

**DataBOOM**: the canon for data science

Databrew

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# Chapter 1

## Welcome!

Welcome to DataBOOM, a curriculum designed to guide you from your very first line of code towards becoming a professional data scientist.

### What this is, and what it isn't

This is not a textbook or a reference manual. It is not exhaustive or comprehensive. It is a *training manual* designed to *empower researchers to do impactful data science*. As such, its tutorials and exercises aim to get you, the researcher, to start writing your own code as quickly as possible and – equally of importance – to *start thinking like a data scientist*, by which we mean tackling ambiguous problems with persistence, independence, and creative problem solving.

Furthermore, this is not a fancy interactive tutorial with bells or whistles. It was purposefully designed to be simple and “analog”. You will not be typing your code into this website and getting feedback from a robot, or setting up an account to track your progress, or getting pretty merit badges or points when you complete each module.

Instead, you will be doing your work on your own machine, working with real folders and files, downloading data and moving it around, etc. – all the things you will be doing as a data scientist in the real world.

### Who this is for

This curriculum covers everything from the absolute basics of writing code in R to machine learning with tensorflow. As such, it is designed to be useful to everyone in some way. But the target audience for these tutorials is the student who *wants* to work with data but has *zero* formal training in programming, computer science, or statistics.

This curriculum was originally developed for the **Sewanee Data Institute for Social Good** at Sewanee: The University of the South, TN, USA.

## What you will learn

- The **Core theory** unit establishes the conceptual foundations and motivations for this work: what data science is, why it matters, and ethical issues surrounding it: the good, the bad, and the ugly.

The next several units comprise a *core* curriculum for tackling data science problems:

- The **Getting started** unit teaches you how to use R (in RStudio) to explore and plot data. Here you will add the first and most important tools to your toolbox: working with variables, vectors, dataframes, scripts, and file directories.
- The **Basic R workflow** unit teaches you how to bring in your own data and work with it in R. You will learn how to format data to simplify analysis and add tools for *data wrangling* (i.e., transforming and re-formatting data to prepare it for plotting and analysis). You will also learn how to conduct basic statistics, from exploratory data analyses (e.g., producing and comparing distributions) to significance testing.
- The **Essential R skills** unit equips you with the tools, tricks, and mindset for tackling the most common tasks in data science. This is where you really begin to cut your teeth on real-world data puzzles: figuring out how to use the R tools in your toolbag to tackle an ambiguous problem and deliver an excellent data product.

The next several units provide a suite of skills essential to any data science professional:

- The **Interactive dashboards** unit teaches you how to make dashboards and websites for projects using shiny in RStudio.
- The **Databases** unit teaches you how to access, create, and work with relational databases online using SQL and its alternatives.
- The **Documenting your work** unit teaches you to use R Markdown to produce beautiful, reproducible data reports. You will also learn about *version control*, using Git and GitHub to collaborate on shared projects and work on data science teams.
- The **Sharing research** unit teaches you to produce publishable research articles and compelling presentations.

The final unit, **Advanced skills**, introduces you to a variety of advanced data science techniques, from interactive maps to iterative simulations to machine learning, that can help you begin to specialize your skillset.

## Who we are

**Joe Brew** is a data scientist, epidemiologist, and economist. He has worked with the Florida Department of Health (USA), the Chicago Department of Public Health (USA), the Barcelona Public Health Agency (Spain), the Tigray Regional Health Bureau (Ethiopia) and the Manhiça Health Research Center (Mozambique). He is a co-founder of Hyfe and DataBrew. His research focuses on the economics of malaria and its elimination. He earned his BA at Sewanee: The University of the South (2008), an MA at the Institut Catholique de Paris (2009) and an MPH at the Kobenhavns Universitet (2013). He is passionate about international development, infectious disease surveillance, teaching, running, and pizza.

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# **Part I**

## **Core theory**



## **Chapter 2**

# **Principles of data science**

**What is data science?**

**What is the data life cycle?**

**What is a pipeline?**

**Data science ‘in the wild’**

**The reproducibility crisis**



# **Chapter 3**

## **Visualizing data**

**3.1 Bad examples**

**3.2 Good exaples**

**3.3 Edward Tufte**

**3.4 Grammar of graphics**

**3.5 Design principles**

**3.6 Plots & power**

The politics of graphics

(Test text)



# **Chapter 4**

## **Data ethics**



## (PART) Getting started



## **Chapter 5**

# **Setting up RStudio**

**First, download and install R:**

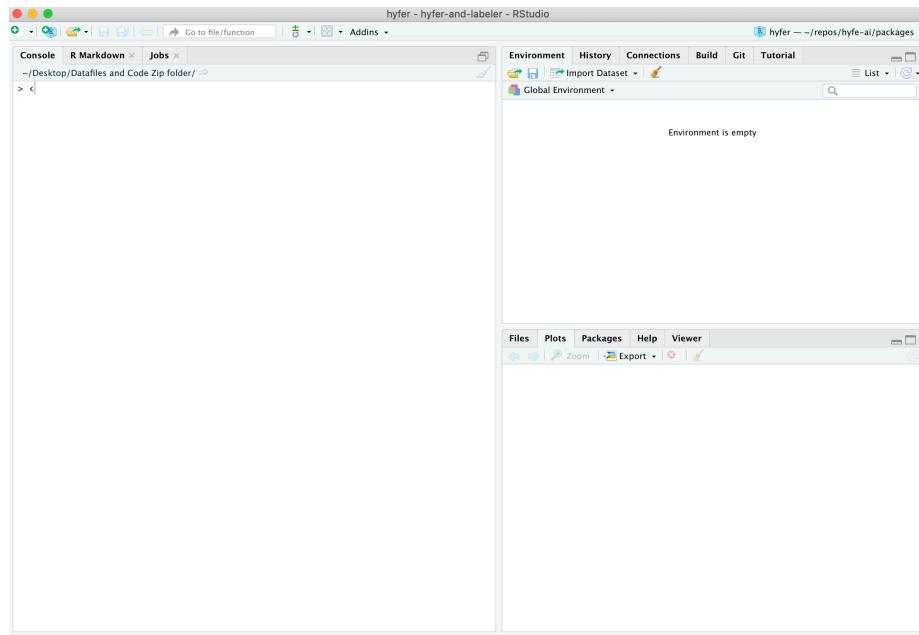
Go to the following website, click the *Download* button, and follow the website's instructions from there. <https://mirrors.nics.utk.edu/cran/>

**Second, download and install RStudio:**

Go to the following website and choose the free Desktop version: <https://rstudio.com/products/rstudio/download/>

**Third, make sure RStudio opens successfully:**

Open the RStudio app. A window should appear that looks like this:



Fourth, make sure R is running correctly in the background:

In RStudio, in the pane on the left (the “Console”), type `2+2` and hit Enter. If R is working properly, the number “4” will be printed in the next line down.

# Boom!

# Chapter 6

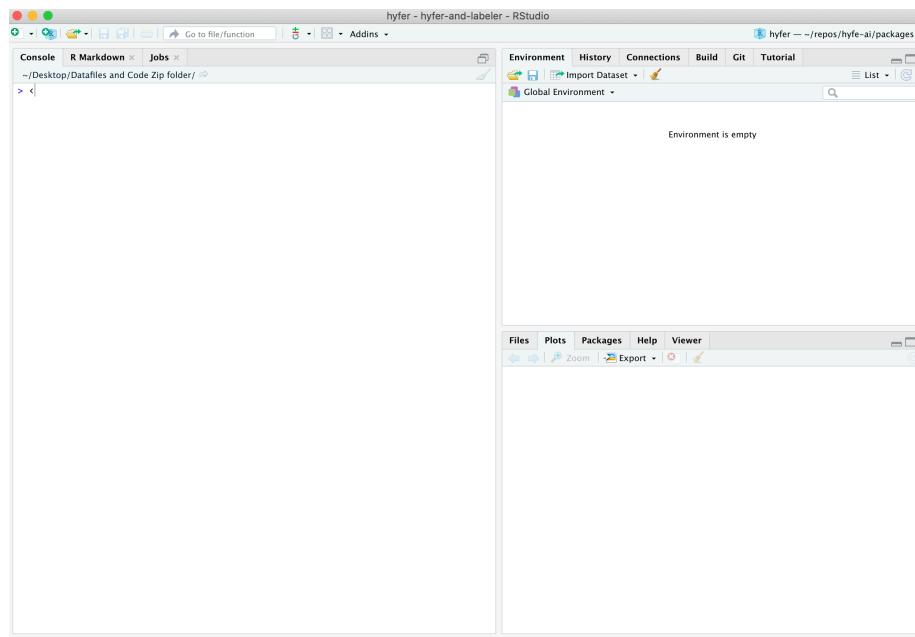
## Running R code

### Learning goals

- Learn how to run code in R
- Learn how to use R as a calculator
- Learn how to use mathematical and logical operators in R

### RStudio's *Console*

When you open RStudio, you see several different panes within the program's window. You will get a tour of RStudio in the next module. For now, look at the left half of the screen. You should see a large pane entitled the *Console*.



RStudio's *Console* is your window into R, the engine under the hood. The *Console* is where you type commands for R to run, and where R prints back the results of what you have told it to do.

## Running code in the *Console*

Type your first command into the *Console*, then press **Enter**:

```
1 + 1
[1] 2
```

When you press **Enter**, R processes the command you fed it, then returns its result (2) just below your command.

Note that spaces don't matter. Both of the following two commands are legible to R and return the same thing:

```
4 + 4
[1] 8

4+4
[1] 8
```

However, it is better to make your code as easy to read as possible, which usually means using spaces.

### Exercise 1

Type a command in the *Console* to determine the sum of 596 and 198.

### Re-running code in the *Console*

If you want to re-run the code you just ran, or if you want to recall the code so that you can adjust it slightly, click anywhere in the *Console* then press your keyboard's Up arrow.

If you keep pressing your Up arrow, R will present you with sequentially older commands.

If you accidentally recalled an old command without meaning to, you can reset the *Console*'s command line by pressing **Escape**.

### Exercise 2

- Re-run the sum of 596 and 198 without re-typing it.
- Recall the command again, but this time adjust the code to find the sum of 596 and 298.
- Practice escaping an accidentally called command: recall your most recent command, then clear the *Console*'s command line.

### Incomplete commands in R

R gets confused when you enter an incomplete command, and will wait for you to write the remainder of your command on the next line in the *Console* before doing anything.

For example, try running this code in your *Console*:

**45 +**

You will find that R gives you a little + sign on the line under your command, which means it is waiting for you to complete your command.

If you want to complete your command, add a number (e.g., 3) and hit **Enter**. You should now be given an answer (e.g., 48).

If instead you want R to stop waiting and stop running, hit the **Escape** key.

### Getting errors in R

R only understands your commands if they follow the rules of the R language (often referred to as its *syntax*). If R does not understand your code, it will throw an error and give up on trying to execute that line of code.

For example, try running this code in your *Console*:

```
4 + 6p
```

You probably received a message in red font stating `Error: unexpected symbol in "4 + 6p"`. That is because R did know how to interpret the symbol `p` in this case.

Get used to errors! They happen all the time, even (especially?) to professionals, and it is essential that you get used to reading your own code to find and fix its errors.

### Exercise 3

Type a command in R that throws an error, then recall the command and revise so that R can understand it.

## Use R like a calculator

As you can tell from those commands you just ran, R is, at heart, a fancy calculator.

Some calculations are straightforward, like addition and subtraction:

```
490 + 1000
[1] 1490

490 - 1000
[1] -510
```

Division is pretty straightforward too:

```
24 / 2
[1] 12
```

For multiplication, use an asterisk (\*):

```
24 * 2
[1] 48
```

R is usually great about following classic rules for Order of Operations, and you can use parentheses to exert control over that order. For example, these two commands produce different results:

```
2*7 - 2*5 / 2
[1] 9

(2*7 - 2*5) / 2
[1] 2
```

You denote exponents like this:

```
2 ^2
[1] 4
2 ^3
[1] 8
2 ^4
[1] 16
```

Finally, note that R is fine with negative numbers:

```
9 + -100
[1] -91
```

#### Exercise 4

- A. Find the sum of the ages of everyone in your immediate family.
- B. Now recall that command and adjust it to determine the *average* age of the members of your family.

## Using operators in R

You can get R to evaluate logical tests using *operators*.

For example, you can ask whether two values are equal to each other.

```
96 == 95
[1] FALSE

95 + 2 == 95 + 2
[1] TRUE
```

R is telling you that the first statement is FALSE (96 is not, in fact, equal to 95) and that the second statement is TRUE (95 + 2 is, in fact, equal to itself).

Note the use of *double* equal signs here. You must use two of them in order for R to understand that you are asking for this logical test.

You can also ask if two values are *NOT* equal to each other:

```
96 != 95
[1] TRUE

95 + 2 != 95 + 2
[1] FALSE
```

This test is a bit more difficult to understand: In the first statement, R is telling you that it is TRUE that 96 is different from 95. In the second statement, R is saying that it is FALSE that 95 + 2 is not the same as itself.

Note that R lets you write these tests another, even more confusing way:

```
! 96 == 95
[1] TRUE

! 95 + 2 == 95 + 2
[1] FALSE
```

The first line of code is asking R whether it is not true that 96 and 95 are equal to each other, which is **TRUE**. The second line of code is asking R whether it is not true that  $95 + 2$  is the same as itself, which is of course **FALSE**.

Other commonly used operators in R include greater than / less than ( $>$  and  $<$ ), and greater/less than or equal to ( $\geq$  and  $\leq$ ).

```
100 > 100
[1] FALSE
100 >= 100
[1] TRUE
```

### Exercise 5

A. Write and run a line of code that asks whether these two calculations return the same result:

```
2*7 - 2*5 / 2
(2*7 - 2*5) / 2
```

B. Now write and run a line of code that asks whether the first calculation is larger than the second:

## Use built-in functions within R

R has some built-in “functions” for common calculations, such as finding square roots and logarithms. Functions are packages of code that take a given value, transform it according to some internal code instructions, and provide an output. You will learn more about functions in a few modules.

```
sqrt(16)
[1] 4

log(4)
[1] 1.386294
```

Note that the function `log()` is the *natural log* function (i.e., the value that  $e$  must be raised to in order to equal 4). To calculate a base-10 logarithm, use `log10( )`.

```
log(10)
[1] 2.302585
```

```
log10(10)
[1] 1
```

Another handy function is `round()`, for rounding numbers to a specific number of decimal places.

```
100/3
[1] 33.33333
round(100/3)
[1] 33
round(100/3,digits=1)
[1] 33.3
round(100/3,digits=2)
[1] 33.33
round(100/3,digits=3)
[1] 33.333
```

Finally, R also comes with some built-in values, such as *pi*:

```
pi
[1] 3.141593
```

### **Exercise 6**

Find the square root of *pi* and round the answer to the 2 decimal places.

#### **Review assignment:**

Show that the following statements are TRUE:

- A. *pi* is greater than the square root of 9
- B. It is FALSE that the square root of 9 is greater than *pi*
- C. *pi* rounded to the nearest whole number equals the square root of 9

#### **Other Resources**

Hobbes Primer, Table 1 (Math Operators, pg. 18) and Table 2 (Logical operators, pg. 22)



# Chapter 7

## Using RStudio and R scripts

### Learning goals

- Understand the difference between R and RStudio
- Understand the RStudio working environment and window panes
- Understand what R scripts are, and how to create and save them
- Understand how to add comments to your code, and why doing so is important
- Understand what a *working directory* is, and how to use it
- Learn basic project work flow

### R and RStudio: what's the difference?

These two entities are similar, but it is important to understand how they are different.

In short, R is a open-source (i.e., free) coding language: a powerful programming engine that can be used to do really cool things with data.

R Studio, in contrast, is a free *user interface* that helps you interact with R. If you think of R as an engine, then it helps to think of RStudio as the car that contains it. Like a car, RStudio makes it easier and more comfortable to use the engine to get where you want to go.

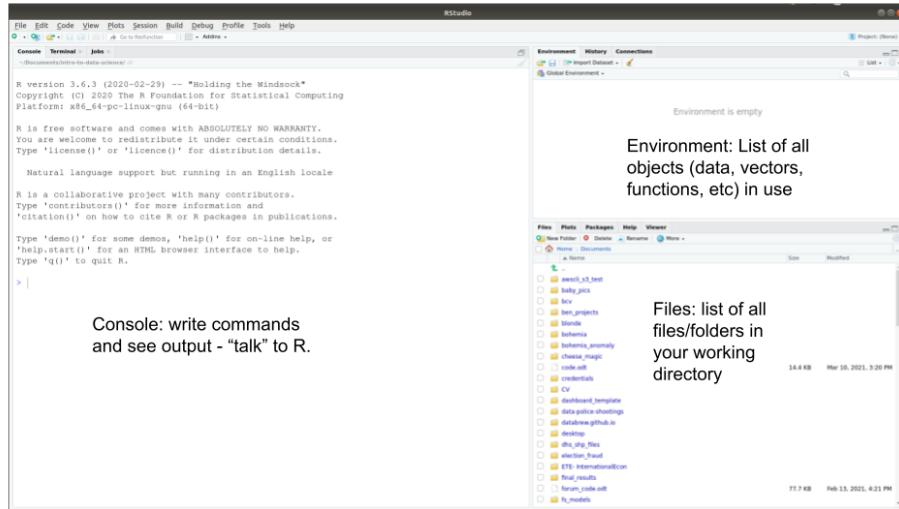
R Studio needs R in order to function, but R can technically be used on its own outside of RStudio if you want. However, just as a good car mechanic can get an engine to run without being installed within a car, using R on its own is a bit clunky and requires some expertise. For beginners (and everyone else, really), R is just so much more pleasant to use when you are operating it from within RStudio.

RStudio also has increasingly powerful *extensions* that make R even more useful and versatile in data science. These extensions allow you to use R to make interactive data dashboards, beautiful and reproducible data reports, presentations, websites, and even books. And new features like these are regularly being added to RStudio by its all-star team of data scientists.

That is why this book *always* uses RStudio when working with R.

## Two-minute tour of RStudio

When you open RStudio for the first time, you will see a window that looks like the screenshot below.



### Console

You are already acquainted with RStudio's *Console*, the window pane on the left that you use to "talk" to R. (See the previous module.)

### Environment

In the top right pane, the *Environment*, RStudio will maintain a list of all the datasets, variables, and functions that you are using as you work. The next modules will explain what variables and functions are.

This is the pane that is used the least often, and if you wish it can simplify your workspace to minimize it.

### Files, Plots, Packages, & Help

You will use the bottom right pane very often.

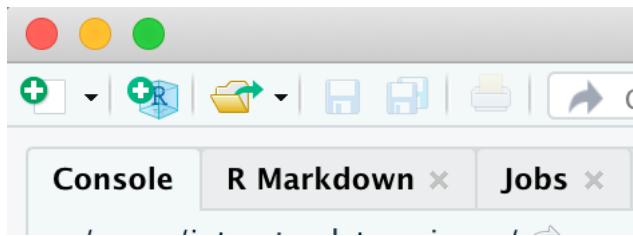
- The **Files** tab lets you see all the files within your **working directory**, which will be explained in the section below.
- The **Plots** tab lets you see the plots you are producing with your code.
- The **Packages** tab lets you see the *packages* you currently have installed on your computer. Packages are bundles of R functions downloaded from the internet; they will be explained in detail a few modules down the road.
- The **Help** tab is very important! It lets you see *documentation* (i.e., user's guides) for the functions you use in your code. Functions will also be explained in detail a few modules down the road.

These three panes are useful, but the most useful window pane of all is actually *missing* when you first open RStudio. This important pane is where you work with **scripts**.

## Scripts

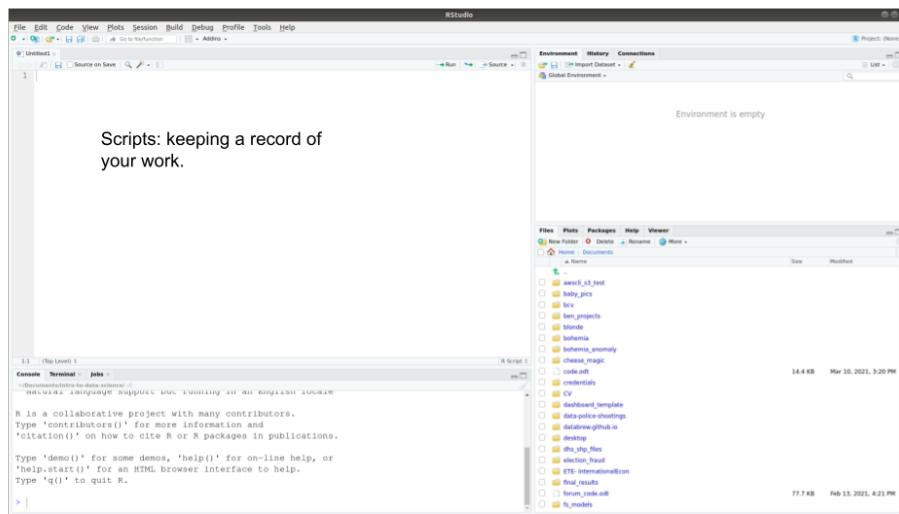
Before explaining what scripts are and why they are awesome, let's start a new script.

**To start a new script**, go to the top left icon in the RStudio window, and click on the green plus sign with a blank page behind it:



A dropdown window will appear. Select "R Script".

A new window pane will then appear in the top left quadrant of your RStudio window:



You now have a blank script to work in!

Now type some simple commands into your script:

```
2 + 10
16 * 32
```

Notice that when you press **Enter** after each line of code, nothing happens in the *Console*. In order to send this code to the Console, press **Enter + Command** at the same time (or **Enter + Control**, if you are on Windows) for each line of code.

To send both lines of code to the *Console* at once, select both lines of code and hit **Enter + Command**.

(To select multiple lines of code, you can (1) click and drag with your mouse or (2) hold down your **Shift** key while clicking your down arrow key. To select *all* lines of code, press **Command + A**.)

### Exercise 1

Add a few more lines to your script, such that your script now looks like this.

```
2 + 10
16 * 32
1080 / 360
500 - 600
```

(A) Run all of these lines of code at once.

(B) Now add 10 to the first number in each row, and re-run all of the code.

Think about how much more efficient part (B) was thanks to your script! If

you had typed all of that directly into your *Console*, you would have to recall or retype each line individually. That difference builds up when your number of commands grows into the hundreds.

## What is an R script, and why are scripts so awesome?

An R script is a file where you can keep a record of your code. Just as a script tells actors exactly what to say and when to say it, an R script tells R exactly what code to run, and in what order to run it.

When working with R, you will almost always type your code into a script first, *then* send it to the *Console*. You can run your code immediately using **Enter + Command**, but you also have a script of what you have done so that you can run the exact same code at a later time

To understand why R scripts are so awesome, consider a typical workflow in *Excel* or *GoogleSheets*. You open a big complicated spreadsheet, spend hours making changes, and save your changes frequently throughout your work session.

The main disadvantages of this workflow are that:

1. There is no detailed record of the changes you have made. You cannot prove that you have made changes correctly. You cannot pass the original dataset to someone else and ask them to revise it in the same way you have. (Nor would you want to, since making all those changes was so time-consuming!) Nor could you take a different dataset and guarantee that you are able to apply the exact same changes that you applied to the first. In other words, your work is not reproducible.
2. Making those changes is labor-intensive! Rather than spend time manually making changes to a single spreadsheet, it would be better to devote that energy to writing R code that makes those changes for you. That code could be run in this one case, but it could also be run at any later time, or easily modified to make similar changes to other spreadsheets.
3. Unless you are an advanced *Excel* programmer, you are probably modifying your original dataset, which is always dangerous and a big No-No in data science. Each time you save your work in *Excel* or *GoogleSheets* (which automatically saves each change you make), the original spreadsheet file gets replaced by the updated version. But if you brought your dataset into R instead, and modified it using an R script, then you leave the raw data alone and keep it safe. (Sure, you can always save different versions of your Excel file, but then you run the risk of mixing up versions and getting confused.)

Working with R scripts allows you to avoid all of these pitfalls. When you write an R script, you are making your work ....

- **Efficient.** Once you get comfortable writing R code, you will be able to write scripts in a few minutes. Those scripts can modify datasets within

seconds (or less) in ways that would take hours (or years) to carry out manually in *Excel* or *GoogleSheets*.

- **Reproducible.** Once you have written an R script, you can reproduce your own work whenever you want to. You can send your script to a colleague so that they can reproduce your work as well. Reproducible work is defensible work.
- **Low-risk.** Since your R script does not make any changes to the original data, you are keeping your data safe. It is *essential* to preserve the sanctity of raw data!

Note that there is nothing fancy or special about an R script. An R script is a simple text file; that is, it only accepts basic text; you can't add images or change font style or font size in an R script; just letters, numbers, and your other keyboard keys. The file's extension, `.R` tells your computer to interpret that text as R code.

## Commenting your code

Another advantage of scripts is that you can include *comments* throughout your code to explain what you are doing and why. A *comment* is just a part of your script that is useful to you but that is ignored by R.

To add comments to your code, use the hashtag symbol (`#`). Any text following a `#` will be ignored by R.

Here is the script above, now with comments added:

```
# Define variable x
x <- 2
x

# Make a new variable, y, based on x
y <- x*56

z <- y / 23 # Make a third variable, z, based on y

x + y + z # Now get the sum of all three variables
```

Adding comments can be more work, but in the end it saves you time and makes your code more effective. Comments might not seem necessary in the moment, but it is amazing how helpful they are when you come back to your code the next day. Frequent and helpful comments make the difference between good and great code. Comment early, comment often!

You can also use lines of hashtags to visually organize your code. For example:

```
#####
# Setup
```

```
#####
# Define variable x
x <- 2
x

# Make a new variable, y, based on x
y <- x*56

z <- y / 23 # Make a third variable, z, based on y

#####
# Get result
#####
x + y + z # Now get the sum of all three variables
```

This might not seem necessary with a 5-line script, but adding visual breaks to your code becomes immensely helpful when your code grows to be hundreds of lines long.

## Saving your work

R scripts are only useful if you save them! Unlike working with *GoogleDocs* or *GoogleSheets*, R will not automatically save your changes; you have to do that yourself. (This is inconvenient, but it is also safer; most of coding is trial and error, and sometimes you want to be careful about what is saved.)

**Where to save your work?** The folder in which you save your R script will be referred to as your *working directory* (see the next section). For the sake of these tutorials, it will be most convenient to save all of your scripts in a single folder that is in an easily accessed location. We suggest making a new folder on your Desktop and naming it `databoom`, but you can name it whatever you want and place it wherever you want.

**How to save your script?** To save the script you have opened and typed a few lines of code into, press `Command + S` (or `Control + S`). Alternatively, go to File > Save. Navigate to the folder you just created and type in a file name that is simple but descriptive. We suggest making a new R script for each module, and naming those scripts according to each module's name. In this case, we recommend naming your script `09_intro_to_rstudio`.

(It is good practice to avoid spaces in your file names; it will be essential later on, so good to begin the correct habit now. Start using an underscore, `_`, instead of a space.)

## Your working directory

When you work with data in R, R will need to know where in your computer to look for that data. The folder it looks in is known as your **working directory**.

To find out which folder R is currently using as your working directory, use the function `getwd()`:

```
getwd()
[1] "/Users/erikeen/repos/intro-to-data-science"
```

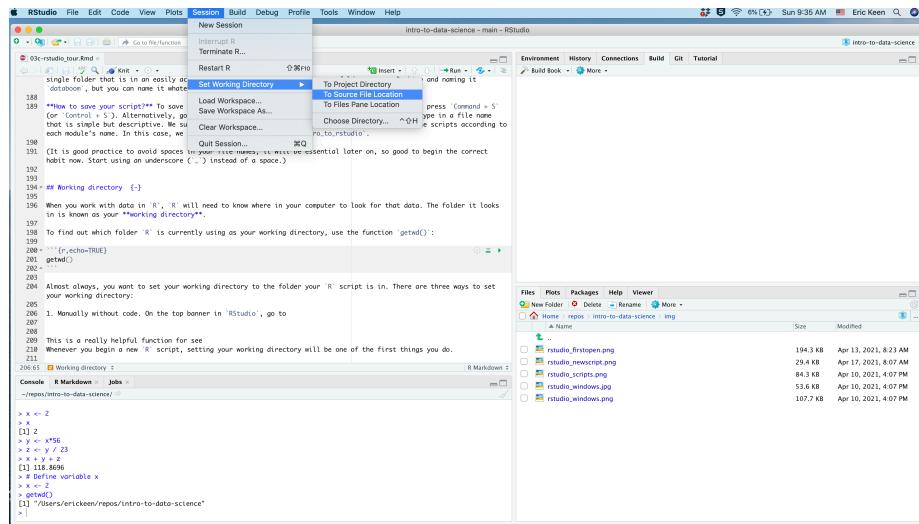
Almost always, you want to set your working directory to the folder your R script is in.

## How to set your working directory

Whenever you begin a new R script, setting your working directory will be one of the first things you do.

There are three ways to set your working directory:

1. **Manually without code.** On the top banner in RStudio, go to *Session > Set Working Directory > To Source File Location*:



This action sets your working directory to the same folder that your R script is in. When you do this, you will see that a command has been entered into your *Console*:

(Note that the filepath may be different on your machine.) This code is using the function `setwd()`, which is also used in the next option.

2. **Manually with code, using `setwd()`:** You can manually provide the filepath you want to set as your working directory. This option allows you

to set your `wd` to whatever folder you want. The character string within the `setwd()` command is the path to a folder. The formatting of this string must be exact, otherwise R will throw an error. Use option 1 at first to get a sense of how your computer formats its folder paths. Copy, paste, and modify the output from option 1 in order to type your path correctly.

3. **Automatically with code:** There is a command you can run that automatically sets your working directory to the folder that your R script is in. This is the most efficient and useful method, in our experience.

To use this command, you must first install a new package. Run this code:

```
install.packages("rstudioapi")
library(rstudioapi)
```

For now, you do not need to understand what this code is doing. We will explain packages and the `library()` function in a later module.

You can now copy, paste, and run this code to set your working directory automatically:

```
setwd(dirname(rstudioapi::getActiveDocumentContext()$path))
```

This is a complicated line of code that you need not understand. As long as it works, it works! Confirm that R is using the correct working directory with the command `getwd()`.

## Typical workflows

Now that you know how to create a script and set your working directory, you are prepared to work on data projects in RStudio.

The workflow for beginning a new data project typically goes like this:

*In your file explorer...*

1. **Create a folder for your project** somewhere on your computer. This will become your working directory.
2. **Create subfolders** within your working directory, if you want. We recommend creating a `data` subfolder, for keeping data, and a `z` subfolder, for keeping miscellaneous documents. The goal is to keep your working directory visually simple and organized; ideally, the only files not within subfolders are your R scripts.
3. **Add data** to your working directory, if you have any.

*In RStudio ...*

4. **Create a new R script.**
5. **Save it** inside your intended working directory.

6. At the top of your script, use comments to **add a title, author info, and brief description.**
7. Add the code to **set your working directory**.
8. **Begin coding!**

### Template R script

Here is a template you can use to copy and paste into each new script you create:

```
#####
# < Add title here >
#####
#
# < Add brief description here >
#
# < Author >
# Created on <add date here >
#
#####
# Set working directory
setwd(dirname(rstudioapi::getActiveDocumentContext()$path))

#####
# Code goes here

#####
# (end of file)
```

### Review assignment:

**Part 1** (*if not already complete*). Create a working directory for this course. Call it whatever you like, but **databoom** could work great. Place it somewhere convenient on your computer, such as your Desktop.

**Part 2.** Within this working directory, create three new folders: (1) a **data** folder, which is where you will store the data files we will be using in subsequent modules; (2) a **modules** folder, which is where you will keep the code you use to work on the material in these modules, and (3) a **project** folder, which is where you will keep all your work associated with your summer project.

**Part 3.** Now follow the *Typical Workflow* instructions above to create a script.

Save it within your `modules` folder. Name it `template.R`. Copy and paste the template R code provided above into this file, and save it. This is now a template that you can use to easily create new scripts for this course.

**Part 4.** Now make a copy of `template.R` to stage a script that you can use in the next module. To do so, in RStudio go to the top banner and click `File > Save As`. Save this new script as `10_variables.R` (because the next module is called *Module 10: Variables in R*).

**Part 5.** Modify the code in `10-variables.R` so that you are prepared to begin the next module. Change the title, and look ahead to *Module 10* to fill in a brief description. Don't forget to add your name as the author and specify today's date.

Boom!

### Other Resources

A Gentle Introduction to R from the RStudio team



# Chapter 8

## Variables in R

### Learning goals

- How to define variables and work with them in R
- Learn the various possible classes of data in R

### Introducing variables

So far we have strictly been using R as a calculator, with commands such as:

```
3 + 5  
[1] 8
```

Of course, R can do much, much more than these basic computations. Your first step in uncovering the potential of R is learning how to use **variables**.

In R, a variable is a convenient way of referring to an underlying value. That value can be as simple as a single number (e.g., 6), or as complex as a spreadsheet that is many Gigabytes in size. It may be useful to think of a variable as a cup; just as cups make it easy to hold your coffee and carry it from the kitchen to the couch, variables make it easy to contain and work with data.

### Declaring variables

To assign numbers or other types of data to a variable, you use the < and - characters to make the arrow symbol <-.

```
x <- 3+5
```

As the direction of the <- arrow suggests, this command stores the result of 3 + 5 into the variable x.

Unlike before, you did not see 8 printed to the *Console*. That is because the result was stored into `x`.

## Calling variables

If you wanted R to tell you what `x` is, just type the variable name into the *Console* and run that command:

```
x  
[1] 8
```

Want to create a variable but also see its value at the same time? Here's a handy trick:

```
x <- 3*12 ; x  
[1] 36
```

The semicolon simulates hitting `Enter`. It says: first run `x <- 3*12`, then run `x`.

You can also update variables.

```
x <- x * 3 ; x  
[1] 108  
x <- x * 3 ; x  
[1] 324
```

You can also add variables together.

```
x <- 8  
y <- 4.5  
x + y  
[1] 12.5
```

## Naming variables

Variables are case-sensitive! If you misspell a variable name, you will confuse R and get an error.

For example, ask R to tell you the value of capital X. The error message will be `Error: object 'X' not found`, which means R looked in its memory for an object (i.e., a variable) named X and could not find one.

You can make variable names as complicated or simple as you want.

```
supercalifragilistic.expiālidocious <- 5  
supercalifragilistic.expiālidocious # still works  
[1] 5
```

Note that periods and underscores can be used in variable names:

```
my.variable <- 5 # periods can be used
my_variable <- 5 # underscores can be used
```

However, hyphens cannot be used since that symbol is used for subtraction.

Also note that variables are case-sensitive! If you name a variable `My_variable`, R will not recognize it if you refer to it as `My_Variable`.

### Naming theory

Naming variables is a bit of an art. The trick is using names that are clear but are not so complicated that typing them is tedious or prone to errors.

Some names need to be avoided, since R uses them for special purposes. For example, `data` should be avoided, as should `mean`, since both are functions built-in to R and R is liable to interpret them as such instead of as a variable containing your data.

Note that R uses a feature called ‘Tab complete’ to help you type variable names. Begin typing a variable name, such as `supercalifragilistic.expialidocious` from the example above, but after the first few letters press the Tab key. R will then give you options for auto-completing your word. Press Tab again, or Enter, to accept the auto-complete. This is a handy way to avoid typos.

### Exercise 1

- A. Estimate how many bananas you’ve eaten in your lifetime and store that value in a variable (choose whatever name you wish).
- B. Now estimate how many ice cream sandwiches you’ve eaten in your lifetime and store that in a different variable.
- C. Now use these variables to calculate your Banana-to-ICS ratio. Store your result in a third variable, then call that variable in the Console to see your ratio.
- D. Who in the class has the highest ratio? Who has the lowest?

## Types of data in R

So far we have been working exclusively with numeric data. But there are many different data types in R. We call these “types” of data **classes**:

- Decimal values like 4.5 are called **numeric** data.
- Natural numbers like 4 are called **integers**. Integers are also numerics.
- Boolean values (TRUE or FALSE) are called **logical** data.
- Text (or string) values are called **character** data.

In order to be combined, data have to be the same class.

R is able to compute the following commands ...

```
x <- 6
y <- 4
x + y
[1] 10
```

... but not these:

```
x <- 6
y <- "4"
x + y
```

That's because the quotation marks used in naming y causes R to interpret y as a **character** class.

To see how R is interpreting variables, you can use the **class()** function:

```
x <- 100
class(x)
[1] "numeric"

x <- "100"
class(x)
[1] "character"

x <- 100 == 101
class(x)
[1] "logical"
```

Another data type to be aware of is **factors**, but we will deal with them later.

## Exercise 2

- A. Assign a **FALSE** statement of your choosing to a variable of whatever name you wish.
- B. Confirm that the class of this variable is “logical.”
- C. Confirm that the variable equals **FALSE**.

### Review assignment

#### Converting Farenheit to Celsius:

- A. Assign a variable **farenheit** the numerical value of 32.
- B. Assign a variable **celsius** to equal the conversion from Fahrenheit to Celsius. Unless you're a meteorology nerd, you may need to Google equation for this conversion.
- C. Print the value of **celsius** to the *Console*.

D. Now use this code to determine the *Celsius* equivalent of 212 degrees *Farenheit*.



# Chapter 9

## Structures for data in R

### Learning goals

- Learn the various structures of data in R
- How to work with vectors in R

### Introducing data structures

Data belong to different *classes*, as explained in the previous module, and they can be arranged into various **structures**.

So far we have been dealing only with variables that contain a single value, but the real value of R comes from assigning *entire sets* of data to a variable.

### Vectors

The simplest data structure in R is a **vector**. A vector is simply a set of values. A vector can contain only a single value, as we have been working with thus far, or it can contain many millions of values.

### Declaring and using vectors

To build up a vector in R, use the function `c()`, which is short for “concatenate”.

```
x <- c(5,6,7,8)
x
[1] 5 6 7 8
```

You can use the `c()` function to concatenate two vectors together:

```
x <- c(5,6,7,8)
y <- c(9,10,11,12)
z <- c(x,y)
z
[1] 5 6 7 8 9 10 11 12
```

You can also use `c()` to add values to a vector:

```
x <- c(5,6,7,8)
x <- c(x,9)
x
[1] 5 6 7 8 9
```

When two vectors are of the same length, you can do arithmetic with them:

```
x <- c(5,6,7,8)
y <- c(9,10,11,12)

x + y
[1] 14 16 18 20
x - y
[1] -4 -4 -4 -4
x * y
[1] 45 60 77 96
x / y
[1] 0.5555556 0.6000000 0.6363636 0.6666667
```

You can also put vectors through logical tests:

```
x <- 1:5
4 == x
[1] FALSE FALSE FALSE TRUE FALSE
```

This command is asking R to tell you whether each element in `x` is equal to 4.

