the data you put into them, it is important to keep your role in mind to recognise when you need to be cautious about what you can learn from the model.

Try this

In activity 8, you should have calculated the effect of condition (`Condition_label`) on estimated calories consumed (`CalEstimate`) for your independent task. Using the model object `lm_cal_est`, work through assumptions for simple linear regression and make a note of whether you think it meets the assumptions, or there might be any problems. Some of the assumptions you consider what you know about the design, while others you need the diagnostic plots.

1. The outcome is interval/ratio level data.
2. The predictor variable is interval/ratio or categorical (with two levels at a time).
3. All values of the outcome variable are independent (i.e., each score should come from a different participant/observation).
4. The predictors have non-zero variance.
5. The relationship between the outcome and predictor is linear.
6. The residuals should be normally distributed.
7. There should be homoscedasticity.

Show me the solution

1. The outcome is interval/ratio level data.

The outcome is nicely ratio as estimated calories have a logical 0 point (no calories) and the units are in equal measurements..

2. The predictor variable is interval/ratio or categorical (with two levels at a time).

Our predictor is categorical with two levels.

3. All values of the outcome variable are independent (i.e., each score should come from a different participant/observation).

The short answer is this appears to be the case in this study. The longer answer is there might have been an issue with the participants apparently completing the study in groups of 3. It is not entirely clear in the data how they recorded this, but grouped data collection does present a potential problem with independence we do not tackle in this course and the original authors did not seem to address it.

4. The predictors have non-zero variance.

We have observations from both levels of the predictor.

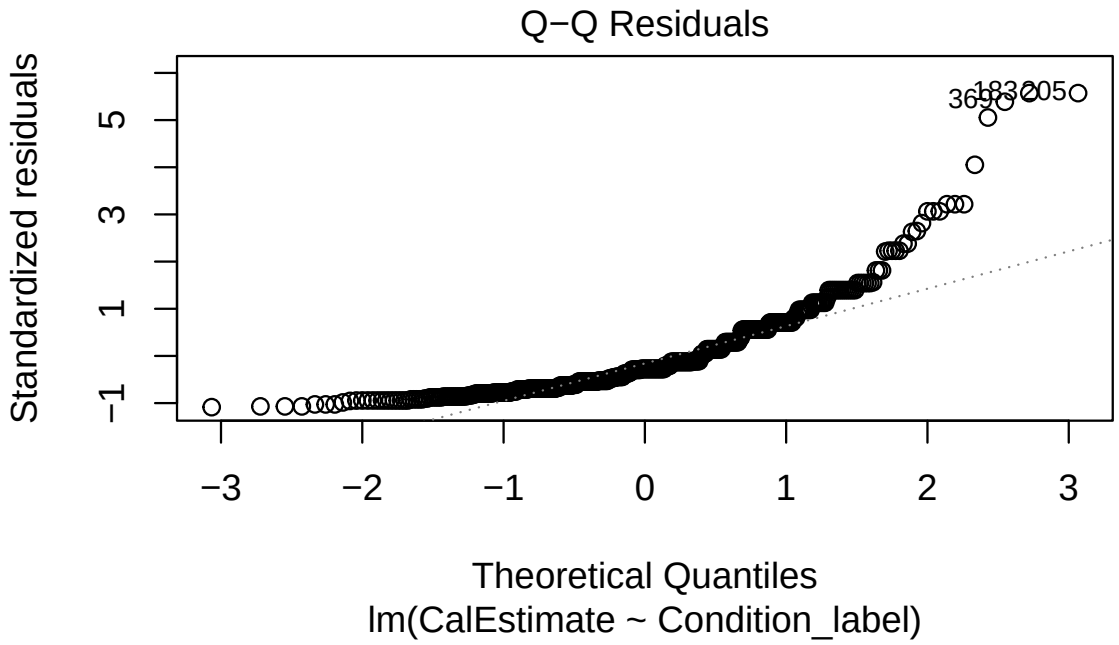
5. The relationship between the outcome and predictor is linear.

We meet linearity by default with two levels, so we do not need the plot here.

6. The residuals should be normally distributed.

Like the actual calories consumed, this is firmly a clear deviation from what we expect and provides a good example of when it does not look right. If we were to analyse the data fully, we would explore the impact of this and alternative models, but for this chapter, we are going to note our concern and remember the authors analysed the data like this.

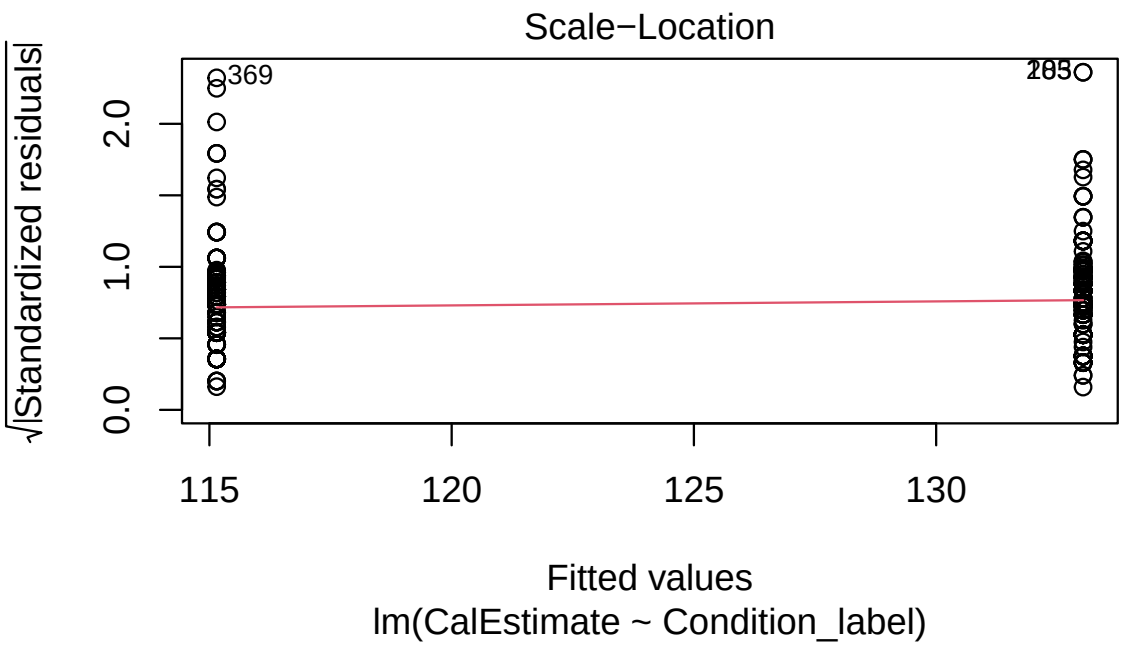
```
plot(lm_cal_est,
     which = 2)
```



7. There should be homoscedasticity.

Looking at the spread of each group, it looks fine with a similar range until both groups are more sparsely distributed above 1.

```
plot(lm_cal_est,
     which = 3)
```



In summary, normality is a clear concern and something we will return to for your options in Chapter 11 and the course materials. For now, we will stick with the model but recognise we should be cautious.

9.5 Reporting your results

Now we have some results to go with, there are a few recommendations on how to communicate that information. If you need a reminder of APA style for formatting numbers, you can see this PDF online for a little cheat sheet for numbers and statistics.

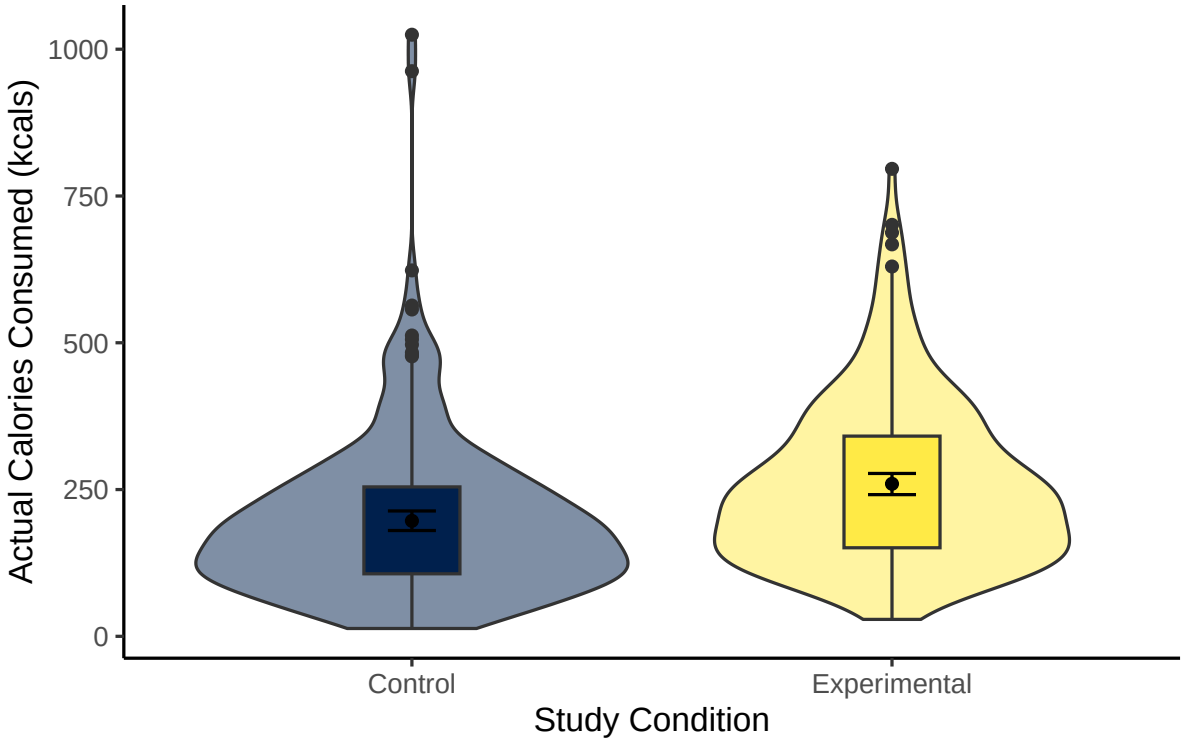
1. Explain to the reader what your linear regression model was. For example, what was your outcome and predictor variable?
2. Report descriptive statistics to help contextualise your findings. For example, the mean/standard deviation for your outcome per group.
3. Provide an appropriate data visualisation to help communciate key patterns to the reader. For example, a violin-boxplot for how each group responded on your outcome.
4. Report all three key inferential statistics concepts for the coefficient: the slope, the confidence interval around your slope, and the p-value for hypothesis testing. When you have one predictor in simple linear regression, you typically focus on the slope as your key effect size that helps address your research question and hypothesis. APA style rounds

numbers to 2 decimal places when numbers can be bigger than 1, and 3 decimals with no leading zero when it cannot be bigger than 1. When you report the unstandardised slope, you use the symbol b_1 but for the standardised slope, you use Beta instead β_1.

5. Provide an overview of the model fit statistics for whether your model explained a significant amount of variance in your outcome. Remember: the p-value for your model will be the same as for the slope in simple linear regression.

For our main example, we could summarise the findings as:

"Our research question was: is there a difference in actual calories consumed between the control and experimental group? To test this, we applied simple linear regression using condition as a predictor with two levels (control and experimental) and actual calories consumed as our outcome. Figure 1 shows a violin-boxplot of the difference between the control and experimental groups.



Our model explained a statistically significant amount of variance in our outcome (adjusted $R^2 = .047$, $F(1, 462) = 23.64$, $p < .001$). Condition was a positive predictor, where the experimental group consumed on average 63 more calories than the control group ($b_1 = 63.05$, 95% CI = [37.57, 88.53], $p < .001$). Expressed as a standardised effect size, the experimental

group consumed 0.44 (95% CI = [0.26, 0.62]) more standard deviations than the control group."

Note: we have not included an APA formatted Figure title here as it is not easy to format in our book, so refer to the course materials for guidance.

9.5.1 Formatting your results reproducibly

Like Chapter 8, we can also make regression models reproducible to add into your reports. For regression models, the first step is saving your model as an object *before* you apply the `summary()` function. We created this in activity 8, but as a reminder:

```
lm_cals_numbers <- lm(formula = F_CaloriesConsumed ~ Condition,
                      data = lopez_clean)
```

To make the reporting flexible, we then separate the model into two components: the overall model and the slope. For the overall model, you must save the reporting function first. Note these are the exact same functions as Chapter 8, so you would not need to duplicate them if you already included them in a file.

```
report_regression_model <- function(regression_object){
  # This function will only work for lm() objects
  # Step 1 = apply the summary function so we have both objects
  model_summary <- summary(regression_object)
  # Step 2 = save all the numbers with formatting
  # Save adjusted R2 with any trailing zeroes
  adj_r2 <- sprintf("%.3f", round(model_summary$adj.r.squared, 3))
  # save model degrees of freedom
  df1 <- model_summary$df[1]
  # save residual degrees of freedom
  df2 <- model_summary$df[2]
  # save F rounded to 2 decimals with any trailing zeroes
  Fval <- sprintf("%.2f", round(model_summary$fstatistic, 2))[1]
  # save p value with formatting if less than .001
  pval <- anova(regression_object)$`Pr(>F)`[1]
  if (pval >= 0.001){
    pval <- str_sub(as.character(pval), 2, 5)
    pval <-  paste0(", *p* = ", pval)
  # If p < .001, manually format as p < .001
  } else if (pval < 0.001){
    pval <- ", *p* < .001"
  }
```

```
  # Step 3 = add them together in APA format
  output <- paste0("adjusted $R^2$ = ",
                   adj_r2,
                   ", ",
                   "F(", df1, ", ", df2, ") = ", Fval,
                   pval)

  return(output)
}
```

Then you can run the function on your regression model.

```
report_regression_model(lm_cals_numbers)
```

```
[1] "adjusted $R^2$ = 0.047, F(2, 462) = 23.64, *p* < .001"
```

For the slope, there is a separate reporting function.

```
report_regression_slope <- function(regression_object){
  # This function will only work for lm() objects
  # Step 1 = apply the summary function so we have both objects
  model_summary <- summary(regression_object)
  # Step 2 = save all the numbers with formatting
  # $b_1 = -0.40$, 95% CI = [-0.44, -0.35], *p* < .001)
  # Save slope with any trailing zeroes
  b_1 <- sprintf("%.2f", round(model_summary$coefficients[2, 1], 2))
  # save p value with formatting if less than .001
  pval <- model_summary$coefficients[2, 4]
  if (pval >= 0.001){
    pval <- str_sub(as.character(pval), 2, 5)
    pval <-  paste0(", *p* = ", pval)
  # If p < .001, manually format as p < .001
  } else if (pval < 0.001){
    pval <- ", *p* < .001"
  }
  # save lower 95% CI
  lower_CI <- round(confint(regression_object)[2, 1], 2)
  # save lower 95% CI
  upper_CI <- round(confint(regression_object)[2, 2], 2)
  # Switch CIs depending on sign
```

```
  b1_CI <- ifelse(b_1 > 0,
                  paste0(lower_CI, ", ", upper_CI),
                  paste0(upper_CI, ", ", lower_CI))

  # Step 3 = add them together in APA format
  output <- paste0("$b_1$ = ",
                   b_1,
                   ", 95% CI = [", b1_CI, "]",
                   pval)

  return(output)
}
```

Then you can run the function on your regression model.

```
report_regression_slope(lm_cals_numbers)
```

```
[1] "$b_1$ = 63.05, 95% CI = [37.57, 88.53], *p* < .001"
```

9.6 Bonus section - One- and paired-samples tests

In this course, we focus on correlational and between-subjects designs, but you might find yourself in a situation where you want to test a continuous variable against a fixed value or compare conditions in the same participants. This is a bonus section if you have time, so you can skip to the Test Yourself section to finish the chapter if you do not.

For this demonstration, we will use data from experiment 1 of Bem (2011), an (in)famous study that almost single-handedly started the replication crisis in psychology. Briefly, participants completed a computer task adapted from priming experiments where they could select one of two windows. They had to guess which window had an image hidden behind it and the images contained different stimuli like erotic or neutral/control images. Across many trials of the participants guessing the location, Bem calculated the proportion of successful trials which could range between 0 (never correct), 50 (50%, chance), and 100 (always correct). The headline finding was participants demonstrated precognition - or the ability to see into the future - to guess above chance levels, but what does the data look like?

We are working with a new data set, so please save the following data file: Bem_2011.csv. Right click the link and select "save link as", or clicking the link will save the files to your Downloads. Make sure that you save the file as ".csv". Save or copy the file to your `data/` folder within `Chapter_09_regression_categorical`. Read in the data file to the object `bem_data` to be consistent with the tasks below.

9.6.1 One-sample comparing against a fixed value

There are scenarios where you want to compare a single continuous variable against a fixed value. For example, do your participants respond significantly above or below chance?

9.6.1.1 Expressed as a t-test

As a t-test, we need to specify two arguments:

- `x` - This is the continuous variable you want to analyse and compare the mean value of. We must use the base R operator `$` to specify the column from your data.
- `mu` - This is the fixed value you want to test your variable against.

In this scenario, we want to compare the hit rate to erotic images against a value of 50. This will tell us if the hit rate is significantly above or below chance.

```
t.test(x = bem_data$Erotic.Hits.PC,
       mu = 50)
```

```
    One Sample t-test

data:  bem_data$Erotic.Hits.PC
t = 2.5133, df = 99, p-value = 0.01358
alternative hypothesis: true mean is not equal to 50
95 percent confidence interval:
 50.66075 55.61703
sample estimates:
mean of x
 53.13889
```

The output is similar to the independent samples t-test. We get the p-value for hypothesis testing, the mean estimate of the variable, and it's 95% confidence interval. To express it as an effect size, you can subtract 50 from each value. So, participants responded 3.14% above chance, statistically significant, but hardly convincing evidence for precognition.

9.6.1.2 Expressed as a linear model

We can also express this as a linear model, but we must first add a small wrangling step. In the one-sample t-test, we can manually enter a fixed value to compare the mean against. In a linear model, we must compare against 0 by subtracting the fixed value from your variable. So, we subtract 50 from all the observations, so they become a kind of deviation from 50.

```
bem_data <- bem_data %>%
  mutate(erotic_deviation = Erotic.Hits.PC - 50)
```

In contrast to previous linear models, we only add a fixed intercept and do not add a predictor. This recreates the one-sample t-test by estimating the mean value of your outcome.

```
lm_erotic <- lm(erotic_deviation ~ 1,
                data = bem_data)

summary(lm_erotic)
```

```
Call:
lm(formula = erotic_deviation ~ 1, data = bem_data)

Residuals:
    Min      1Q  Median      3Q     Max
-28.139  -8.694   2.417   7.972  30.194

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    3.139      1.249   2.513   0.0136 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 12.49 on 99 degrees of freedom
```

This process has the benefit of directly producing your effect size, as the intercept estimate is the deviation from your fixed value (here, 50). As we calculated manually before, the erotic hit rate is 3.14% above your fixed value. If you remember back to the linear model explanations, this is where the p-value for the intercept is finally useful as it tests against 0.

If you compare to the one-sample t-test, all of these values are identical. You also have the option of calculating confidence intervals around the estimate, calculating a standardised effect size, and checking assumptions by applying the previous linear regression activities.

9.6.2 Paired-samples comparing conditions

Alternatively, you might want to compare two conditions from the same participants in paired samples/within-subjects design. For example, is the hit-rate significantly higher for erotic images compared to control images?

9.6.2.1 Expressed as a t-test

To conduct a paired-samples t-test, we must specify three arguments:

- `x` - This is the first level of your condition as a column. You need your data in wide format, so the condition levels are spread across two columns per participant. We must use the base R operator `$` to specify the column from your data.
- `y` - This is the second level of your condition as a column.
- `paired` - This instructs R you want a paired-samples t-test to compare conditions within participants.

In this scenario, we want to compare the hit rate for erotic images to control images.

```
t.test(x = bem_data$Erotic.Hits.PC,
       y = bem_data$Control.Hits.PC,
       paired = TRUE)
```

```
    Paired t-test

data:  bem_data$Erotic.Hits.PC and bem_data$Control.Hits.PC
t = 1.8563, df = 99, p-value = 0.06638
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 -0.2277431  6.8388542
sample estimates:
mean difference
       3.305556
```

The output is almost identical to the one-sample t-test, but this time the effect size is the mean difference between conditions, not just the mean per condition. Behind the scenes, a paired-samples t-test is actually a one-sample t-test in disguise as it uses the difference between conditions as the outcome.

As an aside, Bem (2011) reported a significant difference here, but only because he reported a one-tailed test (`alternative = "greater"`). This is an example where you ideally need a strong (ideally pre-registered) prediction as it makes a material impact on the inferences you would make.

9.6.2.2 Expressed as a linear model

Finally, we can express a paired-samples t-test as a linear model. We must apply a small data wrangling step to calculate a difference score between conditions. This is so the linear model compares the estimate against 0 of no difference. So, for this example, we create a variable for the difference between erotic and control images.

```
bem_data <- bem_data %>%
  mutate(erotic_control = Erotic.Hits.PC - Control.Hits.PC)
```

Like the one-sample scenario, we only add a fixed intercept for the new difference variance and do not add a predictor. This recreates the paired-samples t-test by estimating the mean value of your difference score.

```
lm_paired <- lm(erotic_control ~ 1,
                data = bem_data)

summary(lm_paired)
```

```
Call:
lm(formula = erotic_control ~ 1, data = bem_data)

Residuals:
    Min      1Q  Median      3Q     Max
-58.861  -9.556   2.250   9.194  35.583

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    3.306      1.781   1.856   0.0664 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 17.81 on 99 degrees of freedom
```

This process directly produces your effect size again, as the intercept estimate is the deviation from 0 for your difference score. As we saw in the paired-samples t-test output, there was a 3.31% higher hit rate for erotic images compared to control (as we calculated erotic - control).

If you compare to the paired-samples t-test, all of these values are identical. You also have the option of calculating confidence intervals around the estimate, calculating a standardised effect size, and checking assumptions by applying the previous linear regression activities.

9.7 Test Yourself

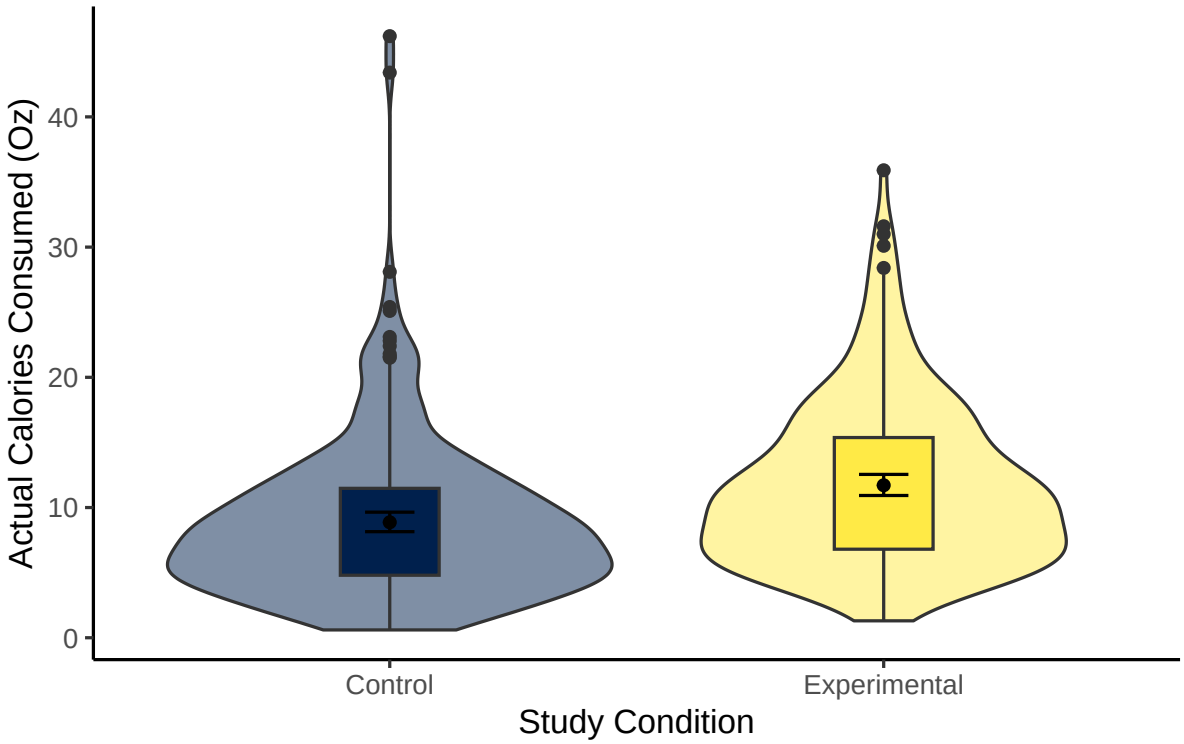
To end the chapter, we have some knowledge check questions to test your understanding of the concepts we covered in the chapter. Compared to previous chapters, there are no error mode questions as the content is so similar to Chapter 8. We are just going to test your understanding of the concepts rather than potential errors.

9.7.1 Knowledge check

For this chapter's knowledge check section, we have something a little different. Instead of purely conceptual questions about functions, we have another example of linear regression from Lopez et al. (2023). Feel free to create this model yourself, but we will show you some output and ask you questions based on it.

For this model, we focus on ounces of soup consumed (`M_postsoup`) rather than calories by each Condition group (`Condition_label`). You might have a good idea about the results based on the chapter, but you will still need to interpret the output accurately.

Question 1. In the violin-boxplot below, the experimental group consumed more soup in ounces than the control group: TRUE / FALSE.



Question 2 For the next few questions, we have the output from a linear regression model and we would like you to interpret it.

```
Call:
lm(formula = M_postsoup ~ Condition_label, data = lopez_clean)

Residuals:
    Min      1Q  Median      3Q     Max
-10.410  -4.467  -1.089   2.833  37.333

Coefficients:
                            Estimate Std. Error t value Pr(>|t|)
(Intercept)                   8.8675     0.4007  22.130  < 2e-16 ***
Condition_labelExperimental   2.8426     0.5846   4.863 1.59e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.285 on 462 degrees of freedom
Multiple R-squared:  0.04869,   Adjusted R-squared:  0.04663
F-statistic: 23.64 on 1 and 462 DF,  p-value: 1.591e-06
```

The outcome variable in this model is

- (A) Actual ounces of soup consumed
- (B) Experimental condition

and the predictor variable is

- (A) Actual ounces of soup consumed
- (B) Experimental condition

.

Question 3 In this model, the reference group is

- (A) Control
- (B) Experimental

and the target group is

- (A) Control
- (B) Experimental

Question 4 Rounded to 2 decimals, we predict a value of _____ for our reference group.

Question 5 The predictor is

- (A) statistically significant
- (B) non-significant

and

- (A) positive
- (B) negative

.

Question 6 The target group consumed on average _____ ounces

- (A) less
- (B) more

soup than the reference group.

9.8 Words from this Chapter

Below you will find a list of words that were used in this chapter that might be new to you in case it helps to have somewhere to refer back to what they mean. The links in this table take you to the entry for the words in the PsyTeachR Glossary. Note that the Glossary is written by numerous members of the team and as such may use slightly different terminology from that shown in the chapter.

term	definition
dummy-coding	Entering a categorical predictor using two values such as 0 and 1.
reference-group	In a dummy-coded variable, the first level of your variable, typically 0.
student-t-test	Calculating a t-value based on the mean difference divided by the pooled standard deviation. In the Student t-test, we times the pooled standard deviation by a term containing the sample sizes of each group.
target-group	In a dummy-coded variable, the second level of your variable, typically 1.
welch-t-test	Calculating a t-value based on the mean difference divided by a term containing the variance of each group. We also correct the degrees of freedom for the difference in variances.

9.9 End of chapter

Well done, you have now completed the first core set of chapters for inferential statistics!

At this point, you can now address a range of research questions by applying variations of the general linear model. As a researcher, the most important thing is starting with your research question (and where applicable, your hypothesis), designing a study to address that research question, and using an appropriate statistical model for your design and research question. But, before you can identify an appropriate statistical model, you need to know what they look like! This is everything we cover in Research Methods 1 to focus on a select range of foundational skills. You will then build on these modelling techniques in Chapters 12-14 for Research Methods 2.

You are now ready to complete the second data analysis journey chapter: Simple Linear Regression. This is where you can test your new skills in a slightly less structured way, from wrangling data, to answering a research question.

In the next core chapter, we turn to statistical power and work on how you can conduct a power analysis in R/RStudio.

10 Statistical Power and Effect Sizes

Until now, a large component of each chapter was dedicated to data wrangling as we must first process raw data into something tidier we can apply our visualisation or modelling steps to. In this chapter, there is no data wrangling, just functions to calculate statistical power in different ways for different tests. Before, the difficulty was in unique problems in wrangling your specific data. In power analysis, the functions are pretty straight forward to use, but deciding what inputs you use are the hard parts as they are your decisions to make.

We adapted a few components of this chapter from J. Bartlett & Charles (2022) and we recommend referring to this article for more information on the concepts behind statistical power. However, the article focuses on the statistics software jamovi, so this chapter focuses on power analysis using the pwr package.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Conduct and interpret an *a priori* power analysis for t-tests, correlations, and regression models.
- Conduct and interpret a sensitivity power analysis for t-tests, correlations, and regression models.
- Report your power analysis to make it reproducible for your reader.

10.1 Chapter preparation

10.1.1 Organising your files and project for the chapter

In contrast to previous chapters, there will be no data wrangling in this chapter, so we do not need to worry about downloading files. We will still be working around some key studies, but we will introduce them as needed. However, you will still be working in an R Markdown document, so you need to make sure your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, create a new folder called `Chapter_10_power`.

2. Create an R Project for `Chapter_10_power` as an existing directory for your chapter folder. This should now be your working directory.
3. Create a new R Markdown document and give it a sensible title describing the chapter, such as `10 Statistical Power and Effect Sizes`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Chapter_10_power` folder.
4. In a code chunk, load the pwr and tidyverse packages. If you need to install any packages, revisit Chapter 1 if you need a refresher, but remember not to install packages on the university computers / online server.

You are now ready to start working on the chapter!

10.2 NHST and statistical power recap

Given there is no data wrangling for this chapter and the functions for power analysis are pretty straight forward, we have a little space to recap the key concepts behind power analysis. Almost all the work here comes into thinking and justifying your decisions, rather than spending lots of time on wrangling and analysis.

The branch of statistics we are using here is Null Hypothesis Significance Testing (NHST). There are two types of hypotheses and what you are trying to establish is the probability of rejecting the null hypothesis. Those two hypotheses are:

- The **null hypothesis** which states that there is no difference ($H_0 : \mu_1 = \mu_2$) or no relationship ($H_0 : r = 0$).
- The **alternative hypothesis** which states that there is a difference ($H_1 : \mu_1 \neq \mu_2$) or there is a relationship ($H_1 : r \neq 0$).

NHST is designed to control error rates associated with two main decisions around these hypotheses:

- **Type I error** - or false positive, is the probability of rejecting the null hypothesis when it should not be rejected (otherwise called alpha or α). In other words, you conclude that there is a real "effect" when in fact there is no effect. The field standard rate of acceptable false positives is $\alpha = .05$, meaning that we would accept 1 in 20 studies may be a false positive.
- **Type II error** - or false negative, is the probability of retaining the null hypothesis when it should be rejected (otherwise called beta or β). In other words, you conclude that there was no real "effect" when in fact there was one. There is less tradition around this, but the most common rule of thumb you will come across is $\beta = .20$, meaning that we would accept 1 in 5 studies may be a false negative.

Statistical power is the opposite of beta and represents the long-run probability of correctly rejecting the null hypothesis when there is a real effect to detect. In other words, how likely are you to detect an effect that is really there? You calculate Power as $1 - \beta$, meaning that if the field standard for beta is $\beta = .20$, then the field standard for power is $1 - .20 = .80$ (80%).

In addition to alpha and beta/power, there are two other key concepts (there are more depending on the test, but we will add them in when we need them):

- **Effect size** - A number that expresses the magnitude of the phenomenon relevant to your research question. In Chapters 8 and 9, we introduced you to different standardised effect sizes such as Pearson's r and Cohen's d.
- **Sample size** - The number of observations (usually participants, but it might be animals or stimuli depending on your topic) in your study.

Critically, there is a relationship between these four concepts, where if you know three, you can calculate the **fourth** in a process called **power analysis**. The two most useful types of power analysis are:

1. **A priori** power analysis: How many participants do I need, for a given alpha, beta/power, and smallest effect size of interest? This is most useful in the design stage to help you plan how many participants you need to design an informative study.
2. **Sensitivity** power analysis: What effect size can I detect, for a given alpha, beta/power, and sample size? This is most useful after you finish collecting data or when you are using secondary data as the sample size is not longer under your control and it helps put your findings in context.

You may now be thinking though, if there is a relationship between all four concepts, could we calculate power for a given alpha, sample size, and effect size? It is a tempting idea and you might see some articles report it, but unfortunately is is misleading and tells you nothing more than the p-value does. The short version is we are typically using a sample to learn something about a population, so there is uncertainty in the estimate. Using the observed effect size in your study assumes this is the true population effect, which is rarely a good assumption. If you are interested, Lakens (2022) is a great resource for sample size justification in general, but also explains why post-hoc power is not a good idea.

After the brief recap, we will now focus on *a priori* and sensitivity power analyses applied to different statistical models.

10.3 Power analysis for t-tests / categorical predictors

10.3.1 Introduction to the study

In this section, imagine we are designing a study to build on Irving et al. (2022) who tested an intervention to correct statistical misinformation. Participants read an article about a new fictional study where one passage falsely concludes watching TV causes cognitive decline. In the correction group, participants receive an extra passage where the fictional researcher explains they only reported a correlation, not a causal relationship. In the no-correction group, the extra passage just explains the fictional researcher was not available to comment. Irving et al. then tested participants' comprehension of the story and coded their answers for mistaken causal inferences. They expected participants in the correction group to make fewer causal inferences than those in the no-correction group, and found evidence supporting this prediction with an effect size equivalent to Cohen's d = 0.64, 95% CI = [0.28, 0.99]. Inspired by their study, we want to design an experiment to correct another type of misinformation in articles.

Irving et al. (2022) themselves provide an excellent example of explaining and justifying the rationale behind their power analysis, so we will walk through the decision making process and how it changes the outputs. For our smallest effect size of interest, our starting point is the estimate of d = 0.64. However, it is worth consulting other sources to calibrate our understanding of effects in the area, such as Irving et al. citing a meta-analysis. For debunking, the average effect across 30 studies was d = 1.14, 95% CI = [0.68, 1.61], so we could use the lower bound of the confidence interval, but this may still represent an overestimate. Irving et al. used the smallest effect (d = 0.54) from the studies most similar to their design which was included in the meta-analysis. As a value slightly smaller than the other estimates, we will also use this as the smallest effect of interest for our study.

Now we have settled on our smallest effect size of interest, we will use d = 0.54 in the following demonstrations. We start with *a priori* and sensitivity power analysis for two independent samples, exploring how the outputs change as we alter inputs like alpha, power, and the number of tails in the test.

10.3.2 A priori power analysis

For an independent samples t-test (we will cover regression shortly), there is the function `pwr.t.test()`. We can enter the following arguments:

- `n`: The number of observations.
- `d`: The effect size as Cohen's d.
- `sig.level`: The alpha level.
- `power`: The power value as 1-β.

- `type`: Whether you want power for a one-, paired-, or independant-samples t-test.
- `alternative`: Whether you have a one- or two-sided hypothesis.

Remember, power analysis works by leaving one argument blank, so for calculating the sample size, we leave `n` blank or enter `NULL` as the argument. As our starting point, we enter d = 0.54, sig.level = .05, power = .90, type = two.sample and alternative = two-sided.

```
pwr.t.test(n = NULL,
           d = 0.54,
           sig.level = .05,
           power = .90,
           type = "two.sample",
           alternative = "two.sided")
```

```

     Two-sample t test power calculation

              n = 73.04123
              d = 0.54
      sig.level = 0.05
          power = 0.9
    alternative = two.sided

NOTE: n is number in *each* group
```

As the note warns us, for an independent-samples t-test, `n` represents the number of observations per group, so we need **74** per group (we round up as we cannot have .04 of a person) or N = **148**.

If you wanted to use these values in inline code, you can save the power analysis object and pick out values to work with.

```
irving_samplesize <- pwr.t.test(n = NULL,
                                d = 0.54,
                                sig.level = .05,
                                power = .90,
                                type = "two.sample",
                                alternative = "two.sided") %>%
  pluck("n") %>%
  ceiling()
```

In this code, we save the power analysis function to an object, use the `pluck()` function to pick out a specific component (the argument name must be spelt exactly), and use the `ceiling()` function to round up. This helps to avoid manually calculating the values as you can use the object.

```
# sample size per group
irving_samplesize

# total sample size
irving_samplesize * 2
```

```
[1] 74
[1] 148
```

The power analysis function is pretty straight forward to work with, it is the thinking and decision making that goes into selecting the value for each argument that is the hardest part here. It is ultimately a subjective decision you must be able to justify in a report and there will always be compromises. You never have unlimited resources, so you are trying to balance designing the most informative study with maximizing the resources available to you.

Try this

With decision making in mind, we can tweak the arguments to see how it affects the sample size we need. We will tweak one argument at a time, so your starting point will be the arguments we started with above.

1. If we used a one-tailed test predicting a positive effect (`"greater"`), we would need ___ participants per group (N = _____).
2. If we wanted to make fewer type I errors and reduce alpha to .005, we would need _____ participants per group (N = _____).
3. If we were happy with a larger beta and reduce power to .80 (80%), we would need ___ participants per group (N = _____).
4. If we wanted to decrease our smallest effect size of interest and set d = .40, we would need _____ participants per group (N = _____).
5. If we thought it was appropriate to change the design to within-subjects and use a paired-samples t-test instead (`"paired"`), we would need ___ participants.

Show me the solution

1. We can calculate sample size for a one-tailed test by entering `alternative = "greater"` or `alternative = "less"`. This must match the effect size direction or you will receive an error.

```
pwr.t.test(n = NULL,
           d = 0.54,
           sig.level = .05,
           power = .90,
           type = "two.sample",
           alternative = "greater") %>%
  pluck("n") %>%
  ceiling()
```

```
[1] 60
```

2. We can decrease alpha by entering `alpha = .005` to calculate the sample size for reducing the type I error rate.

```
pwr.t.test(n = NULL,
           d = 0.54,
           sig.level = .005,
           power = .90,
           type = "two.sample",
           alternative = "two.sided") %>%
  pluck("n") %>%
  ceiling()
```

```
[1] 117
```

3. We can decrease power if we were happy with a larger beta / type II error rate by entering `power = .80`.

```
pwr.t.test(n = NULL,
           d = 0.54,
           sig.level = .05,
           power = .80,
           type = "two.sample",
           alternative = "two.sided") %>%
  pluck("n") %>%
  ceiling()
```

```
[1] 55
```

4. We can decrease the smallest effect size of interest if we wanted the study to be more sensitive by entering `d = .40`.

```
pwr.t.test(n = NULL,
           d = 0.40,
           sig.level = .05,
           power = .90,
           type = "two.sample",
           alternative = "two.sided") %>%
  pluck("n") %>%
  ceiling()
```

```
[1] 133
```

5. If we changed the design and test to within-subjects, we can enter `type = "paired"`.

```
pwr.t.test(n = NULL,
           d = 0.54,
           sig.level = .05,
           power = .90,
           type = "paired",
           alternative = "two.sided") %>%
  pluck("n") %>%
  ceiling()
```

```
[1] 39
```

These are important lessons to recognise which inputs increase and which decrease the sample size you need. For an *a priori* power analysis in the design phase, you can tweak the inputs depending on how sensitive you want your study given the resources available to you. Holding everything else constant, we can summarise the patterns as:

- Using a one-tailed test
- (A) increases
- (B) decreases

the sample size you need.

- Reducing alpha
- (A) decreases
- (B) increases

the sample size you need.

- Reducing power / increasing beta
- (A) increases
- (B) decreases

the sample size you need.