You can create vectors of any data class (i.e., data type).

```
x <- c("Ben", "Joe", "Eric")
x
[1] "Ben"   "Joe"   "Eric"

y <- c(TRUE, TRUE, FALSE)
y
[1] TRUE  TRUE FALSE
```

Note that all values within a vector *must* be of the same class. You can't combine numerics and characters into the same vector. If you did, R would try to convert the numbers to characters. For example:

```
x <- 4
y <- "6"
z <- c(x,y)
z
[1] "4" "6"
```

## Useful functions for handling vectors

**length()** tells you the number of elements in a vector:

```
x <- c(5,6)
y <- c(9,10,11,12)

length(x)
[1] 2
length(y)
[1] 4
```

The **colon symbol** : creates a vector with every integer occurring between a min and max:

```
x <- 1:10
x
[1] 1 2 3 4 5 6 7 8 9 10
```

**seq()** allows you to build a vector using evenly spaced *sequence* of values between a min and max:

```
seq(0,100,length=11)
[1] 0 10 20 30 40 50 60 70 80 90 100
```

In this command, you are telling R to give you a sequence of values from 0 to 100, and you want the length of that vector to be 11. R then figures out the spacing required between each value in order to make that happen.

Alternatively, you can prescribe the interval between values instead of the length:

```
seq(0,100,by=7)
[1] 0 7 14 21 28 35 42 49 56 63 70 77 84 91 98
```

**rep()** allows you to repeat a single value a specified number of times:

```
rep("Hey!",times=5)
[1] "Hey!" "Hey!" "Hey!" "Hey!" "Hey!"
```

**head()** and **tail()** can be used to retrieve the first 6 or last 6 elements in a vector, respectively.

```
x <- 1:1000
head(x)
[1] 1 2 3 4 5 6
tail(x)
[1] 995 996 997 998 999 1000
```

You can also adjust how many elements to return:

```
head(x, 2)
[1] 1 2
tail(x, 10)
[1] 991 992 993 994 995 996 997 998 999 1000
```

**sort()** allows you to order a vector from its smallest value to its largest:

```
x <- c(4, 8, 1, 6, 9, 2, 7, 5, 3)
sort(x)
[1] 1 2 3 4 5 6 7 8 9
```

**rev()** lets you reverse the order of elements within a vector:

```
x <- c(4, 8, 1, 6, 9, 2, 7, 5, 3)
rev(x)
[1] 3 5 7 2 9 6 1 8 4
rev(sort(x))
[1] 9 8 7 6 5 4 3 2 1
```

**which()** allows you to ask, “For which elements of a vector is the following statement true?”

```
x <- 1:10
which(x == 4)
[1] 4
```

If no values within the vector meet the condition, a vector of length zero will be returned:

```
x <- 1:10
which(x == 11)
integer(0)
```

**%in%** is a handy operator that allows you to ask whether a value occurs *within* a vector:

```
x <- 1:10
4 %in% x
[1] TRUE
11 %in% x
[1] FALSE
```

### Exercise 1

- A. Use the colon symbol to create a vector of length 5 between a minimum and a maximum value of your choosing.
- B. Create a second vector of length 5 using the `seq()` function.
- C. Create a third vector of length 5 using the `rep()` function.
- D. Finally, concatenate the three vectors and check that the length makes sense.

### Subsetting vectors

Since you will eventually be working with vectors that contain thousands of data points, it will be useful to have some tools for *subsetting* them – that is, looking at only a few select elements at a time.

You can subset a vector using square brackets [ ].

```
x <- 50:100
x[10]
[1] 59
```

This command is asking R to return the 10th element in the vector x.

```
x[10:20]
[1] 59 60 61 62 63 64 65 66 67 68 69
```

This command is asking R to return elements 10:20 in the vector x.

### Exercise 2

- A. Figure out how to replicate the `head()` function using your new vector subsetting skills.
- B. Now replicate the `tail()` function, using those same skills as well as the `length()` function you just learned.

### Dataframes & other data structures

A **vector** is the most basic data structure in R, and the other structures are built out of vectors.

As a data scientist, the most common data structure you will be working with is a **dataframe**, which is essentially a spreadsheet: a dataset with rows and columns, in which each column represents a vector of the same class of data.

We will explore dataframes in detail later, but here is a sneak peak at what they look like:

```
df <- data.frame(x=300:310,
                  y=600:610)
```

```
df
  x   y
1 300 600
2 301 601
3 302 602
4 303 603
5 304 604
6 305 605
7 306 606
8 307 607
9 308 608
10 309 609
11 310 610
```

In this command, we used the `data.frame()` function to combine two vectors into a dataframe with two columns named `x` and `y`. R then saved this result in a new variable named `df`. When we call `df`, R shows us the dataframe.

The great thing about dataframes is that they allow you to relate different data types to each other.

```
df <- data.frame(name=c("Ben", "Joe", "Eric"),
                  height.inches=c(75,73,80))
df
  name height.inches
1 Ben      75
2 Joe      73
3 Eric     80
```

This dataframe has one column of class `character` and another of class `numeric`.

The two other most common data structures are `matrices` and `lists`, but we will wait on learning about thos. For now, focus on becoming comfortable using vectors and dataframes.

### Exercise 3

Use the `data.frame()` function to create a table (i.e., a dataframe object) listing 10 different pizza toppings and whether or not you like each one.

### Review assignment

*NOTE: UNDER CONSTRUCTION!*

# Chapter 10

## Calling functions

### Learning goals

- Understand what functions are, and why they are awesome
- Understand how functions work
- Understand how to read function documentation

### Introducing R functions

You have already worked with many R functions; commands like `getwd()`, `length()`, and `unique()` are all functions. You know a command is a function because it has parentheses, `()`, attached at its end.

Just as **variables** are convenient names used for calling *objects* such as vectors or dataframes, **functions** are convenient names for calling *processes* or *actions*. An R function is just a batch of code that performs a certain action.

Variables represent data, while functions represent code.

Most functions have three key components: (1) one or more inputs, (2) a process that is applied to those inputs, and (3) an output of the result. When you call a function in R, you are saying, “Hey R, take this information, do something to it, and return the result to me.” You supply the function with the inputs, and the function takes care of the rest.

Take the function `mean()`, for example. `mean()` finds the arithmetic mean (i.e., the average) of a set of values.

```
x <- c(4,6,3,2,6,8,5,3) # create a vector of numbers
mean(x) # find their mean
[1] 4.625
```

In this command, you are feeding the function `mean()` with the input `x`.

## Base functions in R

There are hundreds of functions already built-in to R. These functions are called “*base functions*”. Throughout these modules, we have been – and will continue – introducing you to the most commonly used base functions.

You can access other functions through bundles of external code known as *packages*, which we explain in an upcoming module.

You can also write your *own* functions (and you will!). We provide an entire module on how to do this.

Note that not all functions require an input. The function `getwd()`, for example, does not need anything in its parentheses to find and return current your working directory.

## Saving function output

You will almost always want to save the result of a function in a new variable. Otherwise the function just prints its result to the *Console* and R forgets about it.

You can store a function result the same way you store any value:

```
x <- c(4,6,3,2,6,8,5,3)
x_mean <- mean(x)
x_mean
[1] 4.625
```

## Functions with multiple inputs

Note that `mean()` accepts a second input that is called `na.rm`. This is short for `NA.remove`. When this is set to `TRUE`, R will remove broken or missing values from the vector before calculating the mean.

```
x <- c(4,6,3,2,NA,8,5,3) # note the NA
mean(x,na.rm=TRUE)
[1] 4.428571
```

If you tried to run these commands with `na.rm` set to `FALSE`, R would throw an error and give up.

Note that you provided the function `mean()` with two inputs, `x` and `na.rm`, and that you separated each input with a comma. This is how you pass multiple inputs to a function.

## Function defaults

Note that many functions have default values for their inputs. If you do not specify the input’s value yourself, R will assume you just want to use the default.

In the case of `mean()`, the default value for `na.rm` is `FALSE`. This means that the following code would throw an error ...

```
x <- c(4,6,3,2,NA,8,5,3) # note the NA
mean(x)
[1] NA
```

Because R will assume you are using the default value for `na.rm`, which is `FALSE`, which means you do not want to remove missing values before trying to calculate the mean.

## Function documentation (i.e., getting help)

Functions are designed to accept only a certain number of inputs with only certain names. To figure out what a function expects in terms of inputs, and what you can expect in terms of output, you can call up the function's help page:

When you enter this command, the help documentation for `mean()` will appear in the bottom right pane of your RStudio window:

The screenshot shows the R Help Viewer window. The title bar says "Arithmetic Mean". The menu bar includes "Files", "Plots", "Packages", "Help", and "Viewer". Below the menu is a toolbar with icons for back, forward, search, and help. A search bar says "R: Arithmetic Mean" and a "Find in Topic" button. The main content area has sections: "Description", "Usage", "Arguments", "Value", "References", and "See Also". The "Usage" section contains the R code for the mean function. The "Arguments" section describes the parameters: x (an R object), trim (the fraction of observations to trim from each end), na.rm (logical value for stripping NA values), and ... (further arguments). The "Value" section notes that if trim is zero, the arithmetic mean is computed; if non-zero, a symmetrically trimmed mean is computed. The "References" section lists Becker, Chambers, and Wilks (1988). The "See Also" section lists related functions: weighted.mean, mean.POSIXct, and colMeans.

```

mean(x, ...)

## Default S3 method:
mean(x, trim = 0, na.rm = FALSE, ...)

Arguments

x      An R object. Currently there are methods for numeric/logical vectors and date, date-time and time interval objects. Complex vectors are allowed for trim = 0, only.
trim   the fraction (0 to 0.5) of observations to be trimmed from each end of x before the mean is computed. Values of trim outside that range are taken as the nearest endpoint.
na.rm  a logical value indicating whether NA values should be stripped before the computation proceeds.
...     further arguments passed to or from other methods.

Value

If trim is zero (the default), the arithmetic mean of the values in x is computed, as a numeric or complex vector of length one. If x is not logical (coerced to numeric), numeric (including integer) or complex, NA\_real\_ is returned, with a warning. If trim is non-zero, a symmetrically trimmed mean is computed with a fraction of trim observations deleted from each end before the mean is computed.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) The New S Language. Wadsworth & Brooks/Cole.

See Also

weighted.mean, mean.POSIXct, colMeans for row and column means.

Examples

x <- c(0:10, 50)
xm <- mean(x)
c(xm, mean(x, trim = 0.10))

```

Learning how to read this documentation is essential to becoming competent in using R.

**Be warned:** not all documentation is easy to understand! You will come to really resent poorly written documentation and really appreciate well-written documentation; the few extra minutes taken by the function's author to write good documentation saves users around the world hours of frustration and confusion.

- The **Title** and **Description** help you understand what this function does.
- The **Usage** section shows you how type out the function.
- The **Arguments** section lists out each possible argument (which in R lingo is another word for *input* or *parameter*), explains what that input is asking

for, and details any formatting requirements.

- The **Value** section describes what the function returns as output.
- At the bottom of the help page, example code is provided to show you how the function works. You can copy and paste this code into your own script of *Console* and check out the results.

Note that more complex functions may also include a **Details** section in their documentation, which gives more explanation about what the function does, what kinds of inputs it requires, and what it returns.

## Function examples

R comes with a set of base functions for descriptive statistics, which provide good examples of how functions work and why they are valuable.

We can use the same vector as the input for all of these functions:

```
x <- c(4,6,3,2,NA,8,9,5,6,1,9,2,6,3,0,3,2,5,3,3) # note the NA
```

**mean()** has been explained above.

```
result <- mean(x,na.rm=TRUE)
result
[1] 4.210526
```

**median()** returns the median value in the supplied vector:

```
result <- median(x,na.rm=TRUE)
result
[1] 3
```

**sd()** returns the standard deviation of the supplied vector:

```
result <- sd(x,na.rm=TRUE)
result
[1] 2.594416
```

**summary()** returns a vector that describes several aspects of the vector's distribution:

```
result <- summary(x,na.rm=TRUE)
result
Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
0.000 2.500 3.000 4.211 6.000 9.000 1
```

## Review assignment

*NOTE: Under construction!*



# Chapter 11

## Base plots

### Learning goals

- Make basic plots in R
- Basic adjustments to plot formatting

### Introduction

To learn how to plot, let's first create a dataset to work with:

```
country <- c("USA", "Tanzania", "Japan", "Ctr. Africa Rep.", "China", "Norway", "India")
lifespan <- c(79, 65, 84, 53, 77, 82, 69)
gdp <- c(55335, 2875, 38674, 623, 13102, 84500, 6807)
```

These data come from this publicly available database that compares health and economic indices across countries in 2011.

The `lifespan` column presents the average life expectancy for each country.

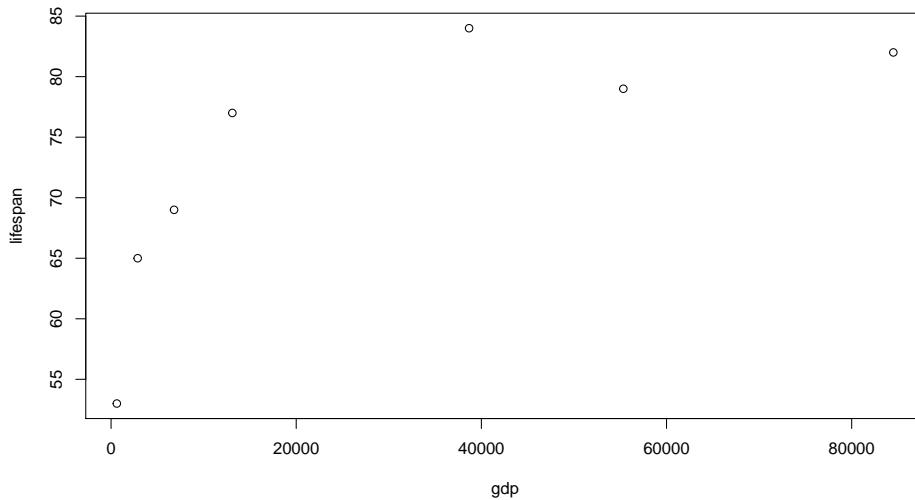
The `gdp` column presents the average GDP per capita within that country, which is a common index for the income and wealth of average citizens.

Let's see if there is a relationship between life expectancy and income.

### Create a basic plot

The simplest way to make a basic plot in R is to use its built-in `plot()` function:

```
plot(lifespan ~ gdp)
```



This syntax is saying this: plot column `lifespan` as a function of `gdp`. The symbol `~` denotes “*as a function of*”. This frames `lifespan` as a dependent variable (y axis) that is affected by the independent variable (x axis), which in this case is `gdp`.

Note that R uses the variable names you provided as the x- and y-axes. You can adjust these labels however you wish (see formatting section below).

You can also produce this exact same plot using the following syntax:

```
plot(y=lifespan, x=gdp)
```

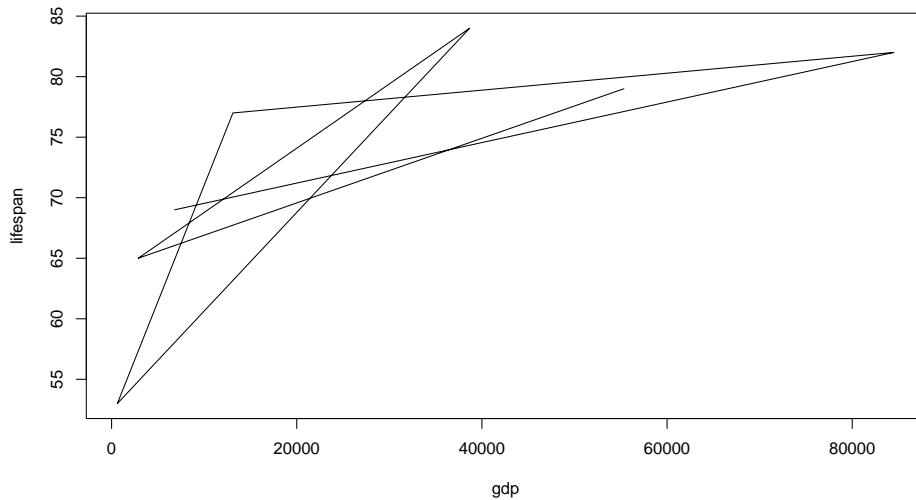
Choose whichever one is most intuitive to you.

## Most common types of plots

The plot above is a **scatter plot**, and is one of the most common types of plots in data science.

You can turn this into a **line plot** by adding a parameter to the `plot()` function:

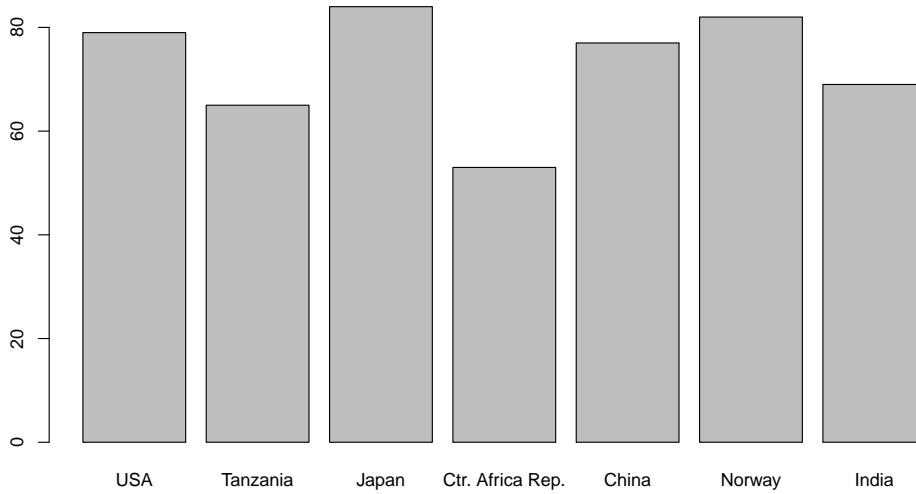
```
plot(lifespan ~ gdp, type="l")
```



*What a mess!* Rather than connecting these values in the order you might expect, R connects them in the order that they are listed in their source vectors. This is why line plots tend to be more useful in scenarios such as time series, which are inherently ordered.

Another common plot is the **bar plot**, which uses a different R function:

```
barplot(height=lifespan,names.arg=country)
```



In this command, the parameter **height** determines the height of the bars, and **names.arg** provides the labels to place beneath each bar.

There are many more plot types out there, but let's stop here now.

### Exercise 1

Produce a bar plot that shows the GDP for each country.

## Basic plot formatting

You can adjust the default formatting of plots by adding other inputs to your `plot()` command. To understand all the parameters you can adjust, bring up the help page for this function:

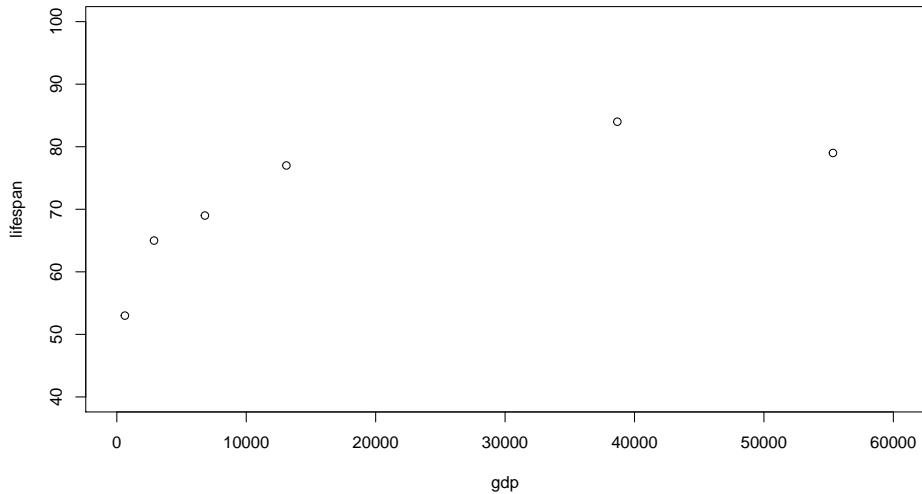
```
?plot
```

If multiple help page options are returned, select the *Generiz X-Y Plotting* page from the `base` package. This is the `plot` function that comes built-in to R.

Here we demonstrate just a few of the most common formatting adjustments you are likely to use:

**Set plot range** using `xlim` (for the x axis) and `ylim` (for the y axis):

```
plot(lifespan ~ gdp, xlim=c(0,60000), ylim=c(40,100))
```



In this command, you are defining axis limits using a 2-element vector (i.e., `c(min, max)`).

Note that it can be easier to read your code if you put each input on a new line, like this:

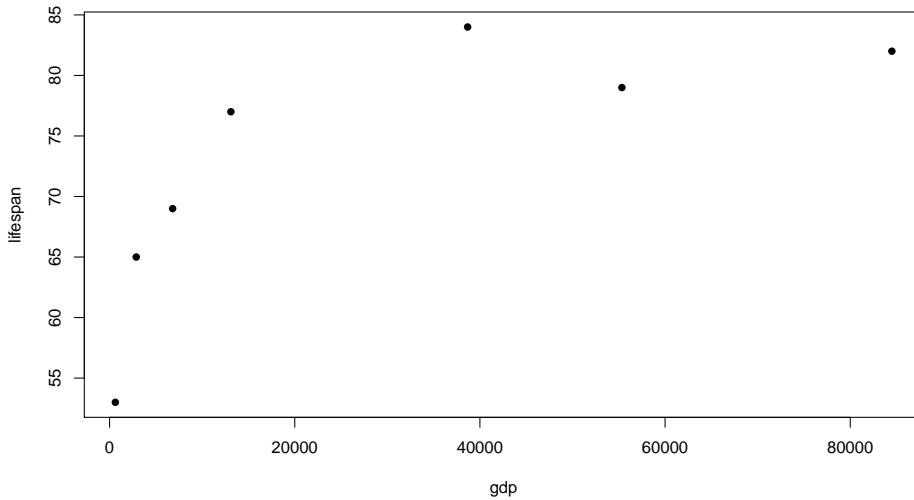
```
plot(lifespan ~ gdp,
      xlim=c(0,60000),
      ylim=c(40,100))
```

Make sure each input line within the function ends with a comma, otherwise

you R will get confused and throw an error.

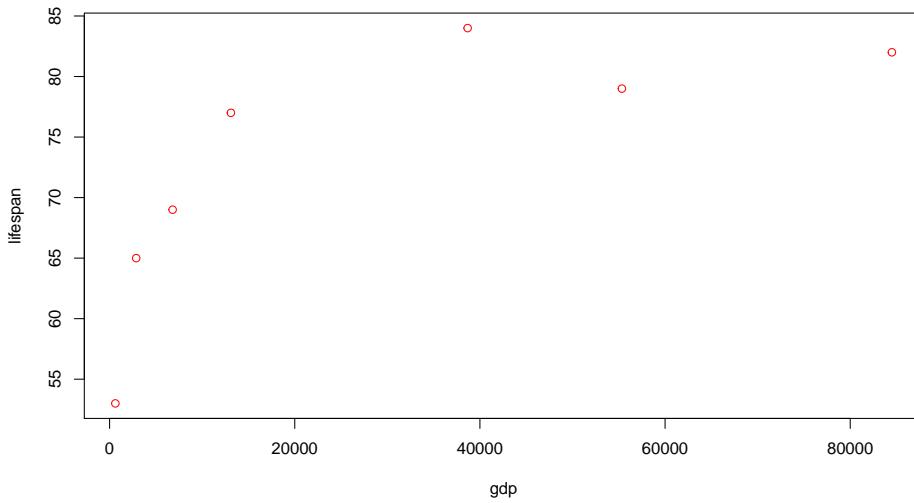
**Set dot type** using the input pch:

```
plot(lifespan ~ gdp,pch=16)
```



**Set dot color** using the input col (the default is col="black")

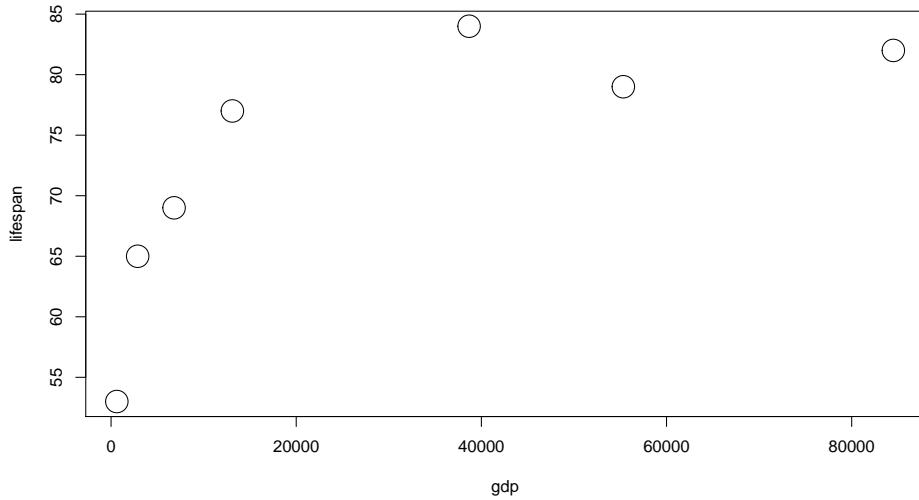
```
plot(lifespan ~ gdp,col="red")
```



Here is a great resource for color names in R.

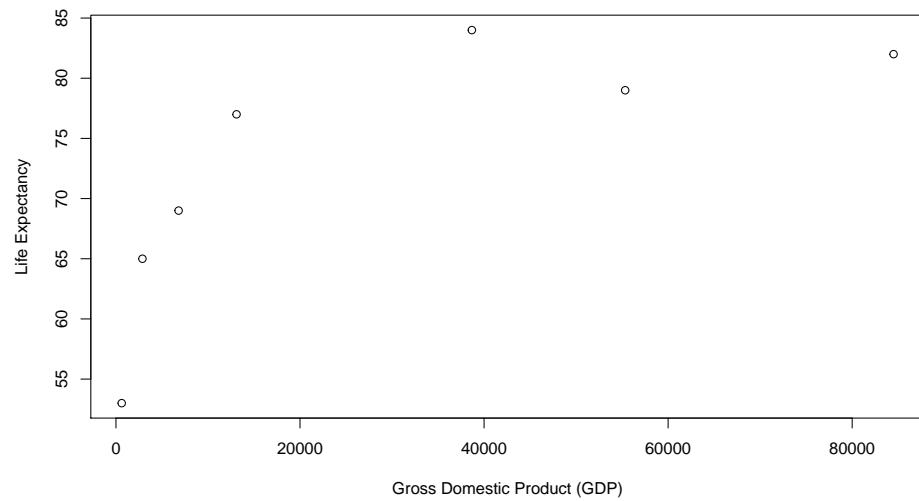
**Set dot size** using the input cex (the default is cex=1):

```
plot(lifespan ~ gdp,cex=3)
```



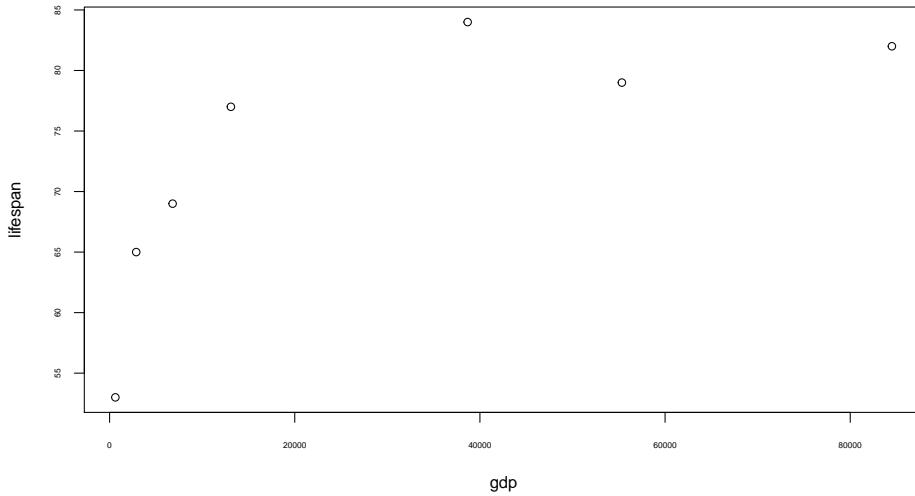
Set axis labels using the inputs `xlab` and `ylab`:

```
plot(lifespan ~ gdp, xlab="Gross Domestic Product (GDP)", ylab="Life Expectancy")
```



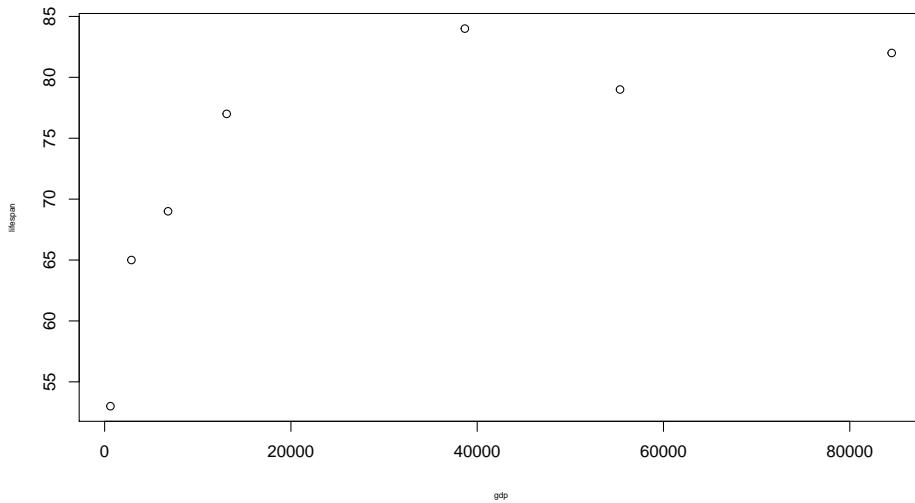
Set axis number size using the input `cex.axis` (the default is `cex.axis=1`):

```
plot(lifespan ~ gdp, cex.axis=.5)
```



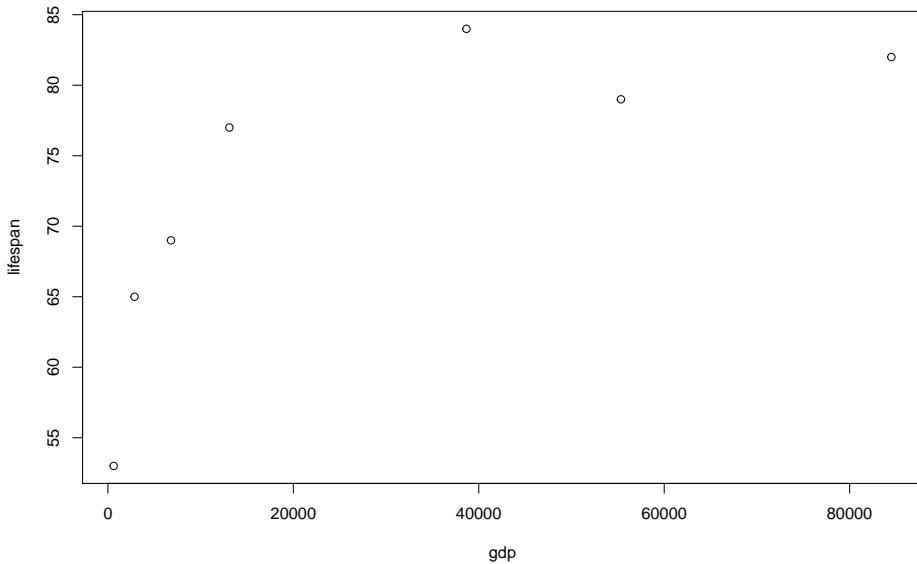
Set axis label size using the input `cex.lab` (the default is `cex.lab=1`):

```
plot(lifespan ~ gdp,cex.lab=.5)
```



Set plot margins using the function `par(mar=c())` before you call `plot()`:

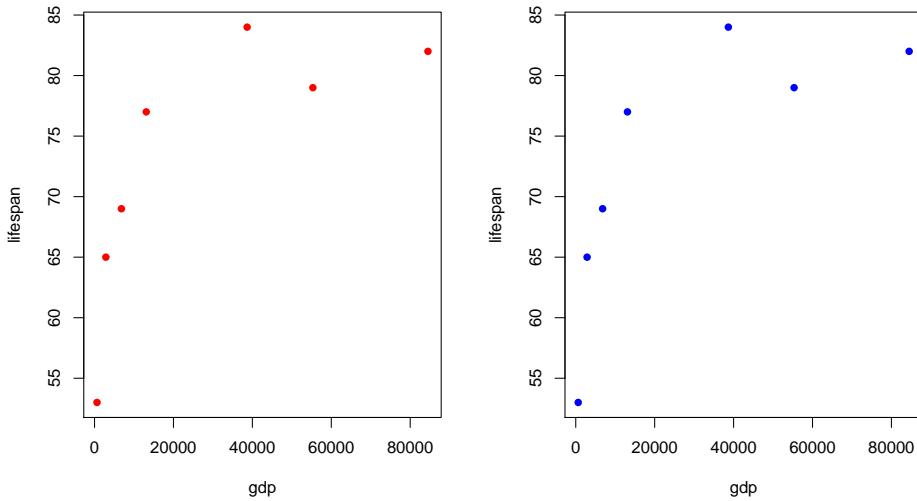
```
par(mar=c(5,5,0.5,0.5))
plot(lifespan ~ gdp)
```



In this command, the four numbers in the vector used to define `mar` correspond to the margin for the bottom, left, top, and right sides of the plot, respectively.

**Create a multi-pane plot** using the function `par(mfrow=c())` before you call `plot()`:

```
par(mfrow=c(1,2))
plot(lifespan ~ gdp, col="red", pch=16)
plot(lifespan ~ gdp, col="blue", pch=16)
```



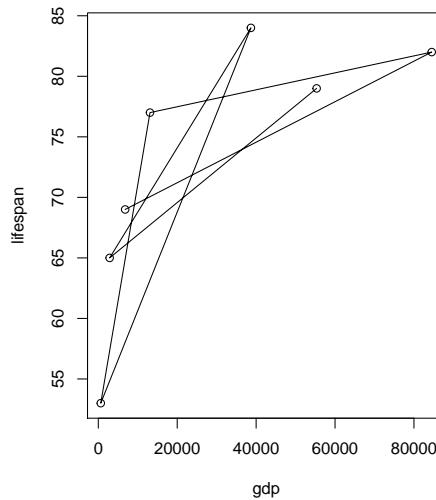
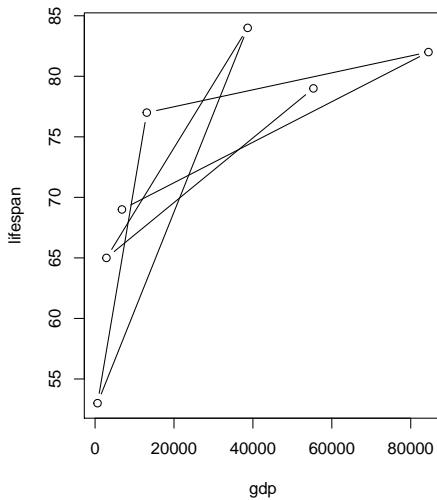
In this command, the two numbers in the vector used to define `mfrow` correspond to the number of rows and columns, respectively, on the entire plot. In this case, you have 1 row of plots with two columns.

Note that you will need to reset the number of panes when you are done with your multi-pane plot!

```
par(mfrow=c(1,1))
```

**Plot dots and lines at once using the input type:**

```
par(mfrow=c(1,2))
plot(lifespan ~ gdp,type="b")
plot(lifespan ~ gdp,type="o")
```

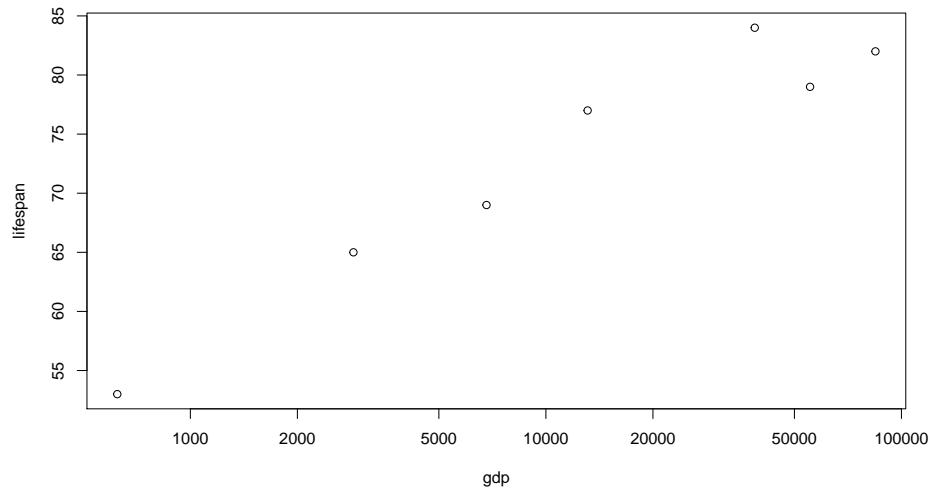


```
par(mfrow=c(1,1))
```

Note the two slightly different formats here.

**Use a logarithmic scale for one or of your axes using the input log**

```
plot(lifespan ~ gdp,log="x")
```



### Exercise 2

Produce a *beautifully* formatted plot that incorporates **all** of these customization inputs explained above into a multi-paned plot.

## Plotting with data frames

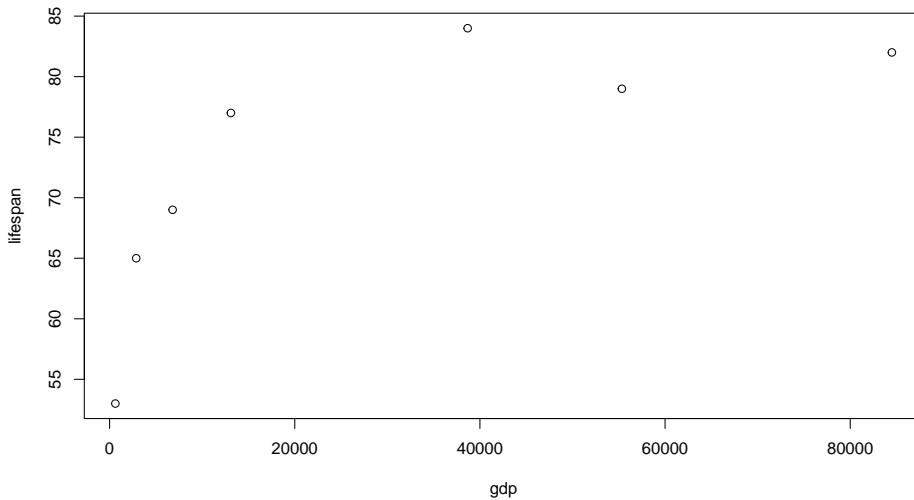
So far in this tutorial we have been using vectors to produce plots. This is nice for learning, but does not represent the real world very well. You will almost always be producing plots using dataframes.