- Reducing the smallest effect size of interest
- (A) decreases
- (B) increases

the sample size you need.

- Switching to a within-subjects design
- (A) decreases
- (B) increases

the sample size you need.

10.3.3 Sensitivity power analysis

Now imagine you already knew the sample size or had access to a population of a known size. In this scenario, you would conduct a sensitivity power analysis. This would tell you what effect sizes your study would be powered to detect for a given alpha, power, and sample size. This is helpful for interpreting your results as you can outline what effect sizes your study was sensitive to and which effects would be too small for you to reliably detect.

Imagine we had finished collecting data and we knew we had 40 participants in each group but did not conduct an *a priori* power analysis when designing the study. Instead of leaving `n` blank, we can leave `d` blank.

```
pwr.t.test(n = 40,
           d = NULL,
           sig.level = .05,
           power = .90,
           type = "two.sample",
           alternative = "two.sided")
```

```
     Two-sample t test power calculation

              n = 40
              d = 0.7339255
      sig.level = 0.05
          power = 0.9
    alternative = two.sided

NOTE: n is number in *each* group
```

The output tells us that the study is sensitive to detect effect sizes of d = 0.73 with 90% power. This helps us to interpret the results if we did not plan with power in mind. If the effect size we could detect with 90% power is larger than our smallest effect size of interest, our study was potentially underpowered. This might sound like post-hoc power we warned you about, but the key difference is you are comparing the effect size your study was sensitive to against your smallest effect size of interest, **not** your observed effect size.

For a sensitivity power analysis, you will often find yourself with unequal sample sizes. The previous function assumes equal sample sizes, but `pwr.t2n.test()` lets you set `n1` and `n2`. For example, imagine we ended up with two groups of 39 and 43 participants.

```
pwr.t2n.test(n1 = 39,
             n2 = 43,
             d = NULL,
             sig.level = .05,
             power = .90,
             alternative = "two.sided") %>%
  pluck("d") %>%
  round(digits = 2)
```

```
[1] 0.73
```

One other key point here is power exists along a curve, there is not just a single value for power once your sample size is fixed. We can visualise this through something called a power curve. Figure 10.1 shows statistical power against Cohen's d as the effect size for a fixed sample of 40 participants per group. We would have 90% power to detect a Cohen's d of 0.75 (the value is a little different here as we set the effect size, rather than calculate it as the output), shown where the two lines meet. You would have more and more power to detect effects larger than 0.75 (follow the curve to the right), but less power to detect effects smaller than 0.75 (follow the curve to the left). The grey shaded region highlights the effects your study would be less sensitive to than your desired value for power.

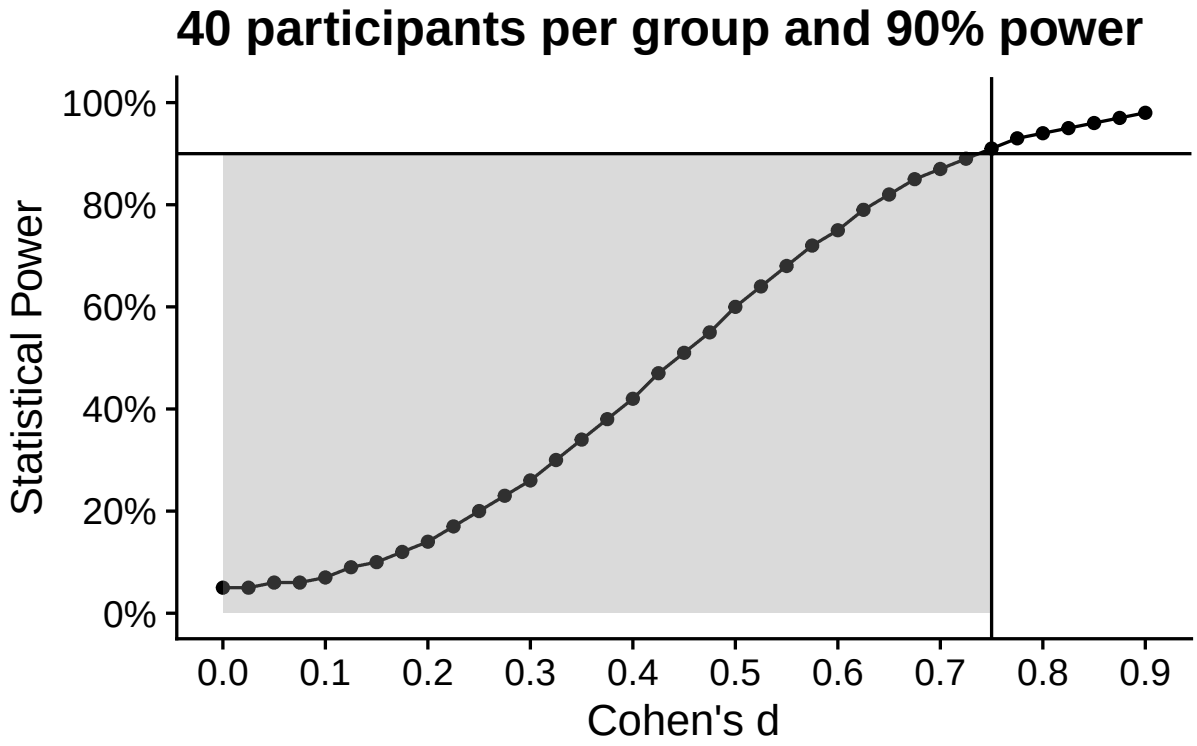


Figure 10.1: Power curve for 40 participants per group and 90% power.

On the other hand, Figure 10.2 shows statistical power against Cohen's d as the effect size for a fixed sample of 80 participants per group. This time, we would have 90% power to detect effects of d = 0.53 and there is a smaller grey region. We would have more power to detect effects larger than d = 0.53 but less power to detect effects smaller than 0.53.

Hopefully, these demonstrations reinforce the idea of sensitivity and how power exists along a curve once you have a fixed sample size.

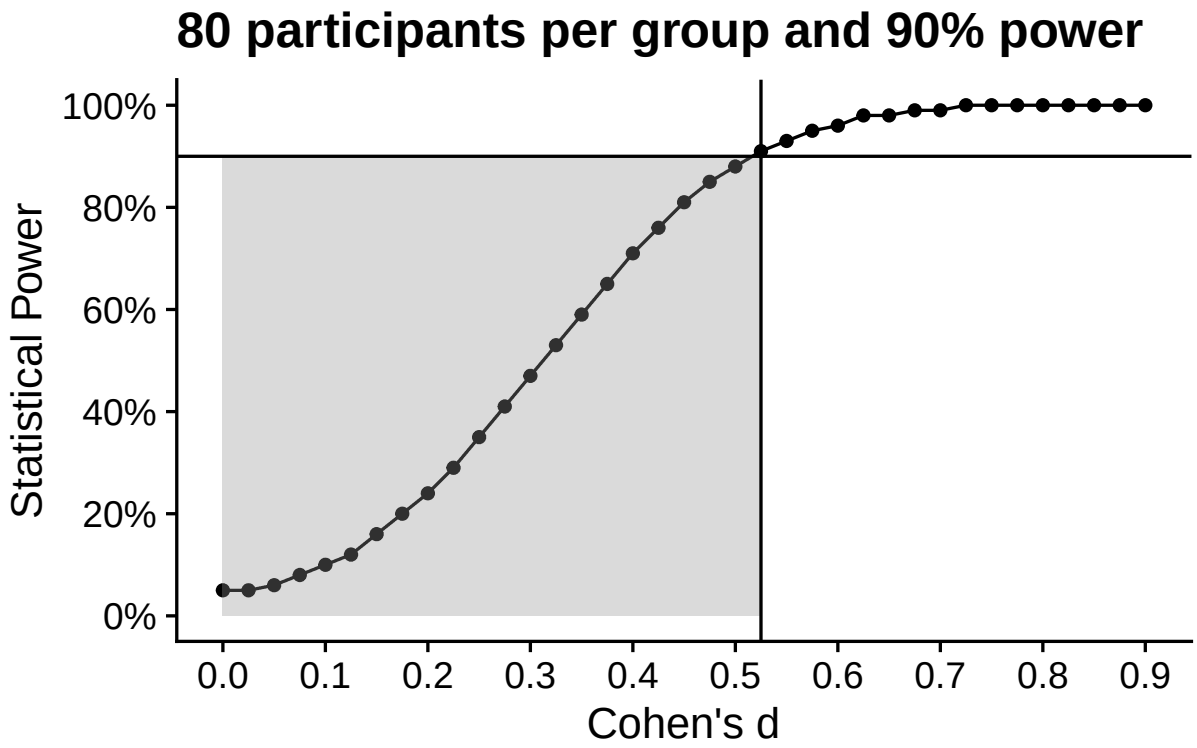


Figure 10.2: Power curve for 80 participants per group and 90% power.

10.3.4 Power for regression with a categorical predictor

In Chapters 8 and 9, we recommended expressing your designs as linear regression models. They have many benefits, but one downside is the effect size and process we need for power analysis is not the most intuitive. Typically, people report effect sizes like Cohen's d when comparing groups, but here we need Cohen's f^2. You can convert between effect sizes and we recommend the website psychometrica.de which has an online calculator for converting effect sizes in section 14. Alternatively, you can use the following code to save f^2 as an object.

```
# enter your Cohen's d value
d <- 0.54

# This calculates f2 from d
f2 <- (d / 2)^2
```

Now we have f^2, we can use the function `pwr.f2.test()` which calculates power for regression models. For the equivalent of a t-test, we have the following new arguments:

- `u`: The numerator degrees of freedom, the number of predictors in your model.
- `v`: The denominator degrees of freedom, a little more awkward but the sample size minus u minus 1.
- `f2`: The effect size f^2, which is a kind of transformed version of R^2 for the amount of variance explained by the model.

For our power analysis, we will save the inputs as objects to make it easier to reuse them, and enter them in the following arguments:

```
# number of predictors
u <- 1

# alpha for type I error rate
alpha <- .05

# power for 1-beta
power <-  .90

pwr.f2.test(u = u,
            v = NULL,
            sig.level = alpha,
            power = power,
            f2 = f2)
```

```
     Multiple regression power calculation

              u = 1
              v = 144.0824
             f2 = 0.0729
      sig.level = 0.05
          power = 0.9
```

Using the objects from the power analysis, we can calculate the sample size we need with a little reorganising.

```
irving_v <- pwr.f2.test(u = 1,
                        v = NULL,
                        sig.level = .05,
                        power = .90,
                        f2 = f2) %>%
  pluck("v")

ceiling(irving_v + u + 1)
```

```
[1] 147
```

In the t-test power analysis function, we needed 148 participants in total, so this is off by 1 participant. There are a few steps for rounding errors here, so this is close enough to show it is the equivalent but more awkward process.

If you wanted to use this function for a sensitivity power analysis, you can convert f^2 back to Cohen's d using psychometrica.de or use the following code:

```
# f2 from the output
f2 <- .073

# convert to d by square root of f2 times 2
d <- sqrt(f2) * 2
```

10.4 Power analysis for correlations / continuous predictors

10.4.1 Introduction to the study

For this section, we need a new study to work with for a correlation / continuous predictor. Wingen et al. (2020) were interested in the relationship between the replication rate in psy-

chology studies and the public trust in psychology research. The replication crisis has led to a lot of introspection in the field to consider how we conduct robust research. However, being honest about the state of the field might be good for science, but perhaps it is related to lower public trust in science. We will focus on study 1 which asked the question: does trust in psychology correlate with expected replicability?

Wingen et al. (2020) reported a power analysis and they aimed for 95% power, 5% alpha, and their smallest effect size of interest was $r = .20$. Like Irving et al. (2022), they chose this value based on a meta-analysis which summarised hundreds of studies across social psychology. We will use these values as a starting point and adapt them to see it's impact on the sample size we need.

10.4.2 A priori power analysis

For Pearson's r correlation, there is the function `pwr.r.test()`. All the arguments are the same as for the t-test, apart from we specify r as an effect size instead of Cohen's d and we do not need to specify the type of test.

```
pwr.r.test(n = NULL,
           r = .20,
           sig.level = .05,
           power = .95,
           alternative = "two.sided")
```

```

     approximate correlation power calculation (arctangh transformation)

              n = 318.2637
              r = 0.2
      sig.level = 0.05
          power = 0.95
    alternative = two.sided
```

As before, we can isolate the sample size we would need for a study sensitive to these inputs.

```
pwr.r.test(n = NULL,
           r = .20,
           sig.level = .05,
           power = .95,
           alternative = "two.sided") %>%
  pluck("n") %>%
  ceiling()
```

```
[1] 319
```

Our starting point is 319 participants to detect our smallest effect size of interest $r = .20$ with 95% power and 5% alpha.

Try this

With decision making in mind, we can tweak the arguments to see how it affects the sample size we need. We will tweak one argument at a time, so your starting point will be the arguments we started with above.

1. If we used a one-tailed test predicting a positive relationship, we would need _____ participants. This reproduces the power analysis from Wingen et al., as they used a one-tailed test.
2. If we wanted to make fewer type I errors and reduce alpha to .005, we would need _____ participants.
3. If we were happy with a larger beta and reduce power to .80 (80%), we would need _____ participants.

Show me the solution

1. We can calculate sample size for a one-tailed test by entering `alternative = "greater"` or `alternative = "less"`. This must match the effect size direction or you will receive an error.

```
pwr.r.test(n = NULL,
           r = .20,
           sig.level = .05,
           power = .95,
           alternative = "greater") %>%
  pluck("n") %>%
  ceiling()
```

```
[1] 266
```

2. We can decrease alpha by entering `alpha = .005` to calculate the sample size for reducing the type I error rate.

```
pwr.r.test(n = NULL,
           r = .20,
           sig.level = .005,
           power = .95,
           alternative = "two.sided") %>%
  pluck("n") %>%
  ceiling()
```

```
[1] 485
```

3. We can decrease power if we were happy with a larger beta / type II error rate by entering `power = .80`.

```
pwr.r.test(n = NULL,
           r = .20,
           sig.level = .05,
           power = .80,
           alternative = "two.sided") %>%
  pluck("n") %>%
  ceiling()
```

```
[1] 194
```

Like for the independent samples t-test, the design phase allows you to carefully consider the inputs you choose and tweak them depending on how sensitive you want your study given the resources available to you. Holding everything else constant, we can summarise the patterns here as:

- Using a one-tailed test
- (A) increases
- (B) decreases

the sample size you need.

- Reducing alpha
- (A) increases
- (B) decreases

the sample size you need.

- Reducing power / increasing beta
- (A) increases
- (B) decreases

the sample size you need.

10.4.3 Sensitivity power analysis

Wingen et al. (2020) is a great example of a sensitivity power analysis in the wild as they are relatively rare to see in published research. They explain they recruited participants online, so they ended up with more participants than they aimed for.

Try this

Their final sample size was **271**, so try and adapt the function to calculate the effect size r they were sensitive to. Both of these answers assume 5% alpha and a one-sided test. To 2 decimal places, they could detect an effect of $r =$ _____ with 80% power and $r =$ _____ with 95% power.

Show me the solution

You should have had this in a code chunk for 80% power:

```
pwr.r.test(n = 271,
           r = NULL,
           sig.level = .05,
           power = .80,
           alternative = "greater") %>%
  pluck("r") %>%
  round(digits = 2)
```

```
[1] 0.15
```

And this in a code chunk for 95% power:

```
pwr.r.test(n = 271,
           r = NULL,
           sig.level = .05,
           power = .95,
           alternative = "greater") %>%
  pluck("r") %>%
  round(digits = 2)
```

```
[1] 0.2
```

10.4.4 Power for regression with a continuous predictor

Like the categorical predictor, we have a mismatch between the effect size you typically see reported (Pearson's r) and the effect size we need for a regression power analysis (f^2). The website psychometrica.de still works for converting effect sizes in section 14. Alternatively, you can use the following code to save f^2 as an object.

```
# effect size as Pearson's r
r <- .20

# convert to f2 by squaring r values
f2 <- r^2 / (1 - r^2)
```

Now we have f^2, we can use the function `pwr.f2.test()` which calculates power for regression models.

```
# number of predictors
u <- 1

# alpha for type I error rate
alpha <- .05

# power for 1-beta
power <-  .95

pwr.f2.test(u = u,
            v = NULL,
            sig.level = alpha,
            power = power,
            f2 = f2)
```

```
     Multiple regression power calculation

              u = 1
              v = 311.807
             f2 = 0.04166667
      sig.level = 0.05
          power = 0.95
```

Using the objects from the power analysis, we can calculate the sample size we need with a little reorganising.

```
wingen_v <- pwr.f2.test(u = 1,
                        v = NULL,
                        sig.level = .05,
                        power = .95,
                        f2 = f2) %>%
  pluck("v")

ceiling(wingen_v + u + 1)
```

```
[1] 314
```

In the Pearson's r power analysis function, we needed 319 participants in total, so the estimate is off by 5 participants this time. We still have a few steps for rounding error, so this is close enough to show it is the equivalent but more awkward process.

If you wanted to use this function for a sensitivity power analysis, you can convert f^2 back to Pearson's r using psychometrica.de or use the following code:

```
# f2 from the output
f2 <- .042

# convert to r from the square root of f2 / f2 + 1
r <- sqrt(f2 / (f2 + 1))
```

10.5 Reporting a power analysis

Bakker et al. (2020) warned that only 20% of power analyses contained enough information to be fully reproducible. To report your power analysis, the reader needs the following four key pieces of information:

- The type of test you based the power analysis on (e.g., t-test, correlation, regression),
- The software used to calculate power (i.e., cite the pwr package, see How to cite R),
- The inputs that you used (alpha, power, effect size, sample size, tails), and
- Why you chose those inputs.

In this chapter, we will only cover the first three. The justification for your inputs comes under evaluation skills, so we will work on that in the course materials. Please note there is no single 'correct' way to report a power analysis, we just provide examples. Just be sure that you have the four key pieces of information.

10.5.1 Reporting a t-test power analysis

For a t-test, the key distinctive input is Cohen's d as the effect size.

> "To detect an effect size of Cohen's d = 0.54 with 90% power (alpha = .05, two-tailed), the pwr package (Champely, 2020) in R (R Core Team, 2024) suggests we would need 74 participants per group (N = 148) for an independent samples t-test."

Alternatively, if you reported a sensitivity power analysis, the emphasis goes to the effect size your study would be sensitive to.

> "With our final sample size of 40 participants per group, a sensitivity power analysis for an independent samples t-test using the pwr package (Champely, 2020; R Core Team, 2024) showed we could detect an effect size of d = 0.73 with 90% power (5% alpha, two-sided)."

10.5.2 Reporting a correlation power analysis

For a correlation, the key distinctive input is Pearson's r as the effect size.

> "To detect an effect size of r = .20 with 95% power (alpha = .05, one-tailed), the pwr package (Champely, 2020) in R (R Core Team, 2024) suggests we would need 266 participants for a Pearson's r correlation."

And for a sensitivity power analysis.

> "With our final sample size of 271 participants, a sensitivity power analysis for a Pearson's r correlation using the pwr package (Champely, 2020; R Core Team, 2024) showed we could detect an effect size of r = .20 with 95% power (5% alpha, one-sided)."

10.5.3 Reporting a regression power analysis

For regression, the key distinctive inputs are f^2 as the effect size, including any details of converting effect sizes, plus the number of predictors.

> "To detect an effect size of Cohen's $f^2 = .073$, we first converted the effect size from d = 0.54. For 90% power (alpha = .05, two-tailed), the pwr package (Champely, 2020) in R (R Core Team, 2024) suggests we would need 147 participants split into two groups for a regression model with one categorical predictor."

For a sensitivity power analysis, remember to include a note of any effect size conversions.

> "We used the pwr package (Champely, 2020; R Core Team, 2024) to conduct a sensitivity power analysis for linear regression with one predictor. With a final sample size of 319, we would be able to detect an effect size of Cohen's $f^2 = .041$ (95% power, 5% alpha). Converted to Pearson's r, this would be an effect size of $r = .20$."

10.6 Test Yourself

To end the chapter, we have some knowledge check questions to test your understanding of the concepts we covered in the chapter. We then have some error mode tasks to see if you can find the solution to some common errors in the concepts we covered in this chapter.

10.6.1 Knowledge check

Question 1. If you want to conduct an *a priori* power analysis , what input do you leave blank to solve for?

- (A) effect size
- (B) power
- (C) sample size
- (D) alpha

Question 2. If you want to conduct a sensitivity power analysis , what input do you leave blank to solve for?

- (A) effect size

- (B) alpha
- (C) power
- (D) sample size

Read the following output for an *a priori* power analysis. The next two questions are based on this output.

```
     Two-sample t test power calculation

              n = 89.95986
              d = 0.42
      sig.level = 0.05
          power = 0.8
    alternative = two.sided

NOTE: n is number in *each* group
```

Question 3. Our smallest effect size of interest is:

- (A) d = 0.80
- (B) d = 0.42
- (C) r = .42
- (D) r = .80

Question 4. For these inputs, we would need to recruit how many participants per group?

- (A) 42
- (B) 80
- (C) 89
- (D) 90

Read the following output for a sensitivity power analysis. The next two questions are based on this output.

```
     approximate correlation power calculation (arctangh transformation)

              n = 72
              r = 0.3695127
      sig.level = 0.05
          power = 0.9
    alternative = two.sided
```

Question 5. Our final sample size was:

- (A) 90
- (B) 50
- (C) 36
- (D) 72

Question 6. For these inputs, what effect size would we be sensitive to detect?

- (A) r = .37
- (B) r = .90
- (C) r = .72
- (D) r = .05

10.6.2 Error mode

The following questions are designed to introduce you to making and fixing errors. For this topic, we focus on simple linear regression between two continuous variables. There are not many outright errors that people make here, more misspecifications that are not doing what you think they are doing.

Create and save a new R Markdown file for these activities. Delete the example code, so your file is blank from line 10. Create a new code chunk to load the packages tidyverse and pwr.

Below, we have several variations of a code chunk error or misspecification. Copy and paste them into your R Markdown file below the code chunk to load tidyverse and pwr. Once you have copied the activities, click knit and look at the error message you receive. See if you can fix the error and get it working before checking the answer.

- unconverted effect sizes

Question 7. Copy the following code chunk into your R Markdown file and press knit. You should get a cryptic sounding error like `Error in uniroot(function(n) eval(p.body) - power, c(4 + 1e-10, 1e+09)): f() values at end points not of opposite sign`.

````
```{r}
pwr.r.test(n = NULL,
           r = .20,
           sig.level = .05,
           power = .95,
           alternative = "less")
```
````

Explain the solution

In this example, we specified a positive effect size but negative one-tailed test. They must be consistent, so you either need to make the hypothesis the same:

```
pwr.r.test(n = NULL,
           r = .20,
           sig.level = .05,
           power = .95,
           alternative = "greater")
```

Or the effect size the same:

```
pwr.r.test(n = NULL,
           r = -.20,
           sig.level = .05,
           power = .95,
           alternative = "less")
```

Both will produce the same sample size as it is the absolute effect which is important, but we recommend making it consistent with your research question / hypothesis.

Question 8. Copy the following code chunk into your R Markdown file and press knit. You want to conduct a sensitivity power analysis when you have unequal sample sizes. You should get the following error: `Error in pwr.t.test(n1 = 40, n2 = 50, d = NULL, sig.level = 0.05, power = 0.9,  : unused arguments (n1 = 40, n2 = 50)`.

```{r}
pwr.t.test(n1 = 40,
           n2 = 50,
           d = NULL,
           sig.level = .05,
           power = .90,
           alternative = "two.sided")
```

Explain the solution

In this example, we used the wrong function. `pwr.t.test()` only accepts `n` as a single argument. If you want a sensitivity power analysis for unequal sample sizes, you need the function `pwr.t2n.test()`:

```
pwr.t2n.test(n1 = 40, n2 = 50,
             d = NULL,
             sig.level = .05,
             power = .90,
             alternative = "two.sided")
```

Question 9. Copy the following code chunk into your R Markdown file and press knit. In your research to establish your smallest effect size of interest, you found a meta-analysis which found the average effect size for your topic was d = 0.54. For your correlational study, you use this effect size for your *a priori* power analysis. This...works, but is this all consistent?

```{r}
pwr.r.test(n = NULL,
           r = .54,
           sig.level = .05,
           power = .95,
           alternative = "two.sided")
```

Explain the solution

In this example, we used the wrong effect size. We see this error a lot when people are looking for past studies to inform their smallest effect size of interest. You find a meta-analysis which is perfect, but it reports Cohen's d when you want Pearson's r for your study. You can convert between effect sizes (with the caveat the studies should be comparable), but the same number means different things. Mistaking d = 0.54 for Pearson's r is going to vastly underestimate the sample size you need, as it would be

converted to $r = .26$.

```
pwr.r.test(n = NULL,
           r = .26,
           sig.level = .05,
           power = .95,
           alternative = "two.sided")
```

10.7 Words from this Chapter

Below you will find a list of words that were used in this chapter that might be new to you in case it helps to have somewhere to refer back to what they mean. The links in this table take you to the entry for the words in the PsyTeachR Glossary. Note that the Glossary is written by numerous members of the team and as such may use slightly different terminology from that shown in the chapter.

term	definition
alpha	(stats) The cutoff value for making a decision to reject the null hypothesis; (graphics) A value between 0 and 1 used to control the levels of transparency in a plot
beta	The false negative rate we accept for a statistical test.
false-negative	When a test concludes there is no effect when there really is an effect
false-positive	When a test concludes there is an effect when there really is no effect
hypothesis	A proposed explanation made on the basis of limited evidence as a starting point for further investigation.
power	The probability of rejecting the null hypothesis when it is false.
probability	A number between 0 and 1 where 0 indicates impossibility of the event and 1 indicates certainty

10.8 End of Chapter

Great work, being able to conduct a power analysis is a great skill to have for designing an informative study. Although things have improved over the years, it is still relatively rare to see a study in the wild report a power analysis to justify their sample size. Keep in mind they involve a lot of subjective decision making as the values you choose for alpha, power, and your smallest effect size have flexibility. A larger sample - and hence more powerful study - would always be useful, but you are never working with unlimited resources. You must make compromises and think about whether you can conduct an informative study with the

resources available to you. This means the hard work comes into making decisions about the values you enter, rather than the data skills for power analysis being difficult.

In the next - and final for the Research Methods 1 component - chapter, we cover screening data and decision making in data analysis. In Chapters 8 and 9, we covered topics like diagnostic checks for statistical models. Some of them looked fine, whereas some looked potentially problematic. In the next chapter, we work through the decisions you must make when analysing data like checking for missing data, outliers, and issues with diagnostic checks. Importantly, we outline the kind of solutions you can consider for those problems which we omitted in previous chapters.

11 Missing data, outliers, and checking assumptions

In this chapter, you will work on decisions that come up in data analysis. In Chapters 8 and 9, you learnt about different inferential statistics and checking assumptions, but not what your options are once you experience different problems. In this final chapter for the Research Methods 1 content, you will learn about identifying and excluding missing data, different strategies for identifying and excluding extreme values or outliers, and your options when checking modelling assumptions.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Identify missing data and justify your strategy for excluding missing data.
- Identify extreme values or outliers and justify your strategy for handling them.
- Justify your choice of statistical test or modelling approach given assumption checks.

11.1 Chapter preparation

11.1.1 Organising your files and project for the chapter

For this chapter, we are going to revisit the data sets you worked with in Chapters 8 (Dawtry et al., 2015) and 9 (Lopez et al., 2023). They each presented some useful examples for checking modelling assumptions and the decisions that go into data analysis. We might not use both data sets for each topic we cover, but they will be useful to demonstrate some of the problems and decisions we highlighted in previous chapters, but did not explore solutions.

Before we can get started, you need to organise your files and project for the chapter, so your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, create a new folder called `Chapter_11_screening_data`. Within `CChapter_11_screening_data`, create two new folders called `data` and `figures`.

2. Create an R Project for `Chapter_11_screening_data` as an existing directory for your chapter folder. This should now be your working directory.
3. Create a new R Markdown document and give it a sensible title describing the chapter, such as `11 Missing Data, Outliers, and Assumptions`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Chapter_11_screening_data` folder.
4. The Dawtry et al. (2015) data wrangling steps were quite long, so please save this clean version of the data to focus on screening data in this chapter: Dawtry_2015_clean.csv. You will also need to save the data from Lopez et al. (2023) if you have not downloaded it yet: Lopez_2023.csv. Right click the link and select "save link as", or clicking the link will save the files to your Downloads. Make sure that you save the files as ".csv". Save or copy the files to your `data/` folder within `Chapter_11_screening_data`.

You are now ready to start working on the chapter!

11.1.2 Activity 1 - Read and wrangle the data

As the first activity, try and test yourself by completing the following task list to read and wrangle the two data files. There is nothing extra to do with this version of the Dawtry data and one small step for the Lopez data.

Try this

To read and wrangle the data, complete the following tasks:

1. Load the following packages:
    - performance
    - tidyverse
2. Read the data file `data/Dawtry_2015_clean.csv` to the object name `dawtry_clean`.
3. Read the data file `data/Lopez_2023.csv` to the object name `lopez_data`.
4. Create a new object called `lopez_clean` based on `lopez_data`:
    - Create a new variable called `Condition_label` by recoding `Condition`. "0" is the "Control" group and "1" is the "Experimental" group.

Show me the solution

You should have the following in a code chunk:

```
# load the relevant packages
library(performance)
library(tidyverse)

# Read the Dawtry_2015_clean.csv file
dawtry_clean <- read_csv("data/Dawtry_2015_clean.csv")

# Read the Lopez_2023.csv file
lopez_data <- read_csv("data/Lopez_2023.csv")

# recode condition
lopez_clean <- lopez_data %>%
  mutate(Condition_label = case_match(Condition,
                                      0 ~ "Control",
                                      1 ~ "Experimental"))
```

11.2 Missing data

Checking whether data are missing are relatively straight forward. **Missing values** in a spreadsheet will be recorded as NA and there are a few ways of identifying them. The much more difficult part of missing data is considering *why* they are missing in the first place. For example, it might be because:

- Your participants accidentally missed a question.
- You made a mistake while setting up your questionnaire/experiment and some responses did not save.
- Your participants intentionally did not want to answer a question.
- Your participants did not turn up to a final testing session.

For the first two reasons, it is not ideal as we are losing data but there is no systematic pattern to why the data is missing. For the latter two reasons, there might be a relationship between a key variable and whether the data are missing. This is where it is particularly important to consider the role of missing data. We are focusing on data skills here rather than the conceptual understanding, but missing data are commonly categorised as:

- **Missing completely at random**.

- **Missing at random**.
- **Missing not at random**.

For this introductory course, we do not have time to investigate strategies to address missing data apart from focusing on complete cases and ignoring missing data, but you might find Jakobsen et al. (2017) useful if you want to explore options like data imputation.

11.2.1 Activity 2 - Identifying missing data

Returning to data skills, the simplest way of getting an overview of whether any data are missing is using the `summary()` function. For this part, we will focus on `dawtry_clean` from Dawtry et al. (2015).

```
summary(dawtry_clean)
```

```
       PS      Household_Income Political_Preference      age
 Min.   :  1   Min.   :    20   Min.   :1.000        Min.   :19.0
 1st Qu.: 77   1st Qu.: 25000   1st Qu.:3.000        1st Qu.:28.0
 Median :153   Median : 42000   Median :4.000        Median :33.5
 Mean   :153   Mean   : 54732   Mean   :4.465        Mean   :37.4
 3rd Qu.:229   3rd Qu.: 75000   3rd Qu.:6.000        3rd Qu.:46.0
 Max.   :305   Max.   :350000   Max.   :9.000        Max.   :69.0
               NA's   :4        NA's   :4            NA's   :1
    gender     Population_Inequality_Gini_Index Population_Mean_Income
 Min.   :1.00   Min.   :14.26                    Min.   : 14205
 1st Qu.:1.00   1st Qu.:31.10                    1st Qu.: 47250
 Median :1.00   Median :35.66                    Median : 58650
 Mean   :1.48   Mean   :35.51                    Mean   : 58605
 3rd Qu.:2.00   3rd Qu.:40.73                    3rd Qu.: 67875
 Max.   :2.00   Max.   :57.45                    Max.   :138645
 NA's   :3
 Social_Circle_Inequality_Gini_Index Social_Circle_Mean_Income
 Min.   : 2.00                       Min.   : 12000
 1st Qu.:19.79                       1st Qu.: 36000
 Median :25.59                       Median : 51060
 Mean   :26.35                       Mean   : 54294
 3rd Qu.:33.27                       3rd Qu.: 66375
 Max.   :61.36                       Max.   :148500

 fairness_satisfaction redistribution
 Min.   :1.000         Min.   :1.00
```

```
1st Qu.:2.000          1st Qu.:3.25
Median :3.000          Median :4.00
Mean   :3.539          Mean   :3.91
3rd Qu.:5.000          3rd Qu.:4.75
Max.   :9.000          Max.   :6.00
```

We get a range of summary statistics for each variable but importantly for our purposes here, the final entry is `NA's`, where relevant. We can see there are 4 missing values for household income, 4 for political preference, 1 for age, and 3 for gender.

Try this

If you explore `lopez_clean` from Lopez et al. (2023), do we have any missing data to worry about?

- (A) Yes
- (B) No

Solution

Yes, it looks like there is also a small amount of missing data here. There is 1 for sex, 2 for estimated ounces, and 3 for estimates calories.

```
summary(lopez_clean)
```

```
 ParticipantID       Sex              Age          Ethnicity
 Min.   :1001   Min.   :0.0000   Min.   :18.00   Min.   :1.000
 1st Qu.:1202   1st Qu.:1.0000   1st Qu.:19.00   1st Qu.:3.000
 Median :1462   Median :1.0000   Median :20.00   Median :3.000
 Mean   :1456   Mean   :0.8099   Mean   :20.47   Mean   :3.261
 3rd Qu.:1704   3rd Qu.:1.0000   3rd Qu.:21.00   3rd Qu.:4.000
 Max.   :1928   Max.   :3.0000   Max.   :54.00   Max.   :8.000
                NA's   :1
   OzEstimate       CalEstimate      M_postsoup     F_CaloriesConsumed
 Min.   :  0.010   Min.   :  1.0   Min.   : 0.600   Min.   :  13.31
 1st Qu.:  2.000   1st Qu.: 50.0   1st Qu.: 5.575   1st Qu.: 123.65
 Median :  4.000   Median : 90.0   Median : 8.700   Median : 192.97
 Mean   :  6.252   Mean   :124.6   Mean   :10.203   Mean   : 226.30
 3rd Qu.:  8.000   3rd Qu.:160.0   3rd Qu.:13.125   3rd Qu.: 291.11
 Max.   :100.000   Max.   :800.0   Max.   :46.200   Max.   :1024.72
```

```
NA's   :2         NA's   :3
  Condition      Condition_label
Min.   :0.0000   Length:464
1st Qu.:0.0000   Class :character
Median :0.0000   Mode  :character
Mean   :0.4698
3rd Qu.:1.0000
Max.   :1.0000
```

11.2.2 Activity 3 - Removing missing data

Once we know whether missing data are present, we must consider what to do with them. For this chapter, we are only going to control removing participants, but you could apply a data imputation technique at this point if appropriate.

For all the modelling techniques we apply in this book, the functions will remove participants who have one or more missing values from any variable involved in the analysis. The functions will give you a warning to highlight when this happens, but it is normally a good idea to remove participants with missing data yourself so you have a note of how many participants you remove.

For `dawtry_clean`, the tidyverse function `drop_na()` is the easiest way of removing missing data, either participants with any missing data or by specifying individual variables.

```
dawtry_all_missing <- dawtry_clean %>%
  drop_na()

dawtry_income_missing <- dawtry_clean %>%
  drop_na(Household_Income)
```

We can compare the number of participants by using the `nrow()` function to count how many rows are in each object.

```
# How many rows in the full data?
nrow(dawtry_clean)

# How many rows when we remove missing data in one variable?
nrow(dawtry_income_missing)

# How many rows when we remove any missing value?
nrow(dawtry_all_missing)
```

```
[1] 305
[1] 301
[1] 294
```

Like most data skills and statistics concepts, the key skill here comes in decision making; documenting and justifying the approach that you take.

11.3 Outliers

The next data screening concept revolves around identifying potential outliers. Like missing data, the difficulty here comes in first deciding what an outlier is and then deciding on what to do with it. Leys et al. (2019) mention one study found 14 definitions and 39 unique ways of identifying outliers, so this is our second key area of decision making. Leys et al. categorise outliers into three types:

1. **Error outliers**.
2. **Interesting outliers**.
3. **Random outliers**.

Even simpler, we can consider values as legitimate or not legitimate. Error outliers would be not legitimate as they represent a mistake or error, so they would potentially provide misleading results. These are values you can justify removing or correcting as they should not be there in the first place.

Interesting and random outliers would be legitimate as they are not clear mistakes or errors; they are just different to the majority of values in the data. In most cases, it is not a good idea to remove these kind of values as they potentially tell you something interesting, but you might need to approach the data analysis in a different way to ensure the results are robust to extreme values.

11.3.1 Activity 4- Identifying error outliers

Unless you can specifically identify values or participants you know contain errors, the main way to check is by ensuring the values are within known limits.

We can look at `dawtry_clean` and the key variables we explored in Chapter 8. Fairness and satisfaction was on a 1-9 scale, so we can check the minimum and maximum values and create a plot. For example, we can isolate the variable and apply the `summary()` function.

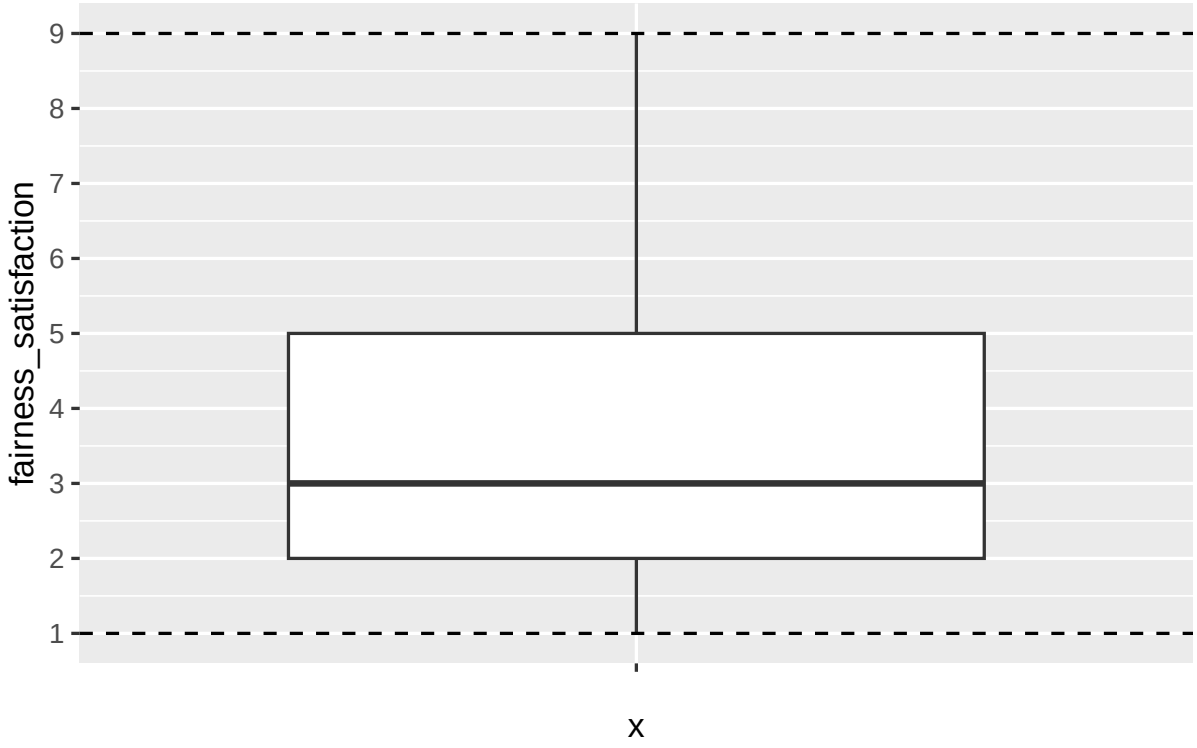
```
dawtry_clean %>%
  select(fairness_satisfaction) %>%
  summary()
```

```
 fairness_satisfaction
 Min.   :1.000
 1st Qu.:2.000
 Median :3.000
 Mean   :3.539
 3rd Qu.:5.000
 Max.   :9.000
```

The minimum and maximum values are nice and consistent with what we expect.

For a visual check, we can also plot the minimum and maximum possible values on a boxplot. This is just a check for you, so you do not need to worry so much about the presentation.

```
dawtry_clean %>%
  ggplot(aes(y = fairness_satisfaction, x = "")) + # make x blank
  geom_boxplot() +
  scale_y_continuous(limits = c(1, 9),
                     breaks = seq(1, 9, 1)) +
  geom_hline(yintercept = c(1, 9), # min and max values
             linetype = 2) # create dashed line
```



Try this

If you explore `redistribution` from `dawtry_clean`, the minimum and maximum values are 1-6. Does it look like there are any problematic looking values?

- (A) Yes
- (B) No

Solution

No, it looks like all values are within the expected 1-6 range.

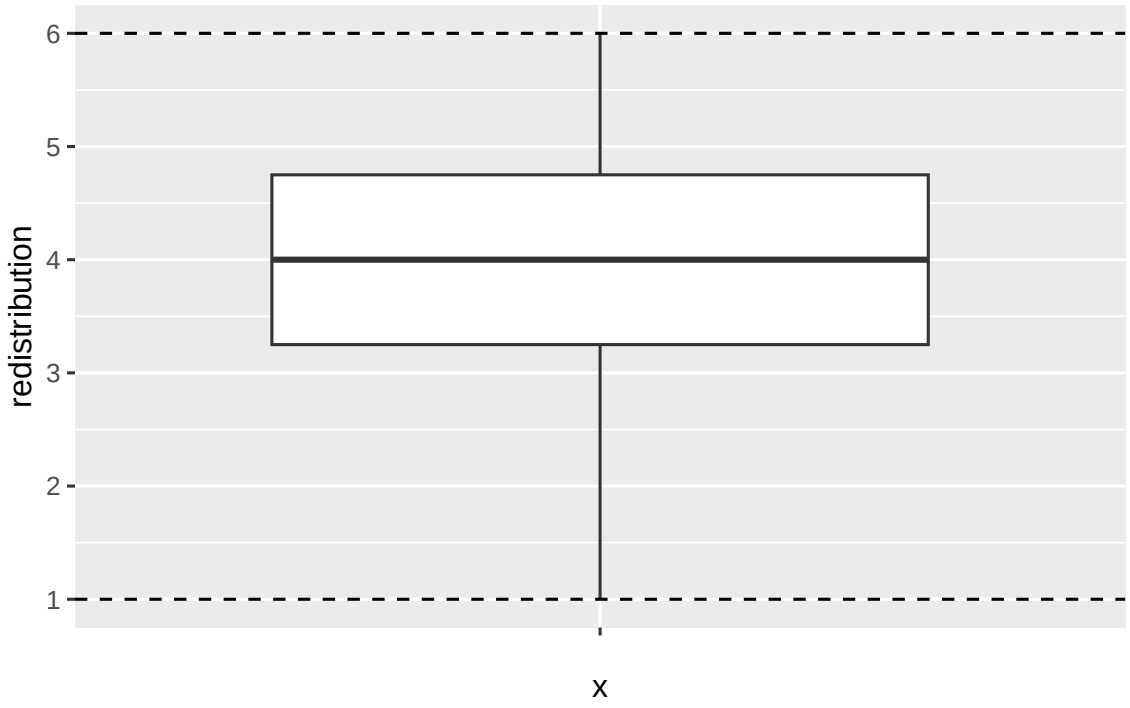
```
dawtry_clean %>%
  select(redistribution) %>%
  summary()
```

```
 redistribution
 Min.   :1.00
 1st Qu.:3.25
```

```
 Median :4.00
 Mean   :3.91
 3rd Qu.:4.75
 Max.   :6.00
```

We can also confirm this with a visual check.

```
dawtry_clean %>%
  ggplot(aes(y = redistribution, x = "")) + # make x blank
  geom_boxplot() +
  scale_y_continuous(limits = c(1, 6),
                     breaks = seq(1, 6, 1)) +
  geom_hline(yintercept = c(1, 6), # min and max values
             linetype = 2) # create dashed line
```



If you did identify error outliers to remove, then you could use `filter()` (Chapter 5) to directly remove values outside your known range, or you could first use `case_when()` to code observations as outliers or not (Chapter 4), before deciding to filter them out.

11.3.2 Activity 5- Identifying interesting or random outliers

Identifying error outliers relies on manually setting known minimum and maximum values, whereas identifying interesting or random outliers relies on data driven boundaries. For this example, we focus on univariate outliers, where we focus on one variable at a time. When we return to checking assumptions of regression models, you can identify interesting or random outliers through observations with large leverage / Cook's distance values.

In general, we recommend not removing outliers providing you are confident they are not errors. It is better to focus on modelling your outcome in a more robust way. However, it is also important you know how to identify errors for strategies you will come across in published research.

We focus here on setting boundaries using the median absolute deviation (MAD) as recommended by Leys et al. (2019). You will see other approaches in the literature, but this method is useful as it's influenced less by the very outliers it is trying to identify. We will use `lopez_clean` from Lopez et al. (2023) for this section.

There are two main steps to this process because we have two groups and each group will have different boundaries. If you only have individual variables, then you could just `mutate()` your data, without the initial `group_by()` and `summarise()` step.

First, we group by the condition to get one value per group. We then calculate a few values for the median ounces of soup, 3 times the MAD in line with Leys et al., then calculating the upper and lower bound using these objects.

```
# create a new object with values per group
mad_bounds <- lopez_clean %>%
  group_by(Condition_label) %>%
  summarise(oz_median = median(M_postsoup), # median of soup in oz
            oz_MAD = 3 * mad(M_postsoup), # 3 times the MAD
            lower = oz_median - oz_MAD, # lower bound
            upper = oz_median + oz_MAD) # upper bound

mad_bounds
```

```
# A tibble: 2 x 5
  Condition_label oz_median oz_MAD lower upper
  <chr>               <dbl>  <dbl> <dbl> <dbl>
1 Control               7.8   14.7 -6.88  22.5
2 Experimental         10.6   17.6 -6.97  28.2
```

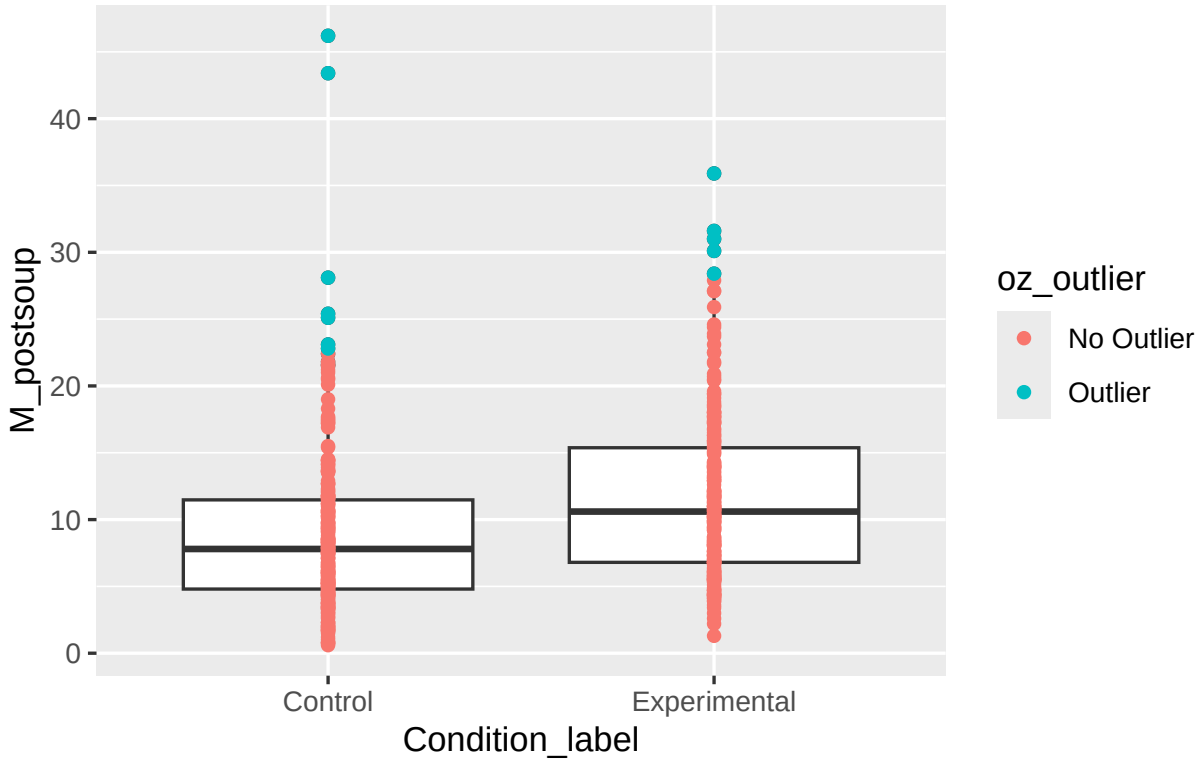
In this example, the lower bound is lower than 0 as the smallest possible value. The upper bounds are then between 22 and 28 depending on the group.

Second, we must add these values to the other information we have available. We join the data sets using `Condition_label`. This adds the relevant values to each group. We then use `mutate()` and `case_when()` to label values as outliers or not. If they are outside the lower and upper bounds, they are labelled as "outlier". If they are inside the lower and upper bounds, they are labelled as "no outlier".

```
lopez_mad <- lopez_clean %>%
  inner_join(mad_bounds, by = "Condition_label") %>%
  mutate(oz_outlier = case_when(M_postsoup < lower | M_postsoup > upper ~ "Outlier",
                                M_postsoup >= lower | M_postsoup <= upper ~ "No Outlier"))
```

We can use these in one of two ways. First, we can visualise the presence of outliers by adding coloured points. These are checks for you again, so you do not need to worry about the plot formatting.

```
lopez_mad %>%
  ggplot(aes(x = Condition_label, y = M_postsoup)) +
  geom_boxplot() +
  geom_point(aes(colour = oz_outlier)) # needs to be within aes to set dynamic values
```



We can see a few values per group flagged as outliers using this criterion. If you did decide to remove outliers, then you could use filter to remove them:

```
lopez_remove <- lopez_mad %>%
  filter(oz_outlier == "No Outlier")
```

Try this

If you switch to `dawtry_clean` from Dawtry et al. (2015), apply the MAD procedure to the variable `fairness_satisfaction`. Does it look like there are any outliers using this criterion?

- (A) Yes
- (B) No

.

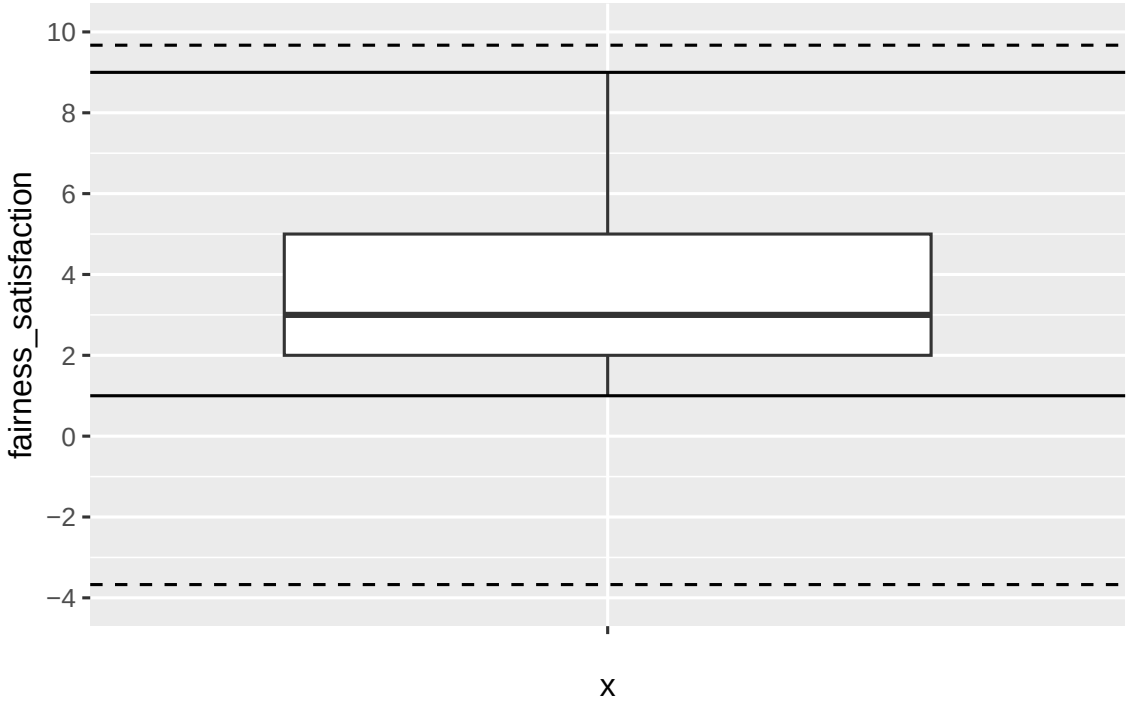
Solution

No, none of the values are outside the MAD thresholds. The thresholds are well beyond the minimum and maximum possible values of 1-9 for this variable.

```
dawtry_mad <- dawtry_clean %>%
  mutate(fs_median = median(fairness_satisfaction), # median of fairness/satisfaction
         fs_MAD = 3 * mad(fairness_satisfaction), # 3 times the MAD
         lower = fs_median - fs_MAD, # lower bound
         upper = fs_median + fs_MAD,  # upper bound
         fs_outlier = case_when(fairness_satisfaction < lower | fairness_satisfaction > upp
                                fairness_satisfaction >= lower | fairness_satisfaction <= u
```

For this variable and it's bounded scale, no value is above or below the thresholds. You can see this in the data, or add horizontal lines in a plot since we are only plotting one variable. The dashed lines are the MAD thresholds and the solid lines are the minimum and maximum possible values.

```
dawtry_mad %>%
  ggplot(aes(y = fairness_satisfaction, x = "")) +
  geom_boxplot() +
  geom_hline(aes(yintercept = lower),
             linetype = 2) + # dashed line
  geom_hline(yintercept = c(1, 9)) +
  geom_hline(aes(yintercept = upper),
             linetype = 2) +
  scale_y_continuous(limits = c(-4, 10),
                     breaks = seq(-4, 10, 2))
```



Remember: identifying outliers is a crucial researcher degree of freedom, so pre-register your choice of outlier detection wherever possible, and document how many outliers you removed. We still recommend favouring a more robust model, but you can make an informed decision now you know how to identify outliers in the data.

11.4 Checking assumptions

The final section revisits checking assumptions from Chapter 8 and 9. In those chapters, we introduced the concepts and stuck with the output regardless of whether we were happy with the assumptions or not. In this chapter, we will introduce potential solutions.

As a reminder, the assumptions for simple linear regression are:

1. The outcome is interval/ratio level data.
2. The predictor variable is interval/ratio or categorical (with two levels at a time).
3. All values of the outcome variable are independent (i.e., each score should come from a different participant/observation).
4. The predictors have non-zero variance.
5. The relationship between the outcome and predictor is linear.
6. The residuals should be normally distributed.
7. There should be homoscedasticity.

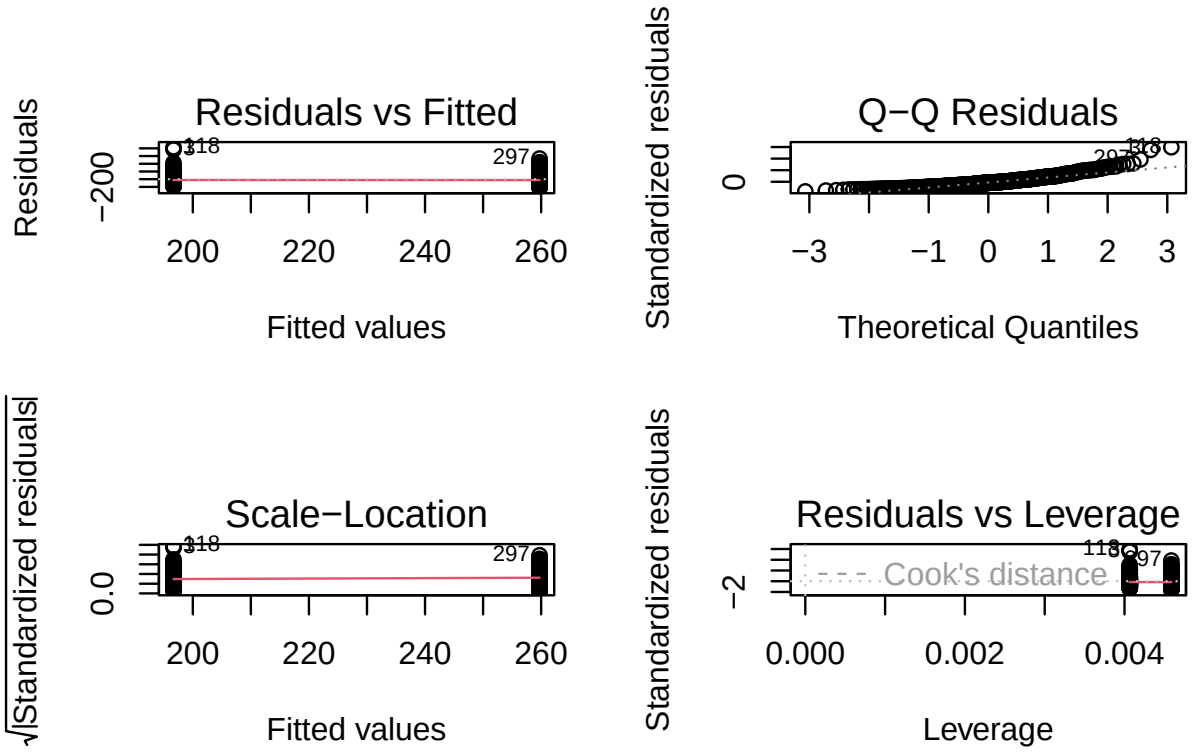
Assumptions 1-4 are pretty straight forward as they relate to your understanding of the design or a simple check on the data. On the other hand, assumptions 5-7 require diagnostic checks.

For this part, we focus on Lopez et al. (2023) as the assumptions did not look quite right in Chapter 9. As a reminder, we can get a quick diagnostic check by running `plot()` on the model object:

```
# Condition as a factor containing 0 and 1
lm_cals_numbers <- lm(formula = F_CaloriesConsumed ~ Condition,
                      data = lopez_clean)

# Change the panel layout to 2 x 2
par(mfrow = c(2,2))

# plot the diagnostic plots
plot(lm_cals_numbers)
```



All of the checks look good apart from normality. We have a clear deviation from the line to curve around at lower and higher values along the x-axis. In Chapter 9, we said we would stick with it as it was consistent with the original article's analyses, but now we will outline options available to you:

1. Parametric tests are robust.
2. Treat the data as non-parametric.
3. Use an alternative model.

11.4.1 Activity 6 - Parametric tests are robust

One get out jail free card is doing nothing as the parametric tests are robust to violations of assumptions. You will often hear this and it is largely true under certain conditions. Knief & Forstmeier (2021) report a simulation study where they explore how violating assumptions like linearity, normality, and outliers affect the results of parametric statistical tests like simple linear regression. They found the tests were robust to violations - particularly normality - apart from when there were extreme outliers which could bias the results.

In the Lopez et al. example, we identified a few outliers using the 3 times the MAD criterion and the strictest Cook's distance cut-off in Chapter 9, but normality was the only notable problem in the diagnostic checks. One option would be to feel reassured the results are robust to minor violations and explain that in your report.

The second option would be checking the results are robust to the presence of outliers. Remember, we advise excluding outliers as a last resort if you consider them legitimate, but it provides a robustness check to see if you get similar conclusions with and without the outliers. For example, we can exclude outliers using the MAD criterion and check the results:

```
# remove outliers under 3 * MAD

lm_cals_outliers <- lm(formula = F_CaloriesConsumed ~ Condition,
                       data = filter(lopez_mad,
                                     oz_outlier == "No Outlier"))

summary(lm_cals_outliers)
```

```
Call:
lm(formula = F_CaloriesConsumed ~ Condition, data = filter(lopez_mad,
    oz_outlier == "No Outlier"))

Residuals:
    Min      1Q  Median      3Q     Max
-220.65  -87.56  -15.30   65.84  369.35

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  182.573      7.485  24.393  < 2e-16 ***
Condition     66.906     10.903   6.136 1.85e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 115.7 on 450 degrees of freedom
Multiple R-squared:  0.07722,   Adjusted R-squared:  0.07517
F-statistic: 37.66 on 1 and 450 DF,  p-value: 1.852e-09
```

The conclusions are very similar. The difference is still statistically significant and instead of a 63 calorie difference for the slope, we get a 67 calorie difference. So, we can stick with the original results and feel reassured that the results are robust to the presence of outliers, given the criterion we used. You would explain to the reader you checked the robustness of the results and what your final conclusion was.

11.4.2 Activity 7 - Treat the data as non-parametric

The second option is switching to a non-parametric statistical test which makes fewer assumptions about the data. In Chapter 8, we introduced the Spearman correlation and in Chapter 9 the Mann-Whitney U as the non-parametric equivalents. For both, instead of doubling the number of non-parametric tests you need to learn, we can apply a similar principle to linear regression and recreate non-parametric equivalents.

In the demonstration by Lindeløv, 2019, common statistical tests you come across are specific applications of the general linear model. Likewise, you can recreate non-parametric tests by converting continuous variables to ranks and using those in the regression model.

For example, instead of a Mann-Whitney U test, you can run wrap the number of calories (`F_CaloriesConsumed`) in the `rank()` function:

```
# Condition_label as numbers
lm_cals_ranks <- lm(formula = rank(F_CaloriesConsumed) ~ Condition,
                    data = lopez_clean)

summary(lm_cals_ranks)
```

```
Call:
lm(formula = rank(F_CaloriesConsumed) ~ Condition, data = lopez_clean)

Residuals:
     Min       1Q   Median       3Q      Max
-261.138 -110.361    1.862  111.467  263.967

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   200.03       8.27  24.188  < 2e-16 ***
Condition      69.11      12.06   5.728 1.84e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 129.7 on 462 degrees of freedom
Multiple R-squared:  0.0663,    Adjusted R-squared:  0.06428
F-statistic: 32.81 on 1 and 462 DF,  p-value: 1.836e-08
```

This means instead of comparing the raw number of calories between groups, you compare the ranks between groups. The logic here is you reduce the impact of extreme values as they become ranks instead of raw numbers, so like using the median over the mean, the difference

between the 99th and 100th number would be one position, instead of a huge difference in actual value. For example, if you had the collection of numbers 1, 2, 3, 4, and 100, there is a difference in raw and ranked values:

```
c(1, 2, 3, 4, 100)

rank(c(1, 2, 3, 4, 100))
```

```
[1]   1   2   3   4 100
[1] 1 2 3 4 5
```

In the write-up, just note you still report the model and null hypothesis significance testing elements like the p-value, but the slope is less interpretable as an effect size. It is now a difference in ranks, so it will be more useful to calculate the difference in medians to present the reader.

Try this

If you switch to `dawtry_clean` from Dawtry et al. (2015), apply the same logic to a correlational design. Is there a significant association between `fairness_satisfaction` and `redistribution` if you convert both variables to ranks in a regression model?

- (A) Yes
- (B) No

.

Solution

Yes, you get a similar finding to the original model where you predict raw values of redistribution from fairness and satisfaction. This time, you are looking at the association in ranks instead. There is still a statistically significant negative relationship and this recreates the process behind the Spearman correlation.

```
# Variables as ranks
lm_dawtry_ranks <- lm(formula = rank(redistribution) ~ rank(fairness_satisfaction),
                      data = dawtry_clean)

summary(lm_dawtry_ranks)
```

```
Call:
```

```
lm(formula = rank(redistribution) ~ rank(fairness_satisfaction),
    data = dawtry_clean)

Residuals:
     Min       1Q   Median       3Q      Max
-217.133  -43.673   -7.611   37.367  228.315

Coefficients:
                             Estimate Std. Error t value Pr(>|t|)
(Intercept)                 257.88387    7.46475   34.55   <2e-16 ***
rank(fairness_satisfaction)  -0.68552    0.04239  -16.17   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 64.56 on 303 degrees of freedom
Multiple R-squared:  0.4633,    Adjusted R-squared:  0.4615
F-statistic: 261.6 on 1 and 303 DF,  p-value: < 2.2e-16
```

For further reinforcement of how this is the same process underlying Spearman's correlation, take the square root of the R^2 value in this model and compare it to the value of r_s from Chapter 8.

11.4.3 Use an alternative model

The third and final option is considering whether a parametric test is the right choice in the first place. The default assumption in psychology research is assuming everything is linear and normal as it is convenient and applies to many scenarios, but there are some outcomes and models which will always be inappropriate to model as linear and normal. For example, if your outcome is dichotomous (0 or 1; correct or incorrect), then you must assume a **binomial distribution** and use something like a **logistic regression** model.

However, these models are beyond the scope of this introductory course. If you are interested, a PsyTeachR book from another one of our courses has a chapter on generalised linear regression for modelling different distributions, but we do not expect you to learn this for RM1 or RM2. As long as you show awareness of checking modelling assumptions and consider the first and second options above, that is all we ask of you.

11.5 Test yourself

To end the chapter, we have some knowledge check questions to test your understanding of the concepts we covered in the chapter. There are no error mode questions in this chapter as we have focused more on decision making around past concepts rather potential errors in new concepts.

11.5.1 Knowledge check

For this chapter's knowledge check section, instead of purely conceptual questions about functions, we have an example model and output and we would like you to consider the presence of missing data, outliers, and modelling assumptions.

We have a simulated study where our research question is "Are scientists perceived to be more objective than highly-educated lay people"? Participants were randomly allocated to rate the characteristics of scientists or highly-educated lay people. The outcome was a 0-10 scale made up of 10 items of how objective they perceive the target to be, from not very objective to very objective.

Question 1. Based on the description of the study, the mostly likely design is:

- (A) One-sample
- (B) Correlational
- (C) Within-subjects
- (D) Between-subjects

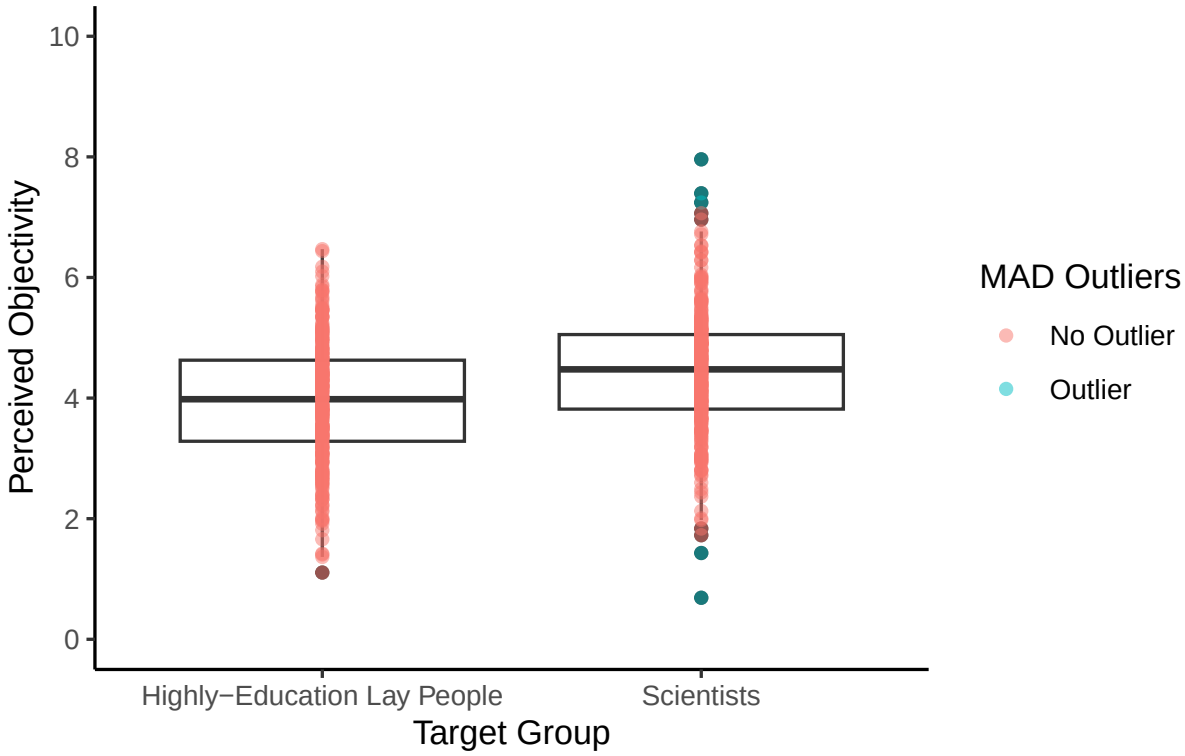
Question 2. Look at the following summary table of the data we are working with. Is there any missing data present?

- (A) Yes
- (B) No

```
     id                  group      objectivity
 Length:600         lay       :300   Min.   :0.689
 Class :character   scientists:300   1st Qu.:3.509
 Mode  :character                    Median :4.232
                                     Mean   :4.190
                                     3rd Qu.:4.897
                                     Max.   :7.959
                                     NA's   :9
```

Question 3. Look at the following boxplot of the data we are working with. We have applied the criterion 3 times the MAD to highlight potential extreme values.

- Looking at the highly-educated group, are there any potential extreme values?
- (A) Yes
- (B) No
- Looking at the scientist group, are there any potential extreme values?
- (A) Yes
- (B) No



Question 4. If we fit a linear regression model, the effect of group is

- (A) statistically significant
- (B) not statistically significant

and the

- (A) highly-educated lay person
- (B) scientist

scored higher on objectivity.

```
Call:
lm(formula = objectivity ~ group, data = df)

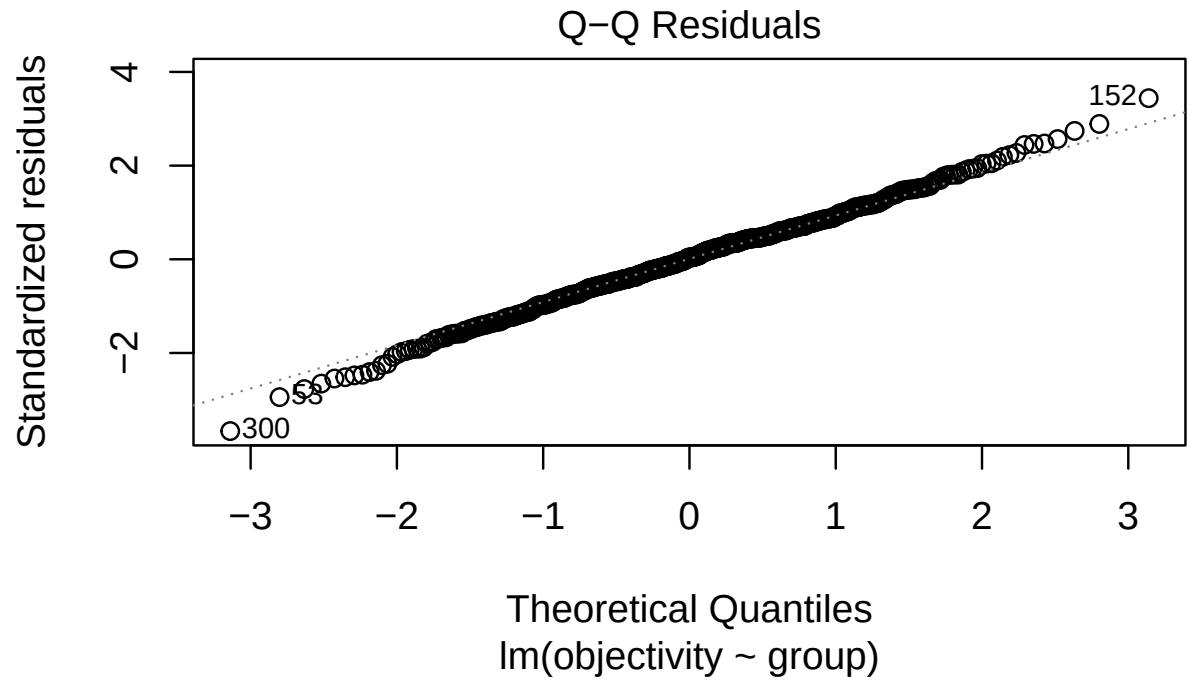
Residuals:
    Min      1Q  Median      3Q     Max
-3.7514 -0.6257  0.0392  0.6479  3.5185

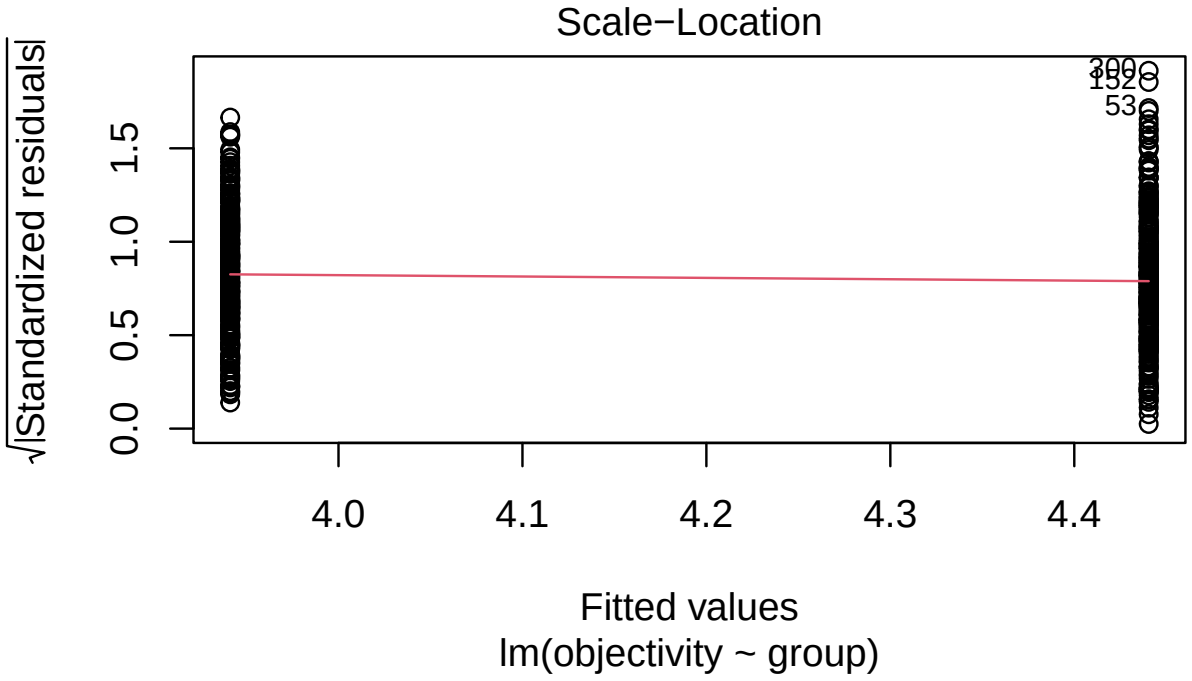
Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)      3.94113    0.05944  66.299  < 2e-16 ***
groupscientists  0.49932    0.08428   5.924 5.33e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.024 on 589 degrees of freedom
  (9 observations deleted due to missingness)
Multiple R-squared:  0.05624,   Adjusted R-squared:  0.05464
F-statistic:  35.1 on 1 and 589 DF,  p-value: 5.331e-09
```

Question 5. If we check the modelling assumptions and focus on normality and homoscedasticity, does it look like we meet the assumptions for linear regression?

- (A) Yes
- (B) No


Q−Q Residuals
Standardized residuals
4
2
0
−2
152
53
300
−3
−2
−1
0
1
2
3
Theoretical Quantiles
lm(objectivity ~ group)


Scale−Location
√|Standardized residuals|
1.5
1.0
0.5
0.0
300
152
53
4.0
4.1
4.2
4.3
4.4
Fitted values
lm(objectivity ~ group)

Explain this answer

For normality in the first plot, it does not look like there is a significant deviation in expected values against observed values. We have a few data points highlighted at the top and bottom of the points, but there is not a consistent deviation to the pattern. Likewise, for homoscedasticity in the second plot, the red line is horizontal and there does not appear to be a noticeable difference in the variance between each group.

Question 6. If you were concerned about the presence of potential outliers from question 3, are the regression results robust if we remove those outliers?

- (A) Yes
- (B) No

```
Call:
lm(formula = objectivity ~ group, data = filter(df, obj_outlier ==
    "No Outlier"))

Residuals:
    Min      1Q  Median      3Q     Max
-2.8339 -0.6167  0.0405  0.6370  2.6338

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)      3.94113    0.05713  68.990  < 2e-16 ***
groupscientists  0.49062    0.08135   6.031 2.89e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.9845 on 584 degrees of freedom
Multiple R-squared:  0.05864,   Adjusted R-squared:  0.05702
F-statistic: 36.38 on 1 and 584 DF,  p-value: 2.887e-09
```

Explain this answer

Yes, there is very little difference in the two results, so you would confident the potential outliers are not driving the results. They are both statistically significant and there is very little different in the main effect size of interest, where the slope changes from 0.499 in question 4 to 0.491 here.

11.6 Words from this Chapter

Below you will find a list of words that were used in this chapter that might be new to you in case it helps to have somewhere to refer back to what they mean. The links in this table take you to the entry for the words in the PsyTeachR Glossary. Note that the Glossary is written by numerous members of the team and as such may use slightly different terminology from that shown in the chapter.

term	definition
binomial-distribution	Instead of the parameters mean and standard deviation in a normal distribution, you have N trials with n number of successes.
error-outliers	A mistake or impossible value in your data.
interesting-outliers	Values in your data that looks extreme until you take another variable or moderator into account.
logistic-regression	Modelling the log-odds of a dichotomous outcome as a linear combination of one or more predictors.
missing-at-random	We can predict the missing value using other variables in the data.
missing-completely-at-random	Whether the data are missing or not is completely unrelated to other variables in the data.
missing-data	If a participant or observation contains no data for one or more cells, they have missing data.
missing-not-at-random	Whether the data are missing or not is causally related to one or more other variables in the data.
random-outliers	Values in your data that are extreme compared to the majority of data points.

11.7 End of Chapter

That is the final chapter you will complete for the Research Methods 1 component of the course!

We hope you take a moment to think about everything you have achieved so far. Think back to how you felt when you were completing Chapters 1 and 2 and learning what a function is. We must get through a huge amount of content in a short space of time on the MSc conversion programmes, so we hope you are all very proud in how far you have come. We cannot guarantee everyone will come out of the course loving R and data skills, but we hope you all recognise you *can* do this.

The next few chapters you will cover in Research Methods 2, so make sure you refresh your memory of the RM1 content prior to starting as the topics build on what you already know around data skills and statistics.

12 One-way ANOVA

This chapter marks the beginning of the content you cover in Research Methods 2. You should be familiar with all the content from Research Methods 1 we covered in Chapters 1 to 11, so please revisit previous chapters if you need a refresher.

In the course materials, you have worked through manually calculating an ANOVA to gain a conceptual understanding. However, when you run an ANOVA, typically the computer does all of these calculations for you. In this chapter, we will show you how to run a one-way ANOVA using the afex package and post-hoc tests using the emmeans package.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Apply and interpret a one-way ANOVA.
- Break down the results of a one-way ANOVA using post-hocs tests and apply a correction for multiple comparisons.
- Conduct a power analysis for a one-way ANOVA.