Let's turn these vectors into a dataframe:

```
df <- data.frame(country, lifespan, gdp)
df
  country lifespan   gdp
1      USA      79 55335
2  Tanzania      65  2875
3      Japan      84 38674
4 Ctr. Africa Rep.      53   623
5      China      77 13102
6     Norway      82 84500
7      India      69  6807
```

To plot data within a dataframe, your `plot()` syntax changes slightly:

```
plot(lifespan ~ gdp, data=df)
```



This syntax is saying this: using the dataframe named `df` as a source, plot column `lifespan` as a function of column `gdp`. The symbol `~` denotes “*as a function of*”. This frames `lifespan` as a dependent variable (y axis) that is affected by the independent variable (x axis), which in this case is `gdp`.

Another way to write this command is as follows:

```
plot(df$lifespan ~ df$gdp)
```

In this command, the `$` symbol is saying, “give me the column in `df` named `lifespan`”. It is a handy way of referring to a column within a dataframe by name. You will learn more about working with dataframes in an upcoming module.

## Exercise 2

- A. Use the `df` dataframe to produce a bar plot that shows life expectancy for each country.
- B. Use the `df` dataframe to produce a jumbled line plot of life expectancy as a function of GDP. Reference the `plot()` documentation to figure out how to change the thickness of the line.

## Next-level plotting

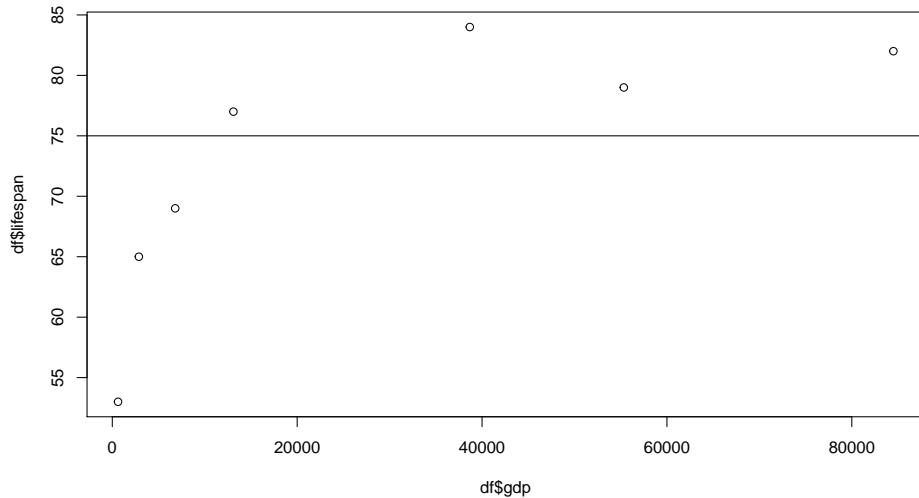
The possibilities for data visualization in R are pretty much limitless, and over time you will become fluent in making gorgeous plots. Here are a few common tools that can take your plots to the next level.

## Adding lines

In some cases it is useful to add reference lines to your plot. For example, what if we wanted to be able to quickly see which countries had life expectancies below 75 years?

You can add a line at `lifespan = 75` using the function `abline()`.

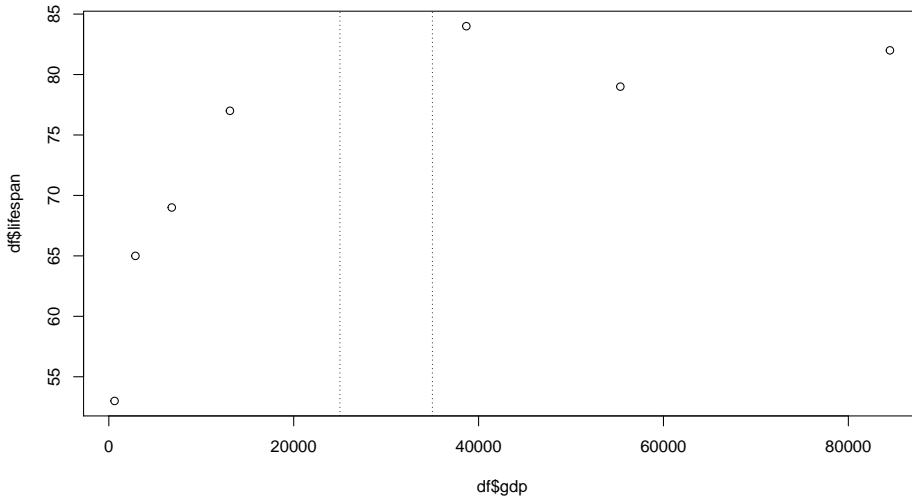
```
plot(df$lifespan ~ df$gdp)
abline(h=75)
```



In this command, the `h` input means “place a horizontal line at this `y` value.”.

Similarly, you can use `v` to specify vertical lines at certain `x` values.

```
plot(df$lifespan ~ df$gdp)
abline(v=c(25000,35000),lty=3)
```



Note here that another input, `lty`, was used to change the type of line printed.  
(Refer to `?abline()` for more details).

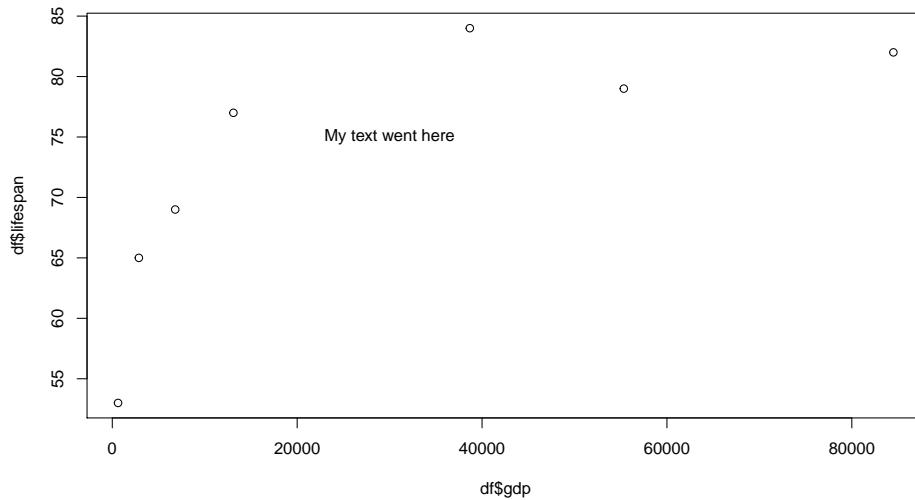
#### Exercise 4

Produce a plot of life expectancy as a function of GDP per capita. Then add a line to your plot that indicates which countries have per-capita GDPs that fall below (or above) the average per-capita GDP for the whole dataset. Make your line dashed and color it red.

#### Adding text

Use the `text()` function to add labels to your plot:

```
plot(df$lifeSpan ~ df$gdp)
text(x=30000,y=75,labels="My text went here")
```



### Exercise 5

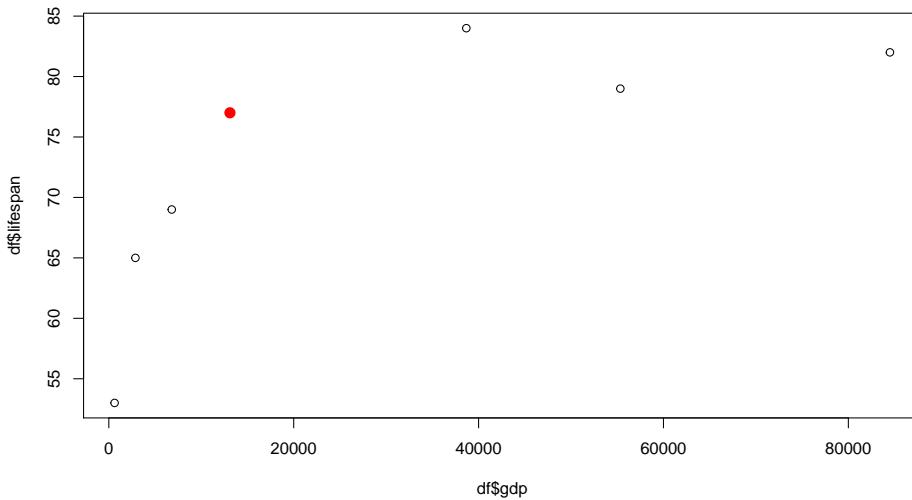
Produce a plot of life expectancy as a function of GDP per capita, then label each point by country. Make the labels small and place them *to the right* of their associated dot (Hint: use `?text` for help).

### Highlighting certain data points

It can be helpful to highlight a certain data point (or group of data points) using a different dot size, format, or color.

To highlight a single data point, here is one approach you can take: first, plot all points, *then* re-plot the point of interest using the `points()` function:

```
plot(df$lifeSpan ~ df$gdp)
points(x=df$gdp[5],y=df$lifeSpan[5],col="red",pch=16,cex=1.5)
```



In this example, we re-plotted the data for the fifth row in the dataframe (in this case, China).

**To highlight a group of data points**, try this approach:

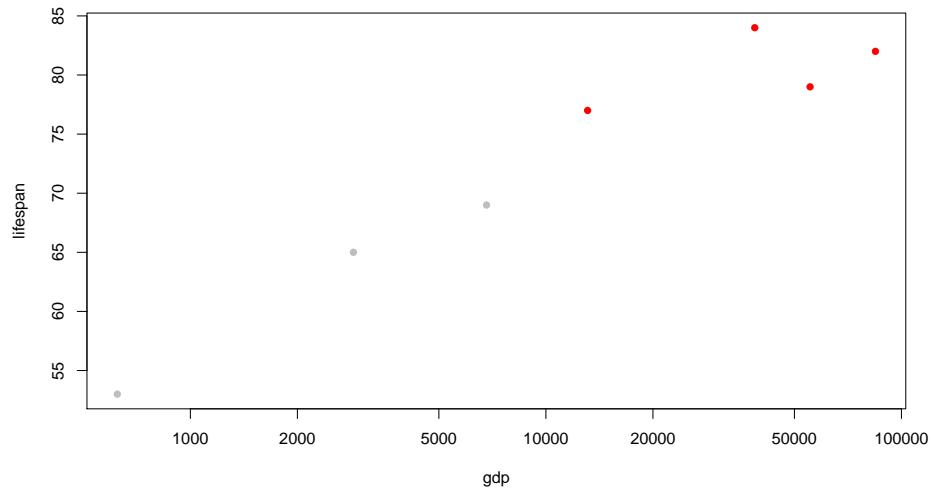
- First, create a vector that will contain the color for each data point.
- Second, determine the color for each data point using a logical test.
- Third, use your vector of colors within your `plot()` command.

For example, let's highlight all countries whose life expectancy is greater than 75.

```
# First
cols <- rep("grey",times=length(lifespan)) # create a vector of colors the length of vector `lifespan` is
cols
[1] "grey" "grey" "grey" "grey" "grey" "grey" "grey" "grey"

# Second
change_these <- which(lifespan > 75)
change_these # these are the elements that we want to highlight
[1] 1 3 5 6
cols[change_these] <- "red" # change the color for these elements to a highlight color

# Third
plot(lifespan ~ gdp,pch=16,col=cols,log="x")
```



### Exercise 6

Produce a plot of life expectancy as a function of GDP per capita, in which all countries with GDPs below \$10,000 have larger dots of a different color.

### Building a plot from the ground up

In many applications it can be helpful to have complete control over the way your plot is built. To do so, you can build your plot from the very bottom up in multiple steps.

The steps for building up your own plot are as follows:

1. **Stage a blank canvas:** A plot begins with a blank canvas that covers a certain range of values for `x` and `y`. To stage a blank canvas, add this parameters to your `plot()` function: `type="n"`, `axes=FALSE`, `ann=FALSE`, `xlim=c(__, __)`, `ylim=c(__, __)`". These commands tell R to plot a blank space, not to print axes, not to print annotations like x- or y-axis labels, and to limit your canvas to a certain coordinate range. Be sure to add numbers to the `xlim()` and `ylim()` commands.
2. **Add your axes**, if you want, using the function `axis()`. The command `axis(1)` prints the x-axis, and `axis(2)` prints the y-axis. This function allows you to define where tick marks occur and other details (see `?axis`).
3. **Add axis titles** using the function `title()`.
4. **Add reference lines**, if you want, using `abline()`. Do this before adding data, since it is usually nice for data points to be superimposed *on top of* your reference lines.
5. **Add your data** using either `points()` or `lines()`.

## 6. Add text labels, if you want, using `text()`.

Here is an example of this process:

```
# 1. Stage a blank canvas
par(mar=c(4.5,4.5,1,1))
plot(1,type="n",axes=FALSE,ann=FALSE,xlim=c(0,100000),ylim=c(40,100))

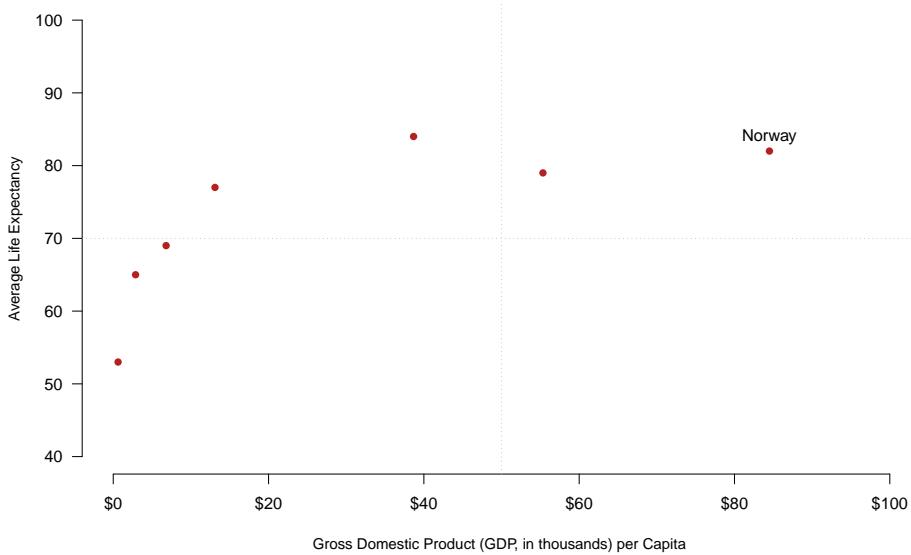
# 2. Add axes
axis(1,at=c(0,20000,40000,60000,80000,100000),labels=c("$0", "$20", "$40", "$60", "$80", "$100"))
axis(2,at=seq(40,100,by=10),las=2)

# 3. Add axis titles
title(xlab="Gross Domestic Product (GDP, in thousands) per Capita ",cex.lab=.9)
title(ylab="Average Life Expectancy",cex.lab=.9)

# 4. Add reference lines
abline(h=70,v=50000,lty=3,col="grey")

# 5. Add data
points(x=gdp,y=lifespan,pch=16,col="firebrick")

# 6. Add text
text(x=gdp[6],y=lifespan[6],labels="Norway",pos=3)
```



## Review assignment

*NOTE: Under construction!*

**Other Resources**

- R color palette
- The R Graph Gallery

# Chapter 12

# Packages

## Learning goals

- Learn what R packages are and why they are awesome
- Learn how to find and read about the packages installed on your machine
- Learn how to install R packages from CRAN
- Learn how to install R packages from GitHub

## Introducing R packages

As established in the **Calling functions** module, R comes with hundreds of built-in base functions and datasets ready for use. You can also write your *own* functions, which we will cover in an upcoming module.

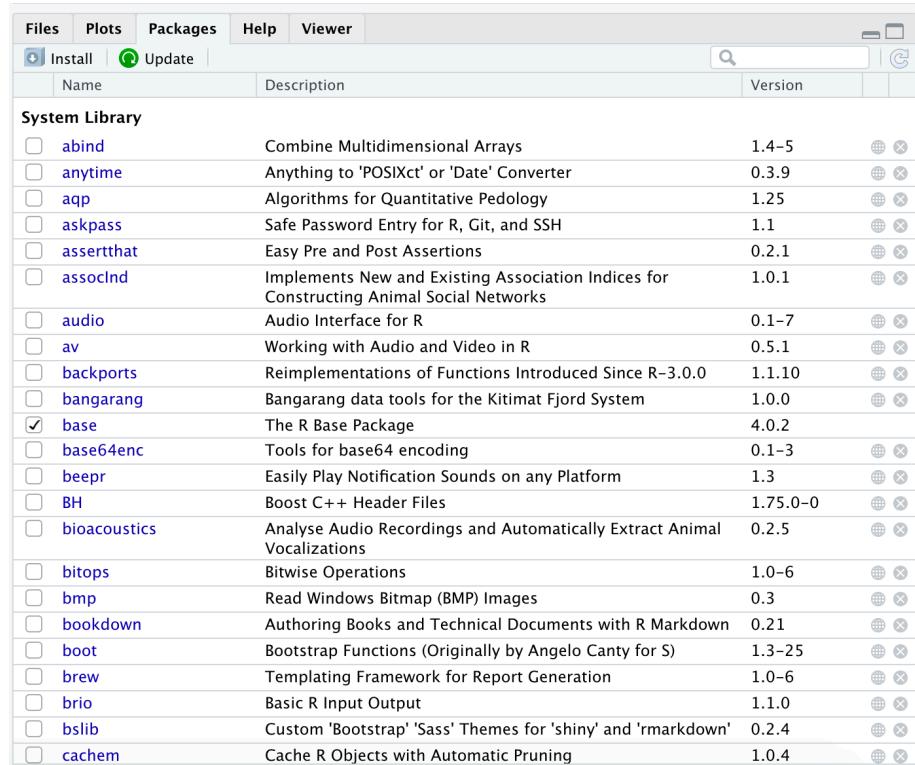
You can also access thousands of other functions and datasets through bundles of external code known as **packages**. Packages are developed and shared by R users around the world – a global community working together to increase R’s versatility and impact.

Some packages are designed to be broadly useful for almost any application, such as the packages you will be learning in this course (`ggplot`, `dplyr`, `stringr`, etc.). Such packages make it easier and more efficient to do your work with R.

Others are designed for niche problems that can be made much more doable with specialized functions or datasets. For example, the package `PBSmapping` contains shoreline, seafloor, and oceanographic datasets and custom mapping functions that make it easier for marine scientists at the Pacific Biological Station (PBS) in British Columbia, Canada, to carry out their work.

## Finding the packages already on your computer

In RStudio, look to the pane in the bottom right and click on the *Packages* tab. You should see something like this:



The screenshot shows the RStudio interface with the 'Packages' tab selected in the top navigation bar. Below the navigation bar, there are two buttons: 'Install' and 'Update'. A search bar and a refresh icon are also present. The main area is titled 'System Library' and displays a table of installed packages. The columns in the table are 'Name', 'Description', and 'Version'. Each package entry includes a checkbox, the package name, its description, its version number, and two small circular icons.

Name	Description	Version	
<b>System Library</b>			
<input type="checkbox"/> <a href="#">abind</a>	Combine Multidimensional Arrays	1.4–5	 
<input type="checkbox"/> <a href="#">anytime</a>	Anything to 'POSIXct' or 'Date' Converter	0.3.9	 
<input type="checkbox"/> <a href="#">aqp</a>	Algorithms for Quantitative Pedology	1.25	 
<input type="checkbox"/> <a href="#">askpass</a>	Safe Password Entry for R, Git, and SSH	1.1	 
<input type="checkbox"/> <a href="#">assertthat</a>	Easy Pre and Post Assertions	0.2.1	 
<input type="checkbox"/> <a href="#">assocInD</a>	Implements New and Existing Association Indices for Constructing Animal Social Networks	1.0.1	 
<input type="checkbox"/> <a href="#">audio</a>	Audio Interface for R	0.1–7	 
<input type="checkbox"/> <a href="#">av</a>	Working with Audio and Video in R	0.5.1	 
<input type="checkbox"/> <a href="#">backports</a>	Reimplementations of Functions Introduced Since R-3.0.0	1.1.10	 
<input type="checkbox"/> <a href="#">bangarang</a>	Bangarang data tools for the Kitimat Fjord System	1.0.0	 
<input checked="" type="checkbox"/> <a href="#">base</a>	The R Base Package	4.0.2	 
<input type="checkbox"/> <a href="#">base64enc</a>	Tools for base64 encoding	0.1–3	 
<input type="checkbox"/> <a href="#">beepR</a>	Easily Play Notification Sounds on any Platform	1.3	 
<input type="checkbox"/> <a href="#">BH</a>	Boost C++ Header Files	1.75.0–0	 
<input type="checkbox"/> <a href="#">bioacoustics</a>	Analyse Audio Recordings and Automatically Extract Animal Vocalizations	0.2.5	 
<input type="checkbox"/> <a href="#">bitops</a>	Bitwise Operations	1.0–6	 
<input type="checkbox"/> <a href="#">bmp</a>	Read Windows Bitmap (BMP) Images	0.3	 
<input type="checkbox"/> <a href="#">bookdown</a>	Authoring Books and Technical Documents with R Markdown	0.21	 
<input type="checkbox"/> <a href="#">boot</a>	Bootstrap Functions (Originally by Angelo Canty for S)	1.3–25	 
<input type="checkbox"/> <a href="#">brew</a>	Templating Framework for Report Generation	1.0–6	 
<input type="checkbox"/> <a href="#">brio</a>	Basic R Input Output	1.1.0	 
<input type="checkbox"/> <a href="#">bslib</a>	Custom 'Bootstrap' 'Sass' Themes for 'shiny' and 'rmarkdown'	0.2.4	 
<input type="checkbox"/> <a href="#">cachem</a>	Cache R Objects with Automatic Pruning	1.0.4	 

This is displaying all the packages already installed in your system.

If you click on one of these packages (try the `base` package, for example), you will be taken to a list of all the functions and datasets contained within it.

The screenshot shows the RStudio interface with the 'Packages' tab selected in the top navigation bar. The main content area displays the documentation for the 'base' package version 4.0.2. The title 'The R Base Package' is at the top, followed by the R logo. Below the title, it says 'Documentation for package ‘base’ version 4.0.2'. There are two small circular icons with arrows below the title. A bulleted list follows: '• DESCRIPTION file.' and '• Code demos. Use `demo()` to run them.' Under the heading 'Help Pages', there is a large list of letters from A to Z, each with a corresponding link. Below this, under the heading '-- A --', there is a list of functions with their descriptions:

<a href="#">abbreviate</a>	Abbreviate Strings
<a href="#">abs</a>	Miscellaneous Mathematical Functions
<a href="#">acos</a>	Trigonometric Functions
<a href="#">acosh</a>	Hyperbolic Functions

When you click on one of these functions, you will be taken to the help page for that function. This is the equivalent of typing `? <function_name>` into the *Console*.

## Installing a new package

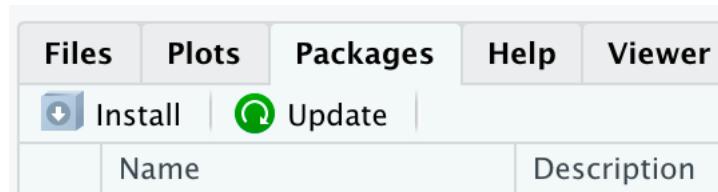
There are a couple ways to download and install a new R packae on your computer. Most packages are available from an open-source repository known as CRAN (which stands for Comprehensive R Archive Network). However, an increasingly common practice is to release packages on a public repository such as GitHub.

### Installing from CRAN

You can install CRAN packages one of two ways:

#### Through clicks:

In RStudio, in the bottom-right pane, return to the *Packages* tab. Click on the “Install” button.



You can then search for the package you wish to install then click **Install**.

#### Through code:

You can download packages from the *Console* using the `install.packages()` function.

```
install.packages('fun')
```

Note that the package name must be in quotation marks.

#### Installing from GitHub

To install packages from GitHub, you must first download a CRAN package that makes it easy to do so:

```
install.packages("devtools")
```

Most packages on GitHub include instructions for downloading it on its GitHub page.

For example, visit this GitHub page to see the documentation for the package **wesanderson**, which provides color palette themes based upon Wes Anderson's films. On this site, scroll down and you will find instructions for downloading the package. These instructions show you how to install this package from your R *Console*:

```
devtools::install_github("karthik/wesanderson")
```

Now go to your *Packages* tab in the bottom-right pane of RStudio, scroll down to find the **wesanderson** package, and click on it to check out its functions.

## Loading an installed package

There is a difference between *installed* and *loaded* packages. Go back to your *Packages* tab. Notice that some of the packages have a checked box next to their names, while others don't.

These checked boxes indicate which packages are currently *loaded*. All packages in the list are *installed* on your computer, but only the checked packages are *loaded*, i.e., ready for use.

To load a package, use the `library()` function.

```
library(fun)
library(wesanderson)
```

Now that your new packages are loaded, you can actually use their functions.

## Calling functions from a package

Most functions from external packages can be used by simply typing the name of the function. For example, the package `fun` contains a function for generating a random password:

```
random_password(length=24)
[1] "@c7dv0+{SAJ#W~<=w:&]Pj;/"
```

Sometimes, however, R can get confused if a new package contains a function that has the same name of some function from a different package. If R seems confused about a function you are calling, it can help to specify which package the function can be found in. This is done using the syntax `<package_name>::<function_name>`. For example, the following command is a fine alternative to the command above:

```
fun::random_password(length=24)
[1] "MtW|2]\\"sh+68,&K)30Yu75EU"
```

Note that this was done in the example above using the `devtools` package.

## Review: the workflow for using a package

To review how to use functions from a non-base package in R, follow these steps (examples provided):

1. Install the package

```
# Example from CRAN
install.packages("wesanderson")

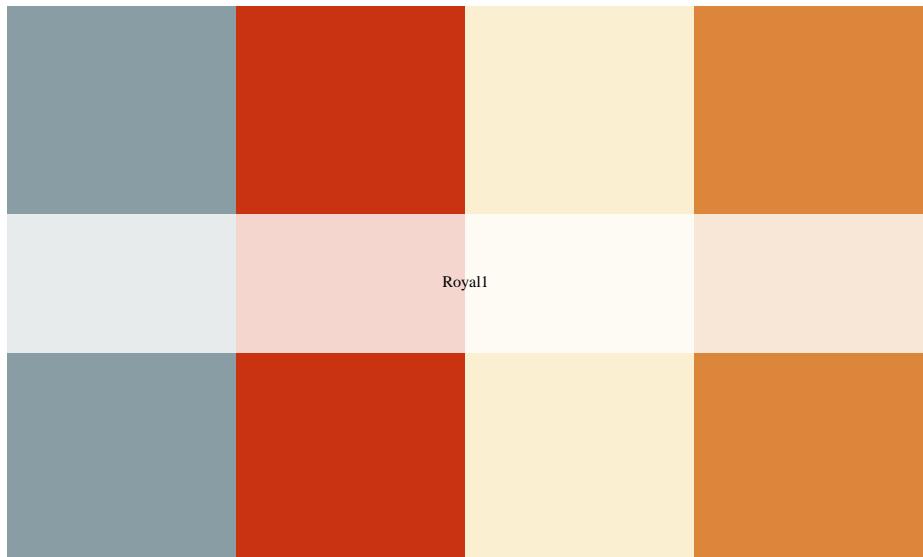
# Example from GitHub
devtools::install_github("karthik/wesanderson")
```

2. Load the package

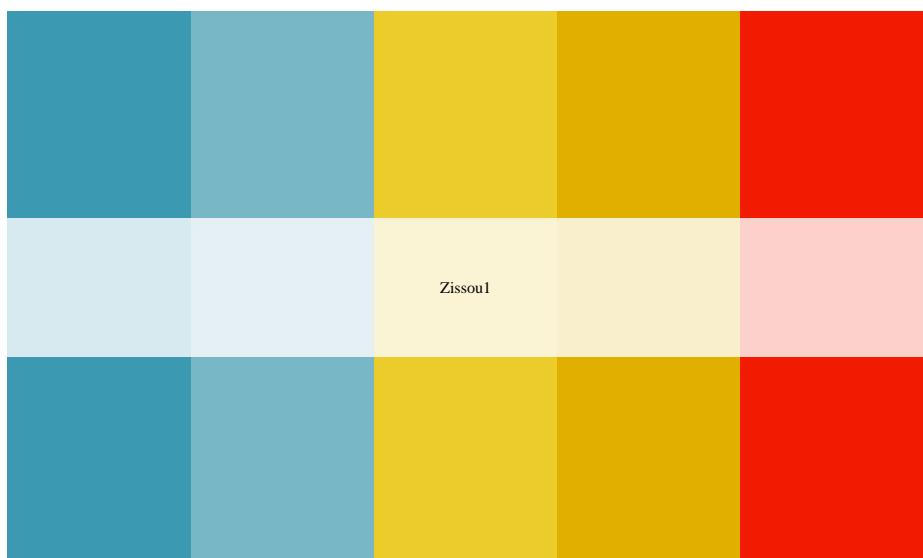
```
# Example
library(wesanderson)
```

3. Call the function.

```
wes_palette("Royal1")
```



```
wesanderson::wes_palette("Zissou1")
```



*(This function creates a plot displaying the different colors contained within the specified palette.)*

## A note on package dependencies

Most packages contain functions that are built using functions built from other packages. Those new functions depend on the functions from those other packages, and that's why those other packages are known as *dependencies*. When you install one function, you will notice that R typically has to install several other packages at the same time; these are the dependencies that allow the package of interest to function.

## A note on package versions

Packages are updated regularly, and sometimes new versions can break the functions that use it as a dependency. Sometimes you may have to install a new version (*or sometimes an older version!*) of a dependency in order to get your package of interest to work as desired.



# Chapter 13

## Basics of ggplot

(Refer heavily to <https://ggplot2-book.org/introduction.html>)

### Learning goals

- Understand what `ggplot2` is and why it's used
- Be able to think conceptually in the framework of the “grammar of graphics”
- Learn the syntax for creating different plots using `ggplot2`

### What is ggplot?

`ggplot2` is an R package. It's one of the most downloaded packages in the R universe, and has become the gold standard for data visualization. It's extremely powerful and flexible, and allows for creating lots of visualizations of different types, ranging from maps to bare-bones academic publications, to complex, paneled charts with labeling, etc. Because the syntax is so different from “base” R, it can give the impression of having a somewhat steep learning curve. But in reality, because the principles are so conceptually simple, learning is fairly fast. Generally those who choose to learn it stick with it; that is, once you go gg, you don't go back.

### The name and concept

“GG” stands for “grammar of graphics”, with “grammar” meaning “the fundamental principles or rules of an art or science” (Wickham, 2010). The most well-known “grammar of graphics” was written in 2005 and laid out some abstract principles for describing statistical graphics (Wilkinson, 2005). The basic

idea is that all graphs can be described using a *layered* grammar, and that all graphs have the same general elements...

- data
- geometric objects
- aesthetics (mapping) of variables to objects

... whereas some graphs have additional elements...

- statistical transformations
- scales
- facets

## A practical example

Let's get practical (we'll get back to the theory later).

First, let's read in some data on health from the World Bank:

Canvas Canvas + variables (mapping) Canvas + variables (mapping) + geometric objects

## Learning examples

### Perfecting the canvas

Adjust y / x limits

Add a different background

Change x / y labels

### Aesthetic attributes of the geoms

A scatterplot

Add a line of best fit

Add title / subtitle / caption

### Review assignment

*Note: Under construction!*

## Other resources

*Note: Under construction!*

## (PART) Basic R workflow



# Chapter 14

## Importing data

### Learning goals

- Understand what a `.csv` file is, and why they are important in data science
- How to format your data for easily importing data in R
- How to load, or “read”, your data into R
- How to set up your project directory and read data from other folders

To work with your own data in R, you need to load your data in R’s memory. This is called **reading in** your data.

Reading in data is simple and easy if your data are saved as a `.csv`, a comma-separated file. You can find functions for reading all sorts of file types into R, but the quickest way to begin working with your own data in R is to maintain that data in `.csv`’s.

### `.csv` files

When you preview a `.csv`, it looks something like this:

station	year	doy	sit	x	y	n	bhvr	id	i
Boat	2004	159	2004060701	-129.1875	53.101	NA	TR	BCY0470	
Boat	2004	189	2004070701	-129.1875	53.101	NA	BNF	BCX0361	
Boat	2004	196	2004071401	-129.1875	53.101	NA	BNF	BCX0361	
Boat	2004	196	2004071401	NA	NA	NA	BNF	BCX0711	
Boat	2004	200	2004071801	-129.1875	53.101	NA	BNF	BCX0275	
Boat	2004	209	2004072701	-129.194	53.1018	NA	MI-FE	BCY0321	
Boat	2004	216	2004080301	-129.1875	53.101	NA	BNF	BCY0049	
Boat	2004	216	2004080301	NA	NA	NA	BNF	BCX0255	
Boat	2004	217	2004080401	-129.1916	53.0696	NA	MI-FE	BCY0117	
Boat	2004	217	2004080401	NA	NA	NA	MI-FE	BCY0189	
Boat	2004	218	2004080501	-129.18067	53.0899	NA	BNF	BCX0083	
Boat	2004	218	2004080501	NA	NA	NA	BNF	BCX0231	
Boat	2004	219	2004080601	-129.1875	53.101	NA	BNF	BCY0013	
Boat	2004	221	2004080801	-129.1875	53.101	NA	TR	BCX0231	
Boat	2004	221	2004080801	NA	NA	NA	TR	BCX0121	
Boat	2004	223	2004081001	-129.1875	53.101	NA	TR	BCX0121	
Boat	2004	227	2004081401	-129.1875	53.101	NA	TR	BCX0171	
Boat	2004	228	2004081501	NA	NA	NA	TR	BCX0022	
Boat	2004	228	2004081502	NA	NA	NA	TR	BCX0121	
Boat	2004	229	2004081601	-129.1875	53.101	NA	TR	BCX0022	
Boat	2004	230	2004081701	-129.1875	53.101	NA	RE-TR	BCY0013	
Boat	2004	230	2004081701	NA	NA	NA	BNF	BCX0171	
Boat	2004	230	2004081701	NA	NA	NA	BNF	BCY0013	
Boat	2004	230	2004081701	NA	NA	NA	BNF	BCX0694	
Boat	2004	230	2004081703	NA	NA	NA	RE-TR	BCX0239	
Boat	2004	230	2004081704	NA	NA	NA	TR	BCY0117	
Boat	2004	231	2004081801	-129.194	53.1018	NA	MI-FE	BCX0567	
Boat	2004	231	2004081802	-129.237	53.068	NA	BNF	BCX0083	
Boat	2004	233	2004082001	NA	NA	NA	TR	BCX0174	
Boat	2004	235	2004082201	-129.1875	53.101	NA	TR	BCX0380	
Boat	2004	235	2004082201	NA	NA	NA	TR	BCX0380	

A neat spreadsheet of rows and columns.