12.1 Chapter preparation

12.1.1 Introduction to the data set

For this chapter, we are using open data from experiment 2 in James et al. (2015). The abstract of their article is:

> Memory of a traumatic event becomes consolidated within hours. Intrusive memories can then flash back repeatedly into the mind's eye and cause distress. We investigated whether reconsolidation - the process during which memories become malleable when recalled - can be blocked using a cognitive task and whether such an approach can reduce these unbidden intrusions. We predicted that reconsolidation of a reactivated visual memory of experimental trauma could be disrupted by engaging in a visuospatial task that would compete for visual working memory resources. We showed that intrusive memories were virtually abolished by playing the computer game Tetris following a memory-reactivation task 24 hr after initial

> exposure to experimental trauma. Furthermore, both memory reactivation and playing Tetris were required to reduce subsequent intrusions (Experiment 2), consistent with reconsolidation-update mechanisms. A simple, non-invasive cognitive-task procedure administered after emotional memory has already consolidated (i.e., > 24 hours after exposure to experimental trauma) may prevent the recurrence of intrusive memories of those emotional events.

In summary, they were interested in whether you can reduce intrusive memories associated with a traumatic event. Participants were randomly allocated to one of four groups and watched a video designed to be traumatic:

1. Control
2. Reactivation + Tetris
3. Tetris
4. Reactivation

They measured the number of intrusive memories prior to the start of the study, then participants kept a diary to record intrusive memories about the film in the 7 days after watching it. The authors were interested in whether the combination of reactivation and playing Tetris would lead to the largest reduction in intrusive memories. You will recreate their analyses using a one-way ANOVA.

12.1.2 Organising your files and project for the chapter

Before we can get started, you need to organise your files and project for the chapter, so your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, create a new folder called `Chapter_12_ANOVA`. Within `Chapter_12_ANOVA`, create two new folders called `data` and `figures`.
2. Create an R Project for `Chapter_12_ANOVA` as an existing directory for your chapter folder. This should now be your working directory.
3. Create a new R Markdown document and give it a sensible title describing the chapter, such as `12 ANOVA`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Chapter_12_ANOVA` folder.
4. We are working with a new data set, so please save the following data file: James_2015.csv. Right click the link and select "save link as", or clicking the link will save the files to your Downloads. Make sure that you save the file as ".csv". Save or copy the file to your `data/` folder within `Chapter_12_ANOVA`.

You are now ready to start working on the chapter!

12.1.3 Activity 1 - Read and wrangle the data

As the first activity, try and test yourself by completing the following task list to practice your data wrangling skills. Create a final object called `james_data` to be consistent with the tasks below.

Try this

To wrangle the data, complete the following tasks:

1. Load the following packages (several of these are new, so revisit Chapter 1 if you need a refresher of installing R packages, but remember not to install packages on the university computers / online server):
    - pwr
    - effectsize
    - broom
    - afex
    - emmeans
    - performance
    - tidyverse
2. Read the data file `data/James_2015.csv` to the object name `james_data`.
3. Create a new variable called `PID` that equals `row_number()` to act as a participant ID which is currently missing from the data set.
4. Convert `Condition` to a factor.
5. Select and rename the following three variables as we do not need the others:
    - `PID`
    - `Condition`
    - Rename `Days_One_to_Seven_Image_Based_Intrusions_in_Intrusion_Diary` to `intrusions`.

Show me the solution

You should have the following in a code chunk:

```r
# Load packages
library(pwr)
library(effectsize)
library(broom)
library(afex)
library(emmeans)
library(performance)
library(tidyverse)

# Read data and add new column
james_data <- read_csv("data/James_2015.csv") %>%
  mutate(PID = row_number(),
         Condition = as.factor(Condition)) %>%
  select(PID,
         Condition,
         intrusions = Days_One_to_Seven_Image_Based_Intrusions_in_Intrusion_Diary)
```

12.1.4 Activity 2 - Create summary statistics

Next, we want to calculate some descriptive statistics to see some overall trends in the data. We are really interested in the scores from each experimental group rather than overall.

Try this

- Summarise the data to show the mean, standard deviation, and standard error for the number of intrusive memories (`intrusions`) grouped by `Condition`.
- Your table should have four columns, `Condition`, `mean`, `sd`, and `se`.

Hint: You can calculate the standard error through: `sd/sqrt(n)` or `sd/sqrt(length(some_variable_name)`.

Show me the solution

You should have the following in a code chunk:

```r
james_data %>%
  group_by(Condition) %>%
  summarise(mean = round(mean(intrusions), 2),
            sd = round(sd(intrusions), 2),
            se = round(sd/sqrt(length(intrusions)), 2))
```

```
# A tibble: 4 x 4
  Condition  mean    sd    se
  <fct>     <dbl> <dbl> <dbl>
1 1          5.11  4.23  1
2 2          1.89  1.75  0.41
3 3          3.89  2.89  0.68
4 4          4.83  3.33  0.78
```

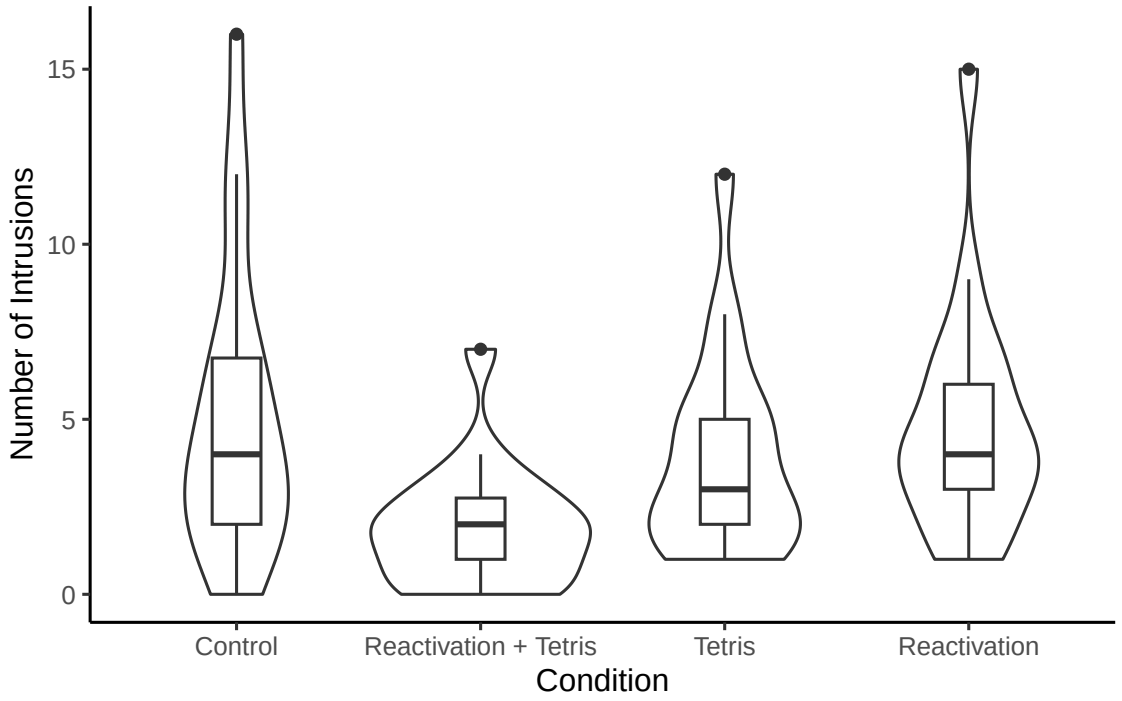
12.1.5 Activity 3 - Visualisation

Now we can visualise the data. In the original paper they use a bar plot, but let's use a better plot that gives us more information about the data.

Try this

- Create a violin-boxplot with the number of intrusive memories on the y-axis and condition on the x-axis (See Chapter 7 if you need a reminder).
- Change the labels on the x-axis to something more informative for the condition names.

Your plot should look like this:



Show me the solution

You should have the following in a code chunk:

```
james_data %>%
  ggplot(aes(x = Condition, y = intrusions))+
  geom_violin()+
  geom_boxplot(width = .2) +
  scale_y_continuous(name = "Number of Intrusions") +
  scale_x_discrete(labels = c("Control", "Reactivation + Tetris", "Tetris", "Reactivation")
  theme_classic()
```

We can see from this plot that there are a few potential outliers in each of the groups. This information is not present in the bar plot, which is why it's not a good idea to use them for this kind of data.

12.2 One-way ANOVA

Now we can run the one-way ANOVA using `aov_ez()` from the afex package and save it to the object `mod`. As well as running the ANOVA, the `aov_ez()` function also conducts a Levene's

test for homogeneity of variance so that we can test our final assumption.

12.2.1 Activity 4 - Running a one-way ANOVA using afex

`aov_ez()` will likely produce some messages that look like errors, do not worry about these, they are just letting you know what it's done. Run the code below to view the results of the ANOVA.

```
mod <- aov_ez(id = "PID", # the column containing the participant IDs
              dv = "intrusions", # the DV
              between = "Condition", # the between-subject variable
              es = "pes", # sets effect size to partial eta-squared
              type = 3, # this affects how the sum of squares is calculated, set this to 3
              include_aov = TRUE,
              data = james_data)

mod
```

```
Anova Table (Type 3 tests)

Response: intrusions
     Effect    df   MSE      F  ges p.value
1 Condition 3, 68 10.09 3.79 * .143    .014
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1
```

Just like with the t-tests and correlations, we can use `tidy()` to make the output easier to work with. Run the below code to transform the output. Do not worry about the warning message, it is just telling you it does not know how to automatically rename the columns so it will keep the original names.

```
mod_output <- mod$anova_table %>%
  tidy()
```

```
Warning in tidy.anova(.): The following column names in ANOVA output were not
recognized or transformed: num.Df, den.Df, MSE, ges
```

```
mod_output
```

```
# A tibble: 1 x 7
  term      num.Df den.Df   MSE statistic   ges p.value
  <chr>      <dbl>  <dbl> <dbl>     <dbl> <dbl>   <dbl>
1 Condition      3     68  10.1      3.79 0.143  0.0141
```

- `term` = the IV

- `num.Df` = degrees of freedom effect
- `den.Df` = degrees of freedom residuals
- `MSE` = Mean-squared errors
- `statistic` = F-statistic
- `ges` = effect size

- `p.value` = p.value

You should refer to the lecture for more information on what each variable means and how it is calculated.

- Is the overall effect of Condition significant?
- (A) Yes

- (B) No
- What is the F-statistics to 2 decimal places? _____
- According to the rules of thumb, the effect size is
- (A) Small

- (B) Medium

- (C) Large

12.2.2 Activity 5 - Checking assumptions for ANOVA

To test the assumptions, we must use the model we created with `aov_ez()`. For a one-way independent ANOVA, the assumptions are the same as for a Student t-test / regression model with a categorical predictor:

1. The DV is interval or ratio data.
2. The observations should be independent.

3. The residuals should be normally distributed.
4. There should be homogeneity of variance between the groups.

We know that 1 and 2 are met because of the design of our study. To test 3, we can look at the qq-plot of the residuals. Instead of saving just the model object, we must specifically select the `aov` component and run our diagnostic plots.

```
plot(mod$aov,
     which = 2)
```

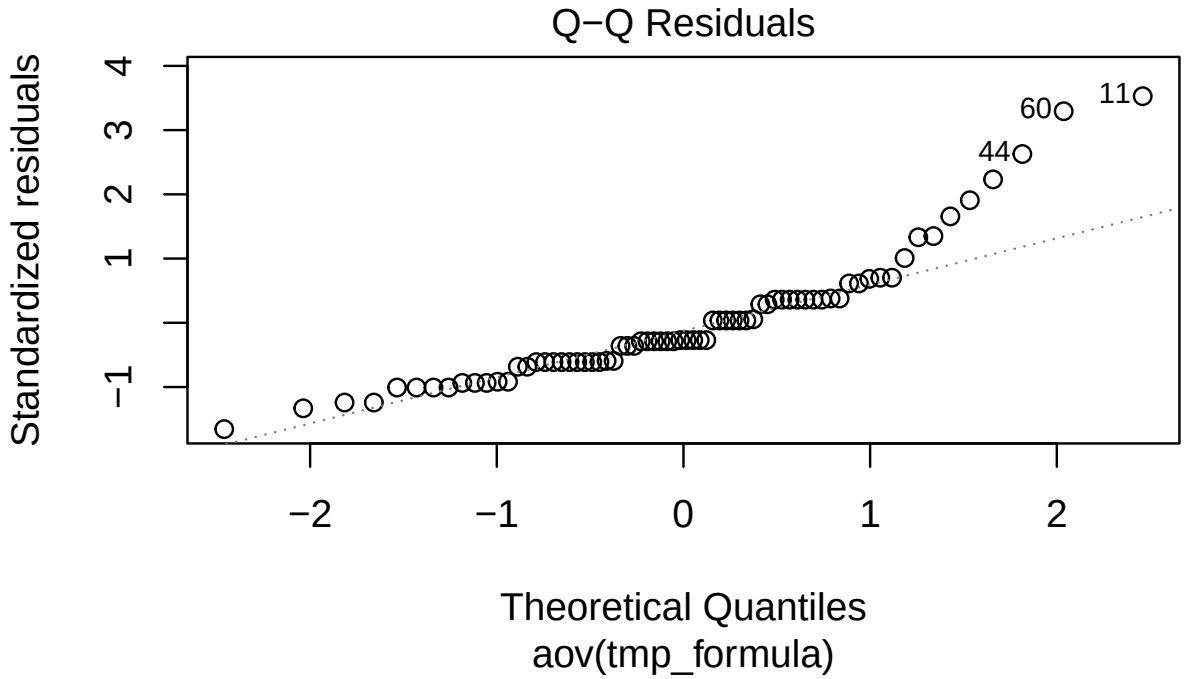


Figure 12.1: qq-plot for model residuals.

The qq-plot shows the assumption of normality might not be ideal. Is this a problem? If the sample sizes for each group are equal, then ANOVA is robust to violations of both normality and of homogeneity of variance. If you are interested, there is a good discussion of these issues in Blanca et al. (2018) and Knief & Forstmeier (2021). We can check how many participants are in each condition using `count()`:

```
james_data %>%
  count(Condition)
```

```
# A tibble: 4 x 2
  Condition     n
  <fct>     <int>
1 1            18
2 2            18
3 3            18
4 4            18
```

Thankfully, the sample sizes are equal, so we should be OK to proceed with the ANOVA. It is not clear whether normality was checked in the original paper.

For the last assumption, we can test homogeneity of variance by checking the third diagnostic plot for the scale against location.

```
plot(mod$aov,
     which = 3)
```

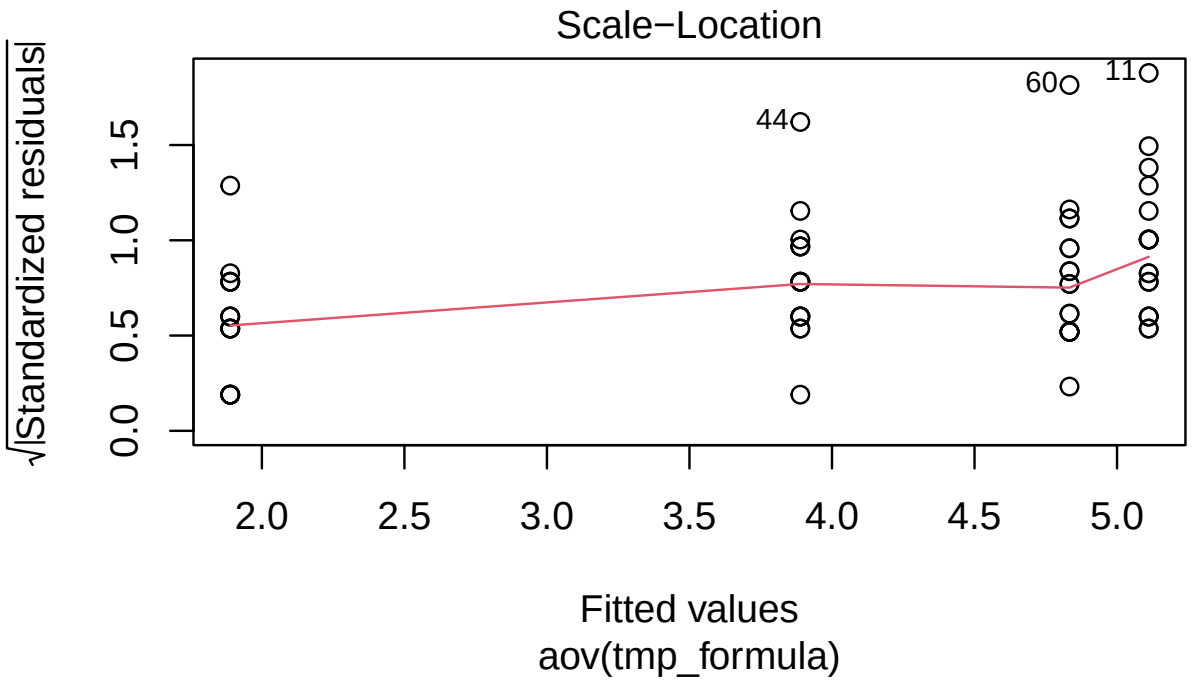


Figure 12.2: Diagnostic plot for homogeneity of variance.

Compared to normality, this assumption looks closer to being supported as the variance of each group is approximately equal. James et al. (2015) suspect there might be issues with this assumption as they mention that the ANOVAs do not assume equal variance, however, the

results of the ANOVA that are reported are identical to our results above where no correction has been made although the post-hoc tests are Welch t-tests (you can tell this because the degrees of freedom have been adjusted and are not whole numbers).

While all of this might seem very confusing - we imagine you might be wondering what the point of assumption testing is given that it seems to be ignored - we are showing you this for three reasons:

1. To reassure you that sometimes the data can fail to meet the assumptions and it is still ok to use the test. To put this in statistical terms, many tests are **robust** to mild deviations of normality and unequal variance, particularly with equal sample sizes.
2. As a critical thinking point, to remind you that just because a piece of research has been published does not mean it is perfect and you should always evaluate whether the methods used are appropriate.
3. To reinforce the importance of pre-registration where these decisions could be made in advance, and/or open data and code so that analyses can be reproduced exactly to avoid any ambiguity about exactly what was done. In this example, given the equal sample sizes and the difference in variance between the groups isn't too extreme, it looks like it is still appropriate to use an ANOVA but the decisions and justification for those decisions could have been more transparent.

> **Note**
>
> The `check_model()` function from performance also works here, so you can see what it looks like if you run:
>
> ```
> check_model(mod$aov)
> ```

12.2.3 Activity 6 - Post-hoc tests

For post-hoc comparisons, the paper appears to have computed Welch t-tests but there is no mention of any multiple comparison correction. We could reproduce these results by using `t.test()` for each of the contrasts.

For example, to compare condition 1 (the control group) with condition 2 (the reactivation plus tetris group) we could run:

```
james_data %>%
  filter(Condition %in% c("1", "2")) %>%
  droplevels() %>% # ignore unused factor levels
  t.test(intrusions ~ Condition,
         data = .)
```

```
    Welch Two Sample t-test

data:  intrusions by Condition
t = 2.9893, df = 22.632, p-value = 0.006627
alternative hypothesis: true difference in means between group 1 and group 2 is not equal to
95 percent confidence interval:
 0.990331 5.454113
sample estimates:
mean in group 1 mean in group 2
       5.111111        1.888889
```

> **!** Important
>
> Because `Condition` has four levels, we cannot just specify `intrustion ~ Condition` because a t-test compares two groups and it would not know which of the four to compare so first we have to filter the data and use a new function `droplevels()`. It's important to remember that when it comes to R there are two things to consider, the data you can see and the underlying structure of that data. In the above code we use `filter()` to select only conditions 1 and 2 so that we can compare them. However, that does not change the fact that R "knows" that `Condition` has four levels - it does not matter if two of those levels do not have any observations any more, the underlying structure still says there are four groups. `droplevels()` tells R to remove any unused levels from a factor. Try running the above code but without `droplevels()` and see what happens.

However, a quicker and better way of doing this that allows you apply a correction for multiple comparisons easily is to use `emmeans()` which computes all possible pairwise comparison t-tests and applies a correction to the p-value.

First, we use `emmeans()` to run the comparisons and then we can pull out the contrasts and use `tidy()` to make it easier to work with.

Run the code below. Which conditions are significantly different from each other? Are any of the comparisons different from the ones reported in the paper now that a correction for multiple comparisons has been applied?

```
mod_pairwise <-emmeans(mod,
                       pairwise ~ Condition,
                       adjust = "bonferroni")

mod_contrasts <- mod_pairwise$contrasts %>%
  tidy()

mod_contrasts
```

```
# A tibble: 6 x 8
  term      contrast   null.value estimate std.error    df statistic adj.p.value
  <chr>     <chr>           <dbl>    <dbl>     <dbl> <dbl>     <dbl>       <dbl>
1 Condition Condition~          0    3.22       1.06    68     3.04        0.0199
2 Condition Condition~          0    1.22       1.06    68     1.15        1
3 Condition Condition~          0    0.278      1.06    68     0.262       1
4 Condition Condition~          0   -2.00       1.06    68    -1.89        0.379
5 Condition Condition~          0   -2.94       1.06    68    -2.78        0.0420
6 Condition Condition~          0   -0.944      1.06    68    -0.892       1
```

> **Warning**
>
> The inquisitive among you may have noticed that `mod` is a list of 5 and seemingly contains the same thing three times: `anova_table`, `aov` and `Anova`. The reasons behind the differences are too complex to go into detail on this course (see The R Companion website here for more information) but the simple version is that `anova_table` and `Anova` use one method of calculating the results (type 3 sum of squares) and `aov` uses a different method (type 1 sum of squares). What's important for your purposes is that you need to use `anova_table` to view the overall results (and replicate the results from papers) and `aov`to run the follow-up tests and to get access to the residuals (or `lm()` for factorial ANOVA). As always, precision and attention to detail is key.

12.2.4 Activity 7 - Power and effect sizes

Finally, we can replicate their power analysis using `pwr.anova.test`from the pwr package.

> On the basis of the effect size of d = 1.14 from Experiment 1, we assumed a large effect size of f = 0.4. A sample size of 18 per condition was required in order to ensure an 80% power to detect this difference at the 5% significance level.

```
pwr.anova.test(k = 4,
               f = .4,
               sig.level = .05,
               power = .8)
```

```
     Balanced one-way analysis of variance power calculation
```

```
              k = 4
              n = 18.04262
              f = 0.4
      sig.level = 0.05
          power = 0.8

NOTE: n is number in each group
```

We have already got the effect size for the overall ANOVA, however, we should also really calculate Cohen's d using `cohens_d()` from effectsize for each of the pairwise comparisons. This code is a little long because you need to do it separately for each comparison, bind them all together and then add them to `mod_contrasts` - just make sure your understand which bits of the code you would need to change to run this on different data. As we are binding rows and columns rather than joining, it is critical the comparisons are already in the correct order.

```
# Calculate Cohen's d for all comparisons
d_1_2 <- cohens_d(intrusions ~ Condition,
                  data = filter(james_data,
                                Condition %in% c(1, 2)) %>%
                    droplevels())

d_1_3 <- cohens_d(intrusions ~ Condition,
                  data = filter(james_data,
                                Condition %in% c(1, 3)) %>%
                    droplevels())

d_1_4 <- cohens_d(intrusions ~ Condition,
                  data = filter(james_data,
                                Condition %in% c(1, 4)) %>%
                    droplevels())

d_2_3 <- cohens_d(intrusions ~ Condition,
                  data = filter(james_data,
                                Condition %in% c(2, 3)) %>%
                    droplevels())

d_2_4 <- cohens_d(intrusions ~ Condition,
                  data = filter(james_data,
                                Condition %in% c(2, 4)) %>%
                    droplevels())
```

```
d_3_4 <- cohens_d(intrusions ~ Condition,
                  data = filter(james_data,
                                Condition %in% c(3, 4)) %>%
                    droplevels())

# Bind all the comparisons in the order of mod_contrasts
pairwise_ds <- bind_rows(d_1_2,
                         d_1_3,
                         d_1_4,
                         d_2_3,
                         d_2_4,
                         d_3_4)

# Bind this object to the mod_contrasts object
mod_contrasts <- mod_contrasts %>%
  bind_cols(pairwise_ds)
```

> **Warning**
>
> What are your options if the data do not meet the assumptions and it's really not appropriate to continue with a regular one-way ANOVA? As always, there are multiple options and it is a judgement call.
>
> 1. You could run a non-parametric test, the Kruskal-Wallis for between-subject designs and the Friedman test for within-subject designs.
> 2. If normality is the problem, you could try transforming the data.
> 3. You could use bootstrapping, which is not something we will cover in this course at all.

12.3 Reporting the results of your ANOVA

The below code replicates the write-up in the paper, although has changed the Welch t-test to the pairwise comparisons from `emmeans()`.

```
Second, and critically, for the 7-day diary postintervention, there was a significant differ
```

If you add that code to your R Markdown document, knitting it should create the following:

> Second, and critically, for the 7-day diary postintervention, there was a significant difference between groups in overall intrusion frequency in daily life, F(3, 68) = 3.79, p = 0.014, p2 = .0.14. Planned comparisons demonstrated that relative to the no-task control group, only those in the reactivation-plus-Tetris group, t(68) = 3.04, p = 0.02, d = 1, experienced significantly fewer intrusive memories; this finding replicated Experiment 1. Critically, as predicted by reconsolidation theory, the reactivation-plus-Tetris group had significantly fewer intrusive memories than the Tetris-only group, t(68) = -1.89, p = 0.38, d = -0.84, as well as the reactivation-only group, t(68) = -2.78, p = 0.04, d = -1.11. Further, there were no significant differences between the no-task control group and the reactivation-only group, t(68) = 0.26, p = 1, or between the no-task control group and the Tetris-only group, t(68) = 1.15, p = 1

12.4 End of chapter

Well done! You have now covered how to run a one-way ANOVA using the afex package. Linear regression models are great for their flexibility, but it is not always simple for expressing a design with several levels. Combining afex and emmeans is a powerful combination when you have categorical independent variables / predictors with several levels.

In the next chapter, we will extend this to when you have multiple independent variables and you want to investigate the interaction between them for how they affect your dependent variable / outcome.

13 Factorial ANOVA

In the previous chapter, you learnt how to conduct and interpret a one-way ANOVA in R. These are flexible models where you have one independent variable (IV) with three or more levels. They get you a long way but sometimes your research question and design calls for multiple IVs or factors.

In this chapter, we extend the ANOVA framework to include two or more IVs/factors and their interaction. We will show you how to run a factorial ANOVA using the afex package and break down interactions through post-hoc tests using the emmeans package. Visualising your data is particularly important for understanding interactions, so we put a lot of emphasis on data visualisation through violin-boxplots and interaction plots.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Apply and interpret a factorial ANOVA.
- Break down the results of a factorial ANOVA using post-hocs tests and apply a correction for multiple comparisons.
- Check statistical assumptions for factorial ANOVA through your understanding of the design and diagnostic plots.
- Visualise the results of a factorial ANOVA through an interaction plot.

13.1 Chapter preparation

13.1.1 Introduction to the data set

For this chapter, we are using open data from experiment 3 in Zhang et al. (2014) which you might remember from Chapter 7. Now you have developed your inferential skills, we can return to reproduce their analyses. The abstract of their article is:

> Although documenting everyday activities may seem trivial, four studies reveal that creating records of the present generates unexpected benefits by allowing future rediscoveries. In Study 1, we used a time-capsule paradigm to show that individuals underestimate the extent to which rediscovering experiences from the past will be curiosity provoking and interesting in the future. In Studies 2 and 3, we found that people are particularly likely to underestimate the pleasure of rediscovering ordinary, mundane experiences, as opposed to extraordinary experiences. Finally, Study 4 demonstrates that underestimating the pleasure of rediscovery leads to time-inconsistent choices: Individuals forgo opportunities to document the present but then prefer rediscovering those moments in the future to engaging in an alternative fun activity. Underestimating the value of rediscovery is linked to people's erroneous faith in their memory of everyday events. By documenting the present, people provide themselves with the opportunity to rediscover mundane moments that may otherwise have been forgotten.

In summary, they were interested in whether people could predict how interested they would be in rediscovering past experiences. They call it a "time capsule" effect, where people store photos or messages to remind themselves of past events in the future. They predicted participants in the ordinary group would underestimate their future feelings (i.e., there would be a bigger difference between time 1 and time 2 measures) compared to participants in the extraordinary group.

Now we are focusing on the analysis rather than just visualisation, we can describe the experiment as a 2 x 2 mixed design. The first IV is time (time1, time2) and is within-subjects. The second IV is type of event (ordinary vs. extraordinary) and is a between-subjects factor. We will then use interest as a DV for a composite measure which took the mean of items on interest, meaningfulness, and enjoyment

13.1.2 Organising your files and project for the chapter

Before we can get started, you need to organise your files and project for the chapter, so your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, create a new folder called `Chapter_13_F_ANOVA`. Within `Chapter_13_F_ANOVA`, create two new folders called `data` and `figures`.
2. Create an R Project for `Chapter_13_F_ANOVA` as an existing directory for your chapter folder. This should now be your working directory.
3. Create a new R Markdown document and give it a sensible title describing the chapter, such as `13 Factorial ANOVA`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Chapter_13_F_ANOVA` folder.

4. If you must download the data again, please save the following file: Zhang_2014.csv. Right click the link and select "save link as", or clicking the link will save the files to your Downloads. Make sure that you save the file as ".csv". Save or copy the file to your `data/` folder within `Chapter_13_F_ANOVA`.

You are now ready to start working on the chapter!

13.1.3 Activity 1 - Load the packages and read the data

We already worked on the data wrangling in Chapter 7, so please type or copy and paste the following code to prepare for the chapter.

```
# Load the packages below
#library("rcompanion")
library(effectsize)
#library("car")
library(broom)
library(afex)
library(emmeans)
library(tidyverse)
library(performance)

# Load the data file
# This should be the Zhang_2014.csv file
zhang_data <- read_csv("data/Zhang_2014.csv")

# Wrangle the data for plotting.
# select and rename key variables
# mutate to add participant ID and recode
zhang_wide <- zhang_data %>%
  select(Gender,
         Age,
         Condition,
         time1_interest = T1_Predicted_Interest_Composite,
         time2_interest = T2_Actual_Interest_Composite) %>%
  mutate(participant_ID = row_number(),
         Condition = case_match(Condition,
                                1 ~ "Ordinary",
                                2 ~ "Extraordinary"))

zhang_long <- zhang_wide %>%
  pivot_longer(cols = time1_interest:time2_interest,
```

```
                names_to = "Time",
                values_to = "Interest")
```

For different functions, we need the data in wide- or long-format, so we have two versions of the data prepared for the chapter. Pay careful attention to when you need one version or the other.

13.1.4 Activity 2 - Calculate descriptive statistics

Try this

Before we start on the inferential statistics, one key part of understanding your data and reporting for context in a report is calculating descriptive statistics like the mean and standard deviation.
For the combination of `Condition` and `Time`, calculate the mean and standard deviation of `Interest`. We will need this at the end of the chapter, so save your results to the object name `zhang_descriptives`.

Show me the solution

You should have the following in a code chunk:

```
zhang_descriptives <- zhang_long %>%
  group_by(Condition, Time) %>%
  summarise(mean = round(mean(Interest, na.rm = TRUE), 2),
            sd = round(sd(Interest, na.rm = TRUE), 2))
```

```
`summarise()` has grouped output by 'Condition'. You can override using the
`.groups` argument.
```

```
zhang_descriptives
```

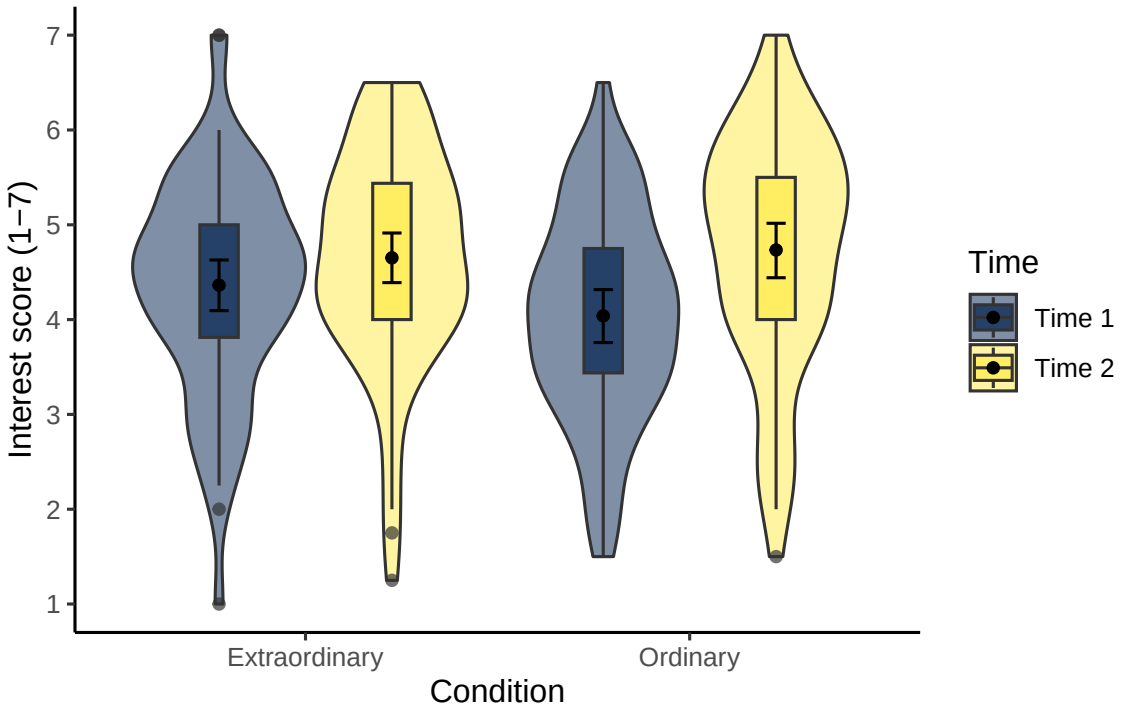
```
# A tibble: 4 x 4
# Groups:   Condition [2]
  Condition     Time            mean    sd
  <chr>         <chr>          <dbl> <dbl>
1 Extraordinary time1_interest  4.36  1.13
2 Extraordinary time2_interest  4.65  1.14
3 Ordinary      time1_interest  4.04  1.09
4 Ordinary      time2_interest  4.73  1.24
```

13.1.5 Activity 3 - Create a violin-boxplot

To communicate your findings, it is also important to visualise your data. Initially, this might be a quick boxplot for exploratory data analysis, but something like a violin-boxplot would be great for communicating your findings in a report.

Try this

Try and recreate the following violin-boxplot that you learnt how to create in Chapter 7. The finer details like the colour scheme are not important, but see how many features you can recreate before checking the code.



Show me the solution

You should have the following in a code chunk:

```r
# specify as an object, so we only change it in one place
dodge_value <- 0.9

zhang_long %>%
  mutate(Time = case_match(Time,
                           "time1_interest" ~ "Time 1",
                           "time2_interest" ~ "Time 2")) %>%
  ggplot(aes(y = Interest, x = Condition, fill = Time)) +
  geom_violin(alpha = 0.5) +
  geom_boxplot(width = 0.2,
               alpha = 0.7,
               fatten = NULL,
               position = position_dodge(dodge_value)) +
  stat_summary(fun = "mean",
               geom = "point",
               position = position_dodge(dodge_value)) +
  stat_summary(fun.data = "mean_cl_boot",
               geom = "errorbar",
               width = .1,
               position = position_dodge(dodge_value)) +
  scale_fill_viridis_d(option = "E") +
  scale_y_continuous(name = "Interest score (1-7)",
                     breaks = c(1:7)) +
  theme_classic()
```

13.2 Factorial ANOVA

To run the factorial ANOVA, we will be using the afex package again. Remember that you must specify both IVs, one of which is between-subjects and the other is within-subjects. Look up the help documentation for `aov_ez` if you need further information.

13.2.1 Activity 4 - Using the `aov_ez()` function.

Before we show you the code, try and complete the following skeleton version first. Think about what variable in the data corresponds to each argument.

Save the ANOVA model to an object called `mod_factorial` to be consistent with explanations below. For making it easier to report the results later, pull out the `mod_factorial$anova_table` component and apply the `tidy()` function from broom as a second step.

```
mod_factorial <- aov_ez(id = "NULL",
                data = NULL,
                between = "NULL",
                within = "NULL",
                dv = "NULL",
                type = 3,
                anova_table = list(es = "NULL"))

factorial_output <- NULL
```

Show me the solution

You should have the following in a code chunk:

```
mod_factorial <- aov_ez(id = "participant_ID",
                        data = zhang_long,
                        between = "Condition",
                        within = "Time",
                        dv = "Interest",
                        type = 3,
                        include_aov = TRUE,
                        anova_table = list(es = "pes"))

factorial_output <- mod_factorial$anova_table %>%
  tidy()
```

We can look at the results of the factorial ANOVA by printing the object.

```
mod_factorial
```

```
Anova Table (Type 3 tests)

Response: Interest
          Effect     df  MSE         F  pes p.value
1      Condition 1, 128 2.05      0.46 .004    .498
2           Time 1, 128 0.61 25.88 *** .168   <.001
3 Condition:Time 1, 128 0.61    4.44 * .034    .037
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1
```

Look at the results. Remember the pre-class information about how to read p-values in scientific notation.

- Is the main effect of Condition significant?
- (A) Yes
- (B) No
- Is the main effect of Time significant?
- (A) Yes
- (B) No
- Is the two-way interaction significant?
- (A) Yes
- (B) No

13.2.2 Activity 5 - Checking assumptions for factorial ANOVA

The assumptions for a factorial ANOVA are the same as the one-way ANOVA.

1. The DV is interval or ratio data.
2. The observations should be independent.
3. The residuals should be normally distributed.
4. There should be homogeneity of variance between the groups.

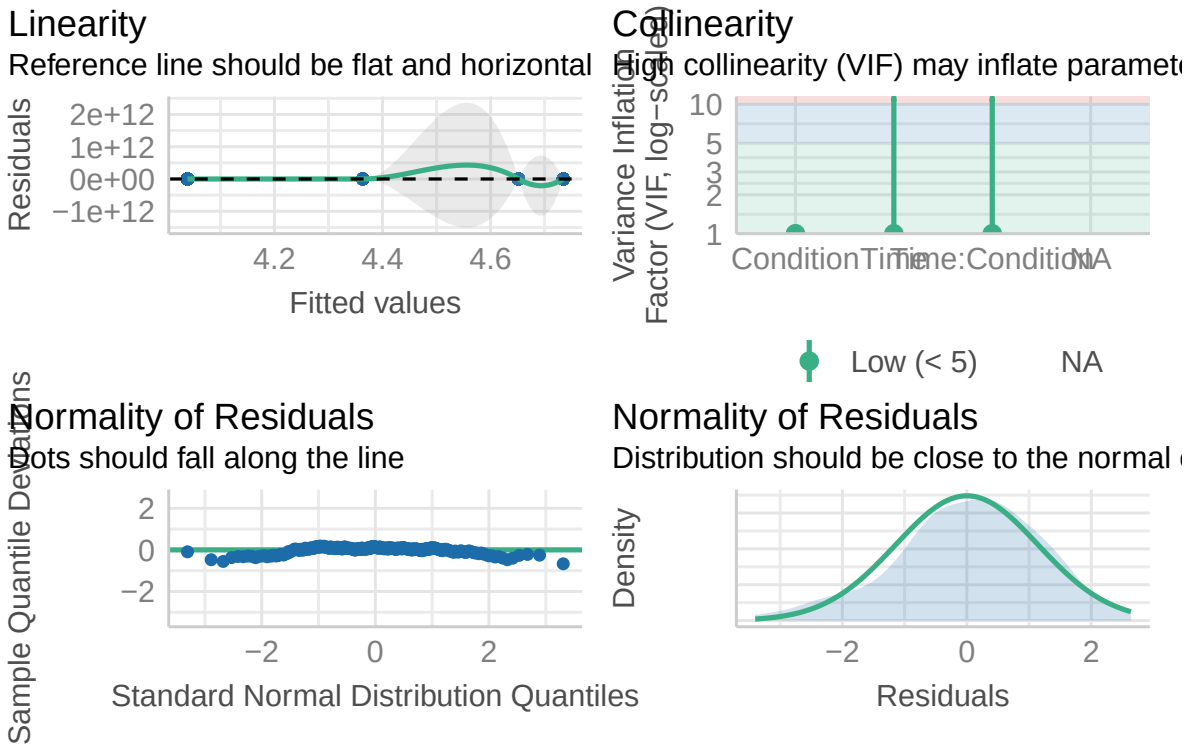
As before, we know assumption 2 is met from the design of the study. Assumption 1 throws up an interesting issue which is the problem of ordinal data. Ordinal data are the kind of data that come from Likert scales and are very common in psychology. The problem is that ordinal data are not interval or ratio data, there's a fixed number of integer values they can take (the values of the Likert scale) and you cannot claim that the distance between the values is equal (is the difference between strongly agree and agree the same as the difference between agree and neutral?).