When you open up this same dataset in a simple text editor, it looks like this:

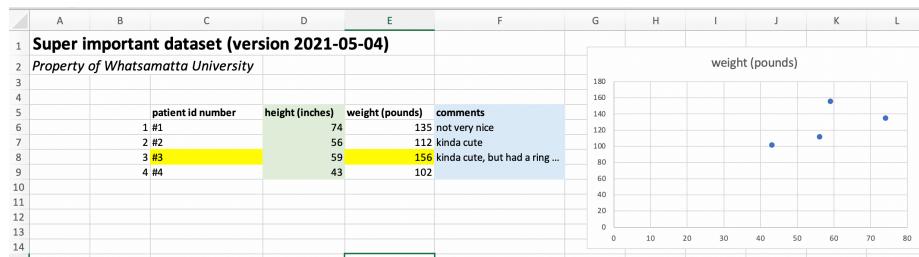
station,year,doy,sit,x,y,n,bhvr,id,name,stage,bhvr2,bhvr3,loc,conf,type,conf,month,dom,date,time
Boat,2004,159,2004060701,-129.1875,53.101,NA,TR,BCY0470,,A,TR,TR,0,1,6,7,6/7/04,16:35
Boat,2004,189,2004070701,-129.1875,53.101,NA,BNF,BCX0361,,F,BNF,BNF,0,1,7,7,7/7/04,13:33
Boat,2004,196,2004071401,-129.1875,53.101,NA,BNF,BCX0361,,F,BNF,BNF,0,1,7,14,7/14/04,14:55
Boat,2004,196,2004071401,NA,NA,BNF,BCX0711,,A,BNF,BNF,0,1,7,14,7/14/04,14:55
Boat,2004,200,2004071801,-129.1875,53.101,NA,BNF,BCX0275,,A,BNF,BNF,0,1,7,18,7/18/04,16:52
Boat,2004,209,2004072701,-129.194,53.1018,NA,MI-FE,BCY0321,,A,MI-FE,MI-FE,0,1,7,27,7/27/04,7:35
Boat,2004,216,2004080301,-129.1875,53.101,NA,BNF,BCY0049,,F,BNF,BNF,0,1,8,3,8/3/04,13:41
Boat,2004,216,2004080301,NA,NA,NA,BNF,BCX0255,,A,BNF,BNF,0,1,8,3,8/3/04,13:41
Boat,2004,217,2004080401,-129.1916,53.0696,NA,MI-FE,BCY0117,,A,MI-FE,MI-FE,0,1,8,4,8/4/04,12:50
Boat,2004,217,2004080401,NA,NA,NA,MI-FE,BCY0189,,F,MI-FE,MI-FE,0,1,8,4,8/4/04,12:50
Boat,2004,218,2004080501,-129.18067,53.0899,NA,BNF,BCX0083,,A,BNF,BNF,0,1,8,5,8/5/04,14:23
Boat,2004,218,2004080501,NA,NA,NA,BNF,BCX0231,,A,BNF,BNF,0,1,8,5,8/5/04,14:23
Boat,2004,219,2004080601,-129.1875,53.101,NA,BNF,BCY0013,,A,BNF,BNF,0,1,8,6,8/6/04,8:19
Boat,2004,221,2004080801,NA,NA,NA,TR,BCX0231,,A,TR,TR,0,1,8,8,8/8/04,12:28
Boat,2004,221,2004080801,NA,NA,NA,TR,BCX0121,,F,TR,TR,0,1,8,8,8/8/04,8:19
Boat,2004,223,2004081001,-129.1875,53.101,NA,TR,BCX0121,,F,TR,TR,0,1,8,10,8/10/04,13:13
Boat,2004,227,2004081401,-129.1875,53.101,NA,TR,BCX0171,,F,TR,TR,0,1,8,14,8/14/04,11:44
Boat,2004,228,2004081501,NA,NA,NA,TR,BCX0022,,A,TR,TR,0,1,8,15,8/15/04,11:44
Boat,2004,228,2004081502,NA,NA,NA,TR,BCX0121,,F,TR,TR,0,1,8,15,8/15/04,18:30
Boat,2004,229,2004081601,-129.1875,53.101,NA,TR,BCX0022,,A,TR,TR,0,1,8,16,8/16/04,9:00
Boat,2004,230,2004081701,-129.1875,53.101,NA,RE-TR,BCY0013,,A,RE-TR,RE-TR,0,1,8,17,8/17/04,7:10
Boat,2004,230,2004081701,NA,NA,NA,BNF,BCX0171,,F,BNF,BNF,0,1,8,17,8/17/04,11:50
Boat,2004,230,2004081701,NA,NA,NA,BNF,BCY0013,,A,BNF,BNF,0,1,8,17,8/17/04,11:50
Boat,2004,230,2004081701,NA,NA,NA,BNF,BCX0094,,A,BNF,BNF,0,1,8,17,8/17/04,11:50
Boat,2004,230,2004081703,NA,NA,NA,RE-TR,BCX0239,,M,RE-TR,RE-TR,0,1,8,17,8/17/04,14:00
Boat,2004,230,2004081704,NA,NA,NA,TR,BCY0117,,A,TR,TR,0,1,8,17,8/17/04,15:30
Boat,2004,231,2004081801,-129.194,53.1018,NA,MI-FE,BCX0567,,A,MI-FE,MI-FE,0,1,8,18,8/18/04,14:36
Boat,2004,231,2004081802,-129.237,53.068,NA,BNF,BCX0083,,A,BNF,BNF,0,1,8,18,8/18/04,14:06
Boat,2004,233,2004082001,NA,NA,NA,TR,BCX0174,,F,TR,TR,0,1,8,20,8/20/04,11:15
Boat,2004,235,2004082201,-129.1875,53.101,NA,TR,BCX0380,,A,TR,TR,0,1,8,22,8/22/04,16:09
Boat,2004,235,2004082201,NA,NA,NA,TR,BCX0380,,A,TR,TR,0,1,8,22,8/22/04,16:09
Boat,2004,236,2004082301,-129.1933,53.0527,NA,RE-TR,BCX0049,,F,RE-TR,RE-TR,0,1,8,23,8/23/04,10:30
Boat,2004,236,2004082303,-129.18067,53.0899,NA,MI-FE,BCX0380,,A,MI-FE,MI-FE,0,1,8,23,8/23/04,13:41
Boat,2004,239,2004082603,-129.237,53.068,NA,BNF,BCX0083,,A,BNF,BNF,0,1,8,26,8/26/04,8:05
Boat,2004,239,2004082605,-129.2113,53.077,NA,TR,BCZ0053,,F,TR,TR,0,1,8,26,8/26/04,9:00
Boat,2004,239,2004082605,-129.1875,53.101,NA,TR,BCZ0053,,F,RE-TR,RE-TR,0,1,8,26,8/26/04,19:12
Boat,2004,239,2004082605,NA,NA,NA,RE-TR,BCY0135,,A,RE-TR,RE-TR,0,1,8,26,8/26/04,19:12
Boat,2004,246,2004090201,-129.1933,53.0527,NA,RE-TR,BCX0049,,A,RE-TR,RE-TR,0,1,9,2,9/2/04,10:40
Boat,2004,246,2004090202,-129.1933,53.0527,NA,RE-TR,BCX0386,,A,RE-TR,RE-TR,0,1,9,2,9/2/04,10:45
Boat,2004,246,2004090203,NA,NA,NA,RE-TR,BCX0144,,A,RE-TR,RE-TR,0,1,9,2,9/2/04,11:00
Boat,2004,246,2004090203,NA,NA,NA,RE-TR,BCX0171,,F,RE-TR,RE-TR,0,1,9,2,9/2/04,11:00
Boat,2004,249,2004090501,-129.1875,53.101,NA,TR,BCY0347,,A,TR,TR,0,1,9,5,9/5/04,0:30
Boat,2004,251,2004090701,NA,NA,NA,TR,BCY0383,,A,TR,TR,0,1,9,7,9/7/04,11:00
Boat,2004,253,2004090902,-129.3198,53.0977,NA,BNF,BCY0013,,A,BNF,BNF,0,1,9,9,9/9/04,13:00
Boat,2004,253,2004090902,NA,NA,NA,BNF,BCX0239,,M,BNF,BNF,0,1,9,9,9/9/04,13:00
Boat,2004,253,2004090902,NA,NA,MI-FE,BCX0239,,C,MI,MI,0,1,9,9,9/9/04,13:00
Boat,2004,253,2004090903,-129.3032,53.0711,NA,TR,BCY0013,,A,TR,TR,0,1,9,9,9/9/04,14:20
Boat,2004,253,2004090903,NA,NA,NA,TR,BCX0171,,F,TR,TR,0,1,9,9,9/9/04,14:20
Boat,2004,253,2004090903,NA,NA,NA,TR,BCX0144,,F,TR,TR,0,1,9,9,9/9/04,14:20
Boat,2004,253,2004090904,-129.2002,53.0472,NA,BNF,BCX0711,,A,BNF,BNF,0,1,9,9,9/9/04,15:30
Boat,2004,254,2004091005,NA,NA,NA,TR,BCX0022,,A,TR,TR,0,1,9,10,9/10/04,15:30
Boat,2004,258,2004091401,-129.2002,53.0472,NA,TR,BCX0567,,A,TR,TR,0,1,9,14,9/14/04,12:12
Boat,2004,258,2004091402,-129.2002,53.0472,NA,BNF,BCY0277,,A,BNF,BNF,0,1,9,14,9/14/04,13:30
Boat,2004,258,2004091402,NA,NA,NA,BNF,BCY0013,,A,BNF,BNF,0,1,9,14,9/14/04,13:30

This looks scary, but it is actually really simple. A .csv is a simple text file in which each row is on a new line and columns of data are separated by commas. As a simple text file, there is no fancy formatting. There are no “Sheets” or “Tabs”, as you would find in GoogleSheets or Excel; it is a simple ‘flat’ file.

One of the major advantages of working with .csv’s is that the format is cross-platform and non-proprietary. That is, they work on Windows, Mac, Linux, and any other common type of computer, and they do not require special software to open.

## Data format requirements

For those of us used to working in *Excel* or *Numbers*, it will take some adjustment to get into the habit of formatting your data for R. We are used to seeing spreadsheets that look something like this:



To read a `.csv` into R without issues or fancy code, this spreadsheet will need to be simplified to look like this:

	A	B	C	D
1	patient_id	height_in	weight_lb	comments
2		1	74	135 not very nice
3		2	56	112 kinda cute
4		3	59	156 kinda cute but had a ring
5		4	43	102

## Workflow for formatting your data

Below is the general workflow for preparing your data for R is the following:

- 1. Get your data into `.csv` format.** In *Excel* and *Numbers*, you can use ‘Save As’ to change the file format. In *GoogleSheets*, you can ‘Download As’ a `.csv`. This will remove any colors, thick lines, special fonts, bold or italicized font styles, and any other special formatting. All that will be left is your data, and that’s the way R likes it.
- 2. Remove blank columns** before and in the middle of your data.
- 3. Remove elements such as graphs.**
- 4. Simplify your ‘header’.** The space above your data is your spreadsheet’s header. It includes column names and metadata like title, author, measurement units, etc. It is possible to read data with complex headers into R, but again we are going for simplicity here, so we suggest (1) simplifying your header to contain column names only, and (2) moving metadata to a `README.txt` file that lives in the same folder as your data.
- 5. Simplify column names.** Remove spaces, or replace them with `,`, `-` or `_`. Make your column names as simple and brief as possible while still being informative. Include units in the column names, as in the screenshot above. Be sure that each column has a name.
- 6. Remove all commas and hashtags from your dataset.** You can do this with the ‘Find & Replace’ feature built-into in most spreadsheet editors.

## Reading in data

The general workflow for reading in data is as follows:

1. In RStudio, set your working directory.
2. Place your data file in your working directory. (See the section below if you want to keep your data somewhere else.)
3. In your R script, read in your data file with one of the core functions below.

You can use this simple data file, , to practice.

## Core functions for reading data

To become agile in reading various types of data into R, there are three key functions you should know:

```
read.csv()
```

This is the base function for reading in a .csv.

```
df <- read.csv("super_data.csv")
```

This function reads in your data file as a dataframe. Save your dataset into R's memory using a variable (in this case, df).

```
df
  patient_id height_in weight_lb           comment
1          1       74      135    not very nice
2          2       56      112        kinda cute
3          3       59      156 kinda cute but had a ring
4          4       43      102            so small!
```

The `read.csv()` function has plenty of other inputs in the event that your data file is unable to follow the formatting rules outlined above (see `?read.csv()`). The three most common inputs you may want to use are `header`, `skip`, and `stringsAsFactors`.

- Use the `header` input when your data does not contain column names. *For example*, `header=FALSE` indicates that your datafile does not have any column names.
- Use the `skip` input when you want to skip some lines of metadata at the top of your file. This is handy if you really don't want to get rid of your metadata in your header. *For example*, `skip=2` skips the first two rows of the datafile before R begins reading data.
- Use the `stringsAsFactors` input when you want to make absolutely sure that R interprets any non-numeric fields as characters rather than factors. We have not focused on factors yet, but it can be frustrating when R

mistakes a column of character strings as a column factors. To avoid any possible confusion, use `stringsAsFactors=TRUE` as an input.

For example, here is how to read in this data without column names:

```
df <- read.csv("super_data.csv", skip=1, header=FALSE)
df
  V1 V2 V3           V4
1  1 74 135      not very nice
2  2 56 112      kinda cute
3  3 59 156 kinda cute but had a ring
4  4 43 102      so small!
```

If you do this without setting header to FALSE, your first row of data gets used as column names and it becomes a big ole mess:

```
df <- read.csv("super_data.csv", skip=1)
df
  X1 X74 X135           not.very.nice
1  2   56   112      kinda cute
2  3   59   156 kinda cute but had a ring
3  4   43   102      so small!
```

#### `readr::read_csv()`

This function, from a package named `readr`, becomes useful when you begin working with (1) data within the `tidyverse`, which you will be introduced to in the next module, and/or (2) very large datasete, since it reads data much more quickly and provides progress updates along the way.

When you use `read_csv()` instead of `read.csv()`, your data are read in as a `tibble` instead of a dataframe. You will be introduced to `tibbles` in the next module on dataframes; for the time being, think of a `tibble` as a fancy version of a dataframe that can be treated exactly as a regular dataframe.

```
df <- readr::read_csv("super_data.csv")
df
# A tibble: 4 x 4
  patient_id height_in weight_lb comment
    <dbl>     <dbl>     <dbl> <chr>
1         1       74      135 not very nice
2         2       56      112 kinda cute
3         3       59      156 kinda cute but had a ring
4         4       43      102 so small!
```

#### `readRDS()`

Another niche function for reading data is `readRDS()`. This function allows you to read in *R data objects*, which have the file extension `.rds`. These data objects

need not be in the same format as a `.csv` or even a dataframe, and that is what makes them so handy. A colleague could send you an `.rds` object of a vector, a list, a plotting function, or any other kind of R object, and you can read it in with `readRDS()`.

For example, contains a `tibble` version of the dataframe above. When you read in that `.rds` file, it is already formatted as a `tibble`:

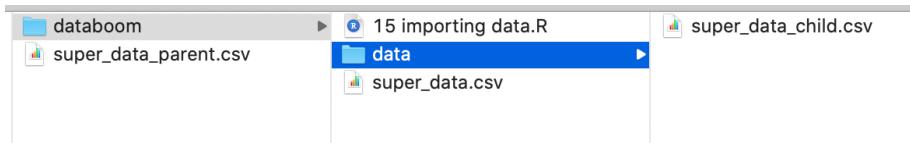
```
df <- readRDS("super_data.rds")
df
# A tibble: 4 x 4
  patient_id height_in weight_lb comment
    <dbl>      <dbl>     <dbl> <chr>
1         1        74       135 not very nice
2         2        56       112 kinda cute
3         3        59       156 kinda cute but had a ring
4         4        43       102 so small!
```

## Reading data from other folders

The data-reading functions above require only a single input: the *path* to your data file. This *path* is relative to the location of your working directory. When your data file is *inside* your working directory, the path simplifies to be the same as the filename of your data:

```
df <- read.csv("super_data.csv")
```

Sometimes, though, you will want to keep your data somewhere nearby but not necessarily *within* your working directory. Consider the following scenario, in which three versions of the “super\_data.csv” dataset occur near a working directory being used for this module:



We have a version within the same directory as our R file (i.e., our working directory), another version within a *child* folder within the directory (i.e., a subfolder), and another version in the *parent* folder of the working directory.

**To read a file from a *child* folder**, add the prefix, `./<child name>/`, to your command:

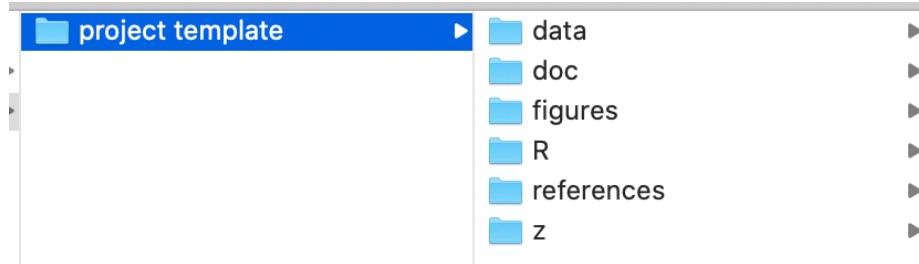
```
df <- read.csv("./data/super_data.csv")
```

**To read a file from a *parent* folder**, add the prefix, `../`, to your command:

```
df <- read.csv("./data/super_data.csv")
```

## Managing files

Now consider the following scenario, in which your project folder structure looks like this:



This structure can be an effective and simple way of organizing your files for a project, and we recommend using it.

Here's what these child folders should contain.

- `./data/` contains data, of course.
- `./doc/` contains documents, such as manuscript drafts.
- `./figures/` contains files for graphs and figures.
- `./R/` contains R scripts, of course.
- `./references/` contains journal articles and other resources you are using in your research.

Since your R code is going into the R child folder, that is what you should set your working directory for those R scripts to. In that case, *how to read data from the data folder*, which is a separate child folder of your parent folder?

Here's how:

```
df <- read.csv("../data/super_data.csv")
```

## Review exercise

*NOTE: Under construction!*

# Chapter 15

## Dataframes

### Learning goals

- Practice exploring, summarizing, and filtering dataframes
- Understand the importance of *tidy* datasets
- Understand what the `tidyverse` is and why it is awesome

In data science, the most common data structure you will be using – by far – is the **dataframe**. You were introduced to this data structure in Module 10, but a more familiar and detailed orientation is worthwhile.

### Subsetting & exploring dataframes

To explore dataframes, let's use a dataset on fuel mileage for all cars sold from 1985 to 2014.

```
library(fueleconomy)
data(vehicles)
head(vehicles)

# A tibble: 6 x 12
  id make model     year class trans drive      cyl displ fuel    hwy    cty
  <dbl> <chr> <chr>   <dbl> <chr> <chr> <chr> <dbl> <dbl> <chr> <dbl> <dbl>
1 13309 Acura 2.2CL/~/ 1997 Subcom~ Autom~ Front~~ 4  2.2 Regu~ 26  20
2 13310 Acura 2.2CL/~/ 1997 Subcom~ Manua~ Front~~ 4  2.2 Regu~ 28  22
3 13311 Acura 2.2CL/~/ 1997 Subcom~ Autom~ Front~~ 6  3   Regu~ 26  18
4 14038 Acura 2.3CL/~/ 1998 Subcom~ Autom~ Front~~ 4  2.3 Regu~ 27  19
5 14039 Acura 2.3CL/~/ 1998 Subcom~ Manua~ Front~~ 4  2.3 Regu~ 29  21
6 14040 Acura 2.3CL/~/ 1998 Subcom~ Autom~ Front~~ 6  3   Regu~ 26  17
```

A dataframe has rows of data organized into columns. In this dataframe, each

row pertains to a single vehicle make/model – i.e., a single *observation*. Each column pertains to a single *type* of data. Columns are named in the *header* of the dataframe.

All the same useful exploration and subsetting functions that applied to vectors now apply to dataframes (see module 10 for a refreshers). In addition to those functions you already know, we've added some new functions to your inventory of useful functions.

## Exploration

```
tail(vehicles) # head() and tail() summarize the beginning and end of the object
# A tibble: 6 x 12
  id make model year class trans drive cyl displ fuel hwy cty
  <dbl> <chr> <chr> <dbl> <chr> <chr> <dbl> <dbl> <chr> <dbl> <dbl>
1 28868 Yugo GV Plu~ 1990 Minico~ Manual~ Front~ 4 1.3 Regu~ 27 21
2 6635 Yugo GV Plu~ 1990 Subcom~ Manual~ Front~ 4 1.3 Regu~ 28 23
3 3157 Yugo GV/GVX 1987 Subcom~ Manual~ Front~ 4 1.1 Regu~ 29 24
4 5497 Yugo GV/GVX 1989 Subcom~ Manual~ Front~ 4 1.1 Regu~ 29 24
5 5498 Yugo GV/GVX 1989 Subcom~ Manual~ Front~ 4 1.3 Regu~ 28 23
6 1745 Yugo Gy/yug~ 1986 Minico~ Manual~ Front~ 4 1.1 Regu~ 29 22

names(vehicles) # get names of columns
[1] "id"      "make"    "model"   "year"    "class"   "trans"   "drive"   "cyl"     "displ"
[10] "fuel"    "hwy"     "cty"

nrow(vehicles) # get number of rows
[1] 33442

ncol(vehicles) # get number of columns
[1] 12
```

Note that `length()` does not work the same on dataframes as it does with vectors. In dataframes, `length()` is the equivalent of `ncol()`; it will *not* give you the number of rows in a dataset.

## Subsetting

Recall that dataframes are filtered by row and/or column using this format: `dataframe[rows,columns]`. To get the third element of the second column, for example, you type `dataframe[3,2]`.

```
vehicles[3,2]
# A tibble: 1 x 1
  make
  <chr>
1 Acura
```

Note that the comma is necessary even if you do not want to specify columns. If you try to type this ...

```
vehicles[3]
```

...R will assume you are asking for the third column, not the third row.

To filter a dataframe to multiple values, you can specify vectors for the `row` and `column`

```
vehicles[1:3,11:12] # can use colons
# A tibble: 3 x 2
  hwy   cty
  <dbl> <dbl>
1    26    20
2    28    22
3    26    18
vehicles[1:3,c(1,11:12)] # can use c()
# A tibble: 3 x 3
  id   hwy   cty
  <dbl> <dbl> <dbl>
1 13309    26    20
2 13310    28    22
3 13311    26    18
```

Columns can also be called according to their names. Use the \$ sign to specify a column.

```
vehicles$hwy[1:5]
[1] 26 28 26 27 29
```

Note that when you use a \$, you will not need to use a comma within your brackets. If you try to run this ...

```
vehicles$hwy[1:5,]
```

...R will throw a fit.

You can use logical tests to filter dataframes to rows that meet certain conditions. For example, to filter to only the rows for cars with better than 100 mpg, you can use this syntax:

```
keeps <- which(vehicles$hwy > 100)
keeps
[1] 6533 10613 10614 16429 16430 24487 24488 24489 28628
vehicles[keeps,]
# A tibble: 9 x 12
  id make   model   year class   trans   drive   cyl displ fuel     hwy   cty
  <dbl> <chr>  <chr>  <dbl> <chr>  <chr>  <chr>  <dbl> <dbl> <chr> <dbl> <dbl>
1 33640 Chevr~ Spark~  2014 Subcom~ Automa~ Front~     NA     NA Elec~    109    128
```

2	33396	Fiat	500e	2013	Minico~	Automa~	Front~	NA	NA	Elec~	108	122
3	34392	Fiat	500e	2014	Minico~	Automa~	Front~	NA	NA	Elec~	108	122
4	33265	Honda	Fit EV	2013	Small ~	Automa~	Front~	NA	NA	Elec~	105	132
5	33905	Honda	Fit EV	2014	Small ~	Automa~	Front~	NA	NA	Elec~	105	132
6	33558	Nissan	Leaf	2013	Midsiz~	Automa~	Front~	NA	NA	Elec~	102	129
7	34699	Nissan	Leaf	2014	Midsiz~	Automa~	Front~	NA	NA	Elec~	101	126
8	34918	Nissan	Leaf	2015	Midsiz~	Automa~	Front~	NA	NA	Elec~	101	126
9	33307	Scion	iQ EV	2013	Minico~	Automa~	Front~	NA	NA	Elec~	105	138

But the above is a long-winded way of doing this. You can also achieve this result as follows:

```
vehicles[which(vehicles$hwy > 100),]
```

You can also get the same result without the `which()` function:

```
vehicles[vehicles$hwy > 100,]
```

The logical test is returning a bunch of TRUEs and FALSEs, one for each row of `vehicles`. Only the TRUE rows will be returned.

### Exercise 1: Reading for errors

What is wrong with these commands? Why will each of them throw an error if you run them, and how can you fix them?

```
# 1
vehicles[1,15,]

# 2
vecihles[1:5,]

# 3
vehicles$hwy[1:5,]

# 4
vehicles[1:5,1:13]
```

### Summarizing

The same summary functions that you have used for vectors work for dataframes, such as:

```
min(vehicles$hwy)
[1] 9
max(vehicles$hwy)
[1] 109
```

```
mean(vehicles$cty)
[1] 17.491
```

You can also use the `summary()` function, which provides summary statistics for each column in your dataframe:

```
summary(vehicles)
      id          make         model        year
Min. : 1  Length:33442  Length:33442  Min. :1984
1st Qu.: 8361  Class :character  Class :character  1st Qu.:1991
Median :16724  Mode  :character  Mode  :character  Median :1999
Mean   :17038
3rd Qu.:25265
Max.   :34932

      class        trans        drive       cyl
Length:33442  Length:33442  Length:33442  Min.  : 2.000
Class :character  Class :character  Class :character  1st Qu.: 4.000
Mode  :character  Mode  :character  Mode  :character  Median : 6.000
                                         Mean   : 5.772
                                         3rd Qu.: 6.000
                                         Max.  :16.000
                                         NA's   :58

      displ        fuel        hwy        cty
Min.  :0.000  Length:33442  Min.  : 9.00  Min.  : 6.00
1st Qu.:2.300  Class :character  1st Qu.:19.00  1st Qu.:15.00
Median :3.000  Mode  :character  Median :23.00  Median :17.00
Mean   :3.353
3rd Qu.:4.300
Max.   :8.400
NA's   :57
```

The function `unique()` returns unique values within a column:

```
unique(vehicles$fuel)
[1] "Regular"                  "Premium"
[3] "Diesel"                   "Premium or E85"
[5] "Electricity"              "Gasoline or E85"
[7] "Premium Gas or Electricity" "Gasoline or natural gas"
[9] "CNG"                      "Midgrade"
[11] "Regular Gas and Electricity" "Gasoline or propane"
[13] "Premium and Electricity"
```

Finally, the `order()` function helps you sort a dataframe according to the values in one of its columns.

```

vehicles_sorted <- vehicles[order(vehicles$hwy), #sort dataframe by highway mileage
                           c(2,3,4,10:12)] # only keep certain columns
head(vehicles_sorted)
# A tibble: 6 x 6
  make       model      year fuel     hwy   cty
  <chr>     <chr>    <dbl> <chr>   <dbl> <dbl>
1 Aston Martin Lagonda 1985 Regular     9     7
2 Aston Martin Lagonda 1985 Regular     9     7
3 Aston Martin Saloon/Vantage/Volante 1985 Regular     9     7
4 Aston Martin Saloon/Vantage/Volante 1985 Regular     9     7
5 Rolls-Royce Camargue 1987 Regular     9     7
6 Rolls-Royce Continental 1987 Regular     9     7

```

Reverse the order by wrapping `rev()` around the `order()` call:

```

vehicles_sorted <- vehicles[rev(order(vehicles$hwy)),
                           c(2,3,4,10:12)]
head(vehicles_sorted)
# A tibble: 6 x 6
  make       model      year fuel     hwy   cty
  <chr>     <chr>    <dbl> <chr>   <dbl> <dbl>
1 Chevrolet Spark EV 2014 Electricity 109    128
2 Fiat      500e      2014 Electricity 108    122
3 Fiat      500e      2013 Electricity 108    122
4 Scion     iQ EV     2013 Electricity 105    138
5 Honda     Fit EV    2014 Electricity 105    132
6 Honda     Fit EV    2013 Electricity 105    132

```

## Building dataframes

To create a new dataframe, use the `data.frame()` function.

	car	mpg_hwy	mpg_city
100	Acura Legend	23	15
101	Acura Legend	22	17
102	Acura Legend	23	16
103	Acura Legend	21	16
104	Acura Legend	22	17
105	Acura Legend	23	16
106	Acura Legend	24	16

Note how the columns were named in the `data.frame()` call, and that each column is separated by a comma.

You can also stage an empty dataframe, which sounds useless but will become very useful as you start working with `for` loops and other higher-order R tools.

```
df <- data.frame()
df
data frame with 0 columns and 0 rows
```

To coerce an object into a format that R interprets as a dataframe, use `as.dataframe()`:

```
df <- as.data.frame(vehicles)
df[1:4,1:4]
  id make      model year
1 13309 Acura 2.2CL/3.0CL 1997
2 13310 Acura 2.2CL/3.0CL 1997
3 13311 Acura 2.2CL/3.0CL 1997
4 14038 Acura 2.3CL/3.0CL 1998
```

You can bind multiple dataframes together using `rbind()`:

```
df1 <- data.frame(name=c("Ben", "Joe", "Eric", "Isabelle"), instrument=c("Nose harp", "Concertina", "Ukelele"))
df1
  name instrument
1 Ben   Nose harp
2 Joe   Concertina
3 Eric   Ukelele
4 Isabelle Drums

df2 <- data.frame(name=c("Matthew"), instrument=c("Washboard"))
rbind(df1, df2)
  name instrument
1 Ben   Nose harp
2 Joe   Concertina
3 Eric   Ukelele
4 Isabelle Drums
5 Matthew Washboard
```

Note that to be combined, two dataframes have to have the exact same number of columns and the exact same column names.

The only exception to this is adding a dataframe with content an empty dataframe. That can work, and that will be helpful in the *R Toolbag* modules ahead.

```
df <- data.frame() # stage empty dataframe
df1 <- data.frame(name=c("Ben", "Joe", "Eric", "Isabelle"), instrument=c("Nose harp", "Concertina", "Ukelele"))
df <- rbind(df, df1)
df
  name instrument
1 Ben   Nose harp
2 Joe   Concertina
```

```
3   Eric    Ukelele
4 Isabelle Drums
```

### Exercise 2: Subsetting and filtering

#### A. Subset one field according to a logical test

With no more than two lines of code, get the number of Honda cars in the `vehicles` dataset.

#### B. Subset one field according to a logical test for a different field.

In a single line of code, show the mileages of all the Toyotas in the dataset.

#### C. Subset a dataframe to a single subgroup

In a single line of code, determine how many different car makes/models were produced in 1995.

#### D. Get the mean value for a subgroup of data

What is the average city mileage for Subaru cars in the dataset?

#### E. Subset a dataframe to only data from between two values

According to this dataset, how many different car makes/models have been produced with highway mileages between 30 and 40 mpg?

## Tidy data

*(Joe writes the remainder of this chapter)*

<https://r4ds.had.co.nz/tidy-data.html>

## Tibbles

*NOTE: Under construction!*

## Tidyverse

*NOTE: Under construction!*

## Tidy transformations

### Mutating

### Grouping

### Arranging

### Review exercise

*NOTE: Under construction!*

# Chapter 16

## Exporting data & plots

### Learning goals

- How to save dataframes as .csv's
- How to save R data objects as .rds's
- How to save plots as .pdf's and .png's

To practice exporting data, let's use the built-in dataset from package `babynames`.

```
install.packages("babynames")
library(babynames)
data(babynames)
```

### `write.csv()`

To write a dataframe to a .csv, use the function `write.csv()`.

```
write.csv(babynames,file="my_babynames.csv",quote=FALSE,row.names=FALSE)
```

This dataset will be saved as the file, `my_babynames.csv` within your parent directory. You can set other destinations using the same rules for child paths, parent paths, and absolute paths from the module on **Importing Data**.

The code above sets a couple parameters that preserves the neat formatting of your dataframe. We recommend using these inputs each time you use `write.csv()` to save a dataframe.

## saveRDS()

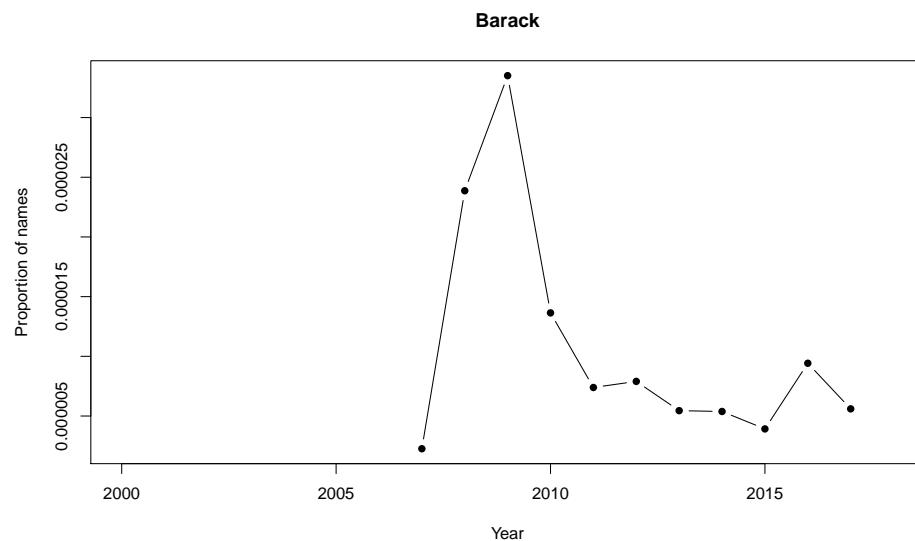
The `saveRDS()` function saves R objects in the `.rds` format, which makes them easier and faster to read into R later on.

```
saveRDS(babynames,file="my_babynames.rds")
```

## pdf() and png()

Let's say you want to plot the prevalence of the name "Barack" in recent U.S history:

```
head(babynames)
# A tibble: 6 x 5
  year sex   name      n    prop
  <dbl> <chr> <chr> <int>  <dbl>
1 1880 F     Mary    7065 0.0724
2 1880 F     Anna    2604 0.0267
3 1880 F     Emma    2003 0.0205
4 1880 F     Elizabeth 1939 0.0199
5 1880 F     Minnie   1746 0.0179
6 1880 F     Margaret 1578 0.0162
baracks <- babynames[babynames$name=="Barack",]
plot(prop~year,data=baracks,
  type="b",pch=16,
  xlim=c(2000,2018),
  xlab="Year",ylab="Proportion of names",main="Barack")
```



To save this as a figure as a `pdf`, preface these lines of code with a `pdf()`

command and add `dev.off()` below those lines. This opens up a `pdf` ‘device’ (i.e., an engine for creating a PDF file), prints the plot to that new file, then closes the device and saves the file.

Saving a pdf:

```
pdf("barack-years.pdf",width=6,height=4)
plot(prop~year,data=baracks,
     type="b",pch=16,
     xlim=c(2000,2018),
     xlab="Year",ylab="Proportion of names",main="Barack")
dev.off()
```

Make sure you add ‘.pdf’ to the end of your filename, and try not to run the `dev.off()` command when you have not first run the `pdf` command. If you do, R will think you are turning off the plotting feature in RStudio and you will have to restart your R session in order to see any more plots.



# Chapter 17

## Exploring data

### Learning goals

- How to go about exploring a dataset and understanding the distribution of your data
- How to produce beautiful histograms and violin plots

Once you get your dataset into R, the first thing you will probably want to do is explore. Until you understand what your data look like, it is difficult to know how to analyze it. **Exploratory data analysis** is the process of becoming familiar with your data - its sample size, its distribution, its central tendencies, and its variation. This module shows you how.

To practice exploring datasets, we will use one of *AirBnB* listings in Amsterdam (go here and download `listings.csv.gz` under the Amsterdam section).

```
# Checkout what the data look like
# use t() to make it easier to read (t = transpose)
t(head(df,1))
  1
id      "2818"
name    "Quiet Garden View Room & Super Fast WiFi"
host_id "3159"
host_name "Daniel"
neighbourhood_group NA
neighbourhood   "Oostelijk Havengebied - Indische Buurt"
latitude     "52.36435"
longitude    "4.94358"
room_type     "Private room"
price        "59"
```

```

minimum_nights           "3"
number_of_reviews         "278"
last_review                "2020-02-14"
reviews_per_month          "1.9"
calculated_host_listings_count "1"
availability_365           "152"

# How much data do we have?
nrow(df)
[1] 17825

```

## Exploring distributions

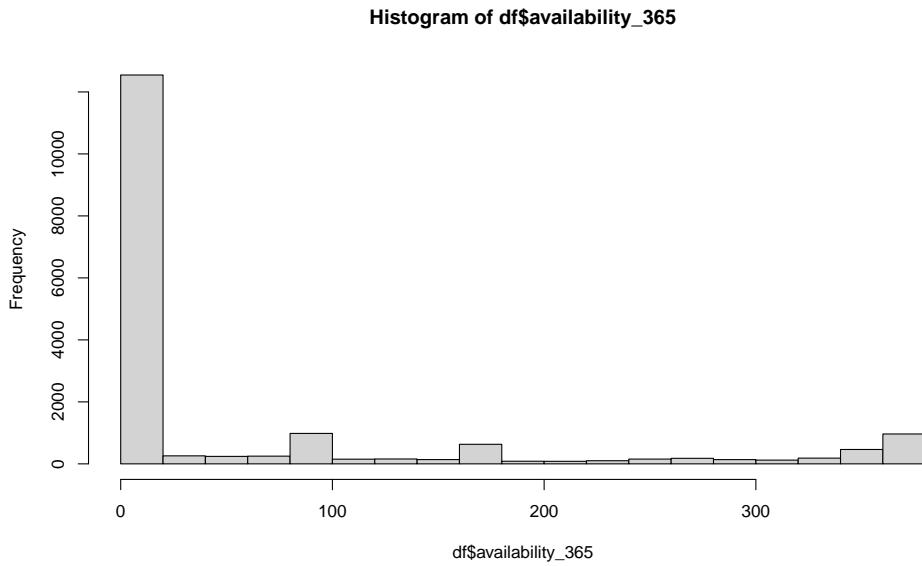
One of the first steps in your data exploration will be to visualize your dataset. There are two main plot types for doing so: **histograms** and **violin plots**.

### Histograms

A histogram sorts your data into bins and counts the number of data points in each bin.

Make histograms in R using the `hist()` function:

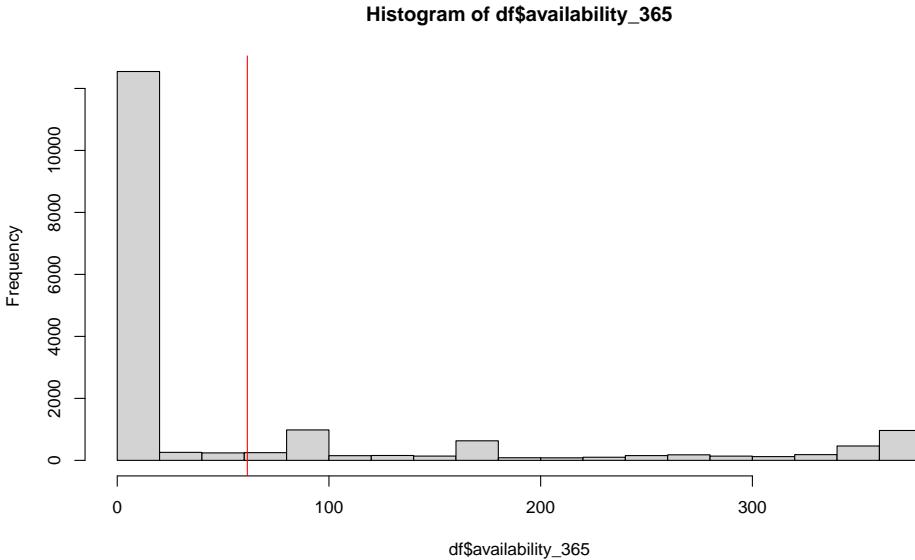
```
hist(df$availability_365)
```



This is a histogram of the number of nights the listings are available for reservation. In a quick glance, you can see that most listings are available for only a few nights, while a small portion have a wide variety of availabilities.

Think about how much more helpful this image is than a simple sample mean. To illustrate that value, let's plot the mean onto this histogram.

```
hist(df$availability_365)
abline(v= mean(df$availability_365), col="red")
```

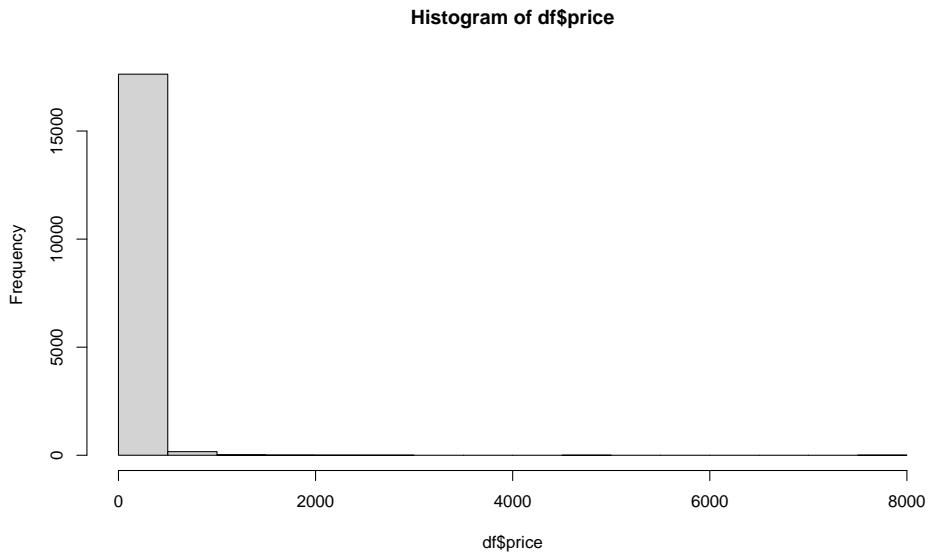


The average value of this dataset is nowhere near the most common values (1 - 20 nights), nor does it capture the fact that there are some listings available for the entire year. **Punchline:** a lot of rich insight is lost when taking an average, which is why a histogram is more useful for displaying distributions than bar graphs (which only show the mean).

### Prettifying histograms

Let's take a look at another variable: the price of lodging per night.

```
hist(df$price)
```

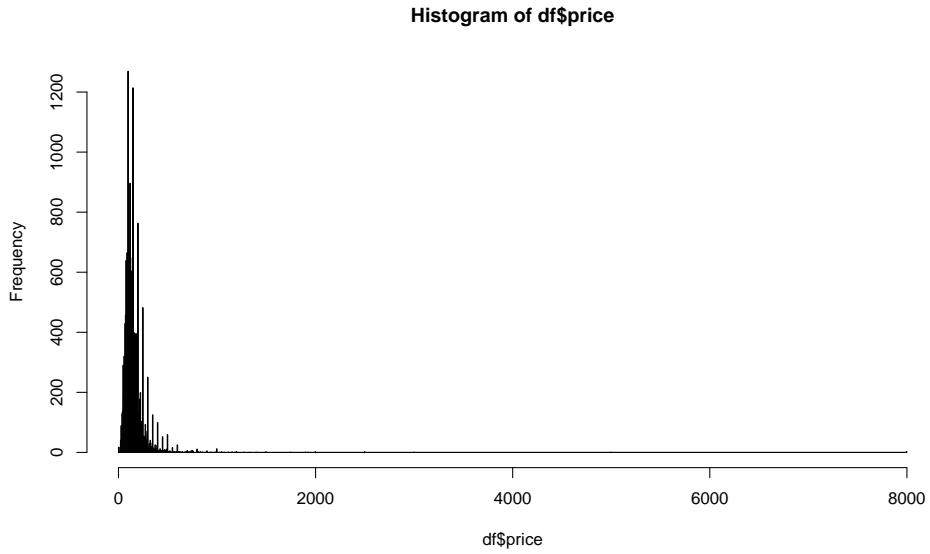


Not a very pretty plot. Since the range in prices is so wide, the default parameters for the `hist()` will need some tweaking.

To make this histogram prettier, first let's manually set the number of "breaks", i.e., the cutoff values for each bin along the x-axis.

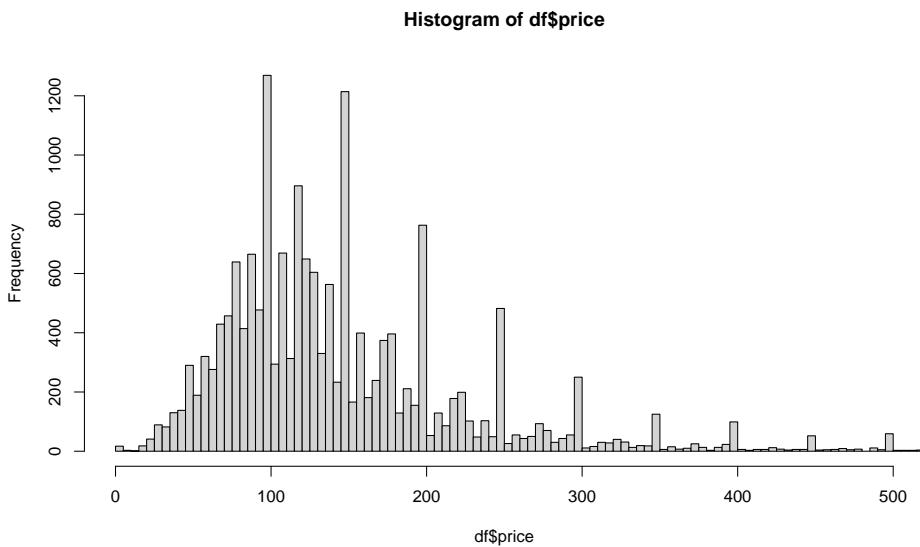
```
# Calculate breaks -- make each bin one day
breaks <- seq(0,max(df$price),by=5)

hist(df$price,
     breaks=breaks)
```



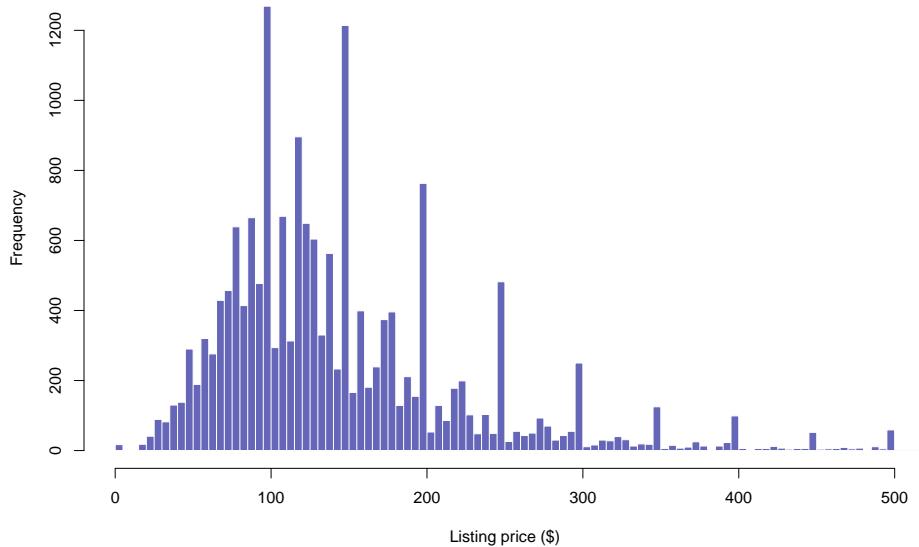
That's better. Let's zoom in on the most common values using `xlim()`.

```
hist(df$price,
     breaks=breaks,
     xlim=c(0,500))
```



Finally, let's improve the labels and colors.

```
par(mar=c(4.2,4.2,.5,.5))
hist(df$price,
     breaks=breaks,
     xlim=c(0,500),
     xlab="Listing price ($)",
     main=NULL,
     col=adjustcolor("darkblue",alpha.f=.6),
     border=adjustcolor("white",alpha.f=.1),
     )
```

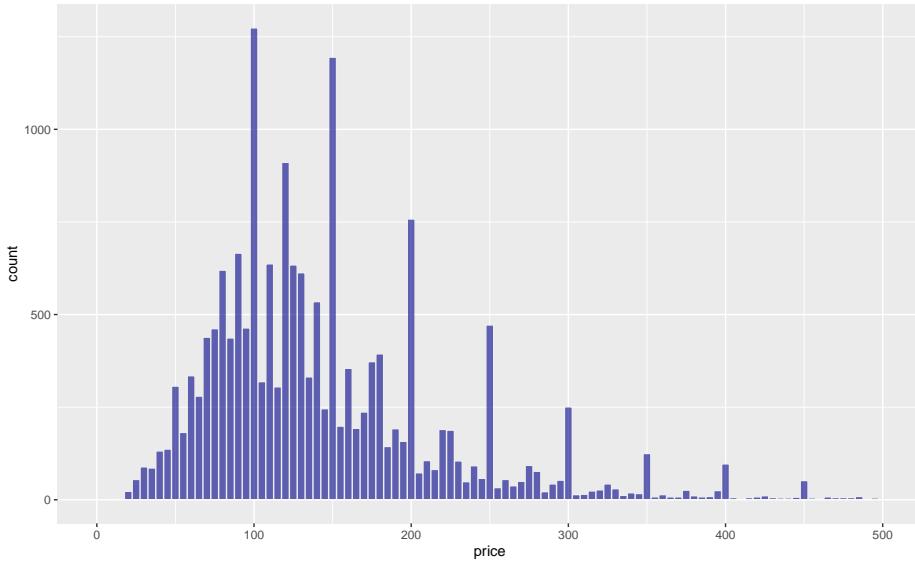


Interesting spikes in the histogram. Why do you think those are occurring? That is a really interesting feature of the dataset that you might never have discovered if you had not plotted your histogram.

### Histograms in ggplot2

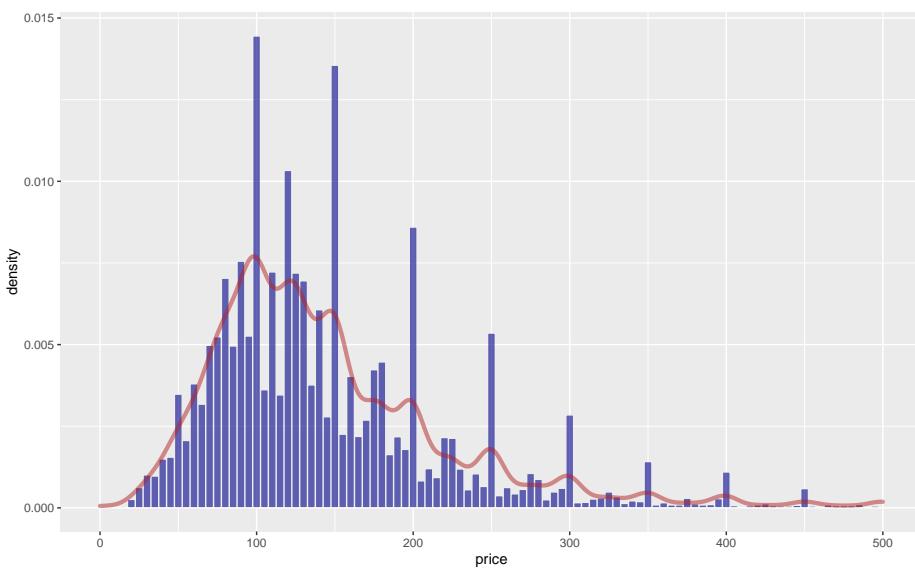
To produce a histogram of the same data in `ggplot2`, use the following code:

```
library(ggplot2)
ggplot(df, aes(x=price)) +
  xlim(0,500) +
  geom_histogram(binwidth=5,
    fill=adjustcolor("darkblue",alpha.f=.6),
    color=adjustcolor("white",alpha.f=.1))
```



`ggplot2` allows you to add some other nice features to histograms, such as a smoothed “density” line:

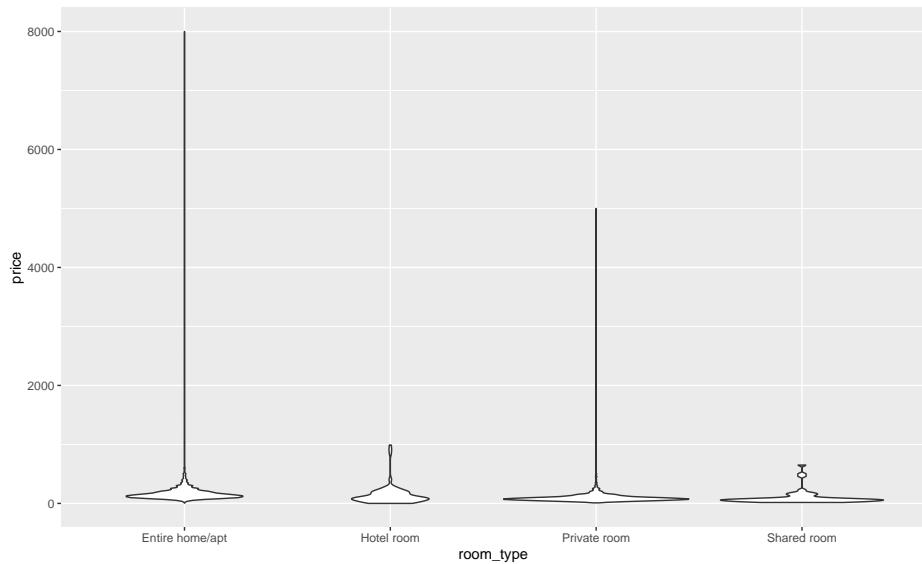
```
ggplot(df, aes(x=price)) +
  xlim(0,500) +
  geom_histogram(binwidth=5,
    fill=adjustcolor("darkblue",alpha.f=.6),
    color=adjustcolor("white",alpha.f=.1),
    aes(y=..density..)) +
  geom_density(alpha=.1,lwd=1.5,col=adjustcolor("firebrick",alpha.f=.5))
```



## Violin Plots

The second most valuable plot for exploring distributions is the **violin plot**.

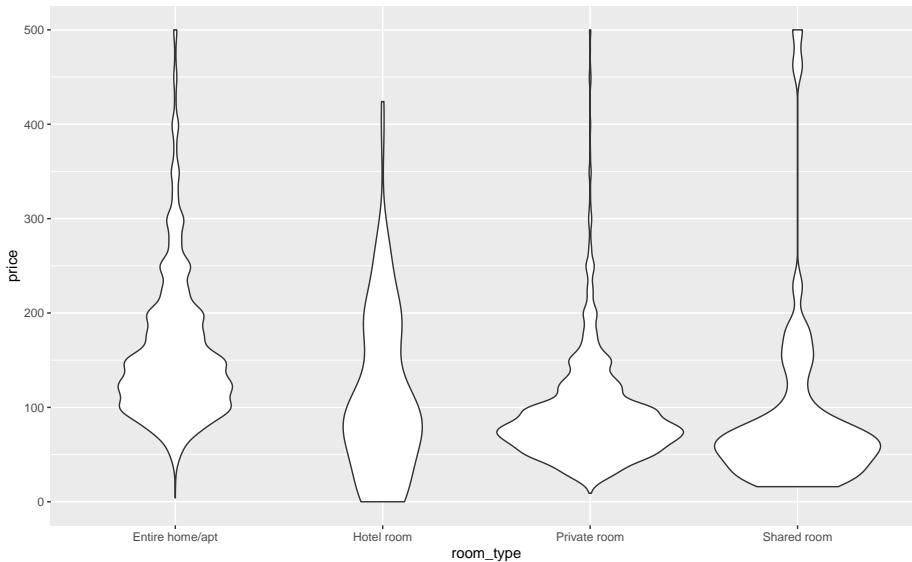
```
ggplot(df, aes(x=room_type,
                y=price)) +
  geom_violin()
```



Violin plots are like *vertical histograms*. Their width indicates where most of your data are clustered, and the shapes also take the shape of a violin – hence the name. Their height shows you your data’s range. Think of a violin plot as the beautiful child of bar graphs and histograms: the best of both worlds.

A major advantage of violin plots is that they allow you two compare multiple distributions with ease. Let’s adjust our `ylim()` to zoom in:

```
ggplot(df,
       aes(x=room_type,
           y=price)) +
  ylim(0,500) +
  geom_violin()
```



If your research question were, “Which type of listing tends to be most affordable?”, think about how easy that is to answer using a plot like this!

## Descriptive statistics

In the Module on Calling Functions, you have already seen some functions for summarizing the trends and variation in your data:

- `mean()`
- `median()`
- `sd()` (standard deviation)
- `summary()` provides descriptive statistics for each column in a dataframe.

Here are a few more:

`var()` provides the sample variance, which is related to standard deviation:

```
var(df$price)
[1] 23766.1
```

`MeanCI()`, from the package `DescTools`, provides 95% confidence intervals for the most common data distributions.

```
install.packages("DescTools")

library(DescTools)
MeanCI(df$price)
  mean    lwr.ci    upr.ci
154.4959 152.2326 156.7592
```

And here are some other useful functions that need not be introduced in detail now. You will encounter them soon.

- `table()` Counts the number of instances of each unique value in a vector.
- `quantile()` Provides the quantiles of a dataset.
- `ecdf()` Plots the empirical cumulative distribution function for a dataset.

### Review exercise

For this exercise, use this dataset on the sale prices of homes in the United States. You can download that dataset directly into R using the following code:

```
library(readr)
df <- readr::read_csv("https://raw.githubusercontent.com/rashida048/Datasets/master/hor...
```

**17.0.0.0.1 Task 1** Create a beautiful histogram of home prices included in this dataset. Only show houses that sold for less than \$2 million USD.

**17.0.0.0.2 Task 2** Create a violin plot that shows the distribution of sale prices for homes with different numbers of bedrooms.

**17.0.0.0.3 Task 3** This task is a bit of review, and a bit of a preview to the next module.

First, create a scatter plot that depicts the relationship between the square footage of a home's living space and its sale price. Do the same for the square footage of the home's lot. Which square footage appears to be a better predictor of sale price?

# Chapter 18

## Significance statistics

### Learning goals

- How to interpret p-values
- How to decide which statistical test to apply to your data
- How to conduct basic significant tests in R
- How to interpret the results of those tests

### p-values

We won't go into statistical theory here. But every statistical test, at the basic level, is asking whether the patterns we observe in our data are actually *meaningful*. Are those *perceived* patterns reflecting *real* patterns, or is it possible to perceive those patterns when the underlying process is purely random chance?

That is what a **p-value** tells you: the probability that the pattern you see in your data is actually the product of random, meaningless chance. The lower the p-value, the less likely it is that the pattern is a product of chance, and the higher the chances that the pattern is real.

Researchers tend to use a p-value of 0.05 as the threshold for a meaningful, or "**significant**" pattern. When a statistical test returns a p-value of 0.05 or less, we consider the pattern to be statistically significant. A p-value of 0.05 means that there is a 5% chance (one in twenty) that the pattern in your data is the product of chance alone.

Please note that there is nothing magical about this number – a p-value of 0.049 is practically the same as 0.051, but only the former would be considered significant. The 0.05 threshold is just a simple heuristic – a way of simplifying your statistical results into a binary concept: significant or not.

Finally, please also note that statistical significance is a tricky thing because it is influenced by *both* the patterns in your data as well as by the *amount* of data you are working with. A larger sample size is going to allow you to identify more nuanced patterns in your data, and those patterns will achieve a lower p-value thanks simply to the number of samples you have.

Conversely, a pattern driven by meaningful real-world processes can be obscured by low sample sizes. If your sample size is too small, you may not be able to produce significant p-values even though the pattern is real.

## Tests for different data types

Most data come in two general forms:

1. **Categorical data** represent categories. For example, we could have a variable named `pet` with a few discrete levels: “dog”, “cat”, etc. The types, or *levels*, of categorical data are also referred to as *treatments*. In R, categorical variables are usually referred to as *factors*.
2. **Continuous data** represent numerical values. For example, let `height` be a variable representing numerical values for people’s height. Note that, for the time being, we will consider integers and count data to fall within this category.

Whenever you plot data or ask a statistical question, you are combining data types in a specific way: a bar graph, for example, compares two *categories* (i.e., the individual bars) of *numerical* data (i.e., bar height). And, by grouping the data by category, you are implying that the category to which a data point belongs has some impact on its value. In other words, the value is **dependent** upon the category. Conversely, the value is assumed to have no impact on category. Category, therefore is the **independent** variable.

Each combination of data types calls for a certain type of plot and a certain type of statistical test.

Here is an overview of what we will cover below:

Question	Independent	Dependent	Test	Plot
Comparing 2 datasets	Categorical	Numerical	t-test	Bar graph or
Comparing 3 or more datasets	Categorical		ANOVA + Tukey HSD	
	Categorical	Categorical	Chi-square	
Association / Relationship	Numerical	Numerical	Regression	Scatterplot

## Comparison tests

To practice basic statistics, we will create our own fake data.

**Scenario:** You are the lead author on a landmark study that investigates the portion sizes in fast food restaurants. You place 50 orders of large fries from one franchise and 50 orders from another, then weigh each order.

We can create a fake dataset by drawing numbers from random distributions:

```
# Set starting point for random number generator
set.seed(2)

# Franchise 1
sample1 <- rnorm(n=50, mean=1, sd=.15)

# Franchise 2
sample2 <- rnorm(n=50, mean=1.1, sd=.15)
```

You can see that we have made these two datasets using slightly different distributions: the mean for Franchise 1 is 1.0 and the mean for Franchise 2 is 1.1. So we know the truth: that these two distributions are, in fact, slightly different. The question is whether we can *conclude* that they are different given the relatively small sample sizes ( $n=50$ ) we are working with.

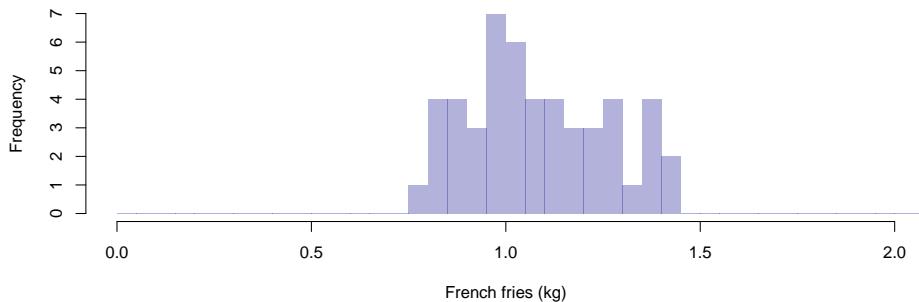
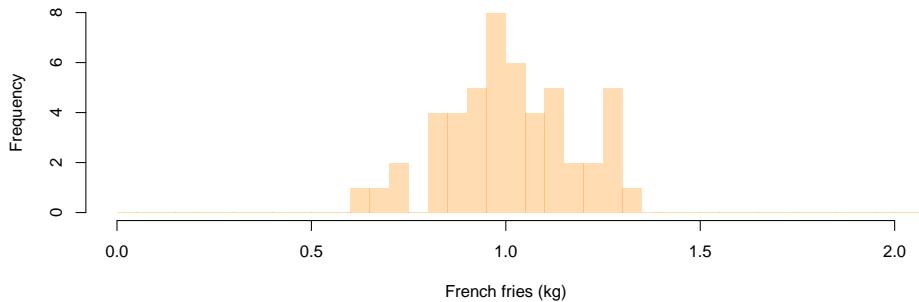
So for now, let's pretend we don't know what the *true* means of these two sample sets are. Let's pretend that all we have done is weighed and eaten a ton of french fries, and now we want to ask some research questions about our sample data.

First, we want to know if there a difference in the amount of food you get from these two franchises? Do the two franchises give you the same amount of food (by weight)? This is a **comparison question**. We are asking: based on our samples, can we conclude that two things (Franchise 1 and Franchise 2) are meaningfully different?

**First, Let's look at our data with some histograms.**

```
par(mfrow=c(2,1))
hist(sample1,
      breaks=seq(0,10,by=.05),
      col=adjustcolor("dark orange",alpha.f=.3),
      border=NA,
      main=NULL,xlab="French fries (kg)",xlim=c(0,2))

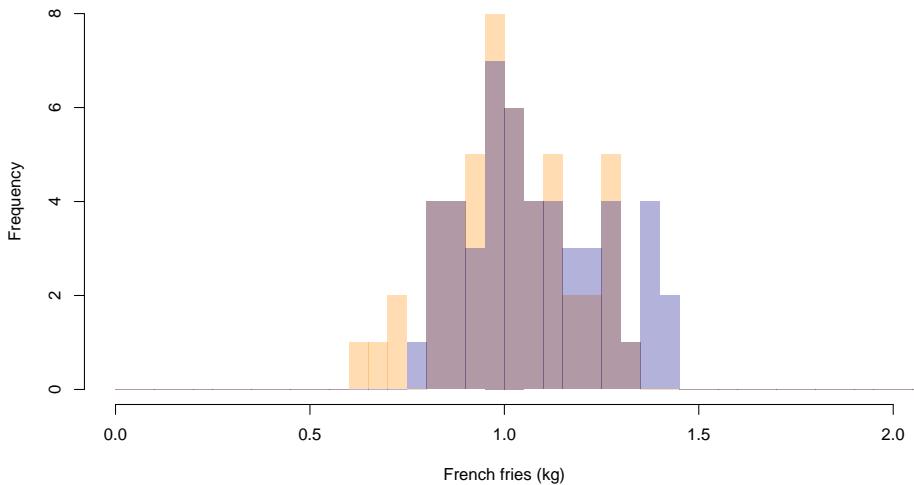
hist(sample2,
      breaks=seq(0,10,by=.05),
      col=adjustcolor("darkblue",alpha.f=.3),
      border=NA,
      main=NULL,xlab="French fries (kg)",xlim=c(0,2))
```



Comparison tests ask whether two distributions are different. It is often easier to gauge that difference when you superimpose one distribution on top of another (we do this by adding `add=TRUE` as an input in the second histogram).

```
hist(sample1,
  breaks=seq(0,10,by=.05),
  col=adjustcolor("dark orange",alpha.f=.3),
  border=NA,
  main=NULL,xlab="French fries (kg)",xlim=c(0,2))

hist(sample2,
  breaks=seq(0,10,by=.05),
  col=adjustcolor("darkblue",alpha.f=.3),
  border=NA,
  main=NULL,xlab="Price",xlim=c(0,2),
  add=TRUE)
```



Okay, these two distributions certainly *look* a bit different, but there is also a high degree of overlap. If we lumped these data together and randomly picked a value from the pile, it would be hard to predict which franchise the data point belongs to.

To add to our uncertainty, maybe the pattern we are seeing here is just a vestige of our relatively low sample size. What if we sampled another 200 restaurants? Are we confident that we would find this same pattern?

Better do a statistical test.

Since these data are normally distributed, the test to use in this scenario is the **t-test**.

```
t.test(sample1,
       sample2)

Welch Two Sample t-test

data: sample1 and sample2
t = -2.0099, df = 97.711, p-value = 0.0472
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-0.139213875 -0.000884483
sample estimates:
mean of x mean of y
1.010371 1.080420
```

This function provides you with a p-value. Based on this p-value, what is your answer to the research question?

## Influence of sample size

To highlight the influence of sample size on your statistical results, let's re-do the analysis above, this time with a larger sample size.

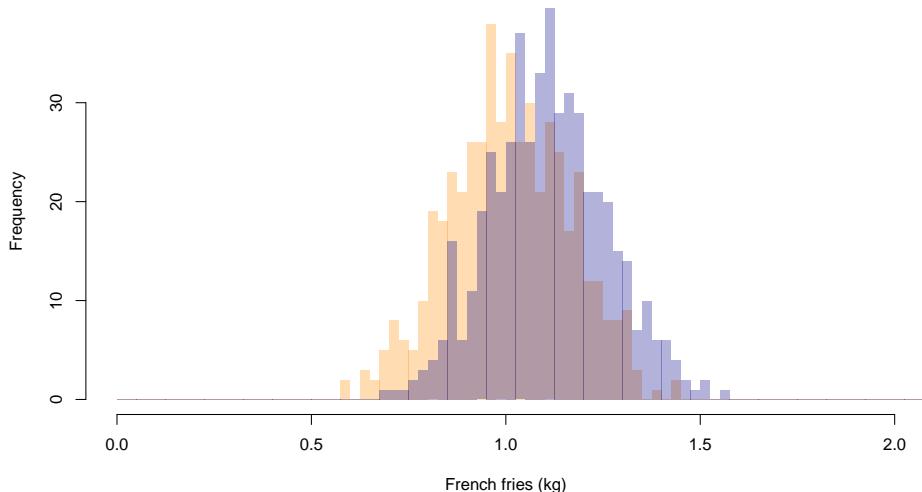
```
# Use same starting point as above
set.seed(2)

# Franchise 1
sample1 <- rnorm(n=500, mean=1, sd=.15)

# Franchise 2
sample2 <- rnorm(n=500, mean=1.1, sd=.15)

hist(sample1,
      breaks=seq(0,10,by=.025),
      col=adjustcolor("dark orange",alpha.f=.3),
      border=NA,
      main=NULL,xlab="French fries (kg)",xlim=c(0,2))

hist(sample2,
      breaks=seq(0,10,by=.025),
      col=adjustcolor("darkblue",alpha.f=.3),
      border=NA,
      main=NULL,xlab="Price",xlim=c(0,2),
      add=TRUE)
```



```
t.test(sample1,
       sample2)
```

```
Welch Two Sample t-test
```

```

data: sample1 and sample2
t = -10.39, df = 996.87, p-value < 0.00000000000000022
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-0.11899609 -0.08118775
sample estimates:
mean of x mean of y
1.009254 1.109346

```

The p-value is now *much* lower! Note that we drew our samples from the *exact same* underlying distributions. But, since we drew many more samples in this second round, the *t-test* was better able to assess the significance of the differences we were seeing between the two sample sets.

## Comparing more than two groups

When you are comparing numerical data in more than two categories, you need to use an **ANOVA**.

Let's say you go out and sample a *third* fast food franchise:

```

# Set starting point for random number generator
set.seed(2)

# Franchise 1
sample1 <- rnorm(n=50, mean=1, sd=.15)

# Franchise 2
sample2 <- rnorm(n=50, mean=1.1, sd=.15)

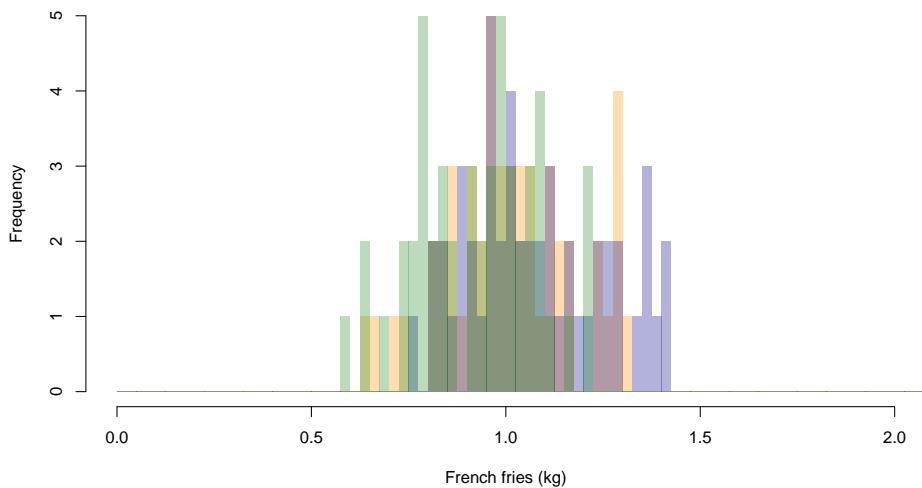
# Franchise 3
sample3 <- rnorm(n=50, mean=0.9, sd=.15)

hist(sample1,
      breaks=seq(0,10,by=.025),
      col=adjustcolor("dark orange",alpha.f=.3),
      border=NA,
      main=NULL,xlab="French fries (kg)",xlim=c(0,2))

hist(sample2,
      breaks=seq(0,10,by=.025),
      col=adjustcolor("darkblue",alpha.f=.3),
      border=NA,
      main=NULL,xlab="Price",xlim=c(0,2),
      add=TRUE)

```

```
hist(sample3,
  breaks=seq(0,10,by=.025),
  col=adjustcolor("forestgreen",alpha.f=.3),
  border=NA,
  main=NULL,xlab="Price",xlim=c(0,2),
  add=TRUE)
```



What a mess! This might be easier to read if we use a **bar graph** instead of layered histograms. (We will add 95% confidence intervals for each bar using the package `DescTools` – be sure to install this package before running this code).

```
install.packages("DescTools")

# Get vector of bar heights
means <- c(mean(sample1),mean(sample2),mean(sample3))

# Get vector of 95% confidence intervals
library(DescTools)
lower_ci <- c(MeanCI(sample1)[2],
  MeanCI(sample2)[2],
  MeanCI(sample3)[2])

upper_ci <- c(MeanCI(sample1)[3],
  MeanCI(sample2)[3],
  MeanCI(sample3)[3])

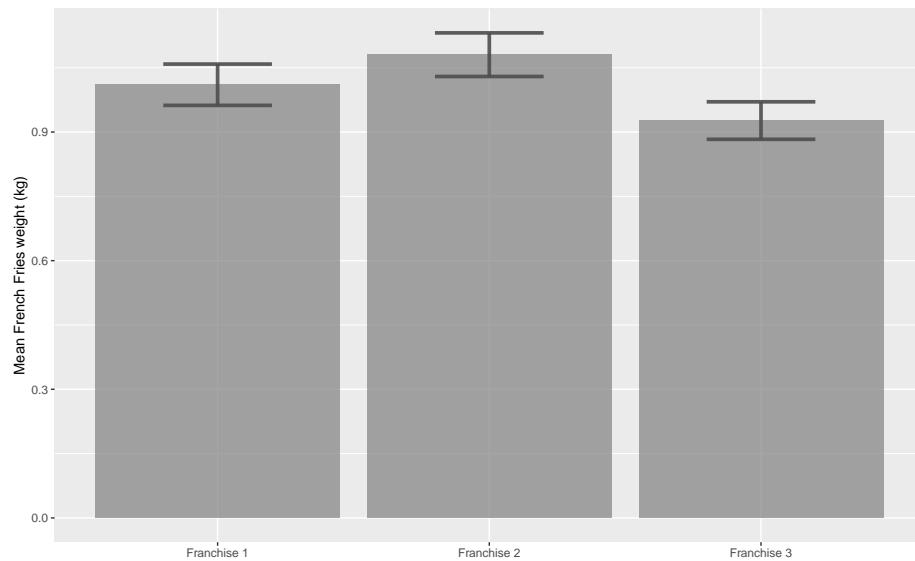
# Create data frame
df <- data.frame(name=paste("Franchise",1:3),
  means,
  lower_ci,
```

```

upper_ci)

# Most basic error bar
library(ggplot2)
ggplot(df) +
  geom_bar( aes(x=name, y=means), stat="identity", fill="grey50", alpha=0.7) +
  geom_errorbar( aes(x=name, ymin=lower_ci, ymax=upper_ci),
                 width=0.4, colour="grey30", alpha=0.9, size=1.3) +
  ylab("Mean French Fries weight (kg)") +
  xlab(NULL)

```



Bar graphs are easier to read, but they do throw about a lot of information. By reducing your samples to a single number (i.e., the sample mean), you are missing out on a lot of interesting detail. Which means that, even though these bars do seem to be of different heights, we better use a statistical test to be sure that these differences are significant.

When we are comparing more than two groups, our question becomes, “Are *any* of these groups different from one another?”

In R, the function for conducting an ANOVA test is `aov()`:

```

Df Sum Sq Mean Sq F value    Pr(>F)
as.factor(franchise)   2  0.592  0.29581   10.51 0.0000542 ***
Residuals              147  4.138  0.02815
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Our p-value is low, which means there are differences between groups. But the

ANOVA doesn't actually tell us which of the pairwise (i.e., two-way) differences are significant. For that we need a follow up test: a *Tukey's HSD test*.

```
TukeyHSD(my_ANOVA)
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = fries ~ as.factor(franchise), data = df_all)

$`as.factor(franchise)`
   diff      lwr       upr     p adj
2-1  0.07004918 -0.009396617  0.149494974 0.0958929
3-1 -0.08358643 -0.163032225 -0.004140635 0.0366717
3-2 -0.15363561 -0.233081404 -0.074189813 0.0000293
```

According to this result, the only sample sets that are statistically different from each other are samples 2 and 3. This makes sense, given our low sample sizes and the innately small differences among the three underlying distributions.

## Comparing categorical counts

Your colleagues have taken an interest in your fast food analyses. One of them wishes to work on an extension study regarding rates of Ketchup packet handouts. Is one franchise more likely to give you free Ketchup with your fries than another?

You go back to your notes and realize that you do indeed have data on ketchup handouts!

```
# (Well, let's fake the data here)

# Setup sample 1
# Create a list of random values between 0 and 1, the same length as sample1
set.seed(2)
randoms <- runif(n=length(sample1),min=0,max=1)

# Stage a `ketchup` vector, the same length as sample1, of all No's
ketchup <- rep("No",times=length(sample1))

# For all indices whose random number is above 0.55, change Ketchup status to Yes.
ketchup[which(randoms > .55)] <- "Yes"

df1 <- data.frame(franchise=1,ketchup)
head(df1)
franchise ketchup
1          1      No
2          1      Yes
3          1      Yes
```

```

4      1      No
5      1      Yes
6      1      Yes

# Repeat for sample 2
set.seed(3)
randoms <- runif(n=length(sample1),min=0,max=1)
ketchup <- rep("No",times=length(sample2))
ketchup[which(randoms > .65)] <- "Yes"
df2 <- data.frame(franchise=2,ketchup)
head(df2)
  franchise ketchup
1          2      No
2          2      Yes
3          2      No
4          2      No
5          2      No
6          2      No

# Combine into single dataframe
study <- rbind(df1,df2)

```

So you pass these data to your colleague and she uses them to produce this summary table:

```

table(study)
  ketchup
franchise No Yes
  1 28 22
  2 39 11

```

This 2x2 table is known as a *contingency table*. It summarizes the interaction of two *categorical* variables (Franchise ID and Ketchup status). To test for differences in ketchup handout rates with these data, we would use a different test called a *Chi-squared test*.

```

# Use the contingency table as input
cst <- chisq.test(table(study))

# Check out results
cst$p.value
[1] 0.03344526
cst$residuals
  ketchup
franchise      No      Yes
  1 -0.9502553 1.3540064
  2  0.9502553 -1.3540064

```

How to interpret:

- Since the p-value of our test is less than 0.05, we conclude that there is indeed a difference in the ketchup handout rates between these two franchises.
- The *positive residuals* indicate positive association: Franchise 1 is less likely to give ketchup.
- The *negative residuals* indicate negative association: Franchise 2 is more likely to give out ketchup.

## Tests of association

Another colleague of yours wants to conduct a separate follow-up study: she suspects there might be a relationship between *how many fries* are included in an order and the *perceived saltiness* of the order. Her hypothesis is that each order is given the same volume of salt. When that salt is distributed across *more* fries, the perceived saltiness of each individual fry declines.

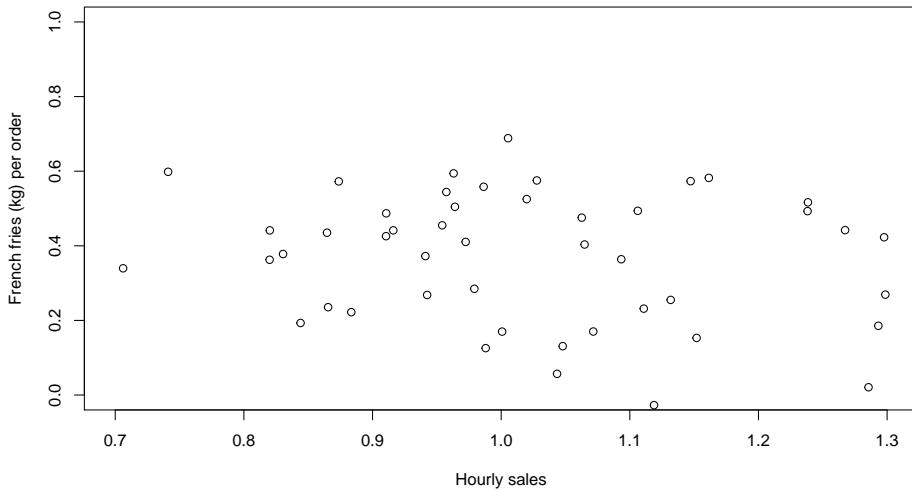
You go back to your notes and realize that you do indeed have data on perceived saltiness!