Technically, we should not use an ANOVA to analyse ordinal data - *but almost everyone does*. Many people argue that if you take the average of multiple Likert scale items, you can interpret the data as if they are interval and they can be normally distributed. Other people argue you should use non-parametric methods or more complex models such as ordinal regression for this type of data, but it is beyond the scope of what we cover in this course (if you are super interested, there is a PsyTeachR book for another course - Statistics and Research Design -

which covers ordinal regression). Whichever route you choose, you should understand the data you have and you should be able to justify your decision.

To test assumption 3, you can run `check_model()` from performance on the model object (`mod_factorial`). Unless you add the argument `re_formula = NA`, you get a little warning saying the function does it anyway. The background of this argument is beyond the scope of this course, but expressed as a linear model, a mixed ANOVA looks like something called a mixed-effects model, so this argument is saying that there is not a formula for it, since we did not have one.

```
check_model(mod_factorial,
            re_formula = NA) # Specify or you get a warning
```



Does it look like we have any obvious problems with normality here?

- (A) Yes
- (B) No

The one annoying thing here is we do not get a diagnostic plot for checking homogeneity of variance / homoscedasticity. We can create our own using the lm component of the model object (`mod_factorial$lm`), but it takes a few steps. In the code below:

- We first isolate the standardised residuals of the model object. We must convert it to a data frame and rename the two columns.
- We combine the residuals with the wide version of the data.
- We pivot the data longer so all the residuals are in one column and create a new variable to take the square root of the absolute residuals. This recreates how the diagnostic plots you saw in Chapters 8, 9, and 12 look.
- Finally, we plot the standardised residuals and add a line to join the means of each group. If the line is roughly flat, we support homoscedasticity. If the line angles up or down substantially, then this points to signs of heteroscedasticity.

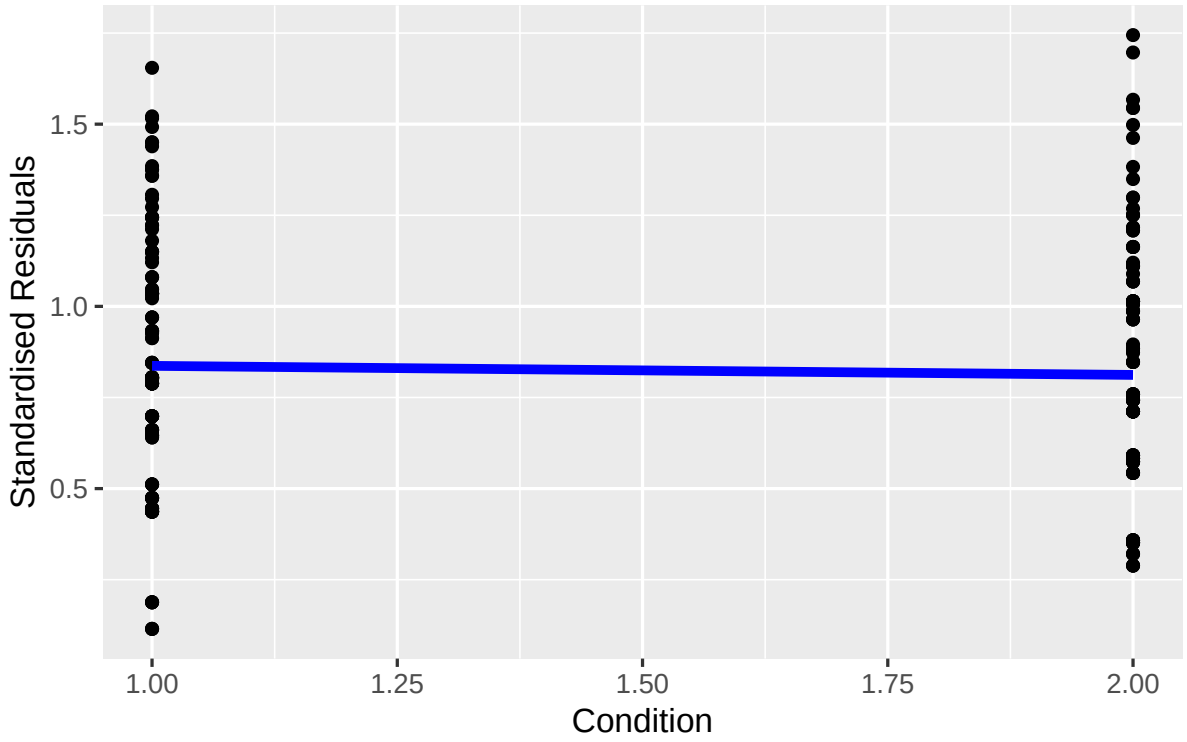
```
# Isolate standardised residuals as a data frame
residuals <- as.data.frame(rstandard(mod_factorial$lm)) %>%
  select(residuals_time1 = time1_interest,
         residuals_time2 = time2_interest)

# add residuals to the wide version of the data, so we have the groups
zhang_wide <- zhang_wide %>%
  bind_cols(residuals)

# Pivot longer and calculate the square root of absolute standardised residuals
residuals_long <- zhang_wide %>%
  pivot_longer(cols = residuals_time1:residuals_time2,
               names_to = "Time",
               values_to = "Residuals") %>%
  mutate(std_residuals = sqrt(abs(Residuals)))

# Plot the residuals
residuals_long %>%
  # we need groups as numbers for the line to plot
  mutate(Condition = case_match(Condition,
                                "Ordinary" ~ 1,
                                "Extraordinary" ~ 2)) %>%
  ggplot(aes(x = Condition, y = std_residuals)) +
  geom_point() +
  # add line joining the mean of residuals per group
  stat_summary(geom = "line",
               fun = mean,
```

```
              color = "blue",
              linewidth = 1.5) +
  labs(x = "Condition", y = "Standardised Residuals")
```



Does it look like we have any obvious problems with homoscedasticity here?

- (A) Yes
- (B) No

13.2.3 Activity 6 - Post-hoc tests

Because the interaction is significant, we should follow this up with post-hoc tests using `emmeans()` to determine which comparisons are significant. If the overall interaction is not significant, you should not conduct additional tests.

`emmeans()` requires you to specify the `aov` object, and then the factors you want to contrast. For an interaction, we use the notation `pairwise ~ IV1 | IV2` and you specify which multiple comparison correction you want to apply.

Run the below code and view the results.

```
# run the tests
posthoc_factorial <- emmeans(mod_factorial,
                             pairwise ~ Time | Condition,
                             adjust = "bonferroni")

posthoc_factorial
```

```
$emmeans
Condition = Extraordinary:
 Time           emmean    SE  df lower.CL upper.CL
 time1_interest   4.36 0.137 128     4.09     4.63
 time2_interest   4.65 0.147 128     4.36     4.94

Condition = Ordinary:
 Time           emmean    SE  df lower.CL upper.CL
 time1_interest   4.04 0.139 128     3.76     4.31
 time2_interest   4.73 0.149 128     4.44     5.03

Confidence level used: 0.95

$contrasts
Condition = Extraordinary:
 contrast                         estimate    SE  df t.ratio p.value
 time1_interest - time2_interest   -0.288 0.136 128  -2.123  0.0357

Condition = Ordinary:
 contrast                         estimate    SE  df t.ratio p.value
 time1_interest - time2_interest   -0.695 0.138 128  -5.049  <.0001
```

In the output, we first get the estimated marginal means for the combination of IVs. We then get the contrasts we requested. This looks at the difference in levels of the first IV for each level of the second IV.

You can use `tidy()` to tidy up the output of the contrasts and save it into a tibble which makes it easier to use in inline code later.

```
# tidy up the output of the tests
contrasts_factorial <- posthoc_factorial$contrasts %>%
  tidy()

contrasts_factorial
```

```
# A tibble: 2 x 9
  Condition term  contrast null.value estimate std.error    df statistic p.value
  <chr>     <chr> <chr>         <dbl>    <dbl>     <dbl> <dbl>     <dbl>   <dbl>
1 Extraord~ Time  time1_i~          0   -0.288     0.136   128     -2.12 3.57e-2
2 Ordinary  Time  time1_i~          0   -0.695     0.138   128     -5.05 1.49e-6
```

Note that because there are two IVs/factors, we could also reverse the order. Above, we get the results contrasting time 1 and time 2 for each event condition. Instead, we could look at the difference between ordinary and extraordinary events at each time point.

Run the code below and compare the output to `contrast_factorial`. Look at how the contrasts are expressed subtly different when you switch the order. Think carefully about your research question and hypotheses for which way around is the most informative.

```
posthoc_factorial2 <- emmeans(mod_factorial,
                              pairwise ~ Condition | Time,
                              adjust = "bonferroni")

posthoc_factorial2

contrasts_factorial2 <- posthoc_factorial2$contrasts %>%
  tidy()

contrasts_factorial2
```

```
$emmeans
Time = time1_interest:
 Condition     emmean    SE  df lower.CL upper.CL
 Extraordinary   4.36 0.137 128     4.09     4.63
 Ordinary        4.04 0.139 128     3.76     4.31

Time = time2_interest:
 Condition     emmean    SE  df lower.CL upper.CL
 Extraordinary   4.65 0.147 128     4.36     4.94
 Ordinary        4.73 0.149 128     4.44     5.03

Confidence level used: 0.95

$contrasts
Time = time1_interest:
 contrast                 estimate    SE  df t.ratio p.value
 Extraordinary - Ordinary   0.3246 0.195 128   1.661  0.0992
```

```
Time = time2_interest:
 contrast                estimate    SE  df t.ratio p.value
 Extraordinary - Ordinary  -0.0829 0.209 128  -0.397  0.6923


# A tibble: 2 x 9
  Time      term  contrast null.value estimate std.error    df statistic p.value
  <chr>     <chr> <chr>         <dbl>    <dbl>     <dbl> <dbl>     <dbl>   <dbl>
1 time1_in~ Cond~ Extraor~          0   0.325      0.195   128     1.66   0.0992
2 time2_in~ Cond~ Extraor~          0  -0.0829     0.209   128    -0.397  0.692
```

Because our main effects (condition and time) only have two levels, we do not need to do any post-hoc tests to determine which conditions differ from each other, however, if one of our factors had three levels then we could use `emmeans()` to calculate the contrast for the main effects, like we did for the one-way ANOVA.

Finally, to calculate standardised effect sizes for the pairwise comparisons, we again need to do this individually using `cohens_d()` from effectsize.

As we have a mixed design, we must follow a slightly different process for each comparison. Cohen's d has a different calculation for between-subjects and within-subjects contrasts, so we must express it differently. For the first comparison, we are interested in the difference between time 1 and time 2 for each group, so this represents a within-subjects comparison.

```
# time 1 vs time 2 for Extraordinary group
d_extraordinary <- cohens_d(x = "time1_interest",
                            y = "time2_interest",
                            paired = TRUE,
                            data = filter(zhang_wide,
                                          Condition == "Extraordinary"))
# time 1 vs time 2 for Ordinary group
d_ordinary <- cohens_d(x = "time1_interest",
                       y = "time2_interest",
                       paired = TRUE,
                       data = filter(zhang_wide,
                                     Condition == "Ordinary"))

# bind together the two contrasts
Condition_ds <- bind_rows(d_extraordinary,
                          d_ordinary)

# add the contrasts to the emmeans tidy table
```

```
contrasts_factorial <- contrasts_factorial %>%
  bind_cols(Condition_ds)

contrasts_factorial
```

```
# A tibble: 2 x 13
  Condition term  contrast null.value estimate std.error    df statistic p.value
  <chr>     <chr> <chr>         <dbl>    <dbl>     <dbl> <dbl>     <dbl>   <dbl>
1 Extraord~ Time  time1_i~          0   -0.288     0.136   128     -2.12 3.57e-2
2 Ordinary  Time  time1_i~          0   -0.695     0.138   128     -5.05 1.49e-6
# i 4 more variables: Cohens_d <dbl>, CI <dbl>, CI_low <dbl>, CI_high <dbl>
```

For the second comparison, we are interested in the difference between ordinary and extraordinary at each time point, so this represents a between-subjects comparison.

```
# Extraordinary vs ordinary at time 1
d_time1 <- cohens_d(time1_interest ~ Condition,
                    data = zhang_wide)

# Extraordinary vs ordinary at time 2
d_time2 <- cohens_d(time2_interest ~ Condition,
                    data = zhang_wide)

# bind the two contrasts together
Time_ds <- bind_rows(d_time1,
                     d_time2)

# add the contrasts to the emmeans tidy table
contrasts_factorial2 <- contrasts_factorial2 %>%
  bind_cols(Time_ds)

contrasts_factorial2
```

```
# A tibble: 2 x 13
  Time      term  contrast null.value estimate std.error    df statistic p.value
  <chr>     <chr> <chr>         <dbl>    <dbl>     <dbl> <dbl>     <dbl>   <dbl>
1 time1_in~ Cond~ Extraor~          0   0.325      0.195   128      1.66   0.0992
2 time2_in~ Cond~ Extraor~          0  -0.0829     0.209   128     -0.397  0.692
# i 4 more variables: Cohens_d <dbl>, CI <dbl>, CI_low <dbl>, CI_high <dbl>
```

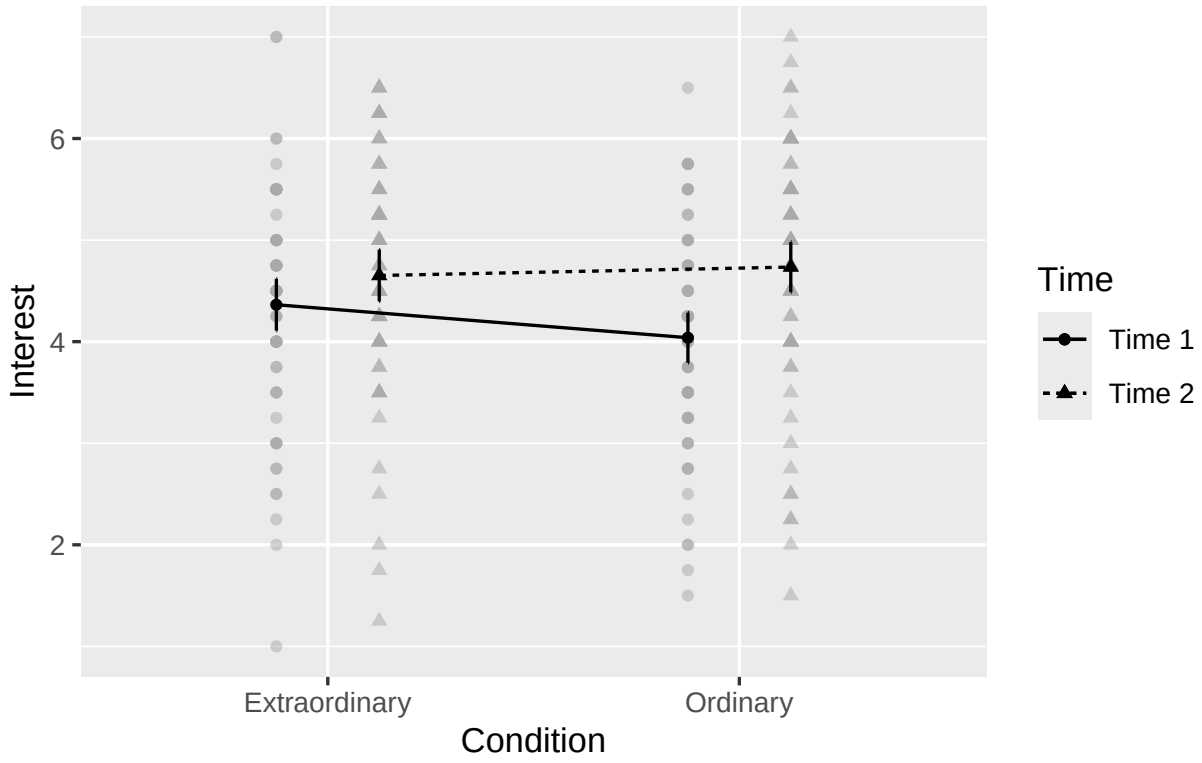
13.2.4 Activity 7 - Creating an interaction plot

When you have a factorial design, one powerful way of visualising the data is through an interaction plot. This is essentially a line graph where the x-axis has one IV and separate lines for a second IV. However, once you have the factorial ANOVA model, you can add confidence intervals to the plot to visualise uncertainty. afex has it's own function called `afex_plot()` which you can use with the model object you created.

In the code below, there are a few key argument to highlight:

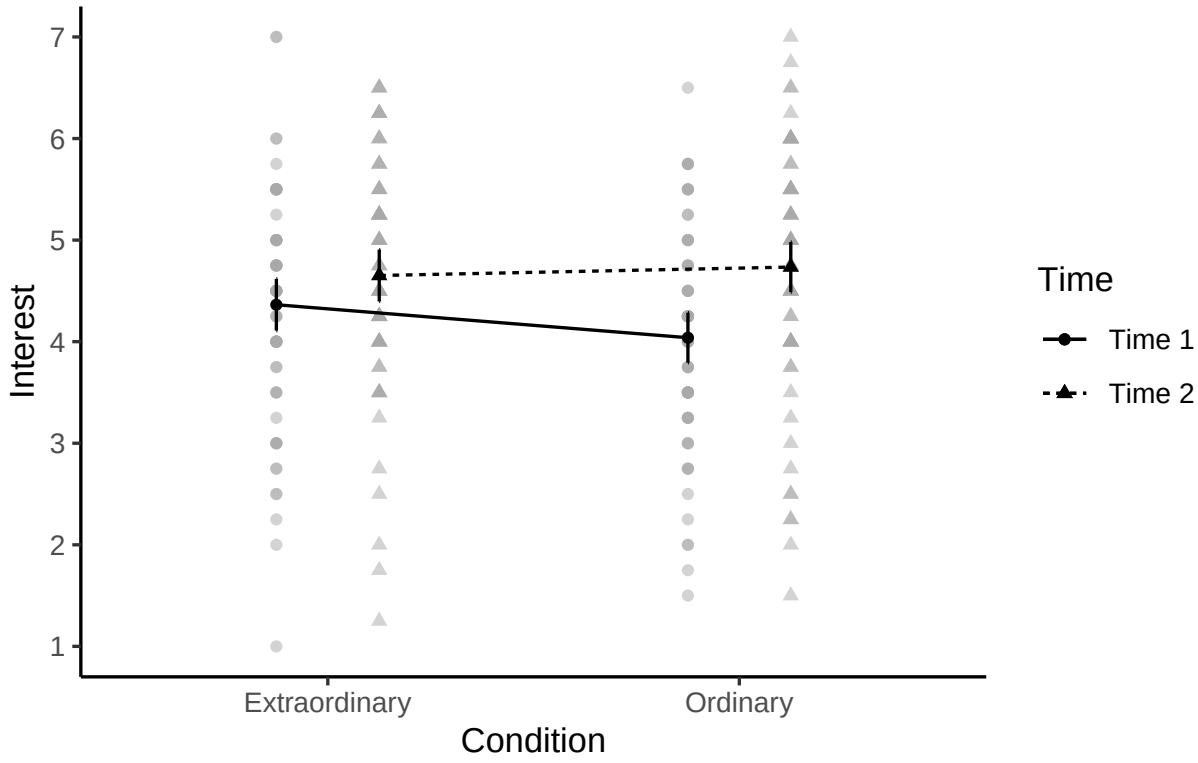
- `object` is the afex model you created.
- `x` is the variable you want on the x-axis.
- `trace` is the variable you want to plot as separate lines.
- `error` controls whether the error bars show confidence intervals for between-subjects or within-subjects. In a mixed design, these have different properties, so you must think about which you want to plot and highlight to the reader.
- `factor_levels` lets you edit the levels of factors you plot, such as renaming or reordering them. You add each factor into a list but check the documentation and vignettes for other options.

```
afex_plot(object = mod_factorial,
          x = "Condition",
          trace = "Time",
          error = "between",
          factor_levels = list(Time = c("Time 1", "Time 2")))
```



One handy feature about this function is it uses ggplot2 in the background, so you can add layers to the initial function like other plots that you have created.

```
afex_plot(mod_factorial,
          x = "Condition",
          trace = "Time",
          error = "between",
          factor_levels = list(Time = c("Time 1", "Time 2"))) +
  theme_classic() +
  scale_y_continuous(breaks = 1:7)
```



> **Note**
>
> Since `afex_plot()` uses ggplot2, you can use `ggsave()` to save your plots and insert them into your work.

13.3 Reporting the results of your factorial ANOVA

Now you have all your values, we can work on the write-up of your results.

In the in-line code demonstration below, we manually entered p-values where they are $<$ .001. There is a way to get R to produce this formatting but it's overly complicated for our purposes in this course. If you want to push yourself, look up the papaja package for creating reproducible manuscripts.

The values of partial eta-squared do not match between our analysis and those reported in the paper. We have not figured out why this is yet, so if you know, please get in touch!

We have also replaced the simple effects in the main paper with our pairwise comparisons.

Copy and paste the text and inline code below into **white-space** in your R Markdown document. If you saved all the descriptives, model, and contrasts using the same object names as us, this should knit.

```
We conducted the same repeated measures ANOVA with interest as the dependent measure and aga
```

> We conducted the same repeated measures ANOVA with interest as the dependent measure and again found a main effect of time, F(1, 128) = 25.88, p < .001, p2 = 0.168; anticipated interest at Time 1 (M = 4.36), SD = 1.13)) was lower than actual interest at Time 2 (M = 4.65, SD = 1.14). We also observed an interaction between time and type of experience, F(1, 128) = 4.445, p = 0.04, p2 = 0.034. Pairwise comparisons revealed that for ordinary events, predicted interest at Time 1 (M = 4.04, SD = 1.09) was lower than experienced interest at Time 2 (M = 4.73, SD = 1.24), t(128) = -5.05, p < .001, d = -0.56. Although predicted interest for extraordinary events at Time 1 (M = 4.36, SD = 1.13) was lower than experienced interest at Time 2 (M = 4.65, SD = 1.14), t(128) = -2.12, p < .001, d = -0.31, the magnitude of underestimation was smaller than for ordinary events.

13.4 End of Chapter

Well done, you have now covered the ANOVA section of the course to learn how to express experimental designs into statistical models. ANOVA and factorial ANOVA are incredibly flexible tools where you can start to combine multiple independent variables. You might have between-subject factors, within-subject factors, or a combination of the two in a mixed design. The most important thing to keep in mind is your research question, hypothesis, and design come first. Factorial ANOVA can get arbitrarily more complicated but try and avoid the temptation to create complex models just because you can. You do not get extra points for complication, it is better to think about which model will let you address your research question.

In the next chapter, we finish the core chapters on the final extension of the general linear model we cover in this course. In Research Methods 1, you learnt about simple linear regression when you only have one predictor. In multiple linear regression, you can add two or more predictors, and even the interaction between predictors.

14 Multiple Regression

In Chapters 8 and 9 from the Research Methods 1 content, we covered simple linear regression to investigate the effect of one predictor on one outcome. At the start of Research Methods 2, we then started to explore ANOVA models to handle more complex designs.

In this chapter, we end the core content on learning how to apply and interpret multiple regression models. This uses the full flexibility of the general linear model to express more complicated designs where you have multiple predictors or interactions between predictors.

Chapter Intended Learning Outcomes (ILOs)

By the end of this chapter, you will be able to:

- Apply and interpret multiple linear regression models.
- Interpret coefficients from individual predictors and interactions.
- Visualise interactions as model predictions to understand and communicate your findings.
- Calculate statistical power for a multiple regression model.

14.1 Chapter preparation

14.1.1 Introduction to the data set

For this chapter, we are using open data from Przybylski & Weinstein (2017). The abstract of their article is:

> Although the time adolescents spend with digital technologies has sparked widespread concerns that their use might be negatively associated with mental well-being, these potential deleterious influences have not been rigorously studied. Using a preregistered plan for analyzing data collected from a representative sample of English adolescents (n = 120,115), we obtained evidence that the links between digital-screen time and mental well-being are described by quadratic functions. Further, our results showed that these links vary as a function of when digital technologies are used (i.e., weekday vs. weekend), suggesting that a full understanding of the impact of these recreational activities will require examining their functionality among other daily pursuits. Overall, the evidence indicated

> that moderate use of digital technology is not intrinsically harmful and may be advantageous in a connected world. The findings inform recommendations for limiting adolescents' technology use and provide a template for conducting rigorous investigations into the relations between digital technology and children's and adolescents' health.

In summary, this was a large-scale study that found support for the "Goldilocks" hypothesis among adolescents: that there is a "just right" amount of screen time, such that any amount more or less than this amount is associated with lower well-being. This was a huge survey study: the data contain responses from over 120,000 participants! In this chapter, we will look at whether the relationship between screen time and well-being is moderated by participants' (self-reported) gender.

The outcome/dependant variable used in the study was the Warwick-Edinburgh Mental Well-Being Scale (WEMWBS). This is a 14-item scale with 5 response categories, summed together to form a single score ranging from 14-70.

Przybylski & Weinstein (2017) looked at multiple measures of screen time, but we will be focusing on smartphone use. They found that decrements in well-being started to appear when respondents reported more than one hour of weekly smartphone use. Our research question is: Does the negative association between hours of use and well-being (beyond the one-hour point) differ for boys and girls?

14.1.2 Organising your files and project for the chapter

Before we can get started, you need to organise your files and project for the chapter, so your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, create a new folder called `Chapter_14_multiple_regression`. Within `Chapter_14_multiple_regressio` create two new folders called `data` and `figures`.
2. Create an R Project for `Chapter_14_multiple_regression` as an existing directory for your chapter folder. This should now be your working directory.
3. Create a new R Markdown document and give it a sensible title describing the chapter, such as `14 Multiple Regression`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Chapter_14_multiple_regression` folder.
4. For this chapter, there are three data files you need. Please save the following files:
    - Przybylski_2017_participants.csv.
    - Przybylski_2017_screentime.csv
    - Przybylski_2017_wellbeing.csv

Right click the link and select "save link as", or clicking the link will save the files to your Downloads. Make sure that you save the files as ".csv". Save or copy the files to your `data/` folder within `Chapter_14_multiple_regression`.

You are now ready to start working on the chapter!

14.1.3 Activity 1 - Load the packages and read the data

As the first activity, try and test yourself by completing the following task list.

Try this

To prepare for wrangling the data, complete the following tasks:

1. Load the following packages (one of these is new, so revisit Chapter 1 if you need a refresher of installing R packages, but remember not to install packages on the university computers / online server):
    - pwr
    - sjPlot
    - performance
    - tidyverse
2. Read the three data files to the following object names to be consistent with the tasks below.

```
# load packages here
?

# read the three data files
# this should be Przybylski_2017_participants.csv
pinfo <- ?

# this should be Przybylski_2017_wellbeing.csv
wellbeing <- ?

# this should be Przybylski_2017_screentime.csv
screen <- ?
```

Show me the solution

You should have the following in a code chunk:

```
# load packages here
library(pwr)
library(sjPlot)
library(performance)
library(tidyverse)

# read the three data files
# this should be Przybylski_2017_participants.csv
pinfo <- read_csv("data/Przybylski_2017_participants.csv")

# this should be Przybylski_2017_wellbeing.csv
wellbeing <- read_csv("data/Przybylski_2017_wellbeing.csv")

# this should be Przybylski_2017_screentime.csv
screen <- read_csv("data/Przybylski_2017_screentime.csv")
```

14.1.4 Activity 2 - Explore the data

Take a look at the resulting tibbles `pinfo`, `wellbeing`, and `screen`. Use functions like `glimpse()` to look at what the data frames contain.

- The `pinfo` data has information on the participant's background.
- The `wellbeing` data has information from the well-being questionnaire.
- The `screen` data has information about screen time use on weekends (variables ending with `we`) and weekdays (variables ending with `wk`) for four types of activities:
  - Using a computer (variables starting with `Comph`; Q10 on the survey)
  - Playing video games (variables starting with `Comp`; Q9 on the survey)
  - Using a smartphone (variables starting with `Smart`; Q11 on the survey)
  - Watching TV (variables starting with `Watch`; Q8 on the survey).

If you want more information about these variables, look at the items 8-11 on pages 4-5 of the the PDF version of the survey on the authors' OSF project.

Once you have explored the objects, try and answer the following questions:

- The variable corresponding to **gender** is located in the object named
- (A) pinfo
- (B) wellbeing
- (C) screen

and this variable is called _____.

- The well-being data is in
- (A) long
- (B) wide

format and contains observations from _____ participants on ___ items.

- Individual participants in this data set are identified by the variable called _____. This variable will allow us to link information across the three tables.
- If you run the function `summary()` on the three data sets, are there any missing data points?
- (A) Yes
- (B) No

14.1.5 Activity 3 - Compute the well-being score for each respondent

Try this

The WEMWBS well-being score is simply the **sum** of all the items.
Wrangle the data to create a new table called `wemwbs`. The data should have two variables:

- `Serial` - the participant ID.
- `total_wellbeing` - the total WEMWBS score.

Think about what wrangling steps you need to apply to achieve this.

Show me some hints

- Gather the data and pivot from wide to long.
- Group the data by a variable.
- Summarise the data to calculate the sum score per participant.

Show me the solution

You should have the following in a code chunk:

```
wemwbs <- wellbeing %>%
  pivot_longer(cols = WBOptimf:WBCheer,
               names_to = "var",
               values_to = "score") %>%
  group_by(Serial) %>%
  summarise(total_wellbeing = sum(score))
```

For a sanity check, verify for yourself that the scores all fall in the 14-70 range. Przybylski & Weinstein (2017) reported a mean of 47.52 with a standard deviation of 9.55. Can you reproduce these values?

Show me the solution

You should have the following in a code chunk:

```
wemwbs %>%
  summarise(mean = mean(total_wellbeing),
            sd = sd(total_wellbeing),
            min = min(total_wellbeing),
            max = max(total_wellbeing))
```

```
# A tibble: 1 x 4
   mean    sd   min   max
  <dbl> <dbl> <dbl> <dbl>
1  47.5  9.55    14    70
```

Now, visualise the distribution of `tot_wellbeing` in a histogram using ggplot2. The distribution of well-being scores is

- (A) symmetric

- (B) negatively skewed
- (C) positively skewed

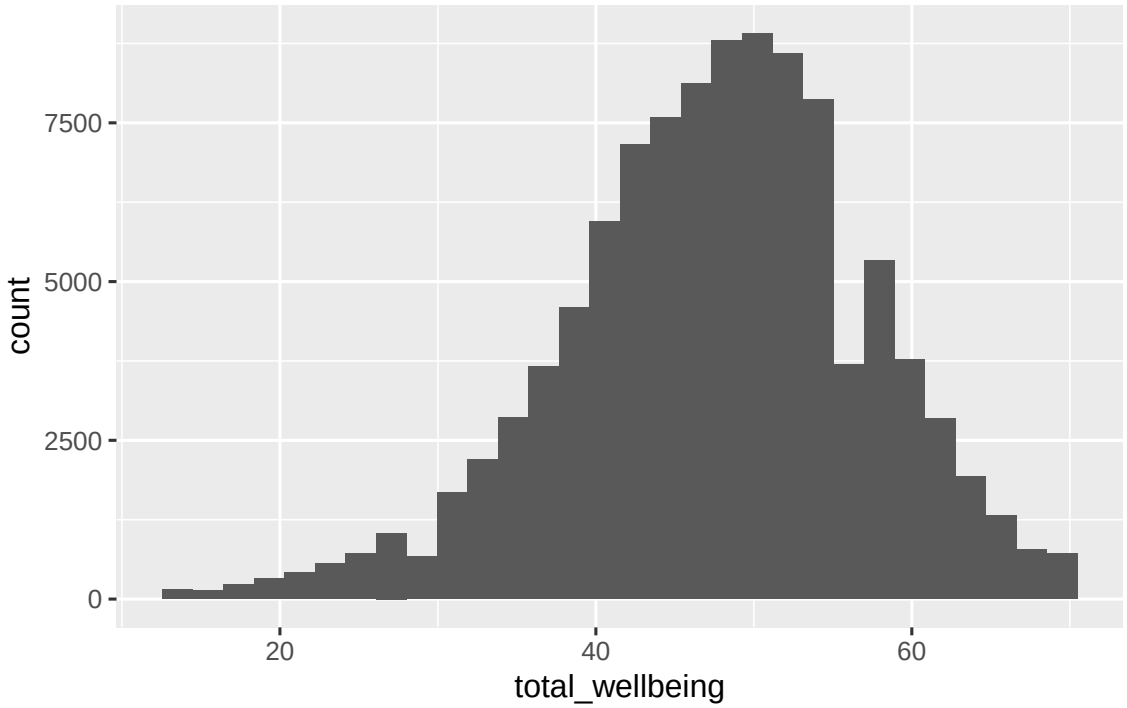
.

Show me the solution

You should have the following in a code chunk:

```
wemwbs %>%
  ggplot(aes(x = total_wellbeing)) +
  geom_histogram()
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



14.1.6 Activity 4 - Wrangle and visualise the data

Before we move onto the final modelling stages, we can wrangle the data to plot the data like the original article. We can plot the relationship between well-being and hours of technology use, split into four categories of technology (video games, computers, smartphones, TV).

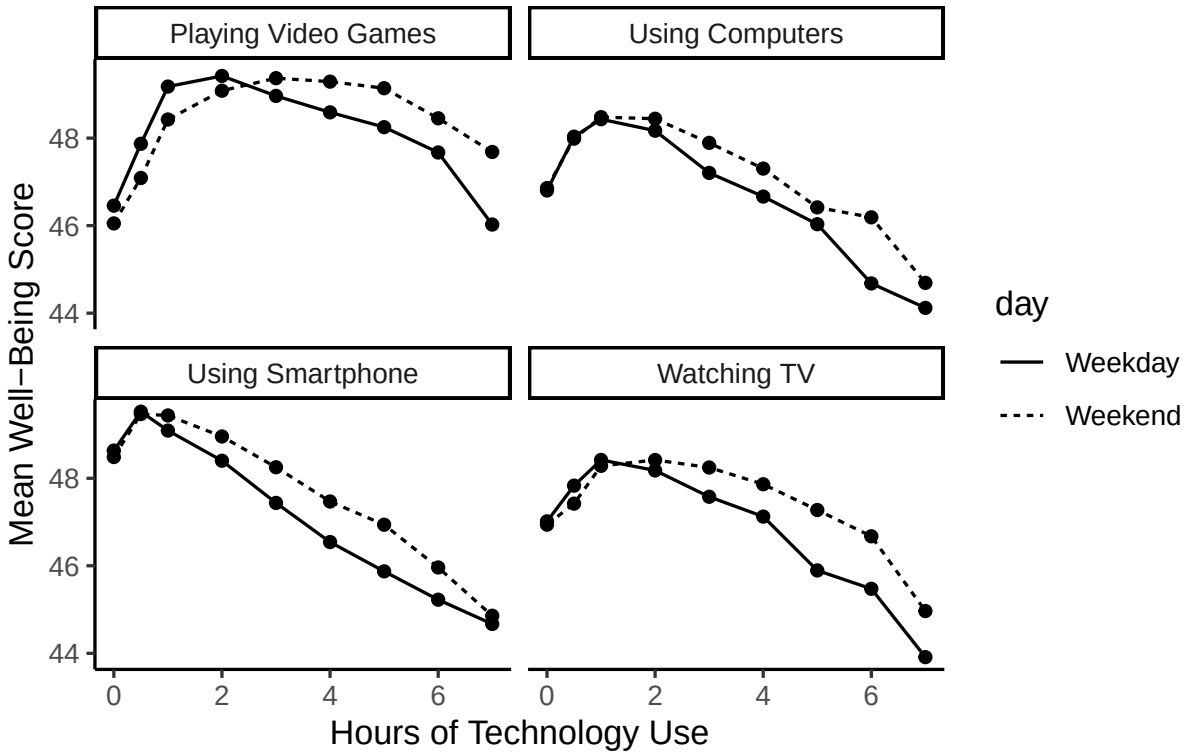
For this step, we are going to give you the code as there are a few new functions we have not taught you about. Make sure as you type the code to question what each line of the code is doing. The functions might be unfamiliar but you should be able to follow what it is doing. We are working with many rows here, so the code might take longer to run than you are used to.

```
# Pivot the screen data longer
# Separate the variable into the category and day of the week
# Recode the new variables
screen_long <- screen %>%
  pivot_longer(cols = Comph_we:Watch_wk,
               names_to = "var",
               values_to = "hours") %>%
  separate(col = var, # split variable name
           into = c("variable", "day"), # split into two components
           sep = "_") %>%  # split when it sees a _
  mutate(variable = case_match(variable,
                               "Watch" ~ "Watching TV",
                               "Comp" ~ "Playing Video Games",
                               "Comph" ~ "Using Computers",
                               "Smart" ~ "Using Smartphone"),
         day = case_match(day,
                          "wk" ~ "Weekday",
                          "we" ~ "Weekend"))

# Join the two data sets together
# group by three variables
# calculate the mean well-being score
dat_means <- wemwbs %>%
  inner_join(screen_long,
             by = "Serial") %>%
  group_by(variable,
           day,
           hours) %>%
  summarise(mean_wellbeing = mean(total_wellbeing))
```

We now have data at the group level rather than per participant. Each row of `dat_means` is a value for mean well-being split by each level of variable (technology type), day (weekday or weekend), and hours of technology use. If you run the following code, we get a line graph showing the relationship split between technology type and day.

```r
dat_means %>%
  ggplot(aes(x = hours, y = mean_wellbeing, linetype = day)) +
  geom_line() +
  geom_point() +
  facet_wrap(~ variable, nrow = 2) +
  theme_classic() +
  labs(x = "Hours of Technology Use",
       y = "Mean Well-Being Score")
```



The graph shows that smartphone use of more than 1 hour per day is associated with increasingly negative well-being. Note that we have combined the tables using an `inner_join()`, such that we only include data for which we have observations across the `wemwbs` and `screen_long` tables.

In the next step, we are going to focus on the smartphone/well-being relationship for our multiple linear regression demonstration.

14.2 Multiple linear regression

Now that we have explored the data, we can start preparing for the analysis. Note that in this analysis, we have:

- A continuous* outcome: well-being.
- One continuous* predictor: screen time.
- One categorical predictor: gender.

*these variables are only quasi-continuous as only discrete values are possible. This returns up to the ordinal dilemma, particularly for the outcome of well-being. However, there are a sufficient number of discrete values that we can treat them as effectively continuous.

We want to estimate two slopes relating screen time to well-being, one for girls and one for boys, and then statistically compare these slopes. So, this problem seems simultaneously like a situation where you would run a regression (to estimate the slopes) but also one where you would need a t-test (to compare two groups). This is the power of regression models as you can look at the interaction between one continuous and one categorical predictor, something that is not possible in factorial ANOVA.

14.2.1 Activity 5 - Complete the final wrangling steps

For this analysis, we are going to average weekday and weekend use for smartphones. We need one final round of wrangling to prepare for creating a multiple linear regression model.

Try this

Step 1. Create a new data object `smarttot` that has the mean number of hours per day of smartphone use for each participant, averaged over weekends/weekdays. Then filter the data to only include those who use a smart phone for more than one hour per day. To do this, you will need to:

- Filter the data `screen_long` to **only** include smartphone use and not other technologies.
- Group the results by the participant ID (`Serial`).
- Summarise the data to calculate the mean number of hours per participant. Call this variable `total_hours`.
- Filter the data to only include participants who use a smartphone for more than 1 hour per day.

The data `smarttot` should have two variables: `Serial` (the participant) and `total_hours`.
Step 2. Once you have `smarttot`, combine (join) this data object with the information in `wemwbs` and `pinfo`. Call this new object `smart_wb`. This is the final object you need for the multiple linear regression model.

Show me the solution

You should have the following in a code chunk:

```
smarttot <- screen_long %>%
  filter(variable == "Using Smartphone") %>%
  group_by(Serial) %>%
  summarise(total_hours = mean(hours)) %>%
  filter(total_hours > 1)

smart_wb <- smarttot %>%
  inner_join(wemwbs,
             by = "Serial") %>%
  inner_join(pinfo,
             by = "Serial")
```

14.2.2 Activity 6 - Mean-centering variables

As we discussed in the course materials, when you have continuous variables in a regression model, it is often sensible to transform them by **mean centering**. We covered this in Chapter 8, but it is particularly important in multiple linear regression. You mean center a predictor `X` by subtracting the mean of the predictor (`X_centered = X - mean(X)`). This has two useful consequences:

- The model intercept reflects the prediction for Y at the mean value of the predictor variable, rather than at the zero value of the unscaled variable.
- If there are interactions in the model, any lower-order effects can be given the same interpretation as they receive in ANOVA (main effects, rather than simple effects).

For categorical predictors with two levels, these become coded as -.5 and .5 (because the mean of these two values is 0).

Try this

Use `mutate()` to add two new variables to `smart_wb`:

- `total_hours_c`: calculated as a mean-centered version of the `total_hours` predictor
- `male_c`: recoded as -.5 for female and .5 for male, and then converts both `male` and `male_c` as factors, so that R knows not to treat them as real numbers.

Show me the solution

You should have the following in a code chunk:

```
smart_wb <- smart_wb %>%
  mutate(total_hours_c = total_hours - mean(total_hours),
         male_c = case_when(male == 1 ~ .5,
                            male == 0 ~ -.5),
         male_c = as.factor(male_c),
         male = as.factor(male))
```

14.2.3 Activity 7 - Running the regression

For the data in `smart_wb`, use the `lm()` function to calculate the multiple regression model:

$Y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + e_i$

where

- Y_i is the well-being score for participant i;
- X_{1i} is the mean-centered smartphone use variable for participant i;
- X_{2i} is gender (-.5 = female, .5 = male);
- X_{3i} is the interaction between smartphone use and gender ($= X_{1i} \times X_{2i}$)

Try this

Save your model to the object `ml_model`.
Save the `summary()` of your model to the object `model_summary`.
Print the `model_summary` to see the results and answer the following questions:

- The interaction between smartphone use and gender is shown by the variable

- (A) thours_c
- (B) male_c
- (C) thours_c:male_c

, and this interaction was

- (A) significant
- (B) non-significant

at the $\alpha = .05$ level.

- To 2 decimal places, adjusted R^2 suggests the overall model explains what percentage of the variance in well-being scores? _____
- The p-value for the overall model fit is `<2e-16`. Is this statistically significant?
- (A) Yes
- (B) No

Show me the solution

You should have the following in a code chunk:

```
ml_model <- lm(formula = total_wellbeing ~ total_hours_c * male_c,
               data = smart_wb)

mod_summary <- summary(ml_model)

mod_summary
```

```
Call:
lm(formula = total_wellbeing ~ total_hours_c * male_c, data = smart_wb)

Residuals:
    Min      1Q  Median      3Q     Max
-36.881  -5.721   0.408   6.237  27.264
```

```
Coefficients:
                          Estimate Std. Error t value Pr(>|t|)
(Intercept)              44.86740    0.04478 1001.87   <2e-16 ***
total_hours_c            -0.77121    0.02340  -32.96   <2e-16 ***
male_c0.5                 5.13968    0.07113   72.25   <2e-16 ***
total_hours_c:male_c0.5   0.45205    0.03693   12.24   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 9.135 on 71029 degrees of freedom
Multiple R-squared:  0.09381,   Adjusted R-squared:  0.09377
F-statistic:  2451 on 3 and 71029 DF,  p-value: < 2.2e-16
```

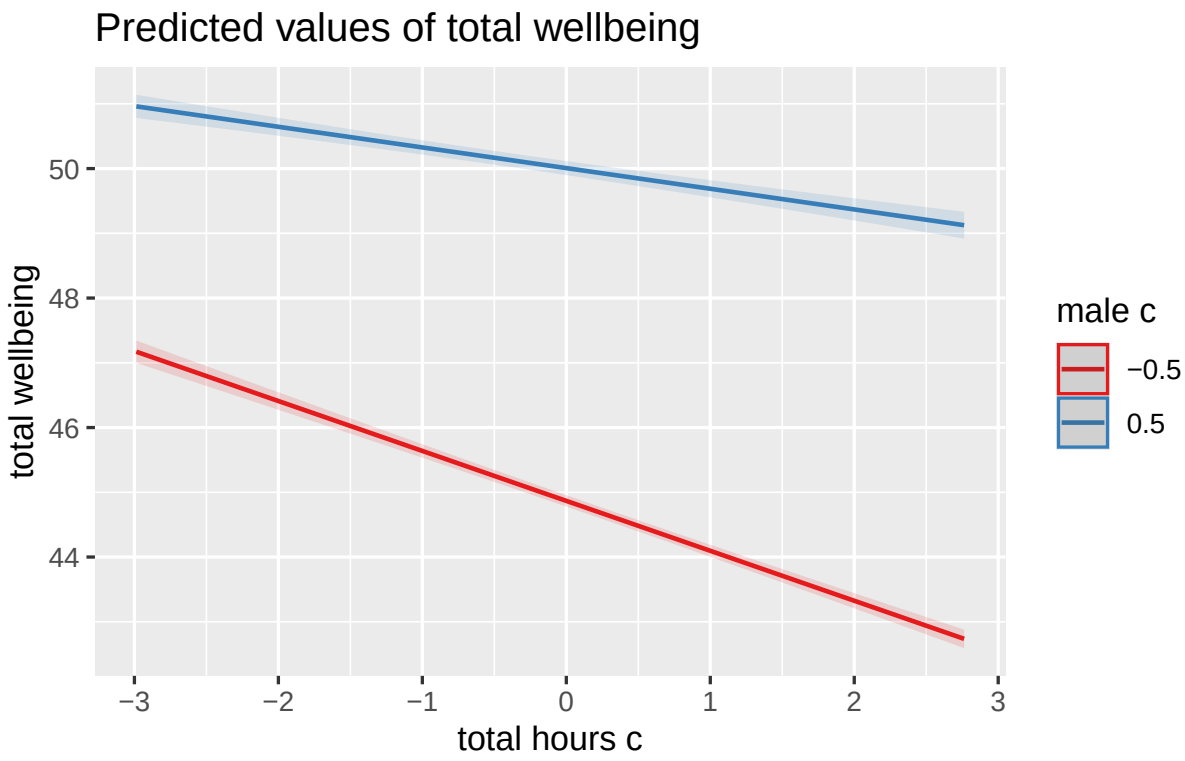
14.2.4 Activity 8 - Visualising interactions

It is very difficult to understand an interaction from the coefficient alone, so your best bet is visualising the interaction to help you understand the results and communicate your results to your readers.

There is a great package called sjPlot which takes regression models and helps you plot them in different ways. We will demonstrate plotting interactions, but for further information and options, see the online documentation.

To plot the interaction, you need the model object (not the summary), specify "pred" as the `type` as we want to plot predictions, and add the `terms` you want to plot.

```
plot_model(ml_model,
           type = "pred",
           terms = c("total_hours_c", "male_c"))
```



What is the most reasonable interpretation of the interaction?

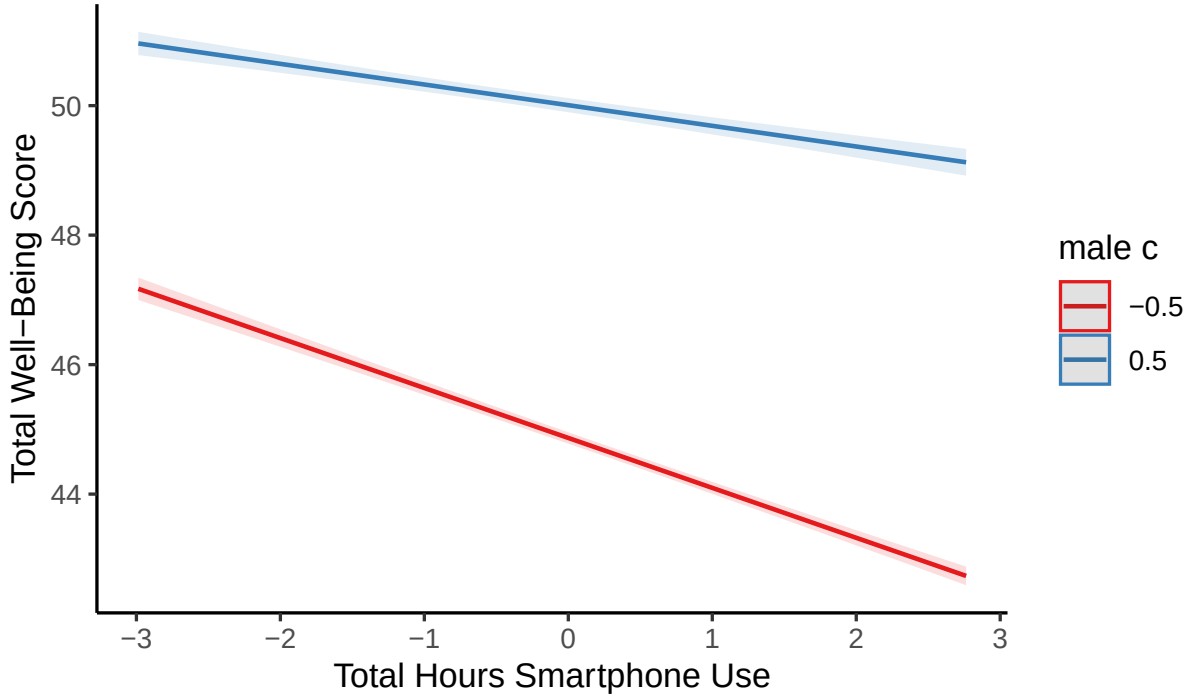
- (A) there is no evidence for gender differences in the relationship between smartphone use and well-being
- (B) smartphone use harms boys more than girls
- (C) smartphone use was more negatively associated with wellbeing for girls than for boys
- (D) smartphone use harms girls more than boys

This is fine for helping you to interpret your model, but you would need to customise it before adding it into a report. Like `afex_plot()` we introduced you to in Chapter 13, `plot_model()` uses ggplot2 in the background. You can add further customisation by adding layers after the initial function.

> **Note**
>
> Since `plot_model()` uses ggplot2, you can use `ggsave()` to save your plots and insert them into your work.

For example, we can tidy up the axis labels and remove the title, and set a theme.

```
plot_model(ml_model,
           type = "pred",
           terms = c("total_hours_c", "male_c")) +
  labs(x = "Total Hours Smartphone Use",
       y = "Total Well-Being Score",
       title = "") +
  theme_classic()
```



For communicating interactions, it is normally better to plot a version using the raw predictors instead of the mean centered versions as the interaction does not change and it will be easier for your readers to understand.

14.2.5 Activity 9 - Assumption checking

Now it's time to test those pesky assumptions. The assumptions for multiple regression are the same as simple regression but there is one additional assumption, that of multicollinearity. This is the idea that predictor variables should not be too highly correlated.

1. The outcome/DV is a interval/ratio level data.

2. The predictor variable is interval/ratio or categorical (with two levels).
3. All values of the outcome variable are independent (i.e., each score should come from a different participant).
4. The predictors have non-zero variance.
5. The relationship between outcome and predictor is linear.
6. The residuals should be normally distributed.
7. There should be homoscedasticity (homogeneity of variance, but for the residuals).
8. Multicollinearity: predictor variables should not be too highly correlated.

From the work we have done so far, we know that we meet assumptions 1 - 4 and we can use the `plot()` function for diagnostic plots, plus `check_model()` from the performance package.

One difference from when we used `check_model()` previously is that rather than just letting it run all the tests it wants, we are going to specify which tests to stop it throwing an error. A word of warning - these assumption tests will take longer than usual to run because it's such a big data set. The first line of code will run the assumption tests and save it to an object, calling the object name will then display the plots.

```
assumptions <- check_model(ml_model,
                           check = c("vif",
                                     "qq",
                                     "normality",
                                     "linearity",
                                     "homogeneity"))

assumptions
```

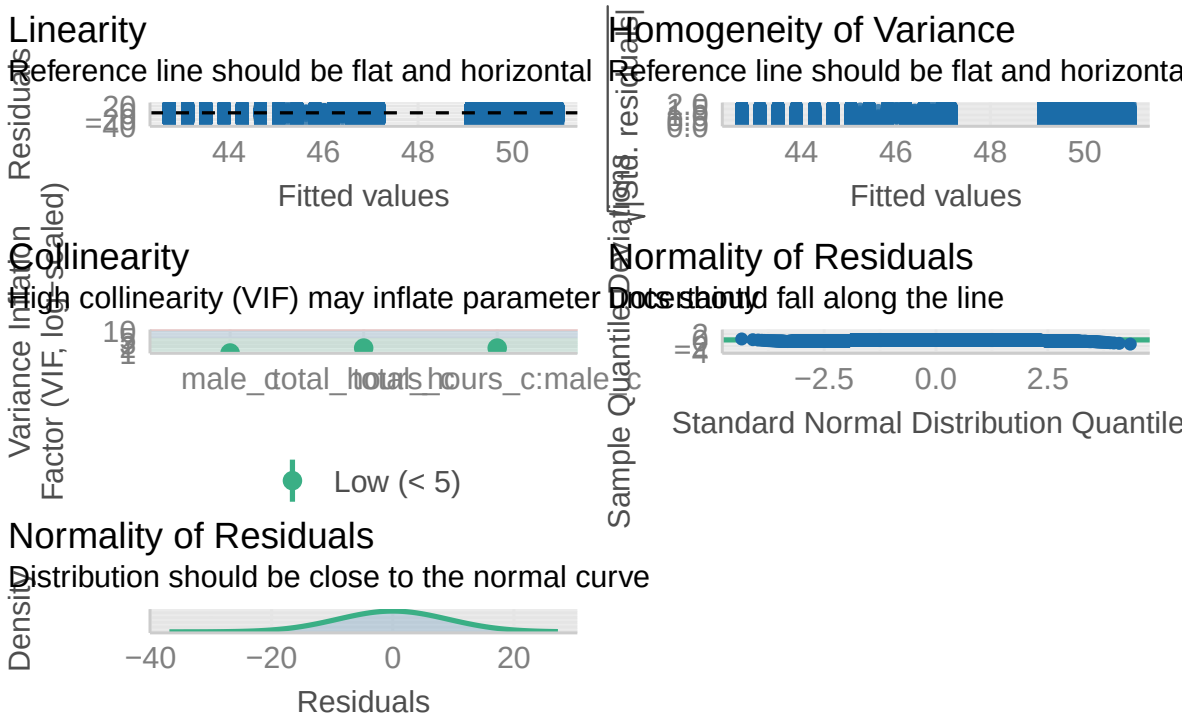


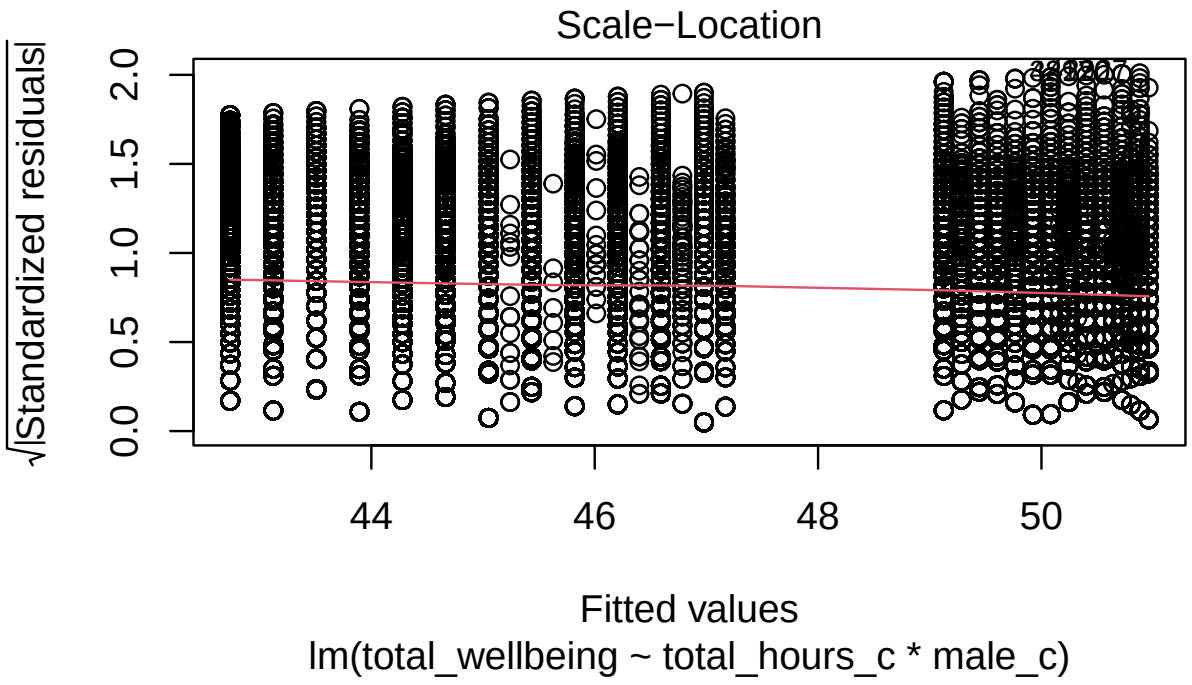
Figure 14.1: Assumption plots from the performance package.

For assumption 5, linearity, we already know from looking at the scatterplot that the relationship is linear, but the residual plot also confirms this.

For assumption 6, normality of residuals, the residuals look good in both plots and this provides an excellent example of why it's often better to visualise than rely on statistics. With a sample size this large, any statistical diagnostic tests will be highly significant as they are sensitive to sample size.

For assumption 7, homoscedasticity, the plot is missing the reference line. Fun fact, this took us several days of our lives and asking for help on social media to figure out. The reason the line is not there is because the data set is so large that is creates a memory issue. However, if you use the `plot()` version, it does show the reference line.

```
plot(ml_model,
     which = 3)
```



It is not perfect, but the reference line is roughly flat to suggest there are no serious issues with homoscedasticity.

Finally, for assumption 8, multicollinearity, the plot also indicates no issues but we can also test this statistically using `check_collinearity()` to produce VIF (variance inflation factor) and tolerance values.

Essentially, this function estimates how much the variance of a coefficient is "inflated" because of linear dependence with other predictors, i.e., that a predictor is not actually adding any unique variance to the model, it's just really strongly related to other predictors. You can read more about this online. Thankfully, VIF is not affected by large samples like other statistical diagnostic tests.

There are various rules of thumb, but most converge on a VIF of above 2 - 2.5 for any one predictor being problematic.

```
check_collinearity(ml_model)
```

```
# Check for Multicollinearity

Low Correlation

                Term  VIF   VIF 95% CI Increased SE Tolerance Tolerance 95% CI
```

```
        total_hours_c 1.72 [1.70, 1.74]         1.31      0.58     [0.57, 0.59]
              male_c 1.04 [1.03, 1.04]         1.02      0.97     [0.96, 0.97]
total_hours_c:male_c 1.72 [1.70, 1.73]         1.31      0.58     [0.58, 0.59]
```

14.2.6 Activity 10 - Power and effect sizes

Finally, we will calculate power and an effect size specific to multiple linear regression. Your coefficients represent the effect size for individual variables, but you can summarise the whole regression model with R^2 and f^2.

Using your understanding of power analysis from Chapter 10 and the function specific to regression models, calculate the minimum effect size we could reliably observe given our sample size and design but for 99% power and 5% alpha.

Hint: for `v`, it is the sample size minus u minus 1 (`N - u - 1`)

```
pwr.f2.test(u = ?,
            v = ?,
            f2 = NULL,
            sig.level = ?,
            power = ?)
```

To 2 decimals, what is the value of f^2 the study would be sensitive to?

Show me the solution

You should have the following in a code chunk:

```
pwr.f2.test(u = 3,
            v = 71029,
            f2 = NULL,
            sig.level = .05,
            power = .99)
```

```
     Multiple regression power calculation

              u = 3
              v = 71029
             f2 = 0.0003673651
      sig.level = 0.05
          power = 0.99
```

The study was incredibly sensitive, where they would detect effects of $f^2 = .0004$ with 99% power.

The effect size f^2 is a kind of transformed version of R^2. You can calculate it through the equation:

$f^2 = \frac{adjR^2}{1-adjR^2}$

Or as code:

```
f2 <- adj_R2/(1 - adj_R2)
```

Try this

Calculate the f^2 value from the multiple regression model using one of these methods. Try and use the values directly from the model object to avoid typing in the values. What is the observed effect size (in f^2) for the study to 2 decimal places? _____

Show me the solution

You should have the following in a code chunk:

```
f2 <- mod_summary$adj.r.squared/(1 - mod_summary$adj.r.squared)

f2
```

```
[1] 0.1034697
```

Comparing the observed effect size against the effect size the study was sensitive to with 99% power, do you think the study was sufficiently powered?

- (A) Yes
- (B) No

14.3 Reporting the results of multiple linear regression

The same as previous chapters like ANOVA and factorial ANOVA, we can use inline code to help with the write-up. First, copy and paste the code below into **white-space** in your R Markdown document and then knit. Note that we enter the p-values manually because of the APA "$p < .001$" formatting.

```
All continuous predictors were mean-centered and deviation coding was used for categorical pr
```

> All continuous predictors were mean-centered and deviation coding was used for categorical predictors. The results of the regression indicated that the model significantly predicted course engagement ($F(3, 7.1029 \times 10^4) = 2450.89$, $p < .001$, Adjusted $R2 = 0.09$, $f^2 = 0.1$), accounting for 9% of the variance. Total screen time was a significant negative predictor of wellbeing scores (= -0.77, $p < .001$, as was gender (= 5.14, $p < .001$, with girls having lower wellbeing scores than boys. Importantly, there was a significant interaction between screentime and gender (= 0.45, $p < .001$), smartphone use was more negatively associated with wellbeing for girls than for boys.

14.4 End of Chapter

You are done!

Not just with this chapter but with the R/RStudio component of Research Methods 2. The progress that you have made is truly astonishing. Even if you struggled with R/RStudio and have not quite understood every single line of code, what you are capable of with data wrangling and visualisation alone makes you some of the most highly competitive psychology graduates in the world. Try and think of everything you have learnt from week 1 of Research Methods 1 to now. Hopefully, you have proved to yourself you can do this.

Regardless of whether you continue with quantitative methods and using R/RStudio, remember the more important critical skills that you have learned as part of this process. The next time you see a data set or you see data being talked about in the news, think about all the work that was put into getting the data into the final format. More importantly, think about all the decisions that the researcher needed to make along the way and how that might have affected the outcome.

Data Analysis Journeys

15 Analysis Journey 1: Data Wrangling

Welcome to the first data analysis journey. We have designed these chapters as a bridge between the structured learning in the core chapters and your assessments. We present you with a new data set, show you what the end product should look like, and see if you can apply your data wrangling, visualisation, and/or analysis skills to get there.

As you gain independence, this is the crucial skill. Data analysis is all about seeing the data you have available to you and identifying what the end product needs to be to apply your visualisation and analysis techniques. You can then mentally (or physically) create a checklist of tasks to work backwards to get there. There might be a lot of trial and error as you try one thing, it does not quite work, so you go back and try something else. If you get stuck though, we have a range of hints and task lists you can unhide, then the solution to check your attempts against.

In this first data analysis journey, we focus on data wrangling to apply all the skills you developed from Chapter 1 to Chapter 6.

15.1 Task preparation

15.1.1 Introduction to the data set

For this task, we are using open data from J. E. Bartlett et al. (2022). The abstract of their article is:

> Both daily and non-daily smokers find it difficult to quit smoking long-term. One factor associated with addictive behaviour is attentional bias, but previous research in daily and non-daily smokers found inconsistent results and did not report the reliability of their cognitive tasks. Using an online sample, we compared daily (n = 106) and non-daily (n = 60) smokers in their attentional bias towards smoking pictures. Participants completed a visual probe task with two picture presentation times: 200ms and 500ms. In confirmatory analyses, there were no significant effects of interest, and in exploratory analyses, equivalence testing showed the effects were statistically equivalent to zero. The reliability of the visual probe task was poor, meaning it should not be used for repeated testing or investigating individual differences. The results can be interpreted in line with contemporary theories of attentional bias where there are unlikely to be stable trait-like differences between

> smoking groups. Future research in attentional bias should focus on state-level differences using more reliable measures than the visual probe task.

To summarise, they compared two daily and non-daily smokers on something called attentional bias. This is the idea that when people use drugs often, things associated with those drugs grab people's attention.

To measure attentional bias, participants completed a dot probe task. This is a computer task where participants see two pictures side-by-side: one related to smoking like someone holding a cigarette and one unrelated to smoking like someone holding a fork. Both the images disappear and a small dot appears in the location of one of the images. Participants must press left or right on the keyboard to identify where the dot appeared. This process is repeated many times for different images, different locations of the dot, and different durations of showing the images. The idea is if smoking images grab people's attention, they will be able to identify the dot location faster on average when it appears in the location of the smoking images compared to when it appears in the location of the the non-smoking images.

Response time tasks like this are incredibly common in psychology and cognitive neuroscience, and being able to wrangle hundreds of trials is a great demonstration of your new data skills. After setting up your files and project for the chapter, we will outline the kind of problems you are trying to solve.

15.1.2 Organising your files and project for the task

Before we can get started, you need to organise your files and project for the task, so your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, create a new folder for the data analysis journey called `Journey_01_wrangling`. Within `Journey_01_wrangling`, create two new folders called `data` and `figures`.
2. Create an R Project for `Journey_01_wrangling` as an existing directory for your chapter folder. This should now be your working directory.
3. Create a new R Markdown document and give it a sensible title describing the chapter, such as `Analysis Journey 1 - Data Wrangling`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Journey_01_wrangling` folder.
4. We are working with data separated into two files. The links are data file one (Bartlett_demographics.csv) and data file two (Bartlett_trials.csv). Right click the links and select "save link as", or clicking the links will save the files to your Downloads. Make sure that both files are saved as ".csv". Save or copy the file to your `data/` folder within `Journey_01_wrangling`.

You are now ready to start working on the task!

15.2 Overview

15.2.1 Load tidyverse and read the data files

Before we explore what wrangling we need to do, load tidyverse and read the two data files. As a prompt, save the data files to these object names to be consistent with the activities below, but you can check the solution if you are stuck.

```
# Load the tidyverse package below
library(tidyverse)

# Load the data files
# This should be the Bartlett_demographics.csv file
demog <- ?

# This should be the Bartlett_trials.csv file
trials <- ?
```

Show me the solution

You should have the following in a code chunk:

```
# Load the tidyverse package below
library(tidyverse)

# Load the data files
# This should be the Bartlett_demographics.csv file
demog <- read_csv("data/Bartlett_demographics.csv")

# This should be the Bartlett_trials.csv file
trials <- read_csv("data/Bartlett_trials.csv")
```

15.2.2 Explore `demog` and `trials`

The data from J. E. Bartlett et al. (2022) is split into two data files. In `demog`, we have the participant ID (`participant_private_id`) and several demographic variables.

```
Rows: 205
Columns: 20
$ participant_private_id <dbl> 631737, 631738, 631741, 631739, 631749, 631746,~
$ consent_given          <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,~
$ age                    <dbl> 46, 54, 23, 34, 38, 19, 25, 21, 28, 35, 47, 45,~
$ cigarettes_per_week    <chr> "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes"~
$ smoke_everyday         <chr> "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes"~
$ past_four_weeks        <chr> "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes"~
$ age_started_smoking    <chr> "12", "17", "17", "16", "15", "16", "22", "11",~
$ country_of_origin      <chr> "United Kingdom", "Germany", "Poland", "Austral~
$ cpd                    <chr> "6", "5", "10", "20", "10", "1", "6", "15", "12~
$ ethnicity              <chr> "White / Caucasian", "White / Caucasian", "Mixe~
$ gender                 <chr> "Female", "Female", "Male", "Female", "Female",~
$ last_cigarette         <chr> "60", "780", "90", "5", "60", "720", "10", "10"~
$ level_education        <chr> "Graduated University / College", "Graduated Un~
$ technical_issues       <chr> "No", "No", "No", "No", "No", "No", "No", "No",~
$ FTND_1                 <dbl> 2, 0, 0, 3, 3, 0, 1, 2, 1, 3, 2, 2, 2, 1, 2, 0,~
$ FTND_2                 <dbl> 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 1, 0, 0,~
$ FTND_3                 <dbl> 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 0, 1, 0,~
$ FTND_4                 <dbl> 0, 0, 1, 1, 0, 1, 1, 0, 0, 0, 1, 1, 1, 0, 1, 1,~
$ FTND_5                 <dbl> 0, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 0, 1, 1, 0, 0,~
$ FTND_6                 <dbl> 0, 0, 0, 1, 0, 0, 0, 1, 1, 1, 1, 1, 1, 0, 0, 0,~
```

The columns (variables) we have in the data set are:

Variable	Type	Description
participant_private_id	double	Participant number.
consent_given	double	1 = informed consent, 2 = no consent.
age	double	Age in Years.
cigarettes_per_week	character	Do you smoke every week? Yes or No.
smoke_everyday	character	Do you smoke everyday? Yes or No.
past_four_weeks	character	Have you smoked in the past four weeks? Yes or No.
age_started_smoking	character	Age started smoking in years.
country_of_origin	character	Country of origin.
cpd	character	How many cigarettes do you smoke per day?
ethnicity	character	What is your ethniciity?
gender	character	What is your gender?

Variable	Type	Description
last_cigarette	character	How long in minutes since your last cigarette?
level_education	character	What is your highest level of education?
technical_issues	character	Did you experience any technical issues? Yes or No
FTND_1 to FTND_6	double	Six items of the Fagerstrom Test for Nicotine Dependence

In `trials`, we then have the participant ID (`participant_private_id`) and trial-by-trial information from the software Gorilla (an online experiment service). This is probably the biggest data set you have come across so far as we have hundreds of trials per participant.

```
Rows: 244,847
Columns: 15
$ participant_private_id <dbl> 631737, 631737, 631737, 631737, 631737, 631737,~
$ trial_number           <chr> "BEGIN TASK", "1", "1", "1", "1", "2", "2", "2"~
$ reaction_time          <dbl> NA, 8007.015, 249.823, 199.765, 1999.671, 249.8~
$ response               <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,~
$ correct                <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
$ display                <chr> NA, "instructions", "practice", "practice", "pr~
$ answer                 <chr> NA, NA, "right", "right", "right", "left", "lef~
$ soa                    <dbl> NA, NA, 200, 200, 200, 200, 200, 200, 500, 500,~
$ screen_name            <chr> NA, "instructions_continue", "Screen 1", "Scree~
$ image_left             <chr> NA, NA, "p1.jpg", "p1.jpg", "p1.jpg", "p1.jpg",~
$ image_right            <chr> NA, NA, "p2.jpg", "p2.jpg", "p2.jpg", "p2.jpg",~
$ dot_left               <chr> NA, NA, "nodot.jpg", "nodot.jpg", "nodot.jpg", ~
$ dot_right              <chr> NA, NA, "dot.jpg", "dot.jpg", "dot.jpg", "nodot~
$ trial_type             <chr> NA, NA, "practice", "practice", "practice", "pr~
$ block                  <dbl> NA, NA, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
```

The columns (variables) we have in the data set are:

Variable	Type	Description
participant_private_id	double	Participant number.
trial_number	character	Trial number as an integer, plus start and end task.
reaction_time	double	Participant response time in milliseconds (ms)

Variable	Type	Description
response	character	Keyboard response from participant. Left or Right.
correct	double	Was the response correct? 1 = correct, 0 = incorrect.
display	character	Trial display: e.g., practice, trials, instructions, breaks.
answer	character	What is the correct answer? Left or Right.
soa	double	Stimulus onset asynchrony. How long the images were shown for: 200ms or 500ms.
screen_name	character	Name of the screen: e.g., screen 1, fixation, stimuli, response.
image_left	character	Name of the image file in the left area.
image_right	character	Name of the image file in the right area.
dot_left	character	Name of the dot image file in the left area.
dot_right	character	Name of the dot image file in the right area.
trial_type	character	Category of the trial: practice, neutral, nonsmoking, smoking.
block	double	Number of the trial block.

Try this

Now we have introduced the two data sets, explore them using different methods we introduced. For example, opening the data objects as a tab to scroll around, explore with `glimpse()`, or even try plotting some of the variables to see what they look like using visualisation skills from Chapter 3.
Do you notice any variables that look the wrong type? Can you see any responses in there that are going to cause problems?

15.3 Wrangling demographics

For this kind of data, we recommend wrangling each file first, before joining them together. Starting with the demographics file, there are a few wrangling steps before the data are ready

to summarise. We are going to show you a preview of the starting data set and the end product we are aiming for.

15.3.0.1 Raw data

```
Rows: 205
Columns: 20
$ participant_private_id <dbl> 631737, 631738, 631741, 631739, 631749, 631746,~
$ consent_given          <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,~
$ age                    <dbl> 46, 54, 23, 34, 38, 19, 25, 21, 28, 35, 47, 45,~
$ cigarettes_per_week    <chr> "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes"~
$ smoke_everyday         <chr> "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes"~
$ past_four_weeks        <chr> "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes"~
$ age_started_smoking    <chr> "12", "17", "17", "16", "15", "16", "22", "11",~
$ country_of_origin      <chr> "United Kingdom", "Germany", "Poland", "Austral~
$ cpd                    <chr> "6", "5", "10", "20", "10", "1", "6", "15", "12~
$ ethnicity              <chr> "White / Caucasian", "White / Caucasian", "Mixe~
$ gender                 <chr> "Female", "Female", "Male", "Female", "Female",~
$ last_cigarette         <chr> "60", "780", "90", "5", "60", "720", "10", "10"~
$ level_education        <chr> "Graduated University / College", "Graduated Un~
$ technical_issues       <chr> "No", "No", "No", "No", "No", "No", "No", "No",~
$ FTND_1                 <dbl> 2, 0, 0, 3, 3, 0, 1, 2, 1, 3, 2, 2, 2, 1, 2, 0,~
$ FTND_2                 <dbl> 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 1, 0, 0,~
$ FTND_3                 <dbl> 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 0, 1, 0,~
$ FTND_4                 <dbl> 0, 0, 1, 1, 0, 1, 1, 0, 0, 0, 1, 1, 1, 0, 1, 1,~
$ FTND_5                 <dbl> 0, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 0, 1, 1, 0, 0,~
$ FTND_6                 <dbl> 0, 0, 0, 1, 0, 0, 0, 1, 1, 1, 1, 1, 1, 0, 0, 0,~
```

15.3.0.2 Wrangled data

```
Rows: 205
Columns: 22
$ participant_private_id <dbl> 631737, 631738, 631741, 631739, 631749, 631746,~
$ consent_given          <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,~
$ age                    <dbl> 46, 54, 23, 34, 38, 19, 25, 21, 28, 35, 47, 45,~
$ cigarettes_per_week    <chr> "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes"~
$ smoke_everyday         <chr> "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes"~
$ past_four_weeks        <chr> "Yes", "Yes", "Yes", "Yes", "Yes", "Yes", "Yes"~
$ age_started_smoking    <int> 12, 17, 17, 16, 15, 16, 22, 11, 18, 15, 18, 19,~
$ country_of_origin      <fct> United Kingdom, Germany, Poland, Australia, Spa~
$ cpd                    <int> 6, 5, 10, 20, 10, 1, 6, 15, 12, 20, 20, 15, 20,~
```

```
$ ethnicity             <fct> White / Caucasian, White / Caucasian, Mixed / m~
$ gender                <fct> Female, Female, Male, Female, Female, Male, Fem~
$ last_cigarette        <dbl> 60, 780, 90, 5, 60, 720, 10, 10, 30, 0, 10, 30,~
$ level_education       <fct> Graduated University / College, Graduated Unive~
$ technical_issues      <chr> "No", "No", "No", "No", "No", "No", "No", "No",~
$ FTND_1                <dbl> 2, 0, 0, 3, 3, 0, 1, 2, 1, 3, 2, 2, 2, 1, 2, 0,~
$ FTND_2                <dbl> 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 1, 0, 0,~
$ FTND_3                <dbl> 1, 0, 1, 1, 1, 1, 1, 0, 1, 1, 1, 0, 1, 0, 1, 0,~
$ FTND_4                <dbl> 0, 0, 1, 1, 0, 1, 1, 0, 0, 0, 1, 1, 1, 0, 1, 1,~
$ FTND_5                <dbl> 0, 0, 0, 1, 1, 1, 0, 1, 1, 1, 1, 0, 1, 1, 0, 0,~
$ FTND_6                <dbl> 0, 0, 0, 1, 0, 0, 0, 1, 1, 1, 1, 1, 1, 0, 0, 0,~
$ daily_smoker          <fct> Daily Smoker, Daily Smoker, Daily Smoker, Daily~
$ FTND_sum              <dbl> 3, 0, 2, 7, 5, 3, 3, 5, 4, 6, 7, 5, 6, 3, 4, 1,~
```

Try this

Before we give you a task list, try and switch between the raw data and the wrangled data. Make a list of all the differences you can see between the two data objects.

1. What type is each variable? Has it changed from the raw data?
2. Do we have any new variables? How could you create these from the variables available to you?

For the variable `daily_smoker`, this has two levels which you cannot see in the preview: "Daily Smoker" and "Non-daily Smoker". Which variable could this be based on?
Try and wrangle the data based on all the differences you notice to create a new object `demog_tidy`.
When you get as far as you can, check the task list which explains all the steps we applied, but not how to do them. Then, you can check the solution for our code.

15.3.1 Task list

Show me the task list

These are all the steps we applied to create the wrangled data object:

1. Convert `age_started_smoking` to an integer (as age is a round number).
2. Convert `cpd` to an integer (as cigarettes per day is a round number). You will notice a warning about introducing an NA as some nonsense responses cannot be converted to a number.

3. Convert `country_of_origin` to a factor (as we have distinct categories).
4. Convert `ethnicity` to a factor (as we have distinct categories).
5. Convert `gender` to a factor (as we have distinct categories).
6. Convert `last_cigarette` to an integer (as time since last cigarette in minutes is a round number). You will notice a warning about introducing an NA as some nonsense responses cannot be converted to a number.
7. Convert `level_education` to a factor (as we have distinct categories).
8. Create a new variable `daily_smoker` by recoding an existing variable. The new variable should have two levels: "Daily Smoker" and "Non-daily Smoker". In the process, convert `daily_smoker` to a factor (as we have distinct categories).
9. Create a new variable `FTND_sum` by taking the sum of the six items `FTND_1` to `FTND_6` per participant.

For some advice, think of everything we covered in Chapters 4 to 6. How could you complete these steps as efficiently as possible? Could you string together functions using pipes, or do you need some intermediary objects? If it's easier for you to complete steps with longer but accurate code, there is nothing wrong with that. You recognise ways to make your code more efficient over time.

15.3.2 Solution

Show me the solution

This is the code we used to create the new object `demog_tidy` using the original object `demog`. As long as you get the same end result, the exact code is not important. In coding, there are multiple ways of getting to the same end result. Maybe you found a more efficient way to complete some of the steps compared to us. Maybe your code was a little longer. As long as it worked, that is the most important thing.