```
# (Well, let's fake the data here)
variability <- rnorm(n=length(sample1),mean=0,sd=.2)
saltiness <- -0.25*sample1 + .6 + variability # y = mx + b + e
```

You pass your colleague the `saltiness` data associated with each sample you collected from Franchise 1. Saltiness is scored from 0 to 1.

Let's check out this data. Since we are now exploring the relationship between two numerical variables, we visualize them with a scatter plot.

```
plot(saltiness ~ sample1,
      ylab="French fries (kg) per order",
      xlab="Hourly sales",
      xlim=c(0.7,1.3),ylim=c(0,1))
```



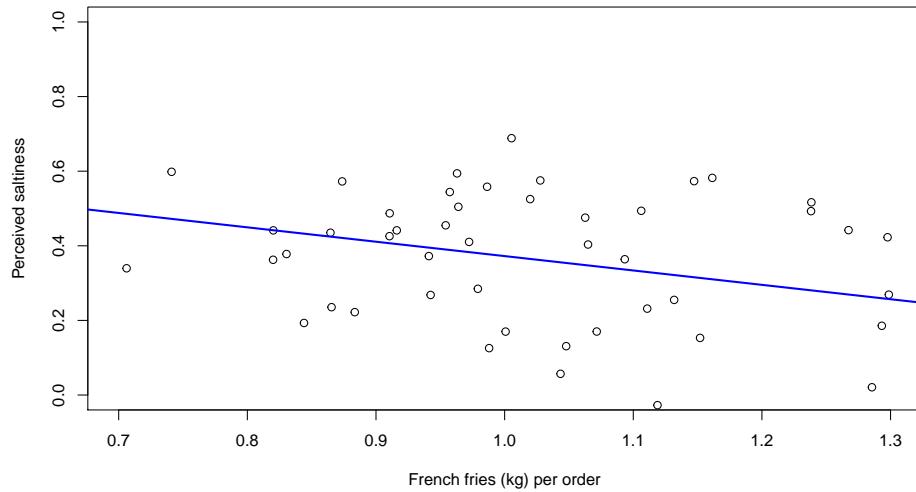
This plot, with French fries on the x-axis, visually implies that saltiness is a function of French Fries weight. Therefore, saltiness is treated as the dependent variable.

Is there a significant relationship between these two variables? We can test that using a **linear regression**, also known as a *linear model*. In R, the function for computing a linear model is `lm()`.

```
salt_lm <- lm(saltiness ~ sample1)
```

*Huzzah!* First, let's add this trend line to our plot:

```
plot(saltiness ~ sample1,
      xlab="French fries (kg) per order",
      ylab="Perceived saltiness",
      xlim=c(0.7,1.3), ylim=c(0,1))
abline(salt_lm, col="blue", lwd=2)
```



Let's interpret the outcome of this linear regression:

```
summary(salt_lm)

Call:
lm(formula = saltiness ~ sample1)

Residuals:
    Min      1Q  Median      3Q     Max 
-0.43303 -0.14105  0.02311  0.15437  0.31810 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 0.7578     0.1564   4.847 0.0000136 ***
sample1     -0.3854     0.1527  -2.524   0.015 *  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.1811 on 48 degrees of freedom
Multiple R-squared:  0.1172,    Adjusted R-squared:  0.09881 
F-statistic: 6.373 on 1 and 48 DF,  p-value: 0.01495
```

- The **Coefficient Estimate** of `sample` is the slope of the trendline. If that estimate were 0.00, the linear model is indicating that there is no relationship between the dependent and independent variables.
- **Adjusted R-squared** indicates the percent of the data's variation “explained” by the trendline. Essentially, this metric compares the average distance of each data point from the trend line to their average distance from a flat line, with a slope of 0.00.

- `p-value` indicates the probability that there is no relationship (i.e., a slope of 0.00).

## Reporting results

When you report the results of your statistical tests within your reports and figure captions, be sure to include the following information:

**t-tests:**

- Type of test used (i.e., t-test)
- Sample sizes of each category
- `p-value`

**ANOVAs:** - Type of test used (i.e., ANOVA)

- Sample sizes of each category
- `df` (i.e., degrees of freedom)
- `p-value`

**Chi-square tests:**

- Type of test used (i.e., Chi-square)
- Sample sizes of each category
- `df` (i.e., degrees of freedom)
- `p-value`

**Linear regressions:**

- Type of test used (i.e., linear regression)
- Sample size
- `p-value`
- R-squared coefficient

For tips on writing these results statements, see the Module on Writing Style for Reports.

### Review exercise

To review these concepts, we will use the same dataset from the previous module: *AirBNB* hosts in Amsterdam.

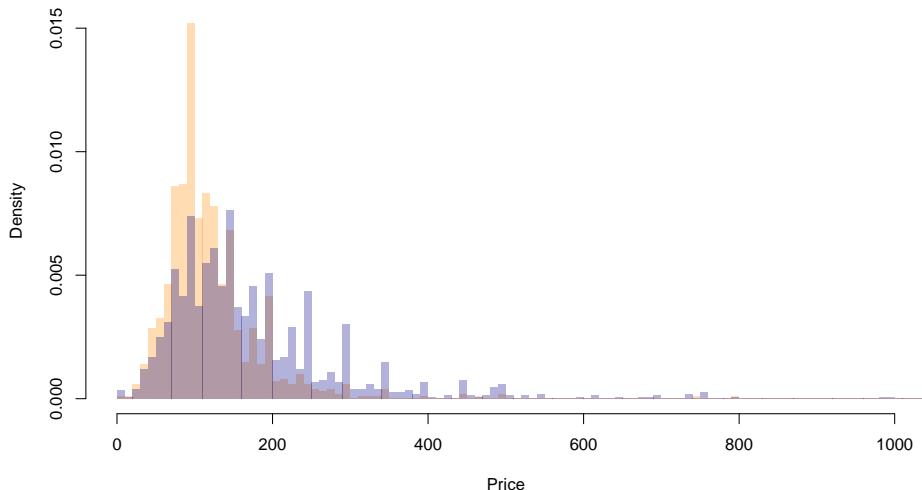
```
df <- read.csv("./data/airbnb-amsterdam.csv")
```

**18.0.0.0.1 Task 1** Two neighborhoods in Amsterdam, “Bos en Lommer” and “Centrum-Oost”, are among the most popular *AirBnB* destinations in the city. But are these two neighbourhoods equally affordable, or does one neighborhood tend to be more expensive?

(a) First, produce a single histogram with the price distributions of listings from these two neighborhoods superimposed upon one another.

```
library(dplyr)
hood1 <- df %>% filter(neighbourhood == "Bos en Lommer")
hood2 <- df %>% filter(neighbourhood == "Centrum-Oost")

hist(hood1$price,
      breaks=seq(0,3000,by=10),
      col=adjustcolor("dark orange",alpha.f=.3),
      border=NA,probability=TRUE,
      main=NULL,xlab="Price",xlim=c(0,1000))
hist(hood2$price,
      breaks=seq(0,3000,by=10),
      col=adjustcolor("darkblue",alpha.f=.3),
      border=NA,probability=TRUE,
      main=NULL,xlab="Price",xlim=c(0,1000),
      add=TRUE)
```



(b) Then conduct a statistical test to answer the task's question.

```
t.test(hood1$price,hood2$price)
```

#### Welch Two Sample t-test

```
data: hood1$price and hood2$price
t = -13.331, df = 2226.1, p-value < 0.0000000000000022
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-65.10065 -48.40420
sample estimates:
mean of x mean of y
```

123.2717 180.0242

- (c) Now properly interpret the test, and write a complete results statement.

**18.0.0.0.2 Task 2** Which neighborhood is more likely to offer a `Private room` instead of an `Entire home/apt`?

- (a) First, produce a single bar graph with the number of room types offered in each neighborhood.

- (b) Then conduct a statistical test to answer the task's question.

```
df1 <- data.frame(hood=hood1$neighbourhood,room=hood1$room_type)
df2 <- data.frame(hood=hood2$neighbourhood,room=hood2$room_type)
df_all <- rbind(df1,df2)
df_all <- df_all %>% filter(room %in% c("Private room","Entire home/apt"))
table(df_all)

            room
hood      Entire home/apt Private room
Bos en Lommer        876       133
Centrum-Oost         1071       402
cst <- chisq.test(table(df_all))
cst$p.value
[1] 0.0000000000000006998397
cst$residuals

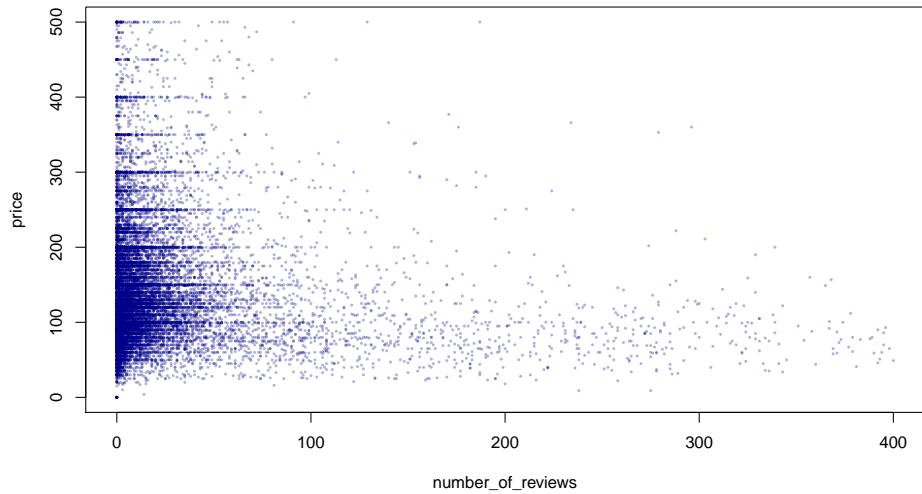
            room
hood      Entire home/apt Private room
Bos en Lommer        3.003223    -5.729196
Centrum-Oost        -2.485603     4.741742
```

- (c) Now properly interpret the test, and write a complete results statement.

**18.0.0.0.3 Task 3** Do listings with more reviews tend to be more expensive? For this analysis, focus on listings priced less than \$500 and less than 400 reviews.

- (a) First, produce a single plot that properly visualizes the data.

```
dfsub <- df[df$price <= 500,]
dfsub <- dfsub[dfsub$number_of_reviews <= 400,]
plot(price ~ number_of_reviews,
  data=dfsub,
  cex=.4,pch=16,
  col=adjustcolor("darkblue",alpha.f=.3),
  ylim=c(0,500))
```

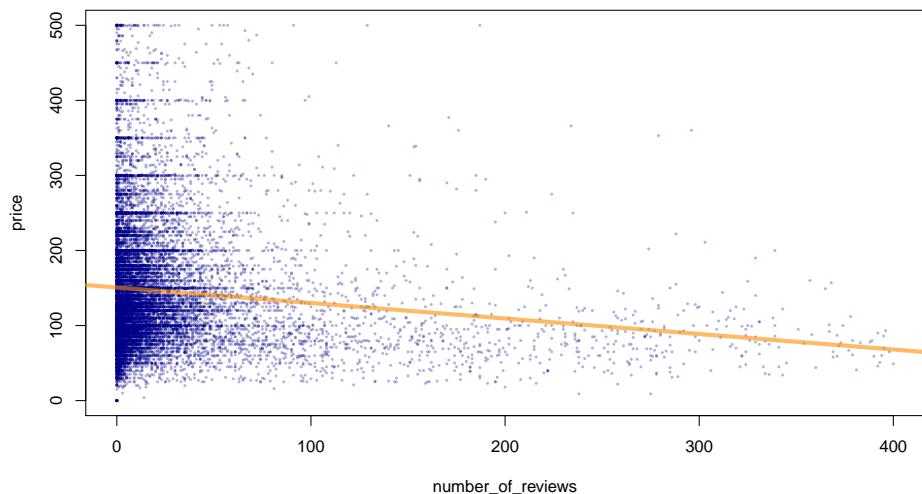


(b) Then conduct a statistical test to answer the task's question.

```
price_lm <- lm(dfsub$price ~ dfsub$number_of_reviews)
```

(c) Add this trendline to your plot.

```
plot(price ~ number_of_reviews,
     data=dfsub,
     cex=.4,pch=16,
     col=adjustcolor("darkblue",alpha.f=.3),
     ylim=c(0,500))
abline(price_lm,col=adjustcolor("dark orange",alpha.f=.6),lwd=4)
```



(d) Now properly interpret the test, and write a complete results statement.

```
summary(price_lm)
```

Call:

```
lm(formula = dfsub$price ~ dfsub$number_of_reviews)
```

Residuals:

Min	1Q	Median	3Q	Max
-150.69	-50.69	-18.84	31.53	387.92

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	150.69465	0.65775	229.10	<0.0000000000000002 ***
dfsub\$number_of_reviews	-0.20649	0.01334	-15.48	<0.0000000000000002 ***

---

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

Residual standard error: 78.02 on 17552 degrees of freedom

Multiple R-squared: 0.01347, Adjusted R-squared: 0.01341

F-statistic: 239.6 on 1 and 17552 DF, p-value: < 0.0000000000000022



## (PART) Essential R skills



# Chapter 19

## Joining datasets

### Learning goals

- How to join together two related datasets efficiently in R

### Joining: the basics

It's not unusual to have data for a project spread out across multiple datasets. The data are all related, but the fact that they are 'packaged' separately into different files can things difficult. To work with such *relational* data in R, you eventually need to merge – or *join* – them into a single dataframe.

For example, say you are studying the economics of professional basketball. In one dataframe, df1, you have the *net worth* of famous players, in millions USD...

```
player <- c("LeBron", "Mugsy", "Shaq", "Jordan", "Hakeem", "Kobe", "Stockton")
worth <- c(500, 14, 400, 1600, 200, 600, 40)
df1 <- data.frame(player, worth)
df1
  player   worth
1  LeBron    500
2   Mugsy     14
3     Shaq    400
4   Jordan   1600
5   Hakeem    200
6     Kobe    600
7 Stockton    40
```

...and in a second dataframe, df2, you have their height.

```
player <- c("Jordan", "Shaq", "Magic", "Hakeem", "Stockton", "Mugsy", "LeBron")
height <- c(78, 85, 81, 84, 73, 63, 81)
```

```
df2 <- data.frame(player,height)
df2
  player height
1  Jordan    78
2   Shaq     85
3   Magic    81
4 Hakeem    84
5 Stockton   73
6  Mugsy    63
7  LeBron    81
```

*Is there a correlation between these players' net worth and their height?* To answer this question you need to join these two datasets together. But the two datasets don't contain the exact same roster of players, and the players are not in the same order. Hmm. Is there an efficient way to join these two datasets?

*Yes!* Thanks to the family of `join()` functions from the package `dplyr`.

```
install.packages("dplyr")
```

These `join()` functions relate two dataframes together according to a common column name. In order for these functions to work, each dataframe has to have a column of the same name. In the case of `df1` and `df2`, that shared column is `player`.

There are four `join()` functions you should know how to use:

`left_join()` joins the two datasets together, keeping all rows in the *first* dataframe you feed it.

```
left_join(df1,df2,by="player")
  player  worth  height
1  LeBron    500     81
2   Mugsy     14      63
3   Shaq     400     85
4  Jordan   1600     78
5  Hakeem    200     84
6   Kobe     600      NA
7 Stockton     40      73
```

Notice that none of the players unique to `df2` made it into this output; only players in `df1` (i.e., the *left* of the two dataframes listed) remain. Also notice that any player from `df1` who was not in `df2` has an `NA` under the column `worth`. That is how these `join()` functions work: it fills in the data where it can, and leaves `NAs` where it can't.

`right_join()` keeps all rows in the *second* dataframe you feed it:

```
right_join(df1,df2,by="player")
  player worth height
1  LeBron   500     81
2   Mugsy    14      63
3    Shaq   400     85
4  Jordan  1600     78
5  Hakeem   200     84
6 Stockton    40     73
7   Magic     NA     81
```

`full_join()` keeping all rows in *both* dataframes:

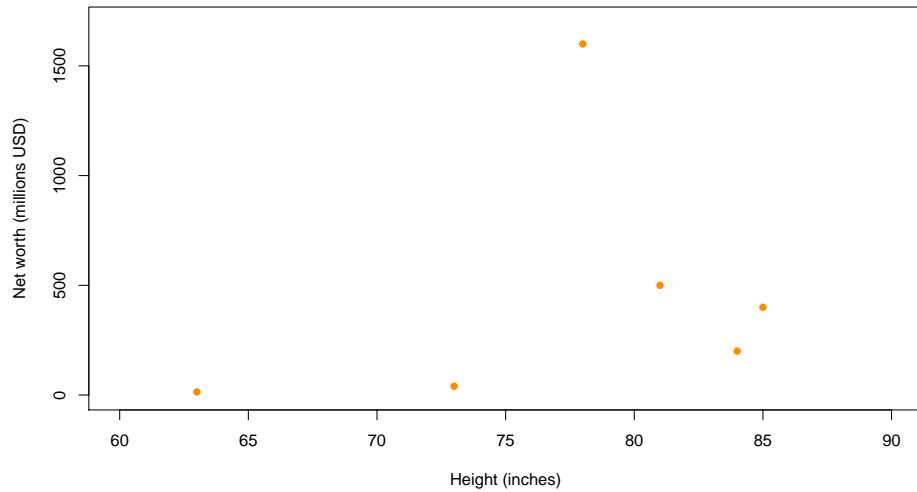
```
full_join(df1,df2,by="player")
  player worth height
1  LeBron   500     81
2   Mugsy    14      63
3    Shaq   400     85
4  Jordan  1600     78
5  Hakeem   200     84
6   Kobe    600     NA
7 Stockton    40     73
8   Magic     NA     81
```

Finally, `inner_join()` keeps only the rows that are *common to both* dataframes:

```
inner_join(df1,df2,by="player")
  player worth height
1  LeBron   500     81
2   Mugsy    14      63
3    Shaq   400     85
4  Jordan  1600     78
5  Hakeem   200     84
6 Stockton    40     73
```

So, to answer our research question about the relationship between player height and net worth, we can now join these data sets and make a nice plot:

```
df3 <- full_join(df1,df2,by="player")
plot(df3$worth ~ df3$height,
  ylim=c(0,1700), xlim=c(60,90),
  pch=16, col="dark orange",
  xlab="Height (inches)",
  ylab="Net worth (millions USD)")
```



Hmm. Looks like we have an outlier!

### Review exercise

This review exercise will involve *both* the joining skills you learned above as well as many of the skills learned in prior modules. But don't worry: as with every exercise in this book, every puzzle here can be solved using the skills you have learned in prior modules.

**Scenario:** A sailing expedition conducted a survey of the whales in the fjords of British Columbia, Canada. That research produced two datasets:

```
env <- read.csv("./data/whales-environment.csv") ; head(env)
  id species year distance seafloor temperature salinity thermocline
1 2014081103      HW 2014  44.1021  352.881   13.49104 25.75687  9.6325
2 2014081104      HW 2014  44.2729  363.563   13.49104 25.75687  9.6325
3 2014081106      HW 2014  46.7883  361.660   13.97642 25.14305  9.7859
4 20140812102     HW 2014  44.9049  317.864   14.11392 22.26935  9.7689
5 20140812104     HW 2014  44.8370  327.717   14.12843 22.21240  9.7689
6 20140812103     HW 2014  44.6589  353.749   14.17754 22.08326  9.7426
  stratification euphotic.depth chlorophyll
1          5.0603       18.2951    81.8442
2          5.0603       18.2951    81.8442
3          5.5067       17.2179    66.1236
4          5.2032       18.0307    76.0000
5          5.2032       18.0307    76.0000
6          5.2039       18.0093    75.9543

dive <-read.csv("./data/whales-dives.csv") ; head(dive)
  id species behavior prey.volume prey.depth dive.time surface.time
1 2014081106      HW     FEED      6.914610     120.76      351.00      237
```

2	20140812104	HW	FEED	7.854762	79.02	281.00	87
3	20140812107	HW	FEED	7.385667	96.92	300.25	80
4	20140812109	FW	FEED	6.626298	105.87	366.00	189
5	20140812131	HW	OTHER	6.356474	123.95	357.00	112
6	20140812140	FW	FEED	3.820782	125.51	408.00	182
blow.interval blow.number							
1	26.833	10.000					
2	14.412	6.667					
3	16.000	6.000					
4	16.273	12.000					
5	25.250	6.000					
6	18.789	11.000					

Each row in these dataframes represent a close encounter with a whale (either a humpback whale, HW, or a fin whale, FW).

The `env` dataset provides details about the habitat in which the whale was found, such as `seafloor` depth and the amount of `chlorophyll` in the water (a proxy for productivity).

The `dive` dataset provides measurements of whale foraging behaviors, such as `dive.time` and the number of breaths at the surface (`blow.number`), as well as the quality of prey in the area (`prey.volume` and `prey.depth`).

Note that these two dataframes are linked by the `id` column, which is a unique code for each whale encounter.

```
head(dive$id)
[1] 20140811106 20140812104 20140812107 20140812109 20140812131 20140812140

head(env$id)
[1] 20140811103 20140811104 20140811106 20140812102 20140812104 20140812103
```

Also note that *some* ids can be found in *both* dataframes. These are the encounters for which we have both foraging behavior data as well as environmental data.

### Task 1. Summarize your dataset.

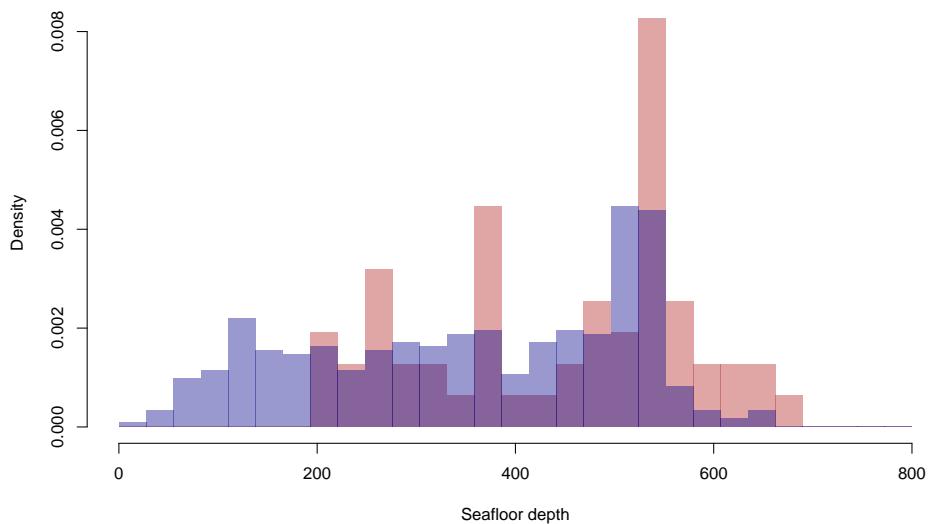
Write the necessary code and fill in the spaces in the data summary statement below:

A total of *BLANK* whale encounters were recorded on *BLANK* separate days in the years *BLANK* - *BLANK*. *BLANK* encounters were with humpback whales (*BLANK* % of all encounters), and *BLANK* were with fin whales (*BLANK* %). Foraging behavior was recorded in *BLANK* % of encounters (*BLANK* % of humpback whale encounters, and *BLANK* % of fin whale encounters).

### Task 2. Research question: Do these two species prefer different seafloor depths?

First, create a nicely formatted histogram that portrays the data relevant to this question.

```
par(mar=c(4.5,4.5,3,1))
hist(env$seafloor[env$species=="FW"],
     xlab="Seafloor depth",
     main=NULL,
     prob=TRUE,
     xlim=c(0,800),
     breaks=seq(0,800,length=30),
     border=NA,
     col=adjustcolor("firebrick",alpha.f=.4))
hist(env$seafloor[env$species=="HW"],
     xlim=c(0,800),
     breaks=seq(0,800,length=30),
     border=NA,
     col=adjustcolor("darkblue",alpha.f=.4),
     prob=TRUE,
     add=TRUE)
```



Provide the code to test this research question statistically, then write a results statement below.

```
t.test(x=env$seafloor[env$species=="FW"],
       y=env$seafloor[env$species=="HW"])

Welch Two Sample t-test

data: env$seafloor[env$species == "FW"] and env$seafloor[env$species == "HW"]
t = 4.7677, df = 78.011, p-value = 0.000008493
```

```

alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 52.84081 128.60877
sample estimates:
mean of x mean of y
445.7157 354.9909

```

**Task 3. Another research question: Is prey volume correlated to chlorophyll concentration?**

Whales eat tiny shrimp-like critters named krill, and krill eat tiny organisms called phytoplankton. Chlorophyll is a proxy measurement for the amount of phytoplankton in the area. Based on these datasets, how good are krill at congregating in areas of high chlorophyll concentration?

First, prepare a plot to visualize what you will be comparing:

```

hwe <- env[env$species=="HW",] ; head(hwe)
  id species year distance seafloor temperature salinity thermocline
1 20140811103    HW 2014  44.1021  352.881   13.49104 25.75687   9.6325
2 20140811104    HW 2014  44.2729  363.563   13.49104 25.75687   9.6325
3 20140811106    HW 2014  46.7883  361.660   13.97642 25.14305   9.7859
4 20140812102    HW 2014  44.9049  317.864   14.11392 22.26935   9.7689
5 20140812104    HW 2014  44.8370  327.717   14.12843 22.21240   9.7689
6 20140812103    HW 2014  44.6589  353.749   14.17754 22.08326   9.7426
  stratification euphotic.depth chlorophyll
1      5.0603        18.2951     81.8442
2      5.0603        18.2951     81.8442
3      5.5067        17.2179     66.1236
4      5.2032        18.0307     76.0000
5      5.2032        18.0307     76.0000
6      5.2039        18.0093     75.9543
hwd <- dive[dive$species=="HW",] ; head(hwd)
  id species behavior prey.volume prey.depth dive.time surface.time
1 20140811106    HW    FEED    6.914610   120.76    351.00       237
2 20140812104    HW    FEED    7.854762    79.02    281.00       87
3 20140812107    HW    FEED    7.385667   96.92    300.25       80
5 20140812131    HW    OTHER   6.356474   123.95    357.00      112
7 20140813105    HW    FEED    7.472343   104.13    365.00       52
8 20140813107    HW    FEED    3.261088   100.19    338.00       20
  blow.interval blow.number
1      26.833      10.000
2      14.412      6.667
3      16.000      6.000
5      25.250      6.000
7      18.610      4.500
8      33.322      1.000

```

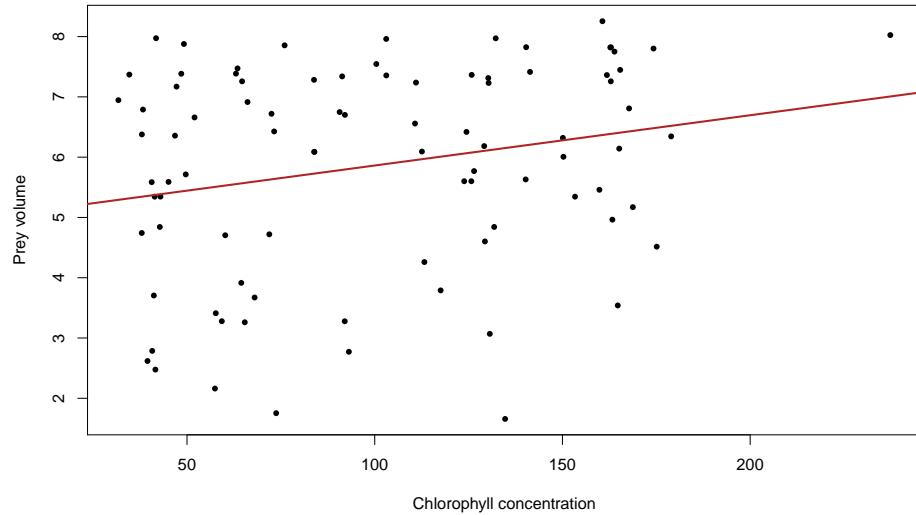
```

nrow(hwe)
[1] 446
hwe <- hwe[hwe$id %in% hwd$id,]
nrow(hwe) ; nrow(hwd)
[1] 89
[1] 89

hwe <- hwe[order(hwe$id),]
hwd <- hwd[order(hwd$id),]
hwd$chl <- hwe$chlorophyll

par(mar=c(4.5,4.5,3,1))
plot(hwd$prey.volume ~ hwd$chl,
      xlab="Chlorophyll concentration",
      ylab="Prey volume",
      pch=16,
      cex=.8)
hwlm <- lm(hwd$prey.volume ~ hwd$chl)
abline(hwlm,col="firebrick",lwd=2)

```



Now carry out your statistical test.

```

summary(hwlm)

Call:
lm(formula = hwd$prey.volume ~ hwd$chl)

Residuals:
    Min     1Q   Median     3Q    Max 
 -1.50  -0.50   0.00  0.50  1.50 

```

```
-4.4931 -1.2639  0.3534  1.3358  2.5978

Coefficients:
            Estimate Std. Error t value      Pr(>|t|)    
(Intercept) 5.027405   0.415675  12.10 <0.0000000000000002 *** 
hwd$chl     0.008340   0.003723   2.24      0.0276 *  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 

Residual standard error: 1.682 on 87 degrees of freedom
Multiple R-squared:  0.05453,  Adjusted R-squared:  0.04366 
F-statistic: 5.018 on 1 and 87 DF,  p-value: 0.02763
```



# Chapter 20

## Writing functions

### Learning goals

- Be able to write your own functions
- Be able to *source* your own functions from separate R files
- Be able to use functions to make your work more efficient, effective, and organized

### First steps

You've already used dozens of functions during your learning in R so far. As you start applying R to your own projects, you will inevitably encounter a puzzle that could be solved by a custom function you write yourself. This module shows you how.

As explained in the **Calling Functions** module, most functions have three key components:

- (1) one or more inputs,
- (2) a process that is applied to those inputs, and
- (3) an output of the result.

When you define your own custom function, these are the three pieces you must be sure to include.

Here is a basic example:

```
my_function <- function(x){  
  y <- 1.3*x + 10  
  return(y)  
}
```

Now use your function:

```
my_function(x=2) # example 1
[1] 12.6
my_function(x=4) # example 2
[1] 15.2
```

Let's break this down.

- `my_function` is the name you are giving your function. It is the command you will use to call your function.
- The `function()` command is what you use to define a function.
- `x` is the variable you are using to represent your input.
- `y <- 1.3x + 10` is the process that you are applying to your input.
- `return(y)` is the command you use to define what the function's output will be.

Note that you are not *required* to write out `x=2` in full when you are calling your function. Just providing 2 can also work:

```
my_function(2)
[1] 12.6
```

## Exercise 1

Define your own basic function and run it to make sure it works.

## Next steps

### Multiple inputs

You can define a function with multiple inputs. Just separate each input with a comma.

To demonstrate this, let's modify the function above to allow you to define any linear regression you wish:

```
my_function <- function(x,a,b){
  y <- a*x + b
  return(y)
}
```

Now call your function:

```
my_function(x=2,a=1.3,b=10) # example 1
[1] 12.6
my_function(x=4,a=5,b=100) # example 2
[1] 120
```

Note that you do not need to write out the name of each input, as long as you provide inputs in the correct order.

```
my_function(2, 1.3, 10) # example 1
[1] 12.6
my_function(4, 5, 100) # example 2
[1] 120
```

But note that it is usually best practice to name each input in your function call, to prevent the possibility of any confusion or mistakes. Also, when you name each input you can provide inputs in whatever order you wish:

```
my_function(x=2, a=1.3, b=10)
[1] 12.6
my_function(a=1.3, b=10, x=2) # different inout order, same output value
[1] 12.6
```

## Providing defaults for inputs

Just as R's base functions include default values for some inputs (think `na.rm=FALSE` for `mean()` and `sd()`), you can define defaults in your own functions.

This version of `my_function` includes default values for inputs `a` and `b`.

```
my_function <- function(x,a=1.3,b=10){
  y <- a*x + b
  return(y)
}
```

When you provide default values, you no longer need to specify those inputs in your function call:

```
my_function(x=2)
[1] 12.6
```

## NULL as a default

Setting the default value for an input to `NULL` can be useful in certain use cases. For example, let's say that if `b` is not defined by the user, you want its value to be set to five times the value of `x`.

```
my_function <- function(x,a=1.3,b=NULL){

  # Handle input `b`
  if(is.null(b)){
    b <- x*5
    print(paste("b was NULL! Setting its value to ", b))
  }
}
```

```
# Now perform process
y <- a*x + b

return(y)
}
```

In this function, a conditional statement is used – `if(is.null(b)){ ... }` – to handle the input `b` when the user does not specify a value for it. When `b` is `NULL`, the logical test `is.null(b)` will be `TRUE`, which will trigger the conditional statement and case `b` to be defined as `x*5`. Conditional statements will be covered in detail in the next modules.

Try running the function with and without providing a value for `b`.

```
my_function(x=2,b=5)
[1] 7.6
my_function(x=2)
[1] "b was NULL! Setting its value to 10"
[1] 12.6
```

Conditional statements such as `if(is.null(x)){ ... }` or `if(is.na(x)){ ... }` will be helpful in dealing with all the possible values that a user can pass to your custom functions.

## Complex inputs

You can pass vectors, dataframes, and any other data structure as inputs in your own custom functions. For example:

```
my_input <- 1:20
my_function(x=my_input,a=1.2,b=10)
[1] 11.2 12.4 13.6 14.8 16.0 17.2 18.4 19.6 20.8 22.0 23.2 24.4 25.6 26.8 28.0
[16] 29.2 30.4 31.6 32.8 34.0
```

## Complex function outputs

At some point you will want multiple objects to be returned by your function. For example, perhaps you want both `y` and `b` to be returned now that you can define `b` according to the value of `x`.

Unfortunately, the `return()` command does not let you include multiple objects. `return(y,b)` will not work. To make it work, you have to place your output objects within a single object, such as a vector, dataframe, or list.

Here is a modification of `my_function()` that allows multiple outputs:

```
my_function <- function(x,a=1.3,b=NULL){
```

```
# Handle input `b`  

if(is.null(b)){  

  b <- x*5  

}  

# Now perform process  

y <- a*x + b  

output <- c("y"=y, "b"=b)  

return(output)  

}
```

Now `my_function()` works like this:

```
my_function(x=5)  

  y      b  

31.5 25.0
```

To get the value of just `y` or just `b`, you can treat the output just like any other vector:

```
my_function(x=5) [1]  

  y  

31.5  

my_function(x=5) [2]  

  b  

25
```

## Adding plots

Plots can be included in the function commands just as in any other context:

```
my_function <- function(x,a=1.3,b=10){  

  y <- a*x + b  

  plot(y ~ x, type="b")  

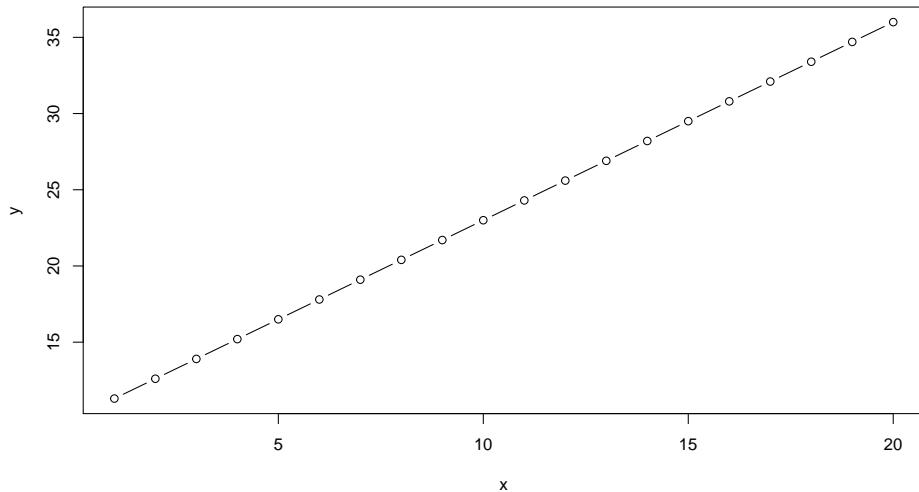
  return(y)  

}  

my_input <- 1:20  

my_function(x=my_input)
```



```
[1] 11.3 12.6 13.9 15.2 16.5 17.8 19.1 20.4 21.7 23.0 24.3 25.6 26.9 28.2 29.5
[16] 30.8 32.1 33.4 34.7 36.0
```

Adding plots to functions can be super useful if you want to make multiple plots with the same formatting specifications. Rather than retyping the same long plot commands multiple times, just write a single function and call the function as many times as you wish.

Let's add some fancy formatting to our plot. Note that we will modify the name of the function to make it more descriptive and helpful. The `lm` in `plot_my_lm` stands for *linear model*, which is what is being defined with the  $y=ax+b$  equation.