```
# Using demog, create a new object demog_tidy
# apply mutate to convert or create variables
demog_tidy <- demog %>%
  mutate(age_started_smoking = as.integer(age_started_smoking),
         cpd = as.integer(cpd),
         country_of_origin = as.factor(country_of_origin),
         ethnicity = as.factor(ethnicity),
         gender = as.factor(gender),
         last_cigarette = as.integer(last_cigarette),
         level_education = as.factor(level_education),
         # we used smoke_everyday to create our daily_smoker variable
         daily_smoker = as.factor(case_match(smoke_everyday,
                                             "Yes" ~ "Daily Smoker",
                                             "No" ~ "Non-daily Smoker")))
# To calculate the sum of the 6 FTND items,
# pivot longer, group by ID, then sum responses.
FTND_sum <- demog_tidy %>%
  pivot_longer(cols = FTND_1:FTND_6,
               names_to = "Item",
               values_to = "Response") %>%
  group_by(participant_private_id) %>%
  summarise(FTND_sum = sum(Response))

# Join this new column back to demog_tidy
demog_tidy <- demog_tidy %>%
  inner_join(y = FTND_sum,
             by = "participant_private_id")
```

15.4 Wrangling trials

Turning to the trials file, there are a few wrangling steps and you will probably need the task list more for this part than you did for demographics. Some of the steps might not be as obvious but it is still important to compare the objects and see if you can identify the changes. We are going to show you a preview of the starting data set, and the end product we are aiming for in step 3.

15.4.0.1 Original raw data

```
Rows: 244,847
```

```
Columns: 15
$ participant_private_id <dbl> 631737, 631737, 631737, 631737, 631737, 631737,~
$ trial_number           <chr> "BEGIN TASK", "1", "1", "1", "1", "2", "2", "2"~
$ reaction_time          <dbl> NA, 8007.015, 249.823, 199.765, 1999.671, 249.8~
$ response               <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,~
$ correct                <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
$ display                <chr> NA, "instructions", "practice", "practice", "pr~
$ answer                 <chr> NA, NA, "right", "right", "right", "left", "lef~
$ soa                    <dbl> NA, NA, 200, 200, 200, 200, 200, 200, 500, 500,~
$ screen_name            <chr> NA, "instructions_continue", "Screen 1", "Scree~
$ image_left             <chr> NA, NA, "p1.jpg", "p1.jpg", "p1.jpg", "p1.jpg",~
$ image_right            <chr> NA, NA, "p2.jpg", "p2.jpg", "p2.jpg", "p2.jpg",~
$ dot_left               <chr> NA, NA, "nodot.jpg", "nodot.jpg", "nodot.jpg", ~
$ dot_right              <chr> NA, NA, "dot.jpg", "dot.jpg", "dot.jpg", "nodot~
$ trial_type             <chr> NA, NA, "practice", "practice", "practice", "pr~
$ block                  <dbl> NA, NA, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
```

15.4.0.2 Step 1

```
Rows: 50,510
Columns: 15
$ participant_private_id <dbl> 631737, 631737, 631737, 631737, 631737, 631737,~
$ trial_number           <chr> "1", "2", "4", "5", "6", "7", "8", "9", "11", "~
$ reaction_time          <dbl> 1486.850, 720.640, 739.635, 668.730, 578.015, 5~
$ response               <chr> "right", "left", "right", "right", "left", "lef~
$ correct                <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,~
$ display                <chr> "trials", "trials", "trials", "trials", "trials~
$ answer                 <chr> "right", "left", "right", "right", "left", "lef~
$ soa                    <dbl> 200, 500, 500, 200, 200, 200, 200, 200, 500, 50~
$ screen_name            <chr> "response", "response", "response", "response",~
$ image_left             <chr> "N14.jpg", "F14.jpg", "F14.jpg", "N4.jpg", "N19~
$ image_right            <chr> "F14.jpg", "N14.jpg", "N14.jpg", "F4.jpg", "F19~
$ dot_left               <chr> "nodot.jpg", "dot.jpg", "nodot.jpg", "nodot.jpg~
$ dot_right              <chr> "dot.jpg", "nodot.jpg", "dot.jpg", "dot.jpg", "~
$ trial_type             <chr> "smoking", "smoking", "nonsmoking", "smoking", ~
$ block                  <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,~
```

15.4.0.3 Step 2

```
Rows: 820
Columns: 5
```

```
$ participant_private_id <dbl> 631737, 631737, 631737, 631737, 631738, 631738,~
$ soa                    <dbl> 200, 200, 500, 500, 200, 200, 500, 500, 200, 20~
$ trial_type             <chr> "nonsmoking", "smoking", "nonsmoking", "smoking~
$ median_RT              <dbl> 444.6275, 452.8675, 456.8900, 449.6650, 638.000~
$ condition              <chr> "nonsmoking200", "smoking200", "nonsmoking500",~
```

15.4.0.4 Step 3

```
Rows: 205
Columns: 5
$ participant_private_id <dbl> 631737, 631738, 631739, 631741, 631746, 631748,~
$ nonsmoking200          <dbl> 444.6275, 638.0000, 516.5375, 410.8250, 375.272~
$ smoking200             <dbl> 452.8675, 703.5000, 529.1300, 433.3175, 367.365~
$ nonsmoking500          <dbl> 456.8900, 700.0000, 517.4775, 427.4100, 363.195~
$ smoking500             <dbl> 449.6650, 725.0000, 514.5050, 421.2250, 355.777~
```

Try this

Before we give you a task list, try and switch between the raw data and the three steps we took for wrangling the data. Make a list of all the differences you can see across the steps.
This part of the data wrangling is quite difficult if you are unfamiliar with dealing with response time tasks as you need to know what the end product should look like to work with later. Essentially, we want the median response time per participant per condition (across trial type and soa). There are rows we do not need, variables to create, and data to restructure. So, it takes all your wrangling skills you have learnt so far.

1. In step 1, how many observations do we have compared to the raw data? Knowing the design is important here, so look at the columns `correct`, `screen_name`, and `trial_type`. What function might reduce the number of observations like this?

2. In step 2, how many observations do we have compared to step 1? How many observations do we have per participant ID? What new variables do we have and how could you make them? Hint: for `condition`, we have not covered this, so look up a function called `paste0()`.

3. In step 3, how many observations do we have compared to step 2? Have we removed any columns compared to step 2? Have the data been restructured?

Try and wrangle the data based on all the differences you notice to create a new object `RT_wide` shown in step 3.
When you get as far as you can, check the task list which explains all the steps we applied, but not how to do them. Then, you can check the solution for our code.

15.4.1 Task list

For this part, we will separate the task list into the three steps in case you want to test yourself at each stage.

Show me the step 1 task list

These are all the steps we applied to create the wrangled data object:

1. Create an object `trials_tidy` using the original `trials` data.
2. Filter observations using three variables:
    - `screen_name` should only include "response".
    - `trial_type` should only include "nonsmoking" and "smoking".
    - `correct` should only include 1 (correct responses).

Show me the step 2 task list

These are all the steps we applied to create the wrangled data object:

1. Create an object `average_trials` using the `trials_tidy` object from step 1.
2. Group observations by three variables: `participant_private_id`, `soa`, and `trial_type`.
3. Summarise the data to create a new variable `median_RT` by calculating the median `reaction_time`.
4. Create a new variable called `condition` by combining the names of the `trial_type` and `soa` columns. Hint: this is a new concept, so try this `paste0(trial_type, soa)`. There are a few ways of dealing with this problem, but we are trying to avoid turning `soa` into variable names, as R does not like having variable names start with or be completely numbers.
5. Ungroup to avoid the groups carrying over into future objects.

Show me the step 3 task list

These are all the steps we applied to create the wrangled data object:

1. Create an object `RT_wide` using the `average_trials` object from step 2.
2. Remove the variables `soa` and `trial_type` to avoid problems with restructuring.

You could use the argument,

3. Restructure the data so your `condition` variable is spread across columns.

15.4.2 Solution

Show me the solution

This is the code we used to create the new object `RT_wide` by following three steps. You could do it in two to combine the first two steps, but we wanted to make the change between filtering and grouping/summarising more obvious before showing you the task list.
Remember: As long as you get the same end result, the exact code is not important. In coding, there are multiple ways of getting to the same end result.

```
# filter trials to focus on correct responses and key trials
trials_tidy <- trials %>%
  filter(screen_name == "response",
         trial_type %in% c("nonsmoking", "smoking"),
         correct == 1)

# Calculate median RT per ID, SOA, and trial type
average_trials <- trials_tidy %>%
  group_by(participant_private_id, soa, trial_type) %>%
  summarise(median_RT = median(reaction_time)) %>%
  mutate(condition = paste0(trial_type, soa)) %>%
  ungroup() # ungroup to avoid it carrying over

# Create wide data by making a new condition variable
# remove soa and trial type
# pivot wider for four columns per participant
RT_wide <- average_trials %>%
  select(-soa, -trial_type) %>%
  pivot_wider(names_from = condition,
              values_from = median_RT)
```

15.5 Combining objects and exclusion criteria

Great work so far! You should now have two wrangled objects: `demog_tidy` and `RT_wide`. The next step is combining them and applying exclusion criteria from the study.

We are going to give you the task list immediately for this as you need to understand the methods to know what criteria to use. We still challenge you to complete the tasks though, before checking your answers against the code we used.

Task list

Complete the following tasks to apply the final data wrangling steps:

1. Create a new object called `full_data` by joining your two data objects`demog_tidy` and `RT_wide` using a common identifier.
2. Filter observations using the following criteria:
    - `consent_given` should only include 1. We only want people who consented.
    - `age` range only between 18 and 60. We do not want people younger or older than this range.
    - `past_four_weeks` should only include "Yes". We do not want people who have not smoked in the past four weeks.
    - `technical_issues` should only include "No". We do not want people who experienced technical issues during the study.

15.5.1 Solution

Show me the solution

This is the code we used to create the new object `full_data` by joining `demog_tidy` and `RT_wide`, and filtering observations based on our four criteria.
As long as you get the same end result, the exact code is not important. In coding, there are multiple ways of getting to the same end result.

```
# create full_data by joining the two objects
# filter data by four criteria
full_data <- demog_tidy %>%
  inner_join(y = RT_wide,
             by = "participant_private_id") %>%
  filter(consent_given == 1,
         age >= 18 & age <= 60,
         past_four_weeks == "Yes",
         technical_issues == "No")
```

15.6 Summarising/visualising your data

That is all the wrangling complete! Hopefully, this reinforces the role of reproducibility and data skills. If you did this in other software like Excel, you might not have a paper trail of all the steps. Like this, you have the full code to apply all the wrangling steps from raw data which you can run every time you need to, and edit it if you found a mistake or wanted to add something new. You can also come back to the file later to add more code (such as after Chapter 7 to plot more of the data, or Chapter 13 for some inferential statistics).

To finish the journey, we have some practice tasks for summarising and visualising the data. The whole purpose of J. E. Bartlett et al. (2022) was to compare daily and non-daily smokers, so we will explore some of the key variables.

All of the questions are based on the final `full_data` object. If your answers differ, check the wrangling steps above. If you are really struggling to identify the difference, or you just wanted to complete these tasks, you can download a spreadsheet version of `full_data` here: Bartlett_full_data.csv.

15.6.1 Demographics

1. How many daily and non-daily smokers were there? There were _____ daily smokers and ___ non-daily smokers.

Show me the solution

```
full_data %>%
  count(daily_smoker)
```

```
# A tibble: 2 x 2
  daily_smoker         n
```

```
  <fct>            <int>
1 Daily Smoker       115
2 Non-daily Smoker    63
```

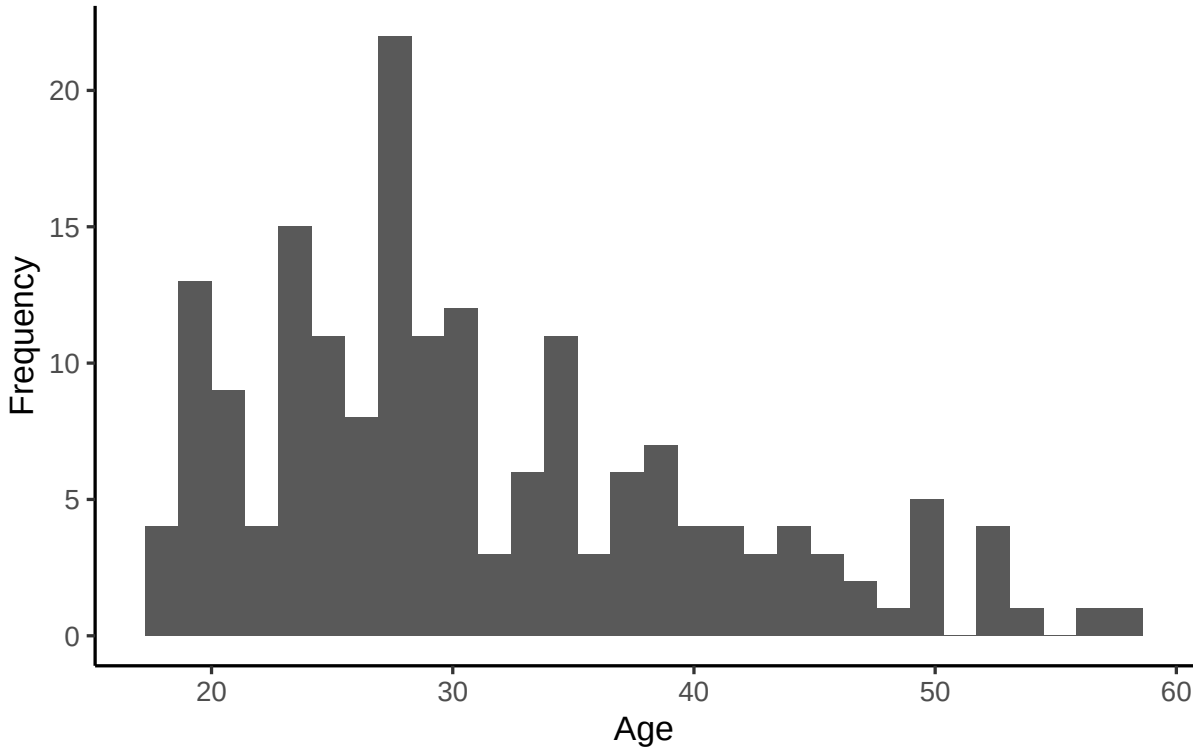
2. To 2 decimal places, the mean age of **all** the participants was _____ (SD = _____).

Show me the solution

```
full_data %>%
  summarise(mean_age = round(mean(age), 2),
            sd_age = round(sd(age), 2))
```

```
# A tibble: 1 x 2
  mean_age sd_age
     <dbl>  <dbl>
1     31.1   9.22
```

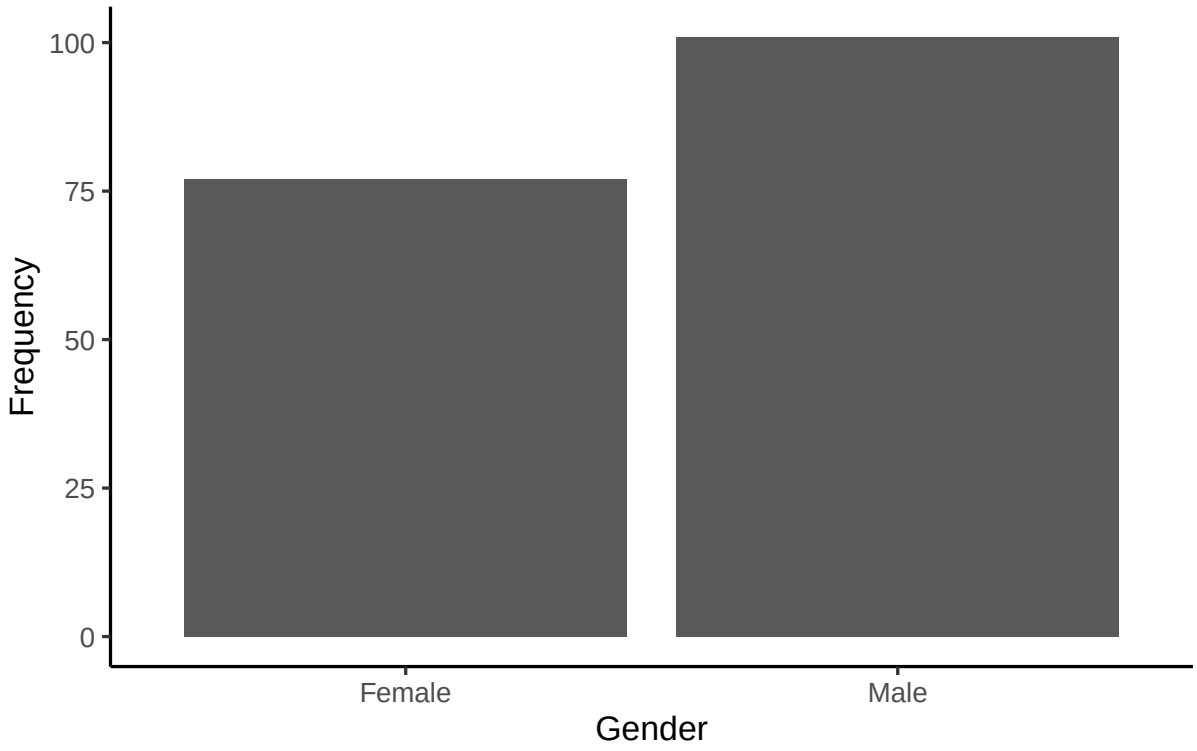
3. A histogram of all the participants' ages looks like:



Show me the solution

```
full_data %>%
  ggplot(aes(x = age)) +
  geom_histogram() +
  scale_x_continuous(name = "Age") +
  scale_y_continuous(name = "Frequency") +
  theme_classic()
```

4. A bar plot of the gender breakdown of the sample would look like:



Show me the solution

```
full_data %>%
  ggplot(aes(x = gender)) +
  geom_bar() +
  scale_x_discrete(name = "Gender") +
  scale_y_continuous(name = "Frequency") +
  theme_classic()
```

15.6.2 Measures of smoking dependence

5. To 2 decimal places, for daily smokers the mean number of cigarettes per day was _____ (SD = _____) and for non-daily smokers the mean number of cigarettes per day was _____ (SD = _____).

Show me the solution

```
full_data %>%
  group_by(daily_smoker) %>%
  summarise(mean_cpd = round(mean(cpd, na.rm = TRUE), 2),
            sd_cpd = round(sd(cpd, na.rm = TRUE), 2))
```

```
# A tibble: 2 x 3
  daily_smoker     mean_cpd sd_cpd
  <fct>               <dbl>  <dbl>
1 Daily Smoker         8.85   6.51
2 Non-daily Smoker     2.32   2.69
```

6. To 2 decimal places, for daily smokers the mean FTND sum score was _____ (SD = ***) and for non-daily smokers the mean number of cigarettes per day was*** _ (SD = _____).

Show me the solution

```
full_data %>%
  group_by(daily_smoker) %>%
  summarise(mean_FTND = round(mean(FTND_sum, na.rm = TRUE), 2),
            sd_FTND = round(sd(FTND_sum, na.rm = TRUE), 2))
```

```
# A tibble: 2 x 3
```

```
  daily_smoker     mean_FTND sd_FTND
  <fct>                <dbl>   <dbl>
1 Daily Smoker          2.61    2.2
2 Non-daily Smoker      0.49    1.28
```

15.6.3 Attentional bias

7. Before answering the following questions, complete one extra data wrangling step to create difference scores where positive values mean attentional bias towards smoking images (faster responses to smoking compared to non-smoking stimuli):

    - Create a new variable called `difference_200` by calculating `nonsmoking200 - smoking200`.
    - Create a new variable called `difference_500` by by calculating `nonsmoking500 - smoking500`.

Show me the solution

```
full_data <- full_data %>%
  mutate(difference_200 = nonsmoking200 - smoking200,
         difference_500 = nonsmoking500 - smoking500)
```

8. To 2 decimal places, the mean difference in attentional bias in the 200ms condition was _____ (SD = _____) for daily smokers and _____ (SD = _____) for non-daily smokers.

Show me the solution

```
full_data %>%
  group_by(daily_smoker) %>%
  summarise(mean_bias_200 = round(mean(difference_200, na.rm = TRUE), 2),
            sd_bias_200 = round(sd(difference_200, na.rm = TRUE), 2))

# A tibble: 2 x 3
  daily_smoker     mean_bias_200 sd_bias_200
  <fct>                    <dbl>       <dbl>
1 Daily Smoker              1.25        23.9
2 Non-daily Smoker         -2.74        21.3
```

9. To 2 decimal places, the mean difference in attentional bias in the 500ms condition was _____ (SD = _____) for daily smokers and _____ (SD = _____) for non-daily smokers.

Show me the solution

```
full_data %>%
  group_by(daily_smoker) %>%
  summarise(mean_bias_500 = round(mean(difference_500, na.rm = TRUE), 2),
            sd_bias_500 = round(sd(difference_500, na.rm = TRUE), 2))
```

```
# A tibble: 2 x 3
  daily_smoker     mean_bias_500 sd_bias_500
  <fct>                    <dbl>       <dbl>
1 Daily Smoker              0.76        21.7
2 Non-daily Smoker         -1.19        14.5
```

If you are currently completing this after Chapter 6, we have not covered visualising continuous data or inferential statistics yet. Try coming back to these tasks to compare these measures when you have finished Chapter 7 for more advanced visualisation and Chapter 13 for factorial ANOVA.

A difference score of 0 means no bias towards smoking or non-smoking images. So, you can see the paper did not find either group showed much attentional bias towards smoking images nor much difference between the groups, hence why it was published in the *Journal of Trial and Error*.

15.7 Conclusion

Well done! Hopefully you recognised how far your skills have come to be able to do this independently, regardless of how many hints you needed.

These are real skills people use in research. If you are curious, J. E. Bartlett et al. (2022) shared their code as a reproducible manuscript, so you can see all the wrangling steps they completed by looking at this file on the Open Science Framework. We did not include all of them here as there are concepts like outliers we had not covered by Chapter 6.

16 Analysis Journey 2: Simple Linear Regression

Welcome to the second data analysis journey. We have designed these chapters as a bridge between the structured learning in the core chapters and your assessments. We present you with a new data set, show you what the end product should look like, and see if you can apply your data wrangling, visualisation, and/or analysis skills to get there.

As you gain independence, this is the crucial skill. Data analysis is all about seeing the data you have available to you and identifying what the end product needs to be to apply your visualisation and analysis techniques. You can then mentally (or physically) create a checklist of tasks to work backwards to get there. There might be a lot of trial and error as you try one thing, it does not quite work, so you go back and try something else. If you get stuck though, we have a range of hints and task lists you can unhide, then the solution to check your attempts against.

In this second data analysis journey, we focus on inferential statistics after some data wrangling to apply all the skills you developed from Chapter 1 to Chapter 9.

16.1 Task preparation

16.1.1 Introduction to the data set

For this task, we are using open data from Binfet et al. (2022), where the authors used the data set to write a separate article on repurposing it for statistics education (Evans et al., 2023), inspiring us to use it in the chapter here. The abstract of their article is:

> Researchers have claimed that canine-assisted interventions (CAIs) contribute significantly to bolstering participants' wellbeing, yet the mechanisms within interactions have received little empirical attention. The aim of this study was to assess the impact of client–canine contact on wellbeing outcomes in a sample of 284 undergraduate college students (77% female; 21% male, 2% non-binary). Participants self-selected to participate and were randomly assigned to one of two canine interaction treatment conditions (touch or no touch) or to a handler-only condition with no therapy dog present. To assess self-reports of wellbeing, measures of flourishing, positive and negative affect, social connectedness, happiness,

integration into the campus community, stress, homesickness, and loneliness were administered. Exploratory analyses were conducted to assess whether these wellbeing measures could be considered as measuring a unidimensional construct. This included both reliability analysis and exploratory factor analysis. Based on the results of these analyses we created a composite measure using participant scores on a latent factor. We then conducted the tests of the four hypotheses using these factor scores. Results indicate that participants across all conditions experienced enhanced wellbeing on several measures; however, only those in the direct contact condition reported significant improvements on all measures of wellbeing. Additionally, direct interactions with therapy dogs through touch elicited greater wellbeing benefits than did no touch/indirect interactions or interactions with only a dog handler. Similarly, analyses using scores on the wellbeing factor indicated significant improvement in wellbeing across all conditions (handler-only, d=0.18, p=0.041; indirect, d=0.38, p<0.001; direct, d=0.78, p<0.001), with more benefit when a dog was present (d=0.20, p<0.001), and the most benefit coming from physical contact with the dog (d=0.13, p=0.002). The findings hold implications for post-secondary wellbeing programs as well as the organization and delivery of CAIs.

In summary, they were interested in the effect of therapy dogs on well-being in undergraduate students. Participants were randomly allocated to one of three groups:

1. Canine interaction touching the dogs (Direct).
2. Canine interaction not touching the dogs (Indirect).
3. Handler-only with no dogs present (Control).

They measured 9 outcomes before and after the intervention including social connectedness, stress, and loneliness. For this journey chapter, we will focus on a constrained set of variables and analyses so it does not take forever, but the process would apply to all the outcomes. The authors posed three hypotheses which we will test after some data wrangling:

1. All treatment groups would have significantly higher measures of well-being and lower measures of ill-being after treatment.
2. The treatment groups that interact with dogs would have significantly higher measures of well-being and lower measures of ill-being compared to the handler-only treatment.
3. Direct contact with a therapy dog would yield greater benefits than indirect contact treatment.

16.1.2 Organising your files and project for the task

Before we can get started, you need to organise your files and project for the task, so your working directory is in order.

1. In your folder for research methods and the book `ResearchMethods1_2/Quant_Fundamentals`, create a new folder for the data analysis journey called `Journey_02_regression`. Within `Journey_02_regression`, create two new folders called `data` and `figures`.
2. Create an R Project for `Journey_02_regression` as an existing directory for your chapter folder. This should now be your working directory.
3. Create a new R Markdown document and give it a sensible title describing the chapter, such as `Analysis Journey 2 - Simple Linear Regression`. Delete everything below line 10 so you have a blank file to work with and save the file in your `Journey_02_regression` folder.
4. We are working with a new data set, so please save the following data file: Evans_2023_raw.csv. Right click the link and select "save link as", or clicking the link will save the files to your Downloads. Make sure that you save the file as ".csv". Save or copy the file to your `data/` folder within `Journey_02_regression`.

You are now ready to start working on the task!

16.2 Overview

16.2.1 Load tidyverse and read the data file

Before we explore what wrangling we need to do, complete the following task list and check the solution if you are stuck.

Try this

Complete the following steps:

1. Load the tidyverse package.
2. Read the data file `data/Evans_2023_raw.csv` to the object name `evans_data`.

Show me the solution

You should have the following in a code chunk:

```r
# load the relevant packages
library(tidyverse)

# Read the Evans_2023_raw.csv file
evans_data <- read_csv("data/Evans_2023_raw.csv")
```

16.2.2 Explore `evans_data`

In `evans_data`, we have the participant ID (`RID`), several demographic variables, and pre- and post-test items for stress, loneliness, and social connectedness. There are 88 variables which would take up loads of space, so we are just showing a preview of the first 20 here. If you use `glimpse()`, you will see all 88.

```
Rows: 284
Columns: 20
$ RID             <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16,~
$ GroupAssignment <chr> "Control", "Direct", "Indirect", "Control", "Direct", ~
$ Age_Yrs         <dbl> 21, 19, 18, 18, 19, 20, 26, 17, 21, 22, 19, 20, 19, 19~
$ Year_of_Study   <dbl> 3, 1, 1, 1, 1, 2, 2, 1, 3, 4, 2, 2, 2, 2, 3, 1, 1, 1, ~
$ Live_Pets       <dbl> 2, 2, 2, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, NA, 2, 2, 1,~
$ Consumer_BARK   <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 1, 1, ~
$ S1_1            <dbl> 2, 2, 4, 2, 3, 4, 4, 3, 2, 2, 3, 2, 3, 4, 3, 2, 4, 2, ~
$ L1_1            <dbl> 3, 3, 3, 4, 2, 4, 3, 2, 3, 4, 3, 3, 4, 4, 4, 2, 3, 4, ~
$ L1_2            <dbl> 3, 2, 3, 2, 3, 3, 2, 3, 4, 1, 3, 3, 2, 3, 1, 4, 3, 2, ~
$ L1_3            <dbl> 4, 3, 2, 2, 3, 3, 1, 3, 3, 1, 2, 2, 1, 3, 1, 3, 3, 1, ~
$ L1_4            <dbl> 3, 3, 3, 3, 3, 3, 3, 3, 4, 1, 2, 3, 2, 3, 2, 4, 3, 2, ~
$ L1_5            <dbl> 2, 4, 3, 4, 4, 3, 2, 4, 4, 4, 4, 4, 4, 4, 4, 2, 3, 4, ~
$ L1_6            <dbl> 3, 3, 4, 4, 3, 2, 3, 3, 3, 4, 3, 3, 4, 3, 4, 2, 2, 4, ~
$ L1_7            <dbl> 1, 2, 2, 1, 2, 2, 4, 2, 2, 1, 3, 2, 3, 2, 2, 2, 3, 3, ~
$ L1_8            <dbl> 2, 2, 3, 3, 2, 3, 2, 3, 3, 2, 3, 2, 2, 3, 2, 4, 3, 2, ~
$ L1_9            <dbl> 3, 4, 3, 3, 3, 3, 3, 3, 2, 4, 3, 3, 4, 4, 4, 3, 2, 3, ~
$ L1_10           <dbl> 4, 3, 3, 4, 2, 2, 3, 3, 3, 4, 4, 3, 4, 4, 4, 2, 2, 3, ~
$ L1_11           <dbl> 3, 2, 2, 2, 4, 3, 4, 2, 2, 1, 3, 2, 2, 2, 2, 4, 3, 2, ~
$ L1_12           <dbl> 1, 2, 2, 1, 4, 3, 2, 2, 1, 1, 2, 2, 1, 2, 2, 1, 3, 1, ~
$ L1_13           <dbl> 3, 1, 2, 2, 4, 3, 3, 3, 4, 1, 3, 4, 2, 2, 2, 4, 3, 2, ~
```

The columns (variables) we have in the data set are:

Variable	Type	Description
RID	double	Participant ID number.
GroupAssignment	character	Randomly allocated study group: Control, Indirect, Direct.
Age_Yrs	double	Age in years.
Year_of_Study	double	Participant's year in college: First (1), Second (2), Third (3), Fourth (4), Fifth or more (5).
Live_Pets	double	Does the participant have a pet back at home: Pet back home (1), no pet back home (2).
Consumer_BARK	double	Is the participant a low (1), medium (2), or high (3) consumer of the BARK program - the therapy dog service.
S1_1	double	Stress scale pre-test, 1 item, 1 (not at all stressed) to 5 (very stressed).
L1_1 to L1_20	double	Loneliness scale pre-test, 20 items, 1 (never) to 4 (often).
SC1_1 to SC1_20	double	Social connectedness scale pre-test, 20 items, 1 (strongly disagree) to 6 (strongly agree).
S2_1	double	Stress scale post-test, 1 item.
L2_1 to L2_20	double	Loneliness scale post-test, 20 items.
SC2_1 to SC2_20	double	Social connectedness scale post-test, 20 items, 1 (strongly disagree) to 6 (strongly agree).

Try this

Now we have introduced the data set, explore them using different methods we introduced. For example, opening the data object as a tab to scroll around, explore with `glimpse()`, or even try plotting some of the individual variables to see what they look like.

16.3 Wrangling

We are going to show you a preview of the starting data set and the end product we are aiming for. For the raw data, we have limited this to the first 20 rows again just so it does not take

up the whole page, but if you use `glimpse()` you will see all 88 variables.

16.3.0.1 Raw data

```
Rows: 284
Columns: 20
$ RID             <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16,~
$ GroupAssignment <chr> "Control", "Direct", "Indirect", "Control", "Direct", ~
$ Age_Yrs         <dbl> 21, 19, 18, 18, 19, 20, 26, 17, 21, 22, 19, 20, 19, 19~
$ Year_of_Study   <dbl> 3, 1, 1, 1, 1, 2, 2, 1, 3, 4, 2, 2, 2, 2, 3, 1, 1, 1, ~
$ Live_Pets       <dbl> 2, 2, 2, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, NA, 2, 2, 1,~
$ Consumer_BARK   <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 1, 1, ~
$ S1_1            <dbl> 2, 2, 4, 2, 3, 4, 4, 3, 2, 2, 3, 2, 3, 4, 3, 2, 4, 2, ~
$ L1_1            <dbl> 3, 3, 3, 4, 2, 4, 3, 2, 3, 4, 3, 3, 4, 4, 4, 2, 3, 4, ~
$ L1_2            <dbl> 3, 2, 3, 2, 3, 3, 2, 3, 4, 1, 3, 3, 2, 3, 1, 4, 3, 2, ~
$ L1_3            <dbl> 4, 3, 2, 2, 3, 3, 1, 3, 3, 1, 2, 2, 1, 3, 1, 3, 3, 1, ~
$ L1_4            <dbl> 3, 3, 3, 3, 3, 3, 3, 3, 4, 1, 2, 3, 2, 3, 2, 4, 3, 2, ~
$ L1_5            <dbl> 2, 4, 3, 4, 4, 3, 2, 4, 4, 4, 4, 4, 4, 4, 4, 2, 3, 4, ~
$ L1_6            <dbl> 3, 3, 4, 4, 3, 2, 3, 3, 3, 4, 3, 3, 4, 3, 4, 2, 2, 4, ~
$ L1_7            <dbl> 1, 2, 2, 1, 2, 2, 4, 2, 2, 1, 3, 2, 3, 2, 2, 2, 3, 3, ~
$ L1_8            <dbl> 2, 2, 3, 3, 2, 3, 2, 3, 3, 2, 3, 2, 2, 3, 2, 4, 3, 2, ~
$ L1_9            <dbl> 3, 4, 3, 3, 3, 3, 3, 3, 2, 4, 3, 3, 4, 4, 4, 3, 2, 3, ~
$ L1_10           <dbl> 4, 3, 3, 4, 2, 2, 3, 3, 3, 4, 4, 3, 4, 4, 4, 2, 2, 3, ~
$ L1_11           <dbl> 3, 2, 2, 2, 4, 3, 4, 2, 2, 1, 3, 2, 2, 2, 2, 4, 3, 2, ~
$ L1_12           <dbl> 1, 2, 2, 1, 4, 3, 2, 2, 1, 1, 2, 2, 1, 2, 2, 1, 3, 1, ~
$ L1_13           <dbl> 3, 1, 2, 2, 4, 3, 3, 3, 4, 1, 3, 4, 2, 2, 2, 4, 3, 2, ~
```

16.3.0.2 Wrangled data

```
Rows: 284
Columns: 12
$ RID             <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16,~
$ GroupAssignment <chr> "Control", "Direct", "Indirect", "Control", "Direct", ~
$ Age_Yrs         <dbl> 21, 19, 18, 18, 19, 20, 26, 17, 21, 22, 19, 20, 19, 19~
$ Year_of_Study   <dbl> 3, 1, 1, 1, 1, 2, 2, 1, 3, 4, 2, 2, 2, 2, 3, 1, 1, 1, ~
$ Live_Pets       <chr> "Does not have a pet back home", "Does not have a pet ~
$ Consumer_BARK   <chr> "Low", "Low", "Low", "Low", "Low", "Low", "Low", "Low"~
$ stress_pre      <dbl> 2, 2, 4, 2, 3, 4, 4, 3, 2, 2, 3, 2, 3, 4, 3, 2, 4, 2, ~
$ stress_post     <dbl> 2, 1, 3, 2, 4, 4, 3, 2, 2, 1, 2, 2, 1, 2, 4, 2, 2, 1, ~
$ lonely_pre      <dbl> 2.25, 1.90, 2.25, 1.75, 2.85, 2.70, 2.40, 2.25, 2.55, ~
$ lonely_post     <dbl> 1.70, 1.60, 2.25, 2.05, 2.70, 2.40, 2.25, 2.00, 2.55, ~
```

```
$ social_pre      <dbl> 3.90, 5.15, 4.10, 4.65, 3.65, 4.35, 4.75, 4.60, 4.20, ~
$ social_post     <dbl> 3.800000, 5.263158, 4.150000, 5.100000, 3.600000, 4.65~
```

Try this

Before we give you a task list, try and switch between the raw data and the wrangled data. Make a list of all the differences you can see between the two data objects.

1. Do the values of variables change from numbers? How might you recode them using the code book above?
2. Looking at the codebook, are some variables the same but renamed?
3. Looking at the codebook, have we calculated the mean of all the items for a scale?

Try and wrangle the data based on all the differences you notice to create a new object `evans_wide`.
For one hint, unless you read the original paper, there are a bunch of items that first need reverse coding you would not know about:

- Loneliness pre-test: L1_1, L1_5, L1_6, L1_9, L1_10, L1_15, L1_16, L1_19, L1_20.
- Loneliness post-test: L2_1, L2_5, L2_6, L2_9, L2_10, L2_15, L2_16, L2_19, L2_20.
- Social connectedness pre-test: SC1_3, SC1_6, SC1_7, SC1_9, SC1_11, SC1_13, SC1_15, SC1_17, SC1_18, SC1_20.
- Social connectedness post-test: SC2_3, SC2_6, SC2_7, SC2_9, SC2_11, SC2_13, SC2_15, SC2_17, SC2_18, SC2_20.

When you get as far as you can, check the task list which explains all the steps we applied, but not how to do them. Then, you can check the solution for our code.

16.3.1 Task list

Show me the task list

These are all the steps we applied to create the wrangled data object:

1. Recode `Live_Pets` to the two labels outlined in the code book.
2. Recode `Consumer_BARK` to the three labels outlined in the code book.

3. Reverse code the loneliness and social connectedness items outlined above. Think of previous examples where we explained reverse coding for how you can do this efficiently.

As one extra piece of advice if you do not want to recode 40 variables one by one, there is a more advanced function you can use within `mutate()`. The function `across()` lets you apply a function or calculation to several columns at once. For example, if we wanted to reverse score items on a 4-point scale, it would look like the following:

```
mutate(across(.cols = c(column1, column2...),
              .fns = ~ 5 - .x))
```

In `.cols`, we enter all the columns we want to apply the function to.
In `.fns` after the `=`, we add the function we want to apply to all the columns we selected. The code is a little awkward as we have a tilde `~`, here the calculation we want to apply, and `.x` in place of the column name. You could summarise it as: for all the columns I select, subtract each value from 5. Once you get used to the format, `across()` is really helpful when you want to do the same thing to multiple columns.

4. After reverse coding the items, calculate the subscale mean scores for loneliness and social connectedness. You must do this twice per scale, as we have the 20 items for the pre-test and 20 items for the post-test per scale.

5. If you calculated the subscale mean scores individually, join them back to the `evans_clean` object you mutated.

6. Select the following columns:

    - `RID` to `Consumer_BARK`.
    - Rename `S1_1` to `stress_pre`.
    - Rename `S2_1` to `stress_post`.
    - Select your four subscale mean score variables.

Remember: If it's easier for you to complete steps with longer but accurate code, there is nothing wrong with that. You recognise ways to make your code more efficient over time.

16.3.2 Solution

Show me the solution

This is the code we used to create the new object `evans_wide` using the original object `evans_data`. As long as you get the same end result, the exact code is not important. In coding, there are multiple ways of getting to the same end result. Maybe you found a more efficient way to complete some of the steps compared to us. Maybe your code was a little longer. As long as it worked, that is the most important thing.