```
plot_my_lm <- function(x,a=1.3,b=10,plot_only=TRUE){

  # Process
  y <- a*x + b

  # Plot
  par(mar=c(4.2,4.2,3,.5)) # set plot margins
  plot(y ~ x, type="o",axes=FALSE,ann=FALSE,pch=16,col="firebrick",xlim=c(-20,20),ylim=
  title(main=paste("y =",a,"x +",b)) # print a dynamic main title
  title(xlab="x",ylab="y") # print axis labels
  axis(1) # print the X axis
  axis(2,las=2) # print the Y axis and turn its labels right-side-up
  abline(h=0,v=0,col="grey70") # add grey lines indicating x=0 and y=0

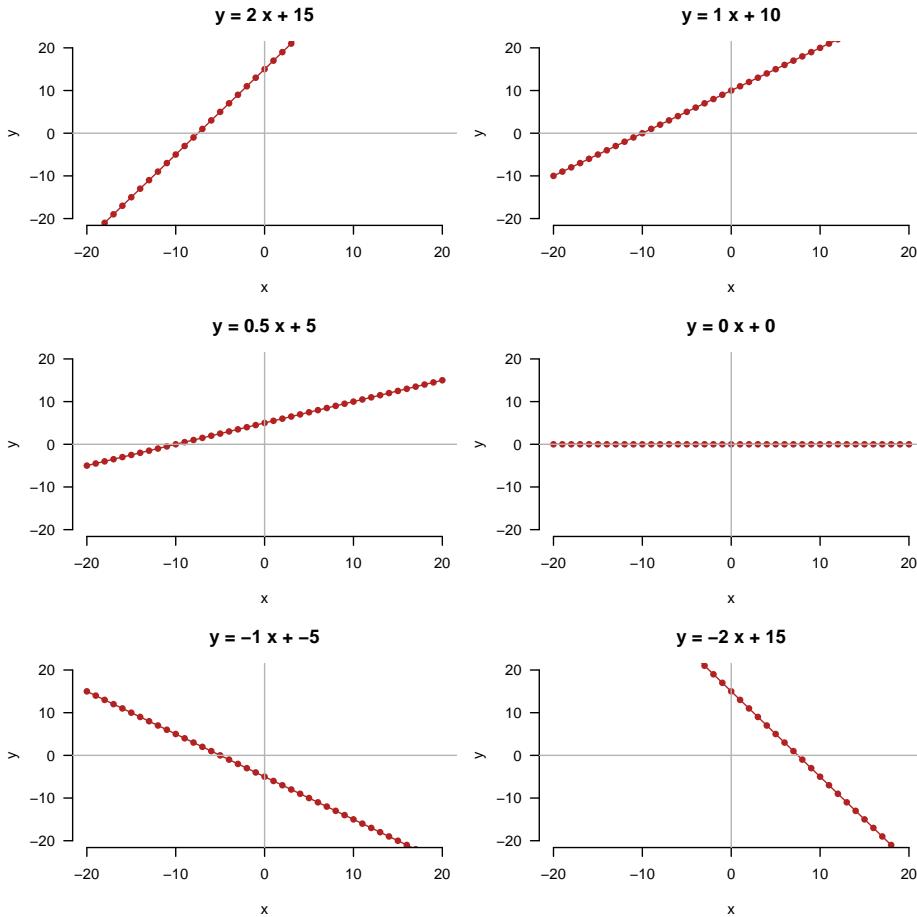
  # Return
  if(plot_only==FALSE){
    return(y)
  }
}
```

Note that we added a parameter, `plot_only`. When it is set to TRUE, the function will not return any numbers.

Now let's call this fancy function a bunch of times:

```
my_input <- -20:20 # define a common x input value

par(mfrow=c(3,2)) # stage a multi-paned plot
plot_my_lm(x=my_input,a=2,b=15)
plot_my_lm(x=my_input,a=1,b=10)
plot_my_lm(x=my_input,a=.5,b=5)
plot_my_lm(x=my_input,a=0,b=0)
plot_my_lm(x=my_input,a=-1,b=-5)
plot_my_lm(x=my_input,a=-2,b=15)
```



Think about how many lines of code would have been needed to write out all of these fancy plots if you did not use a custom function! Think about how cluttered and dizzying your code would look! And think about how many

opportunities for errors and inconsistencies there would have been! That is the advantage of writing your own functions: it makes your work more efficient, more organized, and less prone to errors.

Another major advantage of this approach comes into play when you decide you want to tweak the formatting of your plot. Rather than going through each `plot(...)` command and modifying the inputs in each one, when you write a custom plotting function you just have to make those changes once. Again, using a custom function saves you time and removes the possibility of inconsistencies or mistakes in the plots you are creating.

### Exercise 2

Modify the most recent version of `plot_my_lm` above such that you can specify the color for the plotted line as an input in the function. Then reproduce the multi-paned plot using a different color in each plot. (Here is a good reference for color options in R).

## Sourcing functions

As you advance in your coding, you will likely be writing multiple custom functions within a single R script. It is usually useful to group these functions into the same section of code near the top of your script.

But for even *better* script organization and simplification, you should *source* your functions from a separate R script. This means placing your function code in a separate R script and calling that file from the script in which you are carrying out your analyses. In addition to simplifying your analysis script, keeping your functions in a separate file allows them to be shared or sourced from any number of other scripts, which further organizes and simplifies your project's code and increases the reproducibility of your work.

Here is how sourcing functions can work:

1. Open a new R script. Save it as `functions.R` and save it in the same working directory as the script you are using to work through this module.
2. Copy and paste the `plot_my_lm()` function into your `functions.R` script. Save that script to ensure your code is safe.
3. Now remove the code defining `plot_my_lm()` from your module R script.
4. In its place, type this command:

```
source("functions.R")
```

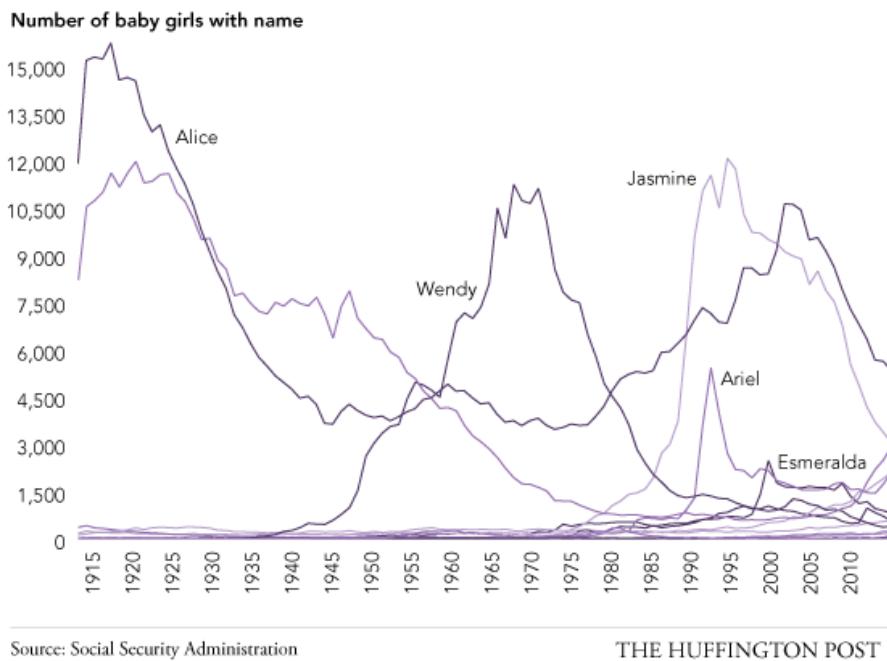
This command tells R to run the code in `functions.R` and store the objects and outputs from it in its active memory. You can now call `plot_my_lm()` from your module script.

### Exercise 3

Carry out the above instructions to ensure that you know how to source a function from a separate R script.

**Review assignment: Baby names over time**

### Female Disney Characters



In this exercise, you will investigate annual trends in the prevalence of six names for babies born in the United States.

**Step 1.** Decide upon five names of interest to you, in addition to your own. Create a vector of these six names.

**Step 2.** Install and load the package `babynames`, which includes the names of each child born in the United States from 1880 to 2017, according to the Social Security Administration.

**Step 3.** This package provides the dataset in a data frame that is also named `babynames`. Familiarize yourself with this dataset using its documentation.

**Step 4.** Before writing any functions, do some basic exploration with this dataset.

- (a) How many different names have been used since 1880?

- (b) What is the most common name (proportionally) ever given to female babies?
- (c) To male babies?
- (d) What was the most common name in 2017?

**Step 5.** Write a function that takes any name and plots its proportional prevalence from 1880 to 2017. Format the plot beautifully. Provide the name as the `main` title of the plot.

**Step 6.** Include an input that allows the user to specify the y axis range. If that input is set to `NULL`, the function should just use the maximum value contained in the data itself, scaled by 1.2 to make the plot prettier. Always use 0 as the lower bound of the y axis.

**Step 7.** Create a multi-pane plot containing six subplots, one for each of your names of interest.

# Chapter 21

## for loops

### Learning goals

- What `for` loops are, and how to use them yourself
- How to use `for` loops for plots that are tricky but super cool.
- How to use `for` loops to summarize subgroups in your data
- How to use nested `for` loops

### Basics

A `for` loop is a super powerful coding tool. In a `for` loop, R loops through a chunk of code for a set number of repetitions.

A super basic example:

```
x <- 1:5
for(i in x){
  print(i)
}
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
```

Here's an example of a pretty useless `for` loop:

```
for(i in 1:5{
  print("I'm just repeating myself.")
}
[1] "I'm just repeating myself."
[1] "I'm just repeating myself."
```

```
[1] "I'm just repeating myself."
[1] "I'm just repeating myself."
[1] "I'm just repeating myself."
```

**This code is saying:**

- For each iteration of this loop, step to the next value in `x` (first example) or `1:5` (second example).
- Store that value in an object `i`,
- and run the code inside the curly brackets.
- Repeat until the end of `x`.

**Look at the basic structure:**

- In the `for( )` parenthetical, you tell R what values to step through (`x`), and how to refer to the value in each iteration (`i`).
- Within the curly brackets, you place the chunk of code you want to repeat.

Another basic example, demonstrating that you can update a variable repeatedly in a loop.

```
x <- 2
for(i in 1:5){
  x <- x*x
  print(x)
}
[1] 4
[1] 16
[1] 256
[1] 65536
[1] 4294967296
```

Another silly example:

```
professors <- c("Keri", "Deb", "Ken")
for(x in professors){
  print(paste0(x, " is pretty cool!"))
}
[1] "Keri is pretty cool!"
[1] "Deb is pretty cool!"
[1] "Ken is pretty cool!"
```

**Exercise 1**

Use this space to practice the basics of `for` loop formatting.

- A. First, create a vector of names (add at least 3)

```
# Add your names to this vector
famous.names <- c("Lady Gaga", "David Haskell", "Tom Cruise")
```

B. Using the examples above as a guide, create a `for` loop that prints the same silly statement about each of these names.

```
# Do your coding here
for(i in famous.names){
  print(paste0(i, " has cooties!"))
}
[1] "Lady Gaga has cooties!"
[1] "David Haskell has cooties!"
[1] "Tom Cruise has cooties!"
```

C. It is usually best practice to write the body of your loop *first*, test it to make sure it works, *then* wrap it in a `for` loop. Use the code chunk below to practice that workflow. Complete each step in the order provided. (This may feel like hand-holding, but this practice will pay off when you dive into more complicated loops)

## for loops in plots

These silly examples above do a poor job of demonstrating how powerful a `for` loop can be. You can use `for` loops with data to do really cool things with relatively simple code.

Thinking in `for` loops, however, can take some getting used to. Learning how to design code with `for` loops is one of the most important milestones on your way to thinking like a data scientist.

## Efficient multi-panel plots

For example, a `for` loop can be a very efficient way of making multi-panel plots.

Let's use a `for` loop to get a quick overview of the variables included in the `airquality` dataset built into R.

```
data(airquality)
head(airquality)
  Ozone Solar.R Wind Temp Month Day
1    41     190  7.4   67     5    1
2    36     118  8.0   72     5    2
3    12     149 12.6   74     5    3
4    18     313 11.5   62     5    4
5    NA      NA 14.3   56     5    5
6    28      NA 14.9   66     5    6
```

Looks like the first four columns would be interesting to plot.

```

par(mfrow=c(2,2)) # Setup a multi-panel plot # format = c(number of rows, number of columns)
par(mar=c(4.5,4.5,1,1)) # Set plot margins

# Loop through the first four columns ...
for(i in 1:4){
  y <- airquality[,i] # Select data in column i
  var.name <- names(airquality)[i] # Get name of that column
  plot(y,xlab="Day",ylab=var.name,pch=16) # Plot data
}




The figure consists of four separate scatter plots arranged in a 2x2 grid. All four plots share a common x-axis labeled 'Day' ranging from 0 to 150. 
  - Top-left plot: Y-axis is 'Ozone', ranging from 0 to 150. The data shows several peaks, notably around day 50, 100, and 120, where ozone levels reach up to 150.
  - Top-right plot: Y-axis is 'Solar.R', ranging from 0 to 250. The data shows a general upward trend from day 0 to 150, with values fluctuating between approximately 50 and 250.
  - Bottom-left plot: Y-axis is 'Wind', ranging from 0 to 20. The data shows a relatively stable pattern with minor fluctuations, mostly between 5 and 15.
  - Bottom-right plot: Y-axis is 'Temp', ranging from 60 to 90. The data shows a clear seasonal pattern with a minimum around day 50 (around 65) and a maximum around day 120 (around 90), with intermediate peaks at day 0 and 150.



```

par(mfrow=c(1,1)) # restore the default single-panel plot

```


```

## Using for loops to plot subgroups of data

for loops are also useful for plotting data in tricky ways. Let's use a different built-in dataset, that shows the performance of various car make/models.

```

data(mtcars)
head(mtcars)

      mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4     21.0   6 160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag 21.0   6 160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710    22.8   4 108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive 21.4   6 258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8 360 175 3.15 3.440 17.02  0  0    3    2
Valiant       18.1   6 225 105 2.76 3.460 20.22  1  0    3    1

```

Let's say we want to see how gas mileage is affected by the number of cylinders

a car has. It would be nice to create a plot that shows the raw data as well as the mean mileage for each cylinder number.

```
# Let's see how many different cylinder types there are in the data
ucyl <- unique(mtcars$cyl) ; ucyl
[1] 6 4 8

# Let's make an empty plot
plot(1,type="n", # tell R not to draw anything
      xlim=c(2,10), ylim=c(0,50),
      xlab="Number of cylinders",
      ylab="Gas mileage (mpg)")

# Write your for loop here to add the actual data

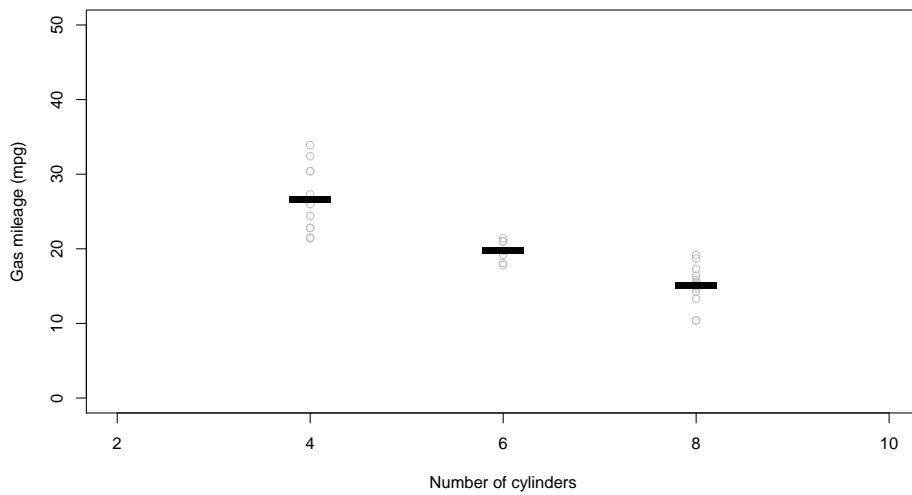
i=ucyl[1] # It's always good to use a known value of i as you build up your for loop

for(i in ucyl){ # Usually helpful to write this line LAST.
    # i.e., write body of loop first, test it, then wrap it in a loop.

    # Subset the dataframe according to number of cylinders
    cari <- mtcars[mtcars$cyl==i,]

    # Plot the raw data
    points(x=cari$cyl,y=cari$mpg,col="grey")

    # Superimpose the mean on top
    points(x=i,y=mean(cari$mpg),col="black",pch="-",cex=5,
    )}
```



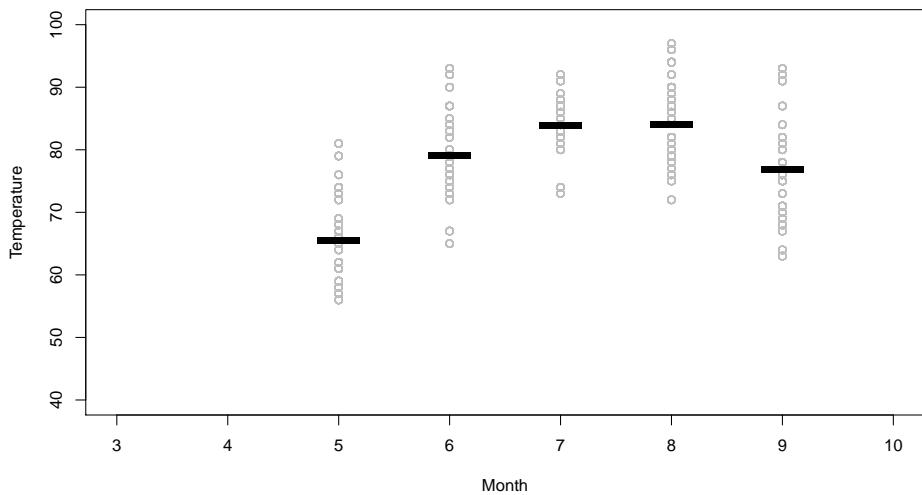
### Exercise 3

Now try to do something similar on your own with the `airquality` dataset. Use `for` loops to create a plot with Month on the x axis and Temperature on the y axis. On this plot, depict all the temperatures recorded in each month in the color grey, then superimpose the mean temperature for each month.

We will provide the empty plot, you provide the `for` loop:

```
plot(1,type="n",
      xlim=c(3,10),ylim=c(40,100),
      xlab="Month",
      ylab="Temperature")

# Write your for loop here to add the actual data
for(i in airquality$Month){
  airi <- airquality[airquality$Month==i,]
  points(x=airi$Month,y=airi$Temp,pch=1,col="grey")
  points(x=i,y=mean(airi$Temp),pch="-",cex=5,col="black")
}
```



### Using `for` loops to layer cyclical or repetitive data

Here's another good example of the power of a good `for` loop.

First, read in some cool data () .

```
kc <- read.csv("./data/keeling-curve.csv") ; head(kc)
  year month day_of_month day_of_year year_dec frac_of_year    CO2
1 1974      5          26   145.4890 1974.399     0.3986 332.95
2 1974      6          2   152.4970 1974.418     0.4178 332.35
3 1974      6          9   159.5050 1974.437     0.4370 332.20
```

```

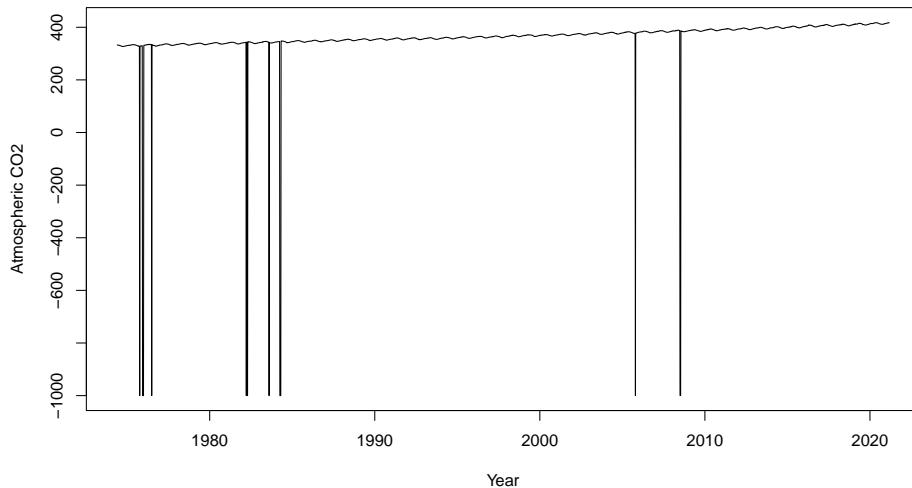
4 1974      6          16    166.5130 1974.456      0.4562 332.37
5 1974      6          23    173.4845 1974.475      0.4753 331.73
6 1974      6          30    180.4925 1974.495      0.4945 331.68

```

This is the famous Keeling Curve dataset: long-term monitoring of atmospheric CO<sub>2</sub> measured at a volcanic observatory in Hawaii.

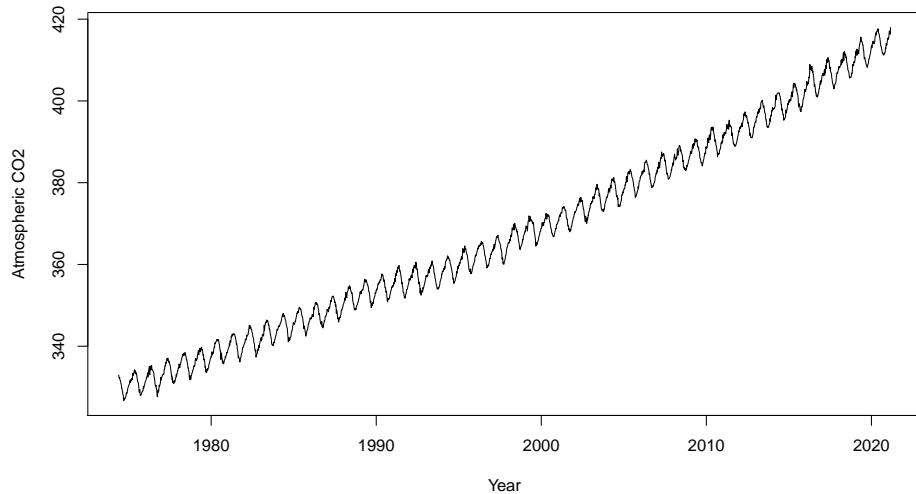
Try plotting the Keeling Curve:

```
plot(kc$CO2 ~ kc$year_dec, type="l", xlab="Year", ylab="Atmospheric CO2")
```



There are some erroneous data points! We clearly can't have negative CO<sub>2</sub> values. Let's remove those and try again:

```
kc <- kc[kc$CO2 > 0,]
plot(kc$CO2 ~ kc$year_dec, type="l", xlab="Year", ylab="Atmospheric CO2")
```



### What's the deal with those squiggles?

They seem to happen every year, cyclically. Let's investigate!

Let's look at the data a different way: *by layering years on top of one another.*

To begin, let's plot data for only a *single* year:

```
# Stage an empty plot for what you are trying to represent
plot(1, # plot a single point
      type="n",
      xlim=c(0,365), xlab="Day of year",
      ylim=c(-5,5), ylab="CO2 anomaly")
abline(h=0,col="grey") # add nifty horizontal line

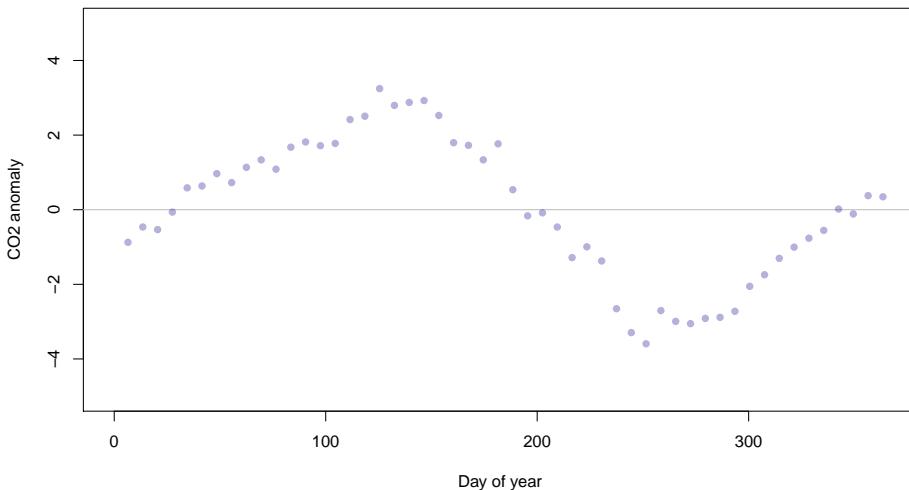
# Reduce the dataset to a single year (any year)
kcy <- kc[kc$year=="1990",] ; head(kcy)
   year month day_of_month day_of_year year_dec frac_of_year   CO2
816 1990      1             7    6.4970 1990.018     0.0178 353.58
817 1990      1            14   13.5050 1990.037     0.0370 353.99
818 1990      1            21   20.5130 1990.056     0.0562 353.92
819 1990      1            28   27.4845 1990.075     0.0753 354.39
820 1990      2             4   34.4925 1990.094     0.0945 355.04
821 1990      2            11   41.5005 1990.114     0.1137 355.09

# Let's convert each CO2 reading to an 'anomaly' compared to the year's average.
CO2.mean <- mean(kcy$CO2,na.rm=TRUE) ; CO2.mean # Take note of how useful that 'na.rm'
[1] 354.4538

y <- kcy$CO2 - CO2.mean ; y # Translate each data point to an anomaly
[1] -0.87384615 -0.46384615 -0.53384615 -0.06384615  0.58615385  0.63615385
```

```
[7] 0.96615385 0.72615385 1.13615385 1.33615385 1.08615385 1.67615385
[13] 1.81615385 1.71615385 1.77615385 2.41615385 2.50615385 3.24615385
[19] 2.79615385 2.87615385 2.92615385 2.52615385 1.79615385 1.72615385
[25] 1.33615385 1.76615385 0.53615385 -0.16384615 -0.08384615 -0.46384615
[31] -1.28384615 -0.99384615 -1.37384615 -2.65384615 -3.29384615 -3.59384615
[37] -2.70384615 -2.99384615 -3.05384615 -2.91384615 -2.88384615 -2.72384615
[43] -2.05384615 -1.74384615 -1.30384615 -1.00384615 -0.76384615 -0.55384615
[49] 0.01615385 -0.11384615 0.37615385 0.34615385 NA
```

# Add points to your plot  
`points(y~kcy$day_of_year,pch=16,col=adjustcolor("darkblue",alpha.f=.3))`



But this only shows one year of data! How can we include the seasonal squiggle from other years?

Let's use a `for` loop!

OK – let's redo that graph and add a `for` loop into the mix:

```
# First, stage your empty plot:
plot(1,type="n",
      xlim=c(0,365),xlab="Day of year",
      ylim=c(-5,5),ylab="CO2 anomaly")

abline(h=0,col="grey")

# Now we will loop through each year of data. First, get a vector of the years included in the data
years <- unique(kc$year) ; years
[1] "1974" "1975" "1976" "1977" "1978" "1979" "1980" "1981" "1982" "1983"
[11] "1984" "1985" "1986" "1987" "1988" "1989" "1990" "1991" "1992" "1993"
[21] "1994" "1995" "1996" "1997" "1998" "1999" "2000" "2001" "2002" "2003"
```

```
[31] "2004" "2005" "2006" "2007" "2008" "2009" "2010" "2011" "2012" "2013"
[41] "2014" "2015" "2016" "2017" "2018" "2019" "2020" "2021" NA

# Now build your for loop.
# Notice that the contents of the `for loop` are exactly the same
# as the single plot above -- with one exception.
# Notice the use of the symbol i

for(i in years){

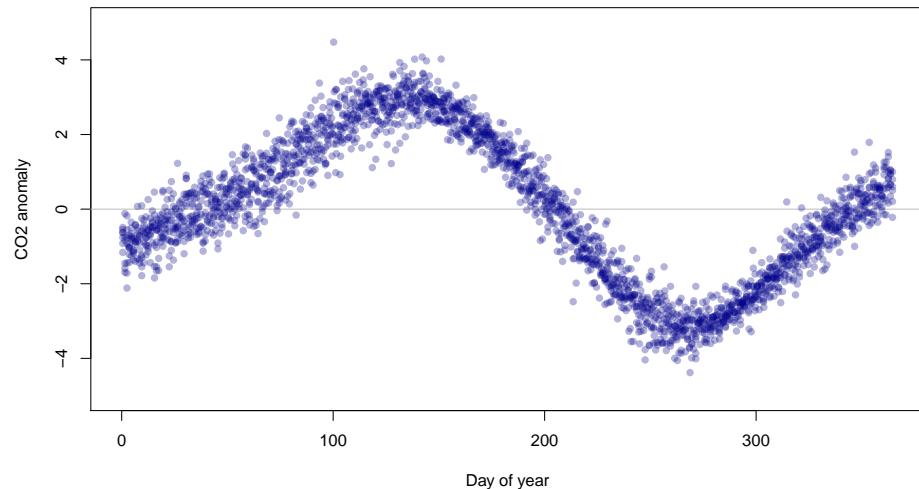
  # Reduce the dataset to a single year
  kcy <- kc[kc$year==i,] ; head(kcy)

  # Let's convert each CO2 reading to an 'anomaly' compared to the year's average.
  CO2.mean <- mean(kcy$CO2,na.rm=TRUE) ; CO2.mean # Get average CO2 for year

  y <- kcy$CO2 - CO2.mean ; y # Translate each data point to an anomaly

  # Add points to your plot
  points(y~kcy$day_of_year,pch=16,col=adjustcolor("darkblue",alpha.f=.3))

}
```



Beautiful! So how do you interpret this graph? Why does the squiggle happen every year?

## Using for loops to process & summarize data

## Using for loops to summarize data subgroups

This is one of the most common uses of `for` loops: you want to summarize information about subgroups in your dataset.

### Example use cases

- You want to summarize sample counts for each day of fieldwork.
- You want to summarize details for each user in your database.
- You want to summarize weather information for each month of the year.

### Workflow

All of these summaries can be achieved with the same basic workflow.

1. Determine how to define the basic unit of summarization (*e.g., each day of fieldwork, each user in your database, or each month of the year*).
2. Stage an empty data object (or multiple objects) in which you will store your summary.
3. Build a `for` loop to iterate through for each unique subgroup value (*e.g., each sampling date or each user or each month*).
4. In each iteration of the loop, subset your data to only the subgroup value of interest.
5. At the end of each iteration, update your data objects with the result from that iteration.
6. Run your `for` loop!
7. After the `for` loop, combine your data objects into a dataframe.

As you are building for loops, it can be very helpful to first start thinking about what needs to happen in each iteration of the loop. So first think about what needs to happen in *Step 4*. Then you go through each step of this workflow to build a loop around that core code.

### Example

The following scenario provides a concrete example of how to do this:

**Scenario:** You participate in a survey of flightless birds in the forests of New Zealand. You conduct thirty days of fieldwork on four species of bird: the kiwi, the weka, the kakapo (*the world's heaviest parrot*), and the kea (*the world's only alpine parrot*).

Your data () look like this:

```

df <- read.csv("./data/nz_birds.csv")
nrow(df)
[1] 406
head(df)
  day species group
1   1     Kiwi    3
2   1      Kea    4
3   1   Kakapo    4
4   1     Weka    2
5   1     Kiwi    1
6   1      Kea    3
tail(df)
  day species group
401 30     Weka    3
402 30     Kiwi    3
403 30     Kiwi    3
404 30   Kakapo    3
405 30   Kakapo    1
406 30      Kea    2

```

Each row contains the data for a single bird group detection.

Your supervisor has tasked you with writing a report of your findings, and she wants to see a table with the number of each species seen on each day of the fieldwork.

You can use a `for` loop to make this table.

But first think about what needs to happen in each iteration of your loop. For each date in the dataset, you want to count the number of sightings for each species.

Let's build our core code using day 10 as a practice date:

```

# Subset to day of interest
dayi <- 10
dfi <- df[df$day == dayi,]

# Tally up counts for each species
kiwi <- length(which(dfi$species=="Kiwi"))
weka <- length(which(dfi$species=="Weka"))
kakapo <- length(which(dfi$species=="Kakapo"))
kea <- length(which(dfi$species=="Kea"))

```

Okay! So our `for` loop needs to contain that basic code, with some minor adjustments in order to save the results from all iterations of the loop instead of just one.

Here is the full code for this `for` loop problem:

```

# 1: determine the unique days in the dataset:
udays <- unique(df$day)

# 2: stage empty results vectors
kiwi <- weka <- kakapo <- kea <- c()

# (create a variable named i to help you test your code as you build it)
i=1

# 3: Start for loop. Loop through each unique day
for(i in 1:length(udays)){

    # 4. Subset to day of interest
    dayi <- udays[i]
    dfi <- df[df$day == dayi,]

    # 5. Tally up birds, add to each vector
    kiwi[i] <- length(which(dfi$species=="Kiwi"))
    weka[i] <- length(which(dfi$species=="Weka"))
    kakapo[i] <- length(which(dfi$species=="Kakapo"))
    kea[i] <- length(which(dfi$species=="Kea"))

}

# 6. Run for loop

# 7. Combine results into a dataframe
results <- data.frame(day=udays, kiwi, weka, kakapo, kea)

# Check it out!
results
  day kiwi weka kakapo kea
1   1     5     6     3     3
2   2     1     3     1     2
3   3     2     4     5     3
4   4     2     3     2     0
5   5     6     6     3     2
6   6     6     2     3     6
7   7     3     1     3     7
8   8     2     6     2     2
9   9     4     1     1     1
10 10     2     0     3     3
11 11     2     2     3     5
12 12     2     3     4     4
13 13     3     3     5     1

```

14	14	7	3	4	6
15	15	3	4	4	5
16	16	4	2	1	4
17	17	3	4	6	2
18	18	3	4	1	1
19	19	4	6	1	6
20	20	2	6	3	1
21	21	4	3	5	6
22	22	4	2	5	5
23	23	4	6	2	4
24	24	1	2	5	2
25	25	4	6	3	1
26	26	4	2	3	5
27	27	8	5	6	7
28	28	8	1	0	2
29	29	6	1	1	3
30	30	4	2	3	4

## Nested for loops

Sometimes you need to summarize your data in such a specific way that you will need to use *nested for* loops, i.e., one **for** loop contained within another.

For example, your supervisor for the New Zealand Flightless Birds Survey has now taken an interest in associations among the four bird species you have been monitoring. For example, are kiwis more abundant on the days when you detect a lot of kakapos?

To answer this question, your supervisor wants to see a table with each species combination (Kiwi - Kakapo, Kiwi - Weka, ... Kakapo - Kea, etc.) and the number of dates in which both species were seen more than 5 times.

You can produce this table using a nested **for** loop. Here is how it's done:

```
uspp <- unique(df$species) # get set of unique species

A <- B <- c() # empty vector for names of each species in the pair
X <- c() # empty vector for number of dates in which both species were common

i=1 ; j=2

# For loop 1
for(i in 1:length(uspp)){
  spi <- uspp[i] # species i
  dfi <- df[df$species == spi,] # subset df to only this species
  counti <- table(dfi$day) # get number of sightings on each day
  dayi <- names(counti)[which(counti >= 5)] ; # get the dates on which this species wa
```

```

# For loop 2
for(j in 1:length(uspp)){
  spj <- uspp[j] # species j
  dfj <- df[df$species == spj,] # subset df to only this species
  countj <- table(dfj$day) # get number of sightings on each day
  dayj <- names(countj)[which(countj >= 5)] ; # get the dates on which this species was seen 5+
  dates_ij <- which(dayi %in% dayj) # get the dates on which both species were seen 5+ times
  Xij <- length(dates_ij) # count the number of these dates

  # Add results to staged objects
  X <- c(X,Xij)
  A <- c(A,spj)
  B <- c(B,spj)
}

# Combine results into a dataframe
results <- data.frame(A, B, X)

# Check it out!
results
      A      B   X
1  Kiwi   Kiwi  7
2  Kiwi    Kea  3
3  Kiwi Kakapo  1
4  Kiwi   Weka  3
5    Kea   Kiwi  3
6    Kea    Kea 10
7  Kea Kakapo  3
8    Kea   Weka  2
9  Kakapo   Kiwi  1
10 Kakapo    Kea  3
11 Kakapo Kakapo  7
12 Kakapo   Weka  1
13  Weka   Kiwi  3
14  Weka    Kea  2
15  Weka Kakapo  1
16  Weka   Weka  8

```

Note that the code for adding the results to the staged objects `X`, `A`, and `B` is contained within the second for loop. This is necessary for producing our results; if we put that code in the first for loop *after* the code for the nested loop, our results would not be complete.

Note that each `for` loop *must* use a different variable to represent each iteration. In this example, the first loop uses `i` and the second uses `j`. If we used `i` for both loops, R would get very confused indeed.

Also note that we used `i` and `j` in the variables specific to each loop (e.g., `dayi` and `dayj`), as a simple way to help us keep track of what each variable is representing.

## Exercise 2

Your supervisor is happy with your pairwise species association dataframe, and wants to use it in an analysis for a publication. However, the R package she wants to use requires that the data be in the format of a square *matrix* with four rows – one for each species – and four columns. Like this:

```
results_matrix <- matrix(data=NA, nrow=4, ncol=4, dimnames=list(uspp,uspp))
results_matrix
  Kiwi Kea Kakapo Weka
Kiwi     NA  NA      NA  NA
Kea      NA  NA      NA  NA
Kakapo   NA  NA      NA  NA
Weka     NA  NA      NA  NA
```

You have not yet worked with matrices in this curriculum (you will in a few modules), but for now think of them as simple dataframes with a single type of data (e.g., all numeric values, like this one). You can subset matrices just as you would a dataframe: `matrix[row, column]`.

The values in this matrix should represent the number of dates in which each species pair was seen 5 times or more. For example, `result[1,2]` would be 3, since the Kiwi and Kea were seen 5+ times on only 3 dates.

She asks you to use the dataframe you just created to create this matrix. Use a nested for loop to do it.

```
# Stage empty results objects
results_matrix <- matrix(data=NA, nrow=4, ncol=4, dimnames=list(uspp,uspp))

# Get unique species
uspp <- unique(c(results$A,results$B))

# Loop 1: each species (row)
for(i in 1:length(uspp)){
  spi <- uspp[i]
  resultsi <- results[results$A==spi,] # subset data to rows where column A equals spe

# Loop 2: each species (column)
for(j in 1:length(uspp)){
  spj <- uspp[j]
```

```

resultsj <- resultsi[resultsi$B==spj,] # subset data from i loop where column B equals species

Xij <- resultsj$X      # Find result

results_matrix[i,j] <- Xij      # Add result to staged object
}
}

results_matrix
  Kiwi Kea Kakapo Weka
Kiwi    7   3     1   3
Kea     3  10     3   2
Kakapo  1   3     7   1
Weka    3   2     1   8

```

Boom!

### Review assignment

First, read in and format some other cool data (). The code for doing so is provided for you here:

```
df <- read.csv("./data/renewable-energy.csv")
```

This dataset, freely available from World Bank, shows the renewable electricity output for various countries, presented as a percentage of the nation's total electricity output. They provide this data as a time series.

**21.0.0.0.1 Summarize columns with a for loop** **Task 1:** Use a for loop to find the change in renewable energy output for each nation in the dataset between 1990 and 2015. Print the difference for each nation in the console.

```

# Write your code here
i=2
for(i in 2:ncol(df)){
  dfi <- df[,i] ; dfi
  diffi <- dfi[length(dfi)] - dfi[1] ; diffi
  print(paste0(names(df)[i]," : ",round(diffi),"% change."))
}
[1] "World : 3% change."
[1] "Australia : 4% change."
[1] "Canada : 1% change."
[1] "China : 4% change."
[1] "Denmark : 62% change."
[1] "India : -9% change."
[1] "Japan : 5% change."

```

```
[1] "New_Zealand : 0% change."
[1] "Sweden : 12% change."
[1] "Switzerland : 7% change."
[1] "United_Kingdom : 23% change."
[1] "United_States : 2% change."
```

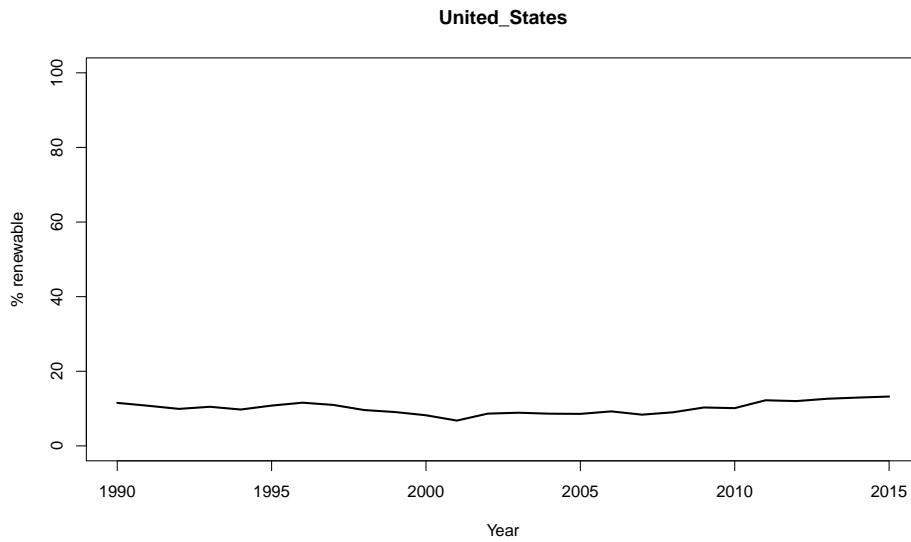
**Task 2:** Re-do this loop, but instead of printing the differences to the console, save them in a vector.