```r
# Initial cleaning step to recode pets and BARK
# then reverse code a bunch of items
evans_clean <- evans_data %>%
  mutate(Live_Pets = case_match(Live_Pets,
                                1 ~ "Has a pet back home",
                                2 ~ "Does not have a pet back home"),
         Consumer_BARK = case_match(Consumer_BARK,
                                    1 ~ "Low",
                                    2 ~ "Medium",
                                    3 ~ "High"),
         # across works with mutate to apply the same function to several columns
         # So, take all the loneliness items to reverse code, then subtract them from 5
         across(.cols = c(L1_1, L1_5, L1_6, L1_9, L1_10, L1_15, L1_16, L1_19, L1_20,
                          L2_1, L2_5, L2_6, L2_9, L2_10, L2_15, L2_16, L2_19, L2_20),
                .fns = ~ 5 - .x),
         # take all the connectedness items to reverse code, then subtract them from 7
         across(.cols = c(SC1_3, SC1_6, SC1_7, SC1_9, SC1_11, SC1_13, SC1_15, SC1_17, SC1_1
                          SC2_3, SC2_6, SC2_7, SC2_9, SC2_11, SC2_13, SC2_15, SC2_17, SC2_1
                .fns = ~ 7 - .x))

# There are more elegant ways around this, but for each set,
# take the 20 items, group by participant ID, and calculate the mean, ignoring missing valu
lonely_pre <- evans_clean %>%
  pivot_longer(cols = L1_1:L1_20,
               names_to = "Item",
               values_to = "Response") %>%
  group_by(RID) %>%
  summarise(lonely_pre = mean(Response, na.rm = TRUE))

# Same thing for post scores
lonely_post <- evans_clean %>%
  pivot_longer(cols = L2_1:L2_20,
               names_to = "Item",
               values_to = "Response") %>%
  group_by(RID) %>%
  summarise(lonely_post = mean(Response, na.rm = TRUE))

# take the 20 items, group by participant ID, and calculate the mean, ignoring missing valu
social_pre <- evans_clean %>%
  pivot_longer(cols = SC1_1:SC1_20,
               names_to = "Item",
               values_to = "Response") %>%
  group_by(RID) %>%
  summarise(social_pre = mean(Response, na.rm = TRUE))

# Same thing for post scores
social_post <- evans_clean %>%
  pivot_longer(cols = SC2_1:SC2_20,
               names_to = "Item",
               values_to = "Response") %>%
  group_by(RID) %>%
  summarise(social_post = mean(Response, na.rm = TRUE))
```

16.4 Summarising/visualising

You should now have an object called `evans_wide` containing 12 variables. If you struggled completing the wrangling steps, you can copy the code from the solution to follow along from this point. In this section, we will calculate some summary statistics and plot the data to see what we can learn. We present you with a list of questions to answer using your wrangling and visualisation skills, interspersed with the solutions to check if you are stuck.

16.4.1 Demographics

For demographics, we will recreate some values from Table 1 from Binfet et al. (2022).

1. How many participants were in each group for `GroupAssignment`?
    - ___ Control
    - ___ Direct
    - ___ Indirect

Show me the solution

This nicely reproduces their values.

```
evans_wide %>%
  count(GroupAssignment)
```

```
# A tibble: 3 x 2
  GroupAssignment     n
  <chr>           <int>
1 Control            94
2 Direct             95
3 Indirect           95
```

2. To 2 decimals, what was the mean and standard deviation age per group?
    - Control: $M =$ _____, $SD =$ _____.
    - Direct: $M =$ _____, $SD =$ _____.
    - Indirect: $M =$ _____, $SD =$ _____.

Show me the solution

Weirdly, this reproduces the standard deviations from Table 1, but not the means.

```
evans_wide %>%
  group_by(GroupAssignment) %>%
  summarise(mean_age = round(mean(Age_Yrs), 2),
            sd_age = round(sd(Age_Yrs), 2))
```

```
# A tibble: 3 x 3
  GroupAssignment mean_age sd_age
  <chr>              <dbl>  <dbl>
1 Control             20.0   2.89
2 Direct              19.8   1.94
3 Indirect            20.0   2.23
```

3. How many participants in each group have a pet at home?

    - ___ Control
    - ___ Direct
    - ___ Indirect

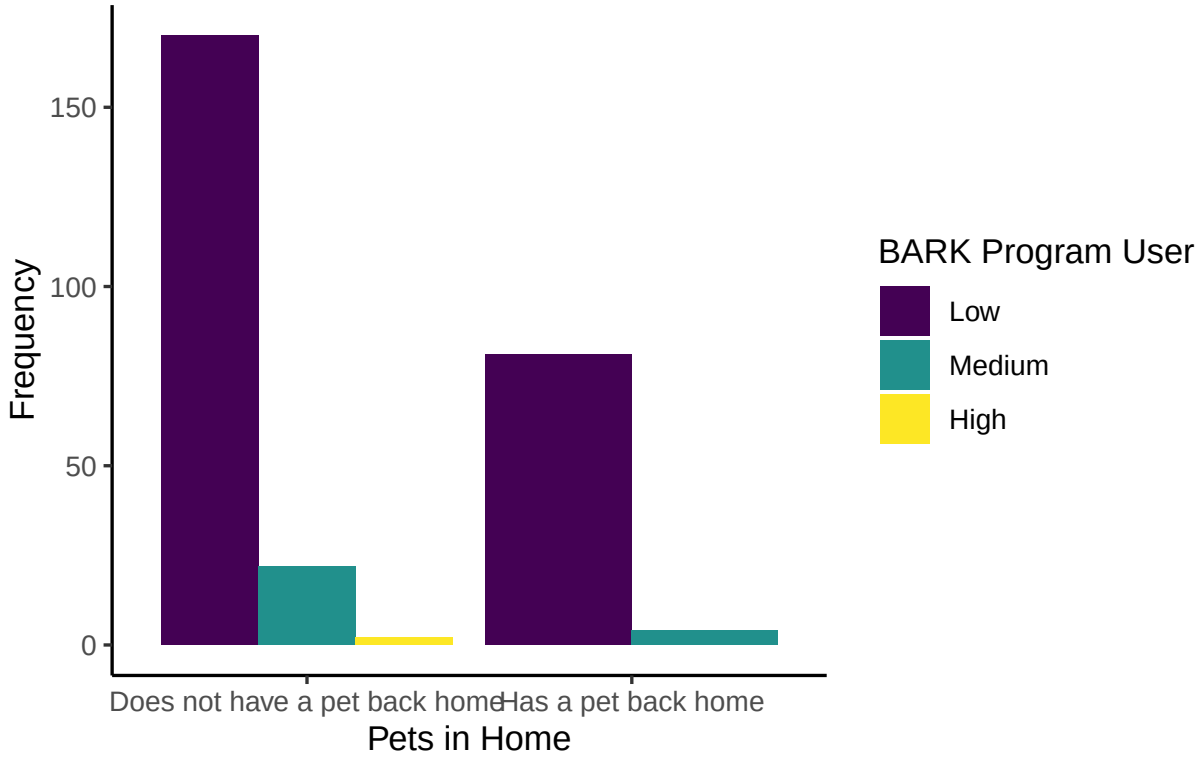
Show me the solution

This nicely reproduces their values.

```
evans_wide %>%
  count(GroupAssignment, Live_Pets)
```

```
# A tibble: 9 x 3
  GroupAssignment Live_Pets                          n
  <chr>           <chr>                          <int>
1 Control         Does not have a pet back home     72
2 Control         Has a pet back home               21
3 Control         <NA>                              1
4 Direct          Does not have a pet back home     63
5 Direct          Has a pet back home               30
6 Direct          <NA>                              2
7 Indirect        Does not have a pet back home     60
8 Indirect        Has a pet back home               34
9 Indirect        <NA>                              1
```

4. This is not part of their article, but one interesting question might be how many people have a pet at home (`Live_Pets`) against how frequently they use the BARK program (`Consumer_BARK`). Try and recreate the following bar plot to visualise this as close as possible. We have intentionally used some features we have not covered in the data visualisation chapters to get you problem solving. For one hint though, we used option D for the viridis colour scheme.



Show me the solution

The new features we hoped you found independently were:

- Setting the factor order to show `Consumer_BARK` as low, medium, then high.
- Set `position = "dodge"` to avoid the stacked bar chart.
- Edited the legend title by using the `name` argument in the `scale_fill` layer.

```r
evans_wide %>%
  drop_na(Live_Pets, Consumer_BARK) %>%
  mutate(Consumer_BARK = factor(Consumer_BARK,
                                levels = c("Low", "Medium", "High"))) %>%
  ggplot(aes(x = Live_Pets, fill = Consumer_BARK)) +
  geom_bar(position = "dodge") +
  labs(x = "Pets in Home",
       y = "Frequency") +
  scale_fill_viridis_d(option = "D",
                       name = "BARK Program User") +
  theme_classic()
```

16.4.2 Wellbeing measures

For wellbeing and ill-being measures, we will recreate some values from Table 2 from Binfet et al. (2022).

5. If you calculate the mean and standard deviation of each variable per group, answer the following questions:

    - Which group has the lowest post-test stress value?

- (A) Control
- (B) Indirect
- (C) Direct

    - Which group has the lowest post-test loneliness value?

- (A) Control
- (B) Direct
- (C) Indirect

    - Which group has the lowest post-test social connectedness value?

- (A) Direct

- (B) Control

- (C) Indirect

Show me the solution

This table calculates the mean and standard score for each variable per group. You can use this to answer the questions above.

```
evans_wide %>%
  pivot_longer(cols = stress_pre:social_post,
               names_to = "Variable",
               values_to = "Value") %>%
  group_by(GroupAssignment, Variable) %>%
  summarise(mean_score = round(mean(Value), 2),
            sd_score = round(sd(Value), 2))
```

```
`summarise()` has grouped output by 'GroupAssignment'. You can override using
the `.groups` argument.
```

```
# A tibble: 18 x 4
# Groups:   GroupAssignment [3]
   GroupAssignment Variable    mean_score sd_score
   <chr>           <chr>            <dbl>    <dbl>
 1 Control         lonely_post       1.96     0.57
 2 Control         lonely_pre        2.02     0.55
 3 Control         social_post       4.49     0.87
 4 Control         social_pre        4.47     0.81
 5 Control         stress_post       2.76     1.08
 6 Control         stress_pre        3.27     1.04
 7 Direct          lonely_post       1.82     0.51
 8 Direct          lonely_pre        2.05     0.56
 9 Direct          social_post       4.64     0.79
10 Direct          social_pre        4.42     0.88
11 Direct          stress_post       1.84     0.76
12 Direct          stress_pre        3.15     0.98
13 Indirect        lonely_post       1.96     0.52
14 Indirect        lonely_pre        2.06     0.48
15 Indirect        social_post       4.5      0.82
16 Indirect        social_pre        4.37     0.79
17 Indirect        stress_post       2.53     1
18 Indirect        stress_pre        3.21     0.9
```

6. Create a scatterplot of the relationship between post-test social connectedness and loneliness. The relationship between the two variables is

- (A) negative
- (B) positive

, meaning that as social connectedness increases, we expect loneliness to

- (A) increase
- (B) decrease

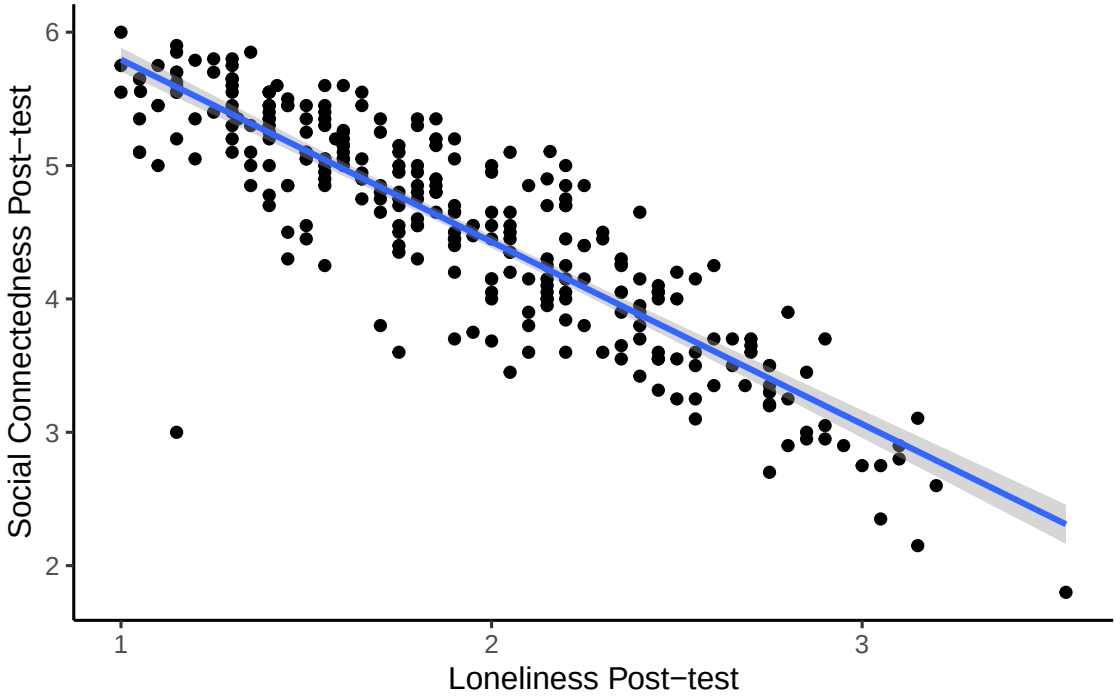
.

Show me the solution

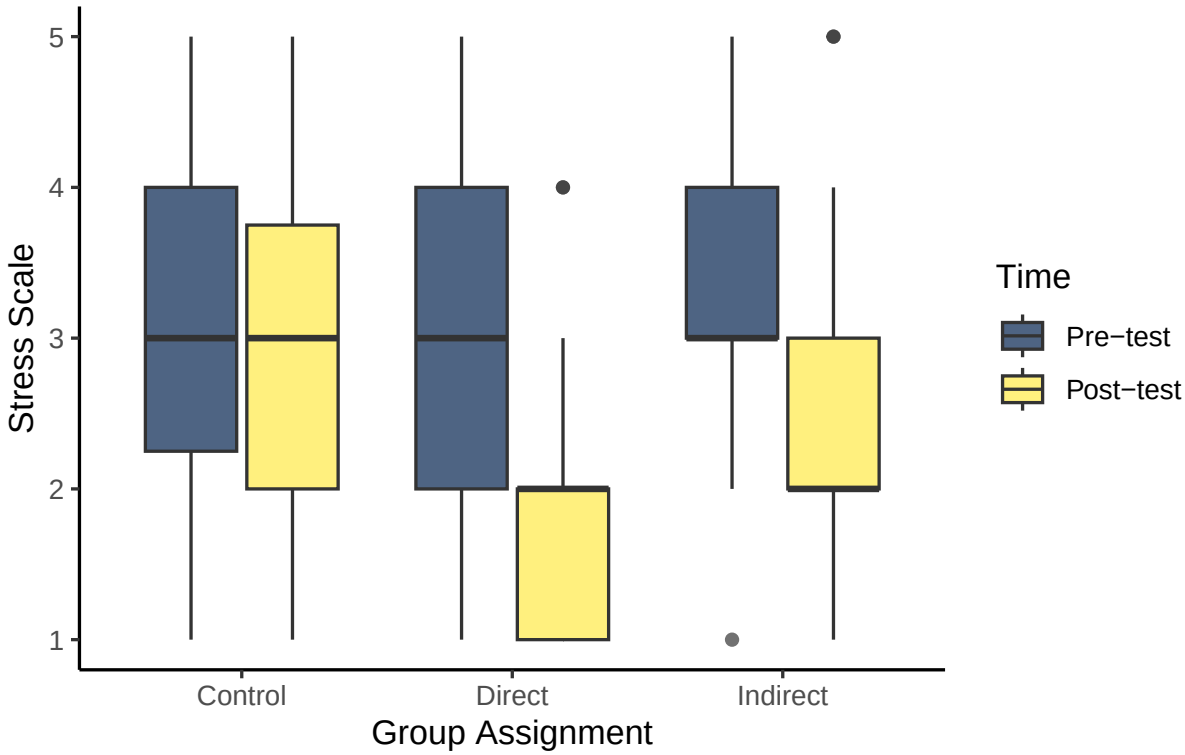
The code here creates a scatterplot for the relationship between post-test social connectedness and loneliness.

```
evans_wide %>%
  ggplot(aes(x = lonely_post, y = social_post)) +
  geom_point() +
  geom_smooth(method = "lm") +
  theme_classic() +
  labs(x = "Loneliness Post-test", y = "Social Connectedness Post-test")
```

```
`geom_smooth()` using formula = 'y ~ x'
```



7. As we start to think about inferential statistics, we can plot the difference between pre- and post-test for each group. For this question, try and recreate the boxplot to visualise stress. Hint: think about if you need to restructure the data, and how you can present the conditions in the appropriate order.

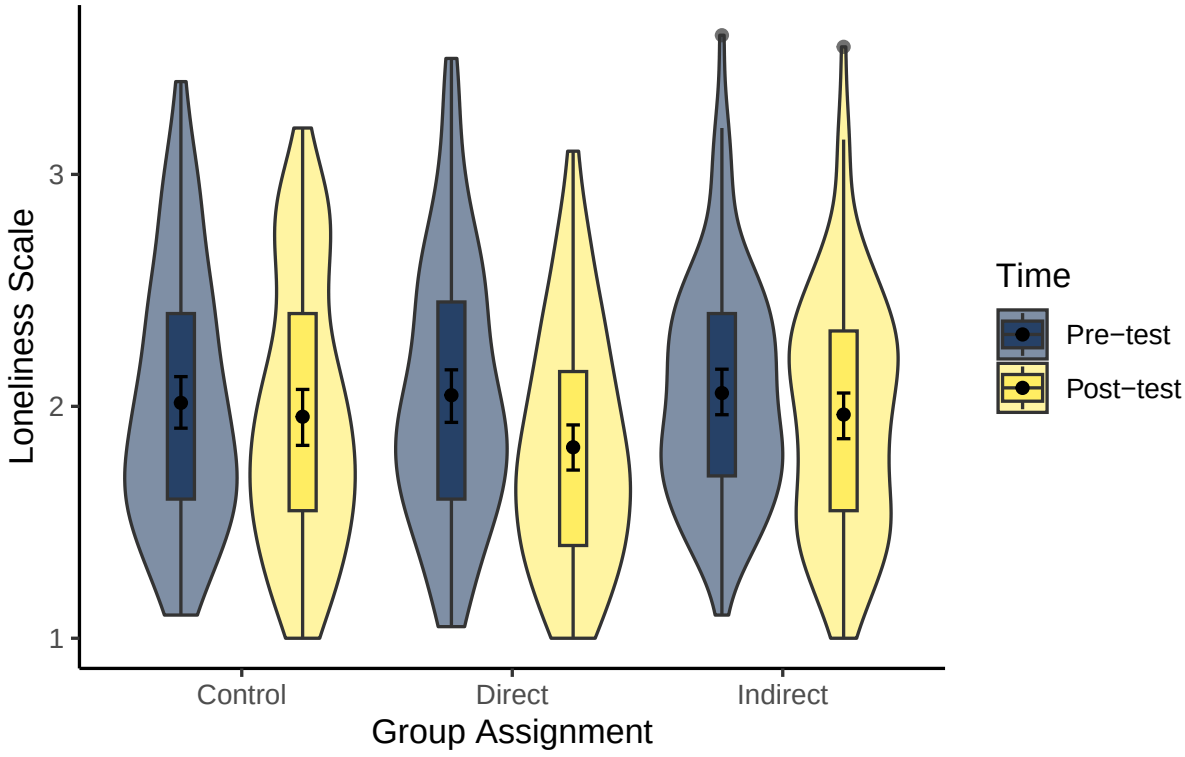


Show me the solution

There are two key steps before you can plot the data. First, you need to restructure the data to long form to get one variable for pre- and post-test. Second, post comes before pre due to alphabetical order, so you need to create a factor to specify the order here.

```
evans_wide %>%
  pivot_longer(cols = stress_pre:stress_post,
               names_to = "Stress",
               values_to = "Value") %>%
  mutate(Stress = factor(Stress,
                         levels = c("stress_pre", "stress_post"),
                         labels = c("Pre-test", "Post-test"))) %>%
  ggplot(aes(x = GroupAssignment, y = Value, fill = Stress)) +
  geom_boxplot(alpha = 0.7) +
  labs(x = "Group Assignment", y = "Stress Scale") +
  scale_fill_viridis_d(option = "E",
                       name = "Time") +
  theme_classic()
```

8. Try and recreate the violin-boxplot to visualise loneliness. Hint: remember how to align the different elements from Chapter 7.



Show me the solution

The same hints apply as question 7 as you need to restructure the data and create a new factor order so pre comes before post. As we have two grouping variables, we must specify a constant position dodge value so it does not plot weird.

```
# specify as an object, so we only change it in one place
dodge_value <- 0.9

evans_wide %>%
  pivot_longer(cols = lonely_pre:lonely_post,
               names_to = "Lonely",
               values_to = "Value") %>%
   mutate(Lonely = factor(Lonely,
                          levels = c("lonely_pre", "lonely_post"),
                          labels = c("Pre-test", "Post-test"))) %>%
  ggplot(aes(x = GroupAssignment, y = Value, fill = Lonely)) +
  geom_violin(alpha = 0.5) +
  geom_boxplot(width = 0.2,
               alpha = 0.7,
               fatten = NULL,
               position = position_dodge(dodge_value)) +
  stat_summary(fun = "mean",
               geom = "point",
               position = position_dodge(dodge_value)) +
  stat_summary(fun.data = "mean_cl_boot",
               geom = "errorbar",
               width = .1,
               position = position_dodge(dodge_value)) +
  scale_fill_viridis_d(option = "E",
                       name = "Time") +
  labs(x = "Group Assignment", y = "Loneliness Scale") +
  theme_classic()
```

16.5 Analysing

Finally, we turn to analysis for inferential statistics. In Evans et al. (2023), they organise the analyses from Binfet et al. (2022) into three hypotheses. You have not covered all the skills in Research Methods 1 to reproduce their analyses exactly, so we will work around an adapted set based on what we currently expect of you.

We present each analysis as an overview so you can think about what techniques from Chapters 8 and 9 would address it, give you instructions on what analysis we have in mind if you need guidance, then present the solution. We focus on one outcome per hypothesis, but once you are confident you are applying and interpreting the appropriate techniques, why not try the other outcomes yourself?

16.5.1 Hypothesis 1

9. Hypothesis 1 is that each treatment group will increase measures of well-being (social connectedness) and decrease measures of ill-being (stress and loneliness). For this question, we focus on stress, so we expected stress to decrease.

Try this

There are two ways you could approach this. Either as the whole sample, or like Evans et al. (2023) present to focus on each group separately. Think about what techniques from Chapters 8 and 9 would let you test the hypothesis that each treatment group will decrease stress at post-test compared to pre-test.

Show me the task list

For the solution below, we are focusing on the whole sample to test whether everyone decreased stress in post-test, but you could approach it by separating the data into the three groups and then testing for the difference per group.
To test whether an outcome decreases between conditions in the same participants, we need a model suitable for a within-subjects design. In Chapter 9, we covered in the bonus section how to test the difference in conditions either through a paired samples-test or linear model with fixed intercept on the difference score.

1. Calculate the difference between stress pre- and post-test.
2. Fit a linear model on the difference score with a fixed intercept and no predictor.
3. Look at the intercept, is it positive or negative? If you calculated pre-test minus post-test, you would be looking for a postive difference as we expect lower stress at post-test. For hypothesis testing, is the p-value lower than alpha?
4. What is the effect size? How much did stress change from pre-test to post-test? What is the confidence interval around the effect size?

Show me the solution

In the code below, we first calculate a difference score by substracting stress post-test from stress pre-test.
We then fit a linear model on this difference score and add a fixed intercept as we have no predictor.
Consistent with hypothesis 1, stress was lower at post-test compared to pre-test across all participants. On average, participants decreased their stress score by 0.83 points (b_0 = 0.83, 95% CI = [0.72, 0.95], $p < .001$).

```r
evans_wide <- evans_wide %>%
  mutate(stress_diff = stress_pre - stress_post)

lm_stress <- lm(stress_diff ~ 1,
                data = evans_wide)

summary(lm_stress)

confint(lm_stress)
```

```
Call:
lm(formula = stress_diff ~ 1, data = evans_wide)

Residuals:
    Min      1Q  Median      3Q     Max
-2.8345 -0.8345  0.1655  0.1655  3.1655

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.83451    0.05657   14.75   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.9534 on 283 degrees of freedom

                2.5 %    97.5 %
(Intercept) 0.7231517 0.9458623
```

16.5.2 Hypothesis 2

10. In Hypothesis 2, we predict that the direct and indirect contact groups will have higher well-being and lower ill-being measures compared to the control group. For this question, we focus on social connectedness at post-test for a measure of well-being, so we expect higher scores in the direct and indirect groups.

> **Try this**
>
> Think about what techniques from Chapters 8 and 9 would let you test the hypothesis that the direct and indirect groups both increase social connectedness at post-test compared

to the control group. Think of how you could focus on two groups at a time per analysis.

Show me the task list

For the solution below, we apply two tests. We focus on the direct and control groups by filtering out indirect, then we focus on indirect and control by filtering out direct.
To test the difference between two groups on one outcome, we need a model suitable for a between-subjects design. In Chapter 9, we covered linear regression with one categorical predictor how to test the difference in an outcome between two groups.

1. Fit a linear model on the outcome social connectedness post-test with a categorical predictor of group. You will need to fit two models, one where you filter out the indirect group and one where you filter out the direct group.
2. Look at the intercept, what is the predicted value for the reference group? Look at the slope, what is the estimated change to the target group? For hypothesis 2, is the direct/indirect group higher on social connectedness compared to control? For hypothesis testing, is the p-value lower than alpha?
3. What is the effect size? How much did the two groups differ on social connectedness? What is the confidence interval around the effect size?

Show me the solution

In the code below, we first fit a linear model on social connectedness post-test and focus on the direct and control groups. There are different ways you could ignore the indirect group, but here we filter the data as we pass the data to the `lm()` function.
The direct group increased social connectedness post-test on average 0.15 points compared to the control group, but the difference was not statistically significant ($b_1 = 0.15$, 95% CI = [-0.09, 0.39], $p = .207$).

```
lm_direct <- lm(social_post ~ GroupAssignment,
                data = filter(evans_wide,
                              GroupAssignment != "Indirect"))

summary(lm_direct)

confint(lm_direct)
```

```
Call:
lm(formula = social_post ~ GroupAssignment, data = filter(evans_wide,
```

```
    GroupAssignment != "Indirect"))

Residuals:
    Min      1Q  Median      3Q     Max
-2.2940 -0.5905  0.1338  0.6560  1.3560

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)           4.49054    0.08596  52.239   <2e-16 ***
GroupAssignmentDirect 0.15349    0.12125   1.266    0.207
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8334 on 187 degrees of freedom
Multiple R-squared:  0.008497,  Adjusted R-squared:  0.003195
F-statistic: 1.603 on 1 and 187 DF,  p-value: 0.2071

                            2.5 %    97.5 %
(Intercept)           4.32096331 4.6601179
GroupAssignmentDirect -0.08569829 0.3926749
```

The indirect group increased social connectedness post-test compared to the control group, but the difference was very small and not statistically significant ($b_1 = 0.01$, 95% CI = [-0.23, 0.25], $p = .936$).

```
lm_indirect <- lm(social_post ~ GroupAssignment,
                  data = filter(evans_wide,
                                GroupAssignment != "Direct"))

summary(lm_indirect)

confint(lm_indirect)
```

```
Call:
lm(formula = social_post ~ GroupAssignment, data = filter(evans_wide,
    GroupAssignment != "Direct"))

Residuals:
     Min       1Q   Median       3Q      Max
-2.70037 -0.59054  0.05946  0.64963  1.34963
```

```
Coefficients:
                          Estimate Std. Error t value Pr(>|t|)
(Intercept)               4.490541   0.087155   51.52   <2e-16 ***
GroupAssignmentIndirect 0.009833   0.122931    0.08    0.936
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.845 on 187 degrees of freedom
Multiple R-squared:  3.422e-05, Adjusted R-squared:  -0.005313
F-statistic: 0.006398 on 1 and 187 DF,  p-value: 0.9363

                              2.5 %    97.5 %
(Intercept)               4.3186067 4.6624745
GroupAssignmentIndirect -0.2326772 0.2523439
```

In Evans et al. (2023), the direct vs control comparison is significant, but they approached the analysis differently using a technique you will not learn until Research Methods 2. They control for pre-test scores by using it as an additional predictor, but you have not learnt about multiple regression yet.

16.5.3 Hypothesis 3

11. Finally, the third hypothesis focuses on the difference between the two contact groups. They predict that the direct contact group will lead to higher well-being and lower ill-being compared to the indirect contact group. For this question, we focus on loneliness post-test for a measure of ill-being, so we expect lower scores in the direct group.

Try this

Think about what techniques from Chapters 8 and 9 would let you test the hypothesis that the direct group decreases loneliness at post-test compared to the indirect group.

Show me the task list

For this analysis, we focus on the final combination of groups, this time ignoring the control group.
To test the difference between two groups on one outcome, we need a model suitable for a between-subjects design. In Chapter 9, we covered linear regression with one categorical predictor how to test the difference in an outcome between two groups.

1. Fit a linear model on the outcome loneliness post-test with a categorical predictor

of group. Filter the data to just focus on the direct and indirect contact groups.

2. Look at the intercept, what is the predicted value for the reference group? Look at the slope, what is the estimated change to the target group? For hypothesis 3, is the direct group lower on loneliness compared to indirect? For hypothesis testing, is the p-value lower than alpha?

3. What is the effect size? How much did the two groups differ on loneliness? What is the confidence interval around the effect size?

Show me the solution

In the code below, we first fit a linear model on loneliness post-test and focus on the direct and indirect groups. There are different ways you could ignore the indirect group, but here we filter the data as we pass the data to the `lm()` function.
The direct group decreased loneliness post-test on average 0.14 points compared to the indirect group, but the difference was not statistically significant ($b_1 = 0.14$, 95% CI = [-0.01, 0.29], $p = .060$).

```
lm_contact <- lm(lonely_post ~ GroupAssignment,
                 data = filter(evans_wide,
                               GroupAssignment != "Control"))

summary(lm_contact)

confint(lm_contact)
```

```
Call:
lm(formula = lonely_post ~ GroupAssignment, data = filter(evans_wide,
    GroupAssignment != "Control"))

Residuals:
     Min       1Q   Median       3Q      Max
-0.96457 -0.42130 -0.06457  0.32645  1.58543

Coefficients:
                          Estimate Std. Error t value Pr(>|t|)
(Intercept)               1.82355    0.05267  34.625   <2e-16 ***
GroupAssignmentIndirect   0.14102    0.07448   1.893   0.0598 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 0.5133 on 188 degrees of freedom
Multiple R-squared:  0.01871,   Adjusted R-squared:  0.01349
F-statistic: 3.585 on 1 and 188 DF,  p-value: 0.05983

                               2.5 %    97.5 %
(Intercept)                1.719655160 1.9274363
GroupAssignmentIndirect -0.005898489 0.2879484
```

Like hypothesis 2, Evans et al. (2023) report the direct vs indirect comparison as significant, but they approached the analysis differently using a technique you will not learn until Research Methods 2. They control for pre-test scores by using it as an additional predictor, but you have not learnt about multiple regression yet.

16.6 Conclusion

Well done! Hopefully you recognised how far your skills have come to be able to do this independently, regardless of how many hints you needed. We are really starting to pile the skills up you have learnt so far, from simply using R Markdown files, to wrangling data, to visualising data, to finally applying modelling techniques for your inferential statistics.

If you are curious, you can read Evans et al. (2023) to see how they walk through wrangling and analysing the data. Some of the techniques we do not cover in Research Methods 1, but they have some great features like highlighting common student mistakes.

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Using our materials

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Licence

Citation

Bartlett, J.E. & Toivo, W. (2024). Fundamentals of Quantitative Analysis (Version 3.0). https://github.com/PsyTeachR/quant-fundamentals-v3

A Additional Resources

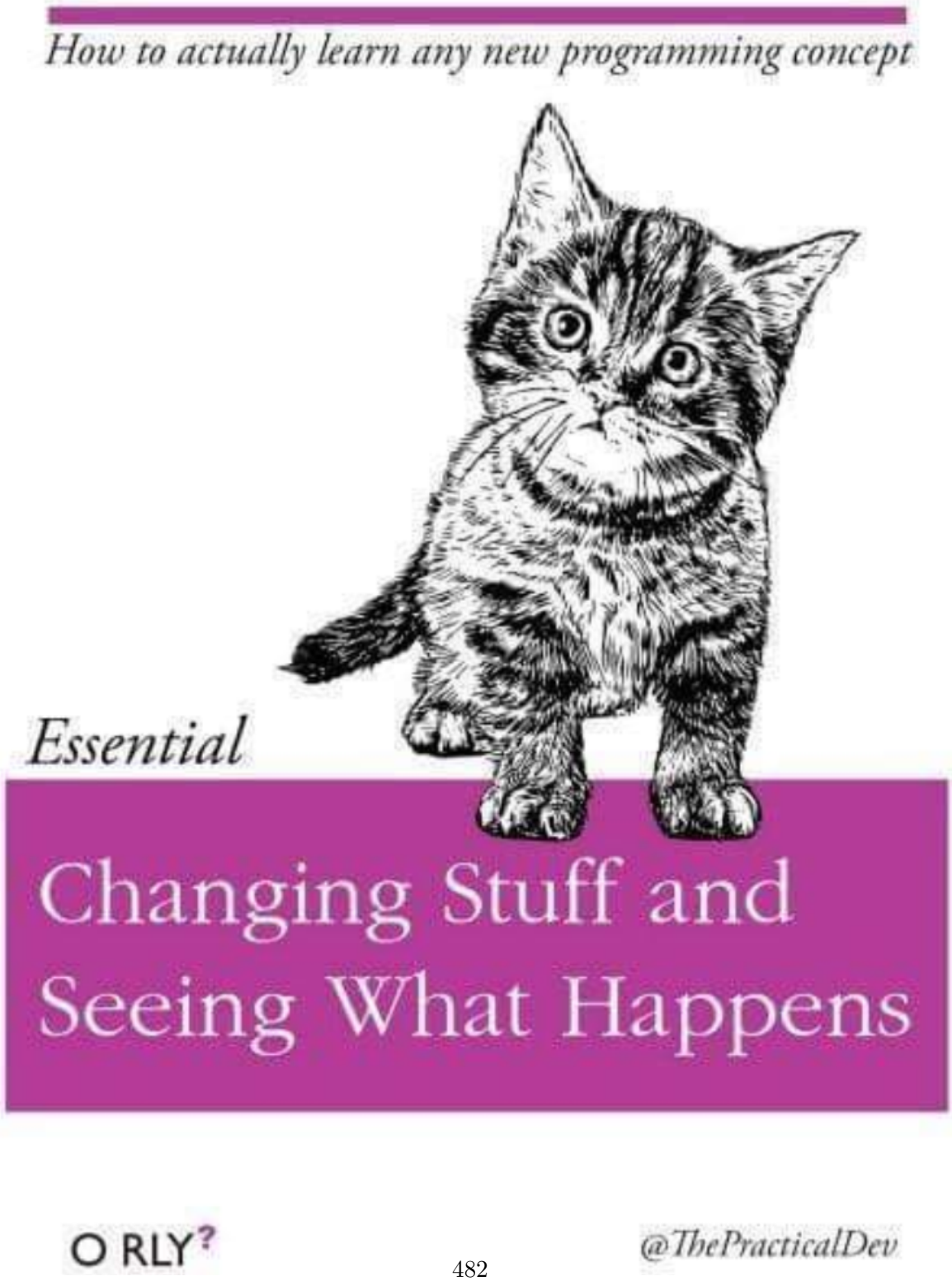

Figure A.1: The truth about programming

If you would like additional practice, you can check out the other UofG PsyTeachR course books.

- Level 1 - Intro to R (overlaps with Msc Conv book), data wrangling, data viz, descriptive statistics

- Level 2 - Our second-year undergraduate course introduces statistical concepts such as permutation tests,t-tests, NHST, alpha, power, effect size, and sample size. Semester 2 focusses on correlations and the general linear model.
- Level 3: This third-year undergraduate course teaches students how to specify, estimate, and interpret statistical models corresponding to various study designs, using a General Linear Models approach.
- MSc Data Skills: This course provides an overview of skills needed for reproducible research and open science using the statistical programming language R. Students will learn about data visualisation, data tidying and wrangling, archiving, iteration and functions, probability and data simulations, general linear models, and reproducible workflows.

We also highly recommend the following, they will help practice your data wrangling skills but also they're great options if you're enjoying R and want to stretch yourself:

- Open Stats Lab - this wonderful resource gives you practice at running statistical tests by providing you with datasets from published papers.
- R for Data Science - written by the authors of the tidyverse, this is a great resource for additional data wrangling practice and more depth on many of the tidyverse functions.
- Text Mining with R - Shows you how to use R to work with text. This isn't something we cover in this course, but it uses the same data wrangling skills and be a very useful additional skill to have.
- How to make BBC style graphics - Ever wondered how the BBC News makes their data visualisation? Well, now you can make your own!
- Data Vizualisation - this is an entire book on data visualisation and goes into detail on how to take `ggplot` to its limits.

B Citing R and RStudio

How to cite R and RStudio

You may be some way off writing a scientific report where you have to cite and reference R, however, when the time comes it is important to do so to give the people who built it (most of them for free!) credit. You should provide separate citations for R, RStudio, and the packages you use.

To get the citation for the version of R you are using, simply run the `citation()` function which will always provide you with the most recent citation.

```
citation()
```

```
To cite R in publications use:

  R Core Team (2024). _R: A Language and Environment for Statistical
  Computing_. R Foundation for Statistical Computing, Vienna, Austria.
  <https://www.R-project.org/>.

A BibTeX entry for LaTeX users is

  @Manual{,
    title = {R: A Language and Environment for Statistical Computing},
    author = {{R Core Team}},
    organization = {R Foundation for Statistical Computing},
    address = {Vienna, Austria},
    year = {2024},
    url = {https://www.R-project.org/},
  }

We have invested a lot of time and effort in creating R, please cite it
when using it for data analysis. See also 'citation("pkgname")' for
citing R packages.
```

To generate the citation for any packages you are using, you can also use the `citation()` function with the name of the package you wish to cite.

```
citation("tidyverse")
```

```
To cite package 'tidyverse' in publications use:

  Wickham H, Averick M, Bryan J, Chang W, McGowan LD, François R,
  Grolemund G, Hayes A, Henry L, Hester J, Kuhn M, Pedersen TL, Miller
  E, Bache SM, Müller K, Ooms J, Robinson D, Seidel DP, Spinu V,
  Takahashi K, Vaughan D, Wilke C, Woo K, Yutani H (2019). "Welcome to
  the tidyverse." _Journal of Open Source Software_, *4*(43), 1686.
  doi:10.21105/joss.01686 <https://doi.org/10.21105/joss.01686>.

A BibTeX entry for LaTeX users is

  @Article{,
    title = {Welcome to the {tidyverse}},
    author = {Hadley Wickham and Mara Averick and Jennifer Bryan and Winston Chang and Lucy
    year = {2019},
    journal = {Journal of Open Source Software},
    volume = {4},
    number = {43},
    pages = {1686},
    doi = {10.21105/joss.01686},
  }
```

To generate the citation for the version of RStudio you are using, you can use the `RStudio.Vesion()` function:

```
RStudio.Version()
```

Finally, here's an example of how that might look in the write-up of your method section:

> Analysis was conducted using R (R Core Team, 2020), RStudio (Rstudio Team, 2020), and the tidyverse package (Wickham, 2017).

As noted, you may not have to do this for a while, but come back to this when you do because it's important to give the open-source community credit for their work.

C Symbols

Symbol	psyTeachR Term	Also Known As
()	(round) brackets	parentheses
[]	square brackets	brackets
{}	curly brackets	squiggly brackets
<>	chevrons	angled brackets / guillemets
<	less than	
>	greater than	
&	ampersand	"and" symbol
#	hash	pound / octothorpe
/	slash	forward slash
\	backslash	
-	dash	hyphen / minus
_	underscore	
*	asterisk	star
^	caret	power symbol
~	tilde	twiddle / squiggle
=	equal sign	
==	double equal sign	
.	full stop	period / point
!	exclamation mark	bang / not
?	question mark	
'	single quote	quote / apostrophe
"	double quote	quote
%>%	pipe	magrittr pipe
|	vertical bar	pipe
,	comma	
;	semi-colon	
:	colon	
@	"at" symbol	various hilarious regional terms
...	`glossary("ellipsis")`	dots

Figure C.1: Image by James Chapman/Soundimals