```
# Write your code here
diffs <- c()
i=2
for(i in 2:ncol(df)){
  dfi <- df[,i] ; dfi
  diffi <- dfi[length(dfi)] - dfi[1] ; diffi
  diffs <- c(diffs,diffi)
}
diffs
[1] 3.49241703 3.98181045 0.63273122 3.51887728 62.33064943 -9.14624362
[7] 4.73004321 0.07524008 12.26263811 7.21543884 23.01128298 1.69994636
```

#### 21.0.0.0.2 Multi-pane plots with for loops

**21.0.0.0.2.1 Practice with a single plot** **Task 3:** First, get your bearings by figuring out how to use the `df` dataset to plot the time series for the United States, for the years 1990 - 2015. Label the x axis “Year” and the y axis “% Renewable”. Include the full name of the country as the `main` title for the plot.

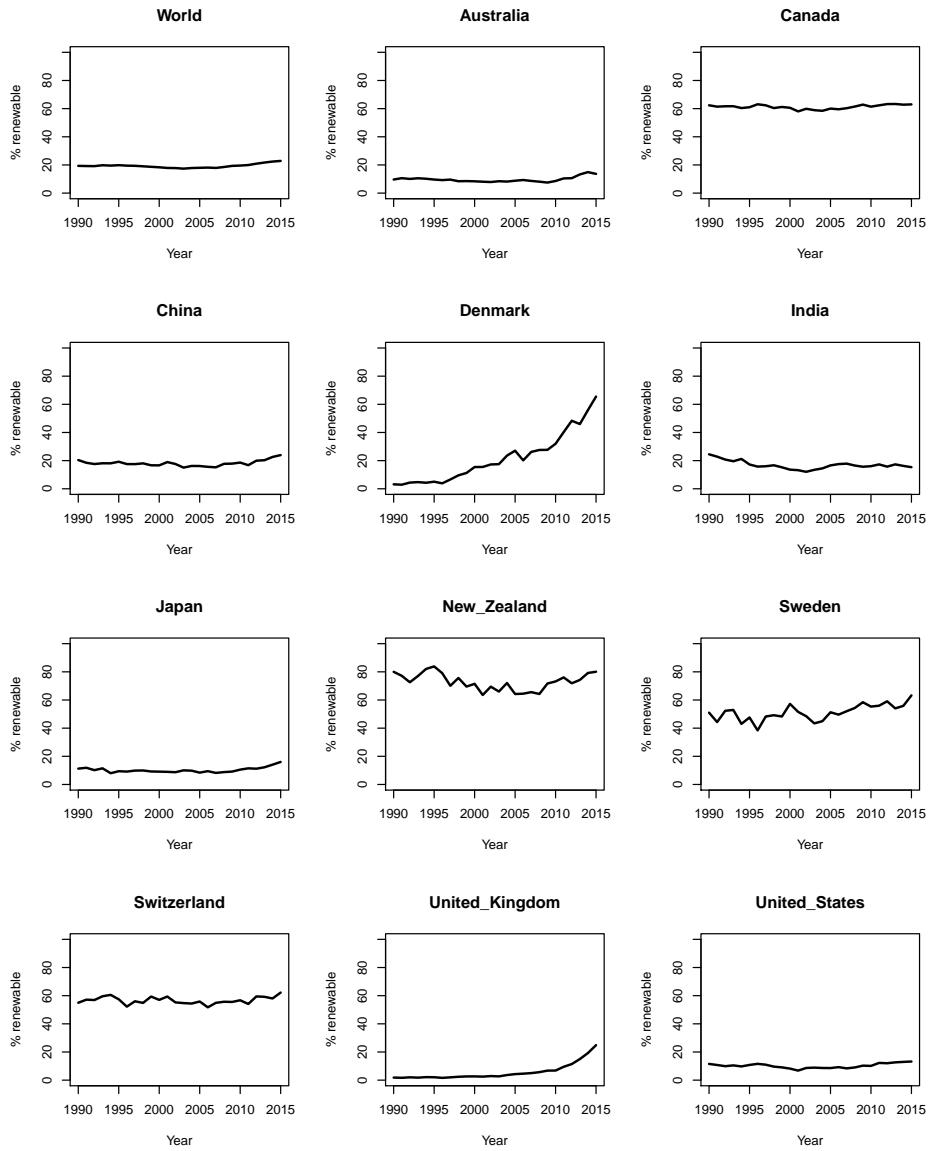
```
# Write code here
dfi <- df[,c(1,13)]
plot(x=dfi[,1],
      y=dfi[,2],
      type="l", lwd=2,
      xlim=c(1990,2015), ylim=c(0,100),
      xlab="Year", ylab="% renewable",
      main=names(dfi)[2])
```



**Now loop it!**

**Task 4:** Use that code as the foundation for building up a `for` loop that displays the same time series for every country in the dataset on a multi-pane graph that with 4 rows and 3 columns.

```
par(mfrow=c(4,3))
i=3
for(i in 2:ncol(df)){
  dfi <- df[,c(1,i)] ; dfi
  plot(x=dfi[,1],
       y=dfi[,2],
       type="l",lwd=2,
       xlim=c(1990,2015),ylim=c(0,100),
       xlab="Year",ylab="% renewable",
       main=names(dfi)[2])
}
```



**21.0.0.0.2.2 Now loop it *in layers!* Task 5:** Now try a different presentation. Instead of producing 12 different plots, superimpose the time series for each country on the *same single plot*.

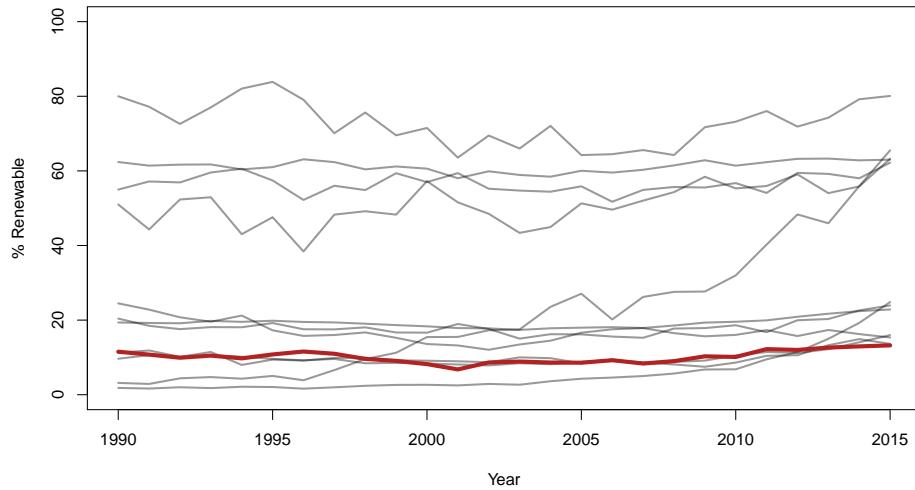
To add some flare, highlight the USA curve by coloring it red and making it thicker.

```
par(mfrow=c(1,1))
plot(1,type="n",lwd=2,
```

```
xlim=c(1990,2015),ylim=c(0,100),
xlab="Year",ylab="% Renewable")

for(i in 2:ncol(df)){
  dfi <- df[,c(1,i)] ; dfi
  lines(dfi[,2]~dfi[,1],lwd=2,col=adjustcolor("black",alpha.f=.4))
}

lines(df$United_States~df$year,lwd=4,col="firebrick")
```





# Chapter 22

## Conditional statements

### Learning goals

- Understand what conditional statements are, and why they are so awesome.
- Be able to write your own conditional statements in R.

### First steps

An example of a conditional statement is, “*If \_\_\_\_\_ happens, do \_\_\_\_\_. Otherwise, do \_\_\_\_\_.*”

In R code, conditional statements work a similar way: they let a variable’s value determine which process to carry out next.

Here is a basic example:

```
x <- 4

if(x==3){
  message("x is equal to 3!")
}else{
  message("x does NOT equal 3!")
}
```

Let’s break this `if` statement down.

- The `if` command opens up a conditional statement.
- The parenthetical (`x==3`) is where the logical test happens. If the result of this test is `TRUE`, then the `if` statement will be processed; if not, the `else` statement will be run instead.
- The curly brackets, `{ }` serve to contain the code that will be run, depending on the outcome of the logical test.

- The `else` command indicates the start of the code that will be run if the logical test's result is `FALSE`.

This code ran the logical test `x==3`, determined its outcome to be `FALSE`, and so it skipped the `if` code and ran the `else` code instead.

Here is another example of the same idea:

```
x <- 4

if(x==3){
  y <- 100
}else{
  y <- 0
}

y # see what y is
[1] 0
```

Since `x==3` returned `FALSE`, `y` was defined as 0 instead of 100.

Note that you do not need to define an `else` statement. If you do not, R will simply do nothing if the logical test is `FALSE`.

```
x <- 4

if(x==3){
  message("x is equal to 3!")
}
```

*(Nothing happened)*

You can also feed the `if` statement a logical object instead of a test.

```
x <- 4
x_test <- x == 3
x_test # check out the value of x_stest
[1] FALSE

if(x_test){
  message("x is equal to 3!")
}
```

Not that, since `x_test` is a logical value (`TRUE` or `FALSE`), you do not need to write out a logical test within the `if` parenthetical. But you are free to do so if you wish:

```
x <- 4
x_test <- x == 3

if(x_test == FALSE){
```

```
    message("x is not equal to 3!")
}
```

This `if` statement is saying that, if it is TRUE that `x_test` is FALSE, print a message saying so.

## Exercise 1

Write out your own basic `if...else` statement and ensure that it works.

## Next steps

### Nested conditions

You can nest conditional statements within others as many times as you wish:

```
x <- 6

if(x==3){
  message("x equals 3")
}else{
  if(x < 3){
    message("x is less than 3")
  }else{
    message("x is greater than 3")
  }
}
```

Note that every open bracket, `{`, needs a corresponding closing bracket `}`. Most errors associated with `if` statements involve missing brackets.

### Handling NAs, NaN's, Infs, and NULLs

`if` statements can be particularly helpful when your dataset contains missing or broken values. R includes base functions that help you carry out logical tests concerning missing values. These three test below can be very helpful within `if` statements.

`is.finite()` tests whether a numeric object is a real, finite number.

```
x <- 0
is.finite(x)
[1] TRUE

y <- 10/x
y
[1] Inf
```

```
is.finite(y)
[1] FALSE
```

Here is an `if` statement making use of `is.finite()`:

```
x <- 0
y <- 10/x
if(is.finite(y)){
  message("y is indeed a finite number!")
}else{
  message("y is not a finite number!")
}
```

`is.na()` tests whether a variable contains a missing or broken object.

```
x <- "eric"
is.na(x)
[1] FALSE

y <- as.numeric(x) # try converting `x` to a numeric value
is.na(y)
[1] TRUE
is.finite(y)
[1] FALSE
```

`NA` stands for “*Not Available*”. `NaN` is also a common sign of a broken value. It stands for *Not a Number*.

`is.null()` tests whether a variable is empty. That is, it has been initiated, but it contains no data.

```
x <- c(4,7,3,1,5) # make a vector of numbers
is.null(x)
[1] FALSE

y <- c() # make an empty vector
is.null(y)
[1] TRUE
```

## Joint conditions

`if` statements can also accommodate joint logical tests. For example, the following `if` statement only returns if a message if *two* tests are true:

```
x <- 6
if(is.finite(x) & x==6){
  message("x is real and equals 6")
}
```

The next `if` statement returns a message if either of the logical statements are true:

```
x <- 6
if(x==3 | x==6){
  message("x is equal to either 3 or 6")
}
```

## Exercise 2

Write a nested `if` statement that produces a message reporting the hemisphere for any GPS position you provide it (a pair of latitude and longitude coordinates, in decimal degrees). The four hemisphere options are as follows:

- *Northwest* (positive latitudes and negative longitudes, e.g., USA)
- *Northeast* (positive latitudes and longitudes, e.g., Russia)
- *Southwest* (negative latitudes and longitudes, e.g., Brazil)
- *Southeast* (negative latitudes and positive longitudes, e.g., New Zealand).

Include the ability to handle missing values (i.e., if an `NA` is provided, return a message saying that values are missing and the hemisphere cannot be determined.)

Provide five examples that demonstrate the functionality for all the possible message options.

## Review assignment

**Note:** This exercise will combine all the skills you've learned for `for` loops, `if` statements, and writing functions into a real-world data science scenario. Buckle up!

You are working at the Center for Disease Control. Your supervisor has asked you to take a look at state-level data on infectious diseases within the United States in the last century. Specifically, she wants you to address the following questions and requests:

1. In the last 90 years, which states have had the highest average prevalence of **measles**, **pertussis** (whooping cough), and **smallpox** in proportion to their population sizes? Which have had the lowest?
2. Provide beautiful plots showing trends in the prevalence of these diseases over the last century. Produce a single plot for each state, with three lines representing the time series for each disease of interest. Save each plot as a `pdf` into a folder named `state-level-summaries`. Name each `pdf` using the state's name.

To do this work, your supervisor asks you to use the `us_contagious_diseases` dataset contained within the R package `dslabs`, which contains disease data from 1928-2011 for all states. To make sure the numbers reflect actual patterns, she asks you to only use prevalence numbers for years in which counts were made in more than 20 weeks out of the year.

# Chapter 23

## Working with text

### Learning goals

- Learn to apply the most common R tools for working with text.

### Basics

If you do not learn how to edit and transform text-based fields within datasets, you will quickly get stuck in R. Think of dates, GPS coordinates, user IDs, group names, plot labels, *etc.* All of these forms of data can contain non-numeric text. Becoming comfortable working with text in R is an essential part of your R toolbag.

Here we will present the most common functions for working with text. Remember that R has a special object class for text, known to as **character** class, and that character objects are often referred to as **strings**.

Most of these functions come pre-installed in R. However, several of the tools we will show here (as well as many other useful tools that we will not detail here) come from the **stringr** package. Go ahead and install **stringr** and load it using `library()`.

```
install.packages("stringr")
library(stringr)
```

### Common tools

`as.character()`: converts a non-character object into a character string.

```
x <- c(1,2,3)
as.character(x)
```

```
[1] "1" "2" "3"

x <- as.factor(c("group1","group2","group3"))
as.character(x)
[1] "group1" "group2" "group3"
```

This can be particularly useful when trying to resolve problems caused by factors. One common issue occurs when R mistakes a set of numbers as a set of factors. Using `as.character()` can set things right:

```
x <- as.factor(c(18,19,20))
x
[1] 18 19 20
Levels: 18 19 20

# If you try to convert straight to numeric, it does not work:
as.numeric(x)
[1] 1 2 3

# So convert to character first
as.numeric(as.character(x))
[1] 18 19 20
```

`paste()` and `paste0()` combines two ore more strings together into a single object:

```
i <- 10
n <- 96
file_name <- "this_file.csv"

paste(i,"of",n,": Processing",file_name,". . . ") # paste assumes each object is separated by a space
[1] "10 of 96 : Processing this_file.csv . . . "
paste0(i,"of",n,": Processing",file_name,". . . ") # paste0 assumes no space between objects
[1] "10of96: Processingthis_file.csv. . . "
paste0(i," of ",n,": Processing ",file_name," . . . ") # this paste0 version matches the output of paste()
[1] "10 of 96: Processing this_file.csv . . . "
```

You can also use `paste()` to collapse multiple objects into a single string.

```
x <- 1:10
paste(x,collapse="-")
[1] "1-2-3-4-5-6-7-8-9-10"
```

`tolower()` and `toupper()` forces all text in a string to lower case or upper case, respectively:

```
x <- "That Tree Is Far Away."
tolower(x)
```

```
[1] "that tree is far away."
toupper(x)
[1] "THAT TREE IS FAR AWAY."
```

`nchar()` returns the number of characters within a string:

```
x <- "That Tree Is Far Away."
nchar(x)
[1] 22
```

`substr()` trims a string according to a start and end character position:

```
dates <- c("2021-03-01", "2021-03-02", "2021-03-03")
substr(dates, 1, 4) # years
[1] "2021" "2021" "2021"
substr(dates, 6, 7) # months
[1] "03" "03" "03"
substr(dates, 9, 10) # days
[1] "01" "02" "03"
```

`grep()` returns the elements in a character vector that contain a given pattern:

```
years <- 1900:1999

# Which elements correspond to the 1980s?
eighties <- grep("198", years)

years[eighties]
[1] 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989
```

`gsub()` replaces a given pattern with another in a character vector.

```
dates <- c("2021-03-01", "2021-03-02", "2021-03-03")
gsub("-", "/", dates)
[1] "2021/03/01" "2021/03/02" "2021/03/03"
```

`stringr::str_pad()`: standardize the lengths of strings by “padding” it (e.g., with zeroes) :

```
days <- as.character(1:15)
days
[1] "1"  "2"  "3"  "4"  "5"  "6"  "7"  "8"  "9"  "10" "11" "12" "13" "14" "15"
stringr::str_pad(days, width=2, side="left", pad="0")
[1] "01" "02" "03" "04" "05" "06" "07" "08" "09" "10" "11" "12" "13" "14" "15"
```

`stringr::str_split()`: split a string into several strings at the occurrence of a specified character.

```
dates <- c("2021-03-01", "2021-03-02", "2021-03-03")
splits <- stringr::str_split(dates, "-")
```

```
splits
[[1]]
[1] "2021" "03"   "01"

[[2]]
[1] "2021" "03"   "02"

[[3]]
[1] "2021" "03"   "03"
```

This function returns a *list* for every element in the original vector. A common need is to retrieve one item from each of the elements in this list. For example, let's say you are trying to retrieve the months of each element in the `dates` vector. The list structure makes this tricky to retrieve. Here's the way to do it by drawing upon the `apply()` family of functions:

```
sapply(splits, "[[", 2) # Months
[1] "03" "03" "03"

# now get years and days
sapply(splits, "[[", 1) # years
[1] "2021" "2021" "2021"
sapply(splits, "[[", 3) # days
[1] "01" "02" "03"
```

### Review assignment

- A. For a given dataset, print informative status update for each iteration in a `for` loop.
- B. Modify the above to only print an update at every integer percentage point (i.e., at 1% and 2% but not at 1.233%, etc.)
- C. Your collaborator sends you a dataset containing columns for `Date`, `Latitude`, and `Longitude`. Formatting varies in these fields. Fix it. (can use `hw-raw.csv` file. - Eric)

## **Chapter 24**

# **Working with dates & times**



## Chapter 25

# Working with factors



# Chapter 26

## Matrices & lists

### Learning goals

- What R lists are, how to work with them, and when they are useful
- What R matrices are, how to work with them, and when they are useful

As a data scientist, you will almost always be working exclusively with dataframes. But there are occasions when you will need other complex data structures – **lists** and **matrices** – to get a job done.

Here we show you what these data structures are like, how to work with them, and when to use them.

### Lists

Think of lists as complicated vectors. Instead of being a set of single values, which is what a vector is, a list is a set of complex data structures. In fact, a better analogy may be that lists are like shopping carts. You can put a lot of different things in there.

To see what we mean, stage an empty list:

```
x <- list()
```

Now add a simple vector to it:

```
x$vector <- 1:10
```

Now add a dataframe to it.

```
x$dataframe <- data.frame(name=c("Ben", "Joe", "Eric"),
                           height.inches=c(75,73,80))
```

Now add a new list to it.

```
x$list <- list()
```

Now add a vector to that new list:

```
x$list$vector <- 10:20
```

Okay! Nice shopping spree. Let's see what we have:

```
$vector
[1] 1 2 3 4 5 6 7 8 9 10

$dataframe
  name height.inches
1 Ben            75
2 Joe            73
3 Eric           80

$list
$list$vector
[1] 10 11 12 13 14 15 16 17 18 19 20
```

This is a list: a lot of complicated data structures, all contained in a single variable.

As you saw above, you can access the items in your list using the same dollar sign, \$, that we use to access columns in a dataframe:

```
x$vector
[1] 1 2 3 4 5 6 7 8 9 10
```

You can do the same with lists within your list:

```
x$list$vector
[1] 10 11 12 13 14 15 16 17 18 19 20
```

Alternatively, you can subset lists using double brackets, [[ ]].

```
x[[1]]
[1] 1 2 3 4 5 6 7 8 9 10
x[[3]]
$vector
[1] 10 11 12 13 14 15 16 17 18 19 20
```

Finally, you can create a list from scratch like so:

```
y <- list("vector1"=1:10,
          "vector2"=11:20)
y
$vector1
[1]  1  2  3  4  5  6  7  8  9 10

$vector2
[1] 11 12 13 14 15 16 17 18 19 20
```

## Use cases for lists

Common use cases for lists include:

- Keeping track of a bunch of related dataframes (i.e., by storing each dataframe as an element in a list).
- Several R functions return lists as outputs. For example, when you split up a vector of strings using `stringr::str_split()`, the output is a list that is the same length as your original vector.
- Returning complex outputs from your own custom functions. Since functions can return only a single object, you can stuff a bunch of different objects into a list and return the list.

## Matrices

Matrices are like dataframes, except that they can only contain a single data type. Dataframes can have a column with text and another with numbers, but a matrix will only handle one type.

Here's a simple dataframe containing two classes of data:

```
df <- data.frame(name=c("Ben", "Joe", "Eric"),
                  height.inches=c(75, 73, 80))
df
  name height.inches
1 Ben        75
2 Joe        73
3 Eric       80
```

When you coerce this dataframe into a matrix (using the function `as.matrix()`), the numeric data get coerced into text:

```
mdf <- as.matrix(df)
mdf
  name   height.inches
[1,] "Ben"  "75"
```

```
[2,] "Joe"  "73"
[3,] "Eric" "80"
```

Other than that, you can treat a variable of class `matrix` similarly to a dataframe.

Subsetting is the same: `matrix[rows,columns]`

```
mdf[2,]
      name height.inches
      "Joe"        "73"
mdf[,2]
[1] "75" "73" "80"
mdf[2,2]
height.inches
"73"
```

To build a matrix from scratch, use the `matrix()` function.

```
mx <- matrix(data=1:12,
              nrow=4,
              ncol=3)
mx
 [,1] [,2] [,3]
[1,]    1    5    9
[2,]    2    6   10
[3,]    3    7   11
[4,]    4    8   12
```

The `data` input takes a vector of data and sorts it into a matrix with rows and columns. It starts “laying down” your data in the first column, then wraps to the second column, etc.

You can also define names for the rows and columns in a matrix:

```
mx <- matrix(data=1:12,
              nrow=4,
              ncol=3,
              dimnames=list(c("row1","row2","row3","row4"),
                            c("col1","col2","col3")))
mx
      col1 col2 col3
row1    1    5    9
row2    2    6   10
row3    3    7   11
row4    4    8   12
```

The `dimnames` input takes a list with two vectors: the first contains row names, the second contains column names.

Note, however, that you cannot subset a matrix according to their column names. `mx$col1`, for example, will not work.

One more tool worth knowing for matrices is the function `diag()`, which returns the values that fall along the matrix's diagonal ([1,1], [2,2], [3,3], etc.).

```
mx
  col1 col2 col3
row1   1    5    9
row2   2    6   10
row3   3    7   11
row4   4    8   12

diag(mx)
[1] 1 6 11
```

The `diag()` function comes in handy in most use cases for matrices in R (see next section).

## Use cases for matrices

Common use cases for matrices include:

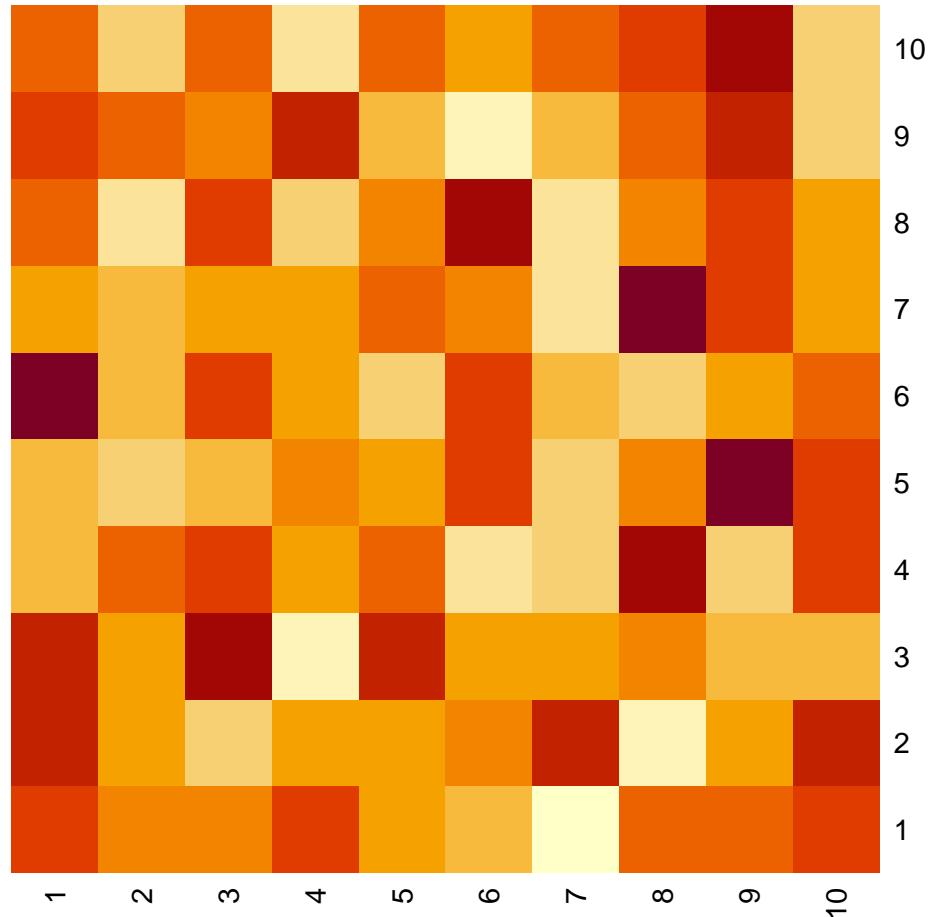
- Matrix algebra applications (*duh*), such as life history tables in biology.
- Using certain packages whose inputs require matrix objects. Matrices are particularly common in analyses of social networks.
- Producing images (after all, an image is just a matrix in which each value is a pixel color.)

To practice the latter use case, let's build up a simple matrix using a random number generator:

```
mx <- matrix(data=round(rnorm(100,50,10)),
              nrow=10,
              ncol=10)

mx
 [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
 [1,]  57   50   49   56   45   42   26   54   52   57
 [2,]  62   52   45   52   50   54   64   38   51   62
 [3,]  54   41   55   31   52   43   41   44   40   39
 [4,]  40   54   59   43   52   33   37   69   37   57
 [5,]  48   41   48   55   49   62   41   54   75   62
 [6,]  67   41   56   45   35   57   38   37   43   52
 [7,]  46   40   46   47   54   51   30   76   59   46
 [8,]  57   43   61   46   55   65   40   55   60   52
 [9,]  62   61   56   66   45   34   48   59   66   44
[10,]  58   46   60   43   57   51   59   61   68   45

heatmap(mx, Rowv=NA, Colv=NA)
```



To see a real-world example of a matrix in action, here is a dataset containing rates of social associations, scaled between 0 and 0.5, among humpback whales in the fjords of British Columbia, Canada: .

```
sociality <- readRDS("./data/humpback-sociality.rds")
```

Let's look at the first 5 rows and columns of this dataset:

```
sociality[1:5,1:5]
      id1      id2      id3      id4      id5
id1 0.50000000 0.02758621 0.00000000 0.00000000 0.00000000
id2 0.02758621 0.50000000 0.02424242 0.00000000 0.02439024
id3 0.00000000 0.02424242 0.50000000 0.00000000 0.00000000
id4 0.00000000 0.00000000 0.00000000 0.50000000 0.02631579
id5 0.00000000 0.02439024 0.00000000 0.02631579 0.50000000
```

Notice that this matrix is *symmetrical*. That is, the number of rows equals the number of columns. It is an  $N \times N$  matrix.

Also note that the row names and column names are the same. Each element in the matrix is the rate of association between the row's whale ID and the column's whale ID. This means that all of the values along this matrix's diagonal will be 0.5, which is the max association rate in this example:

```
diag(sociality)[1:10]
id1  id2  id3  id4  id5  id6  id7  id8  id9  id10
0.5  0.5  0.5  0.5  0.5  0.5  0.5  0.5  0.5  0.5
```

The fact that this matrix is symmetrical with identical rows and columns also means that all the data in the *bottom* half of the matrix (i.e., *below* the diagonal) are the *mirror image* of the data in the top half.

Look again at the first few rows and columns:

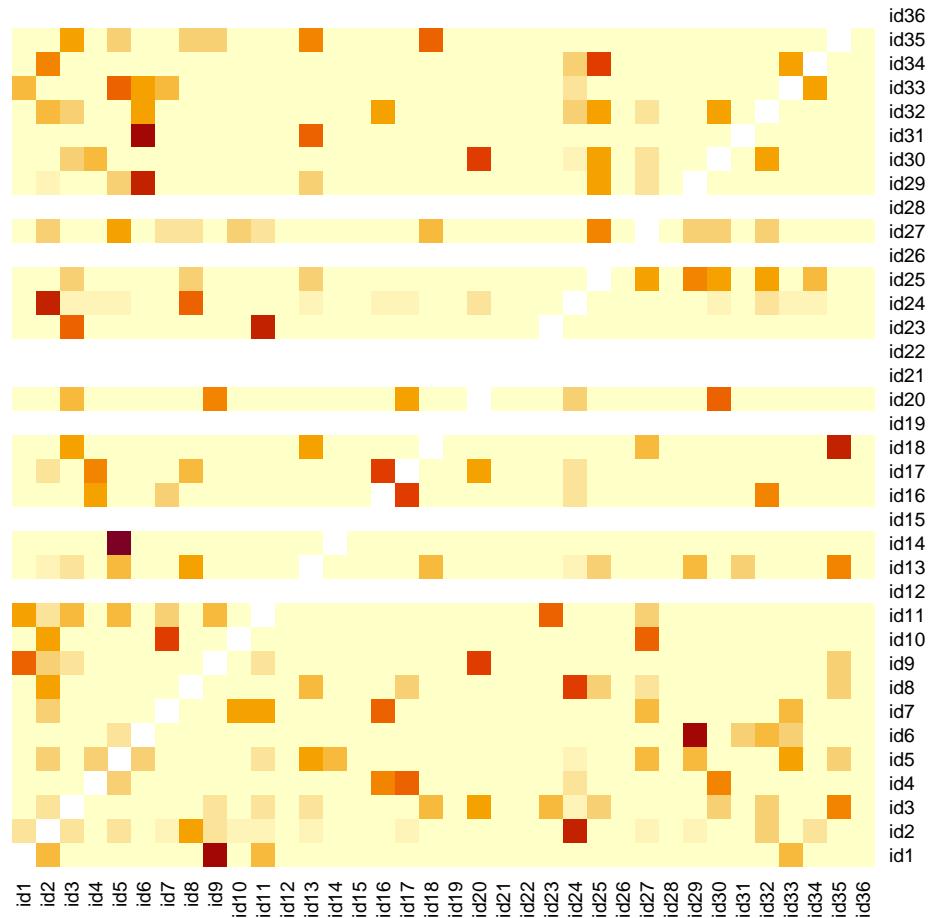
```
sociality[1:3,1:3]
      id1      id2      id3
id1 0.50000000 0.02758621 0.00000000
id2 0.02758621 0.50000000 0.02424242
id3 0.00000000 0.02424242 0.50000000
```

If we don't like the fact that the diagonal has large values (after all, it doesn't make much sense to quantify how much an individual associates with itself), we can use the `diag()` function to replace those diagonal values with `NA`:

```
diag(sociality) <- NA
sociality[1:5,1:5]
      id1      id2      id3      id4      id5
id1      NA 0.02758621 0.00000000 0.00000000 0.00000000
id2 0.02758621      NA 0.02424242 0.00000000 0.02439024
id3 0.00000000 0.02424242      NA 0.00000000 0.00000000
id4 0.00000000 0.00000000 0.00000000      NA 0.02631579
id5 0.00000000 0.02439024 0.00000000 0.02631579      NA
```

Now that we've cancelled out the diagonal, a heatmap of this dataset will show us which whales are involved in the strongest social associations:

```
heatmap(sociality, Rowv=NA, Colv=NA)
```



### Review exercise

**26.0.0.0.1 Task 1** Write a function that uses `for` loop techniques to convert any matrix, such as the `sociality` matrix above, into a dataframe. This dataframe must have a row for each value in the matrix, with three columns: `row_name`, `col_name`, and `data`.

The output of your function must be a list with two elements, `raw_matrix` and `df` (which contains your new dataframe).

Demonstrate that your function works using the `sociality` dataset above.

**26.0.0.0.2 Task 2** Then, write a function that reverses your work: this new function will take the `dataframe` output of your first function and revert your dataframe back into a matrix. The output of this function will also be a list with two elements, `raw_df` and `matrix` (which contains your new dataframe).

In this function, include an input option giving you the choice of setting the diagonal in your matrix to NA.

Demonstrate that the matrix output of your second function is the same as the original **sociality** dataset, and demonstrate that the diagonal input works as well.



# Chapter 27

## Cleaning messy data

### Learning goals

- This is a review exercise: learn the skills introduced in the previous modules by applying them to a universal data science scenario: cleaning up messy data.

### Your mission

In the module on joining datasets, we introduced a dataset of whale diving behaviour:

```
dives <- read.csv("./data/whales-dives.csv")  
  
head(dives)  
  id species behavior prey.volume prey.depth dive.time surface.time  
1 2014081106      HW    FEED     6.914610    120.76    351.00      237  
2 2014081204      HW    FEED     7.854762     79.02    281.00       87  
3 2014081207      HW    FEED     7.385667    96.92    300.25       80  
4 20140812109     FW    FEED     6.626298   105.87    366.00      189  
5 20140812131     HW    OTHER    6.356474   123.95    357.00      112  
6 20140812140     FW    FEED     3.820782   125.51    408.00      182  
  blow.interval blow.number  
1        26.833      10.000  
2        14.412      6.667  
3        16.000      6.000  
4        16.273      12.000  
5        25.250      6.000  
6        18.789      11.000
```

This dataframe is nice and tidy. Here are a few of its many tidy features:

- Each row is a single observation.

- There is not a single missing value anywhere in the dataset.
- The rows are organized from earliest to most recent, based on the data embedded in the `sit` column.
- Categorical columns have standardized formatting. In the `species` column, there are two levels: HW (humpback whale) and FW (fin whale). In the `behavior` column, there are also two levels: FEED and OTHER.

But this dataset was not always so pretty. Here is the link to the **original** data file:

**Your task in this review exercise is to write a script that carries out the necessary data cleaning steps to get this dataset from its original form to its tidy form.**

Test your work along the way, then demonstrate its completion, using the `identical()` function. If your `my_dives` version of the dataset is identical to the `dives` data above, the following logical test will be TRUE:

```
identical(dives,my_dives)
```

Enjoy!

## Chapter 28

# Excel files & GoogleSheets

Learning goals



## **Part II**

# **Interactive dashboards**



## Chapter 29

# Intro to Shiny apps



## Chapter 30

# Shiny dashboards



## **Chapter 31**

### **Data entry apps**



# **Part III**

# **Databases**



# **Chapter 32**

## **Introduction**

- 32.1 What**
- 32.2 Why**
- 32.3 When**
- 32.4 When not**



# Chapter 33

## Platforms

33.1 PostgreSQL

33.2 mySQL

33.3 SQLite



## Chapter 34

# Alternatives

### 34.1 NoSQL



# **Chapter 35**

## **Practices**

Spinning up a local DB



## **Part IV**

# **Documenting your work**



## **Chapter 36**

### **R Markdown**



## **Chapter 37**

# **Reproducible research**



## **Chapter 38**

# **Automated reporting**



## **Chapter 39**

# **Formatting standards**

**39.1 Tables**

**39.2 Figures**

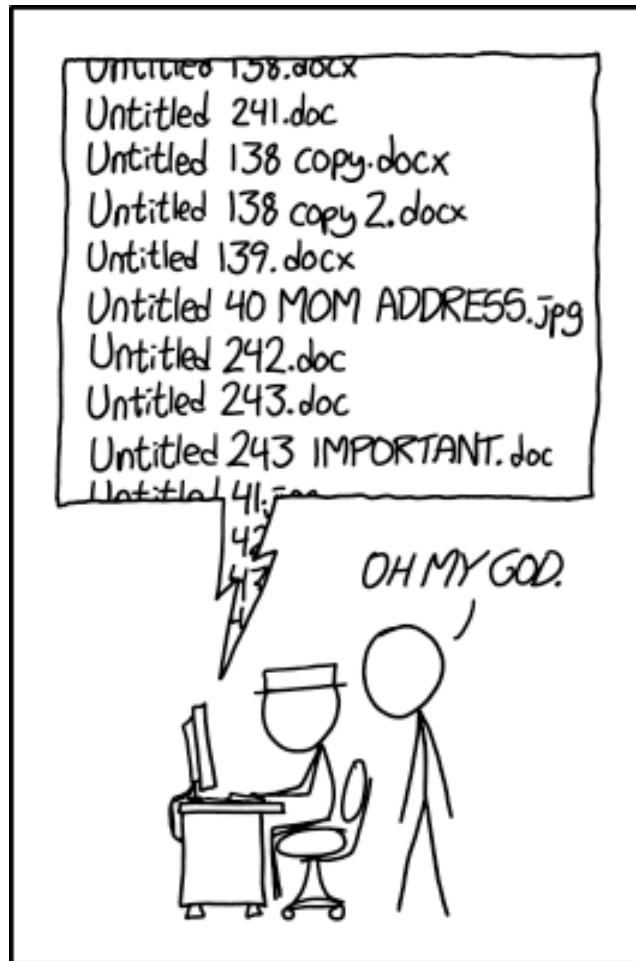
**39.3 Captions**



## **Chapter 40**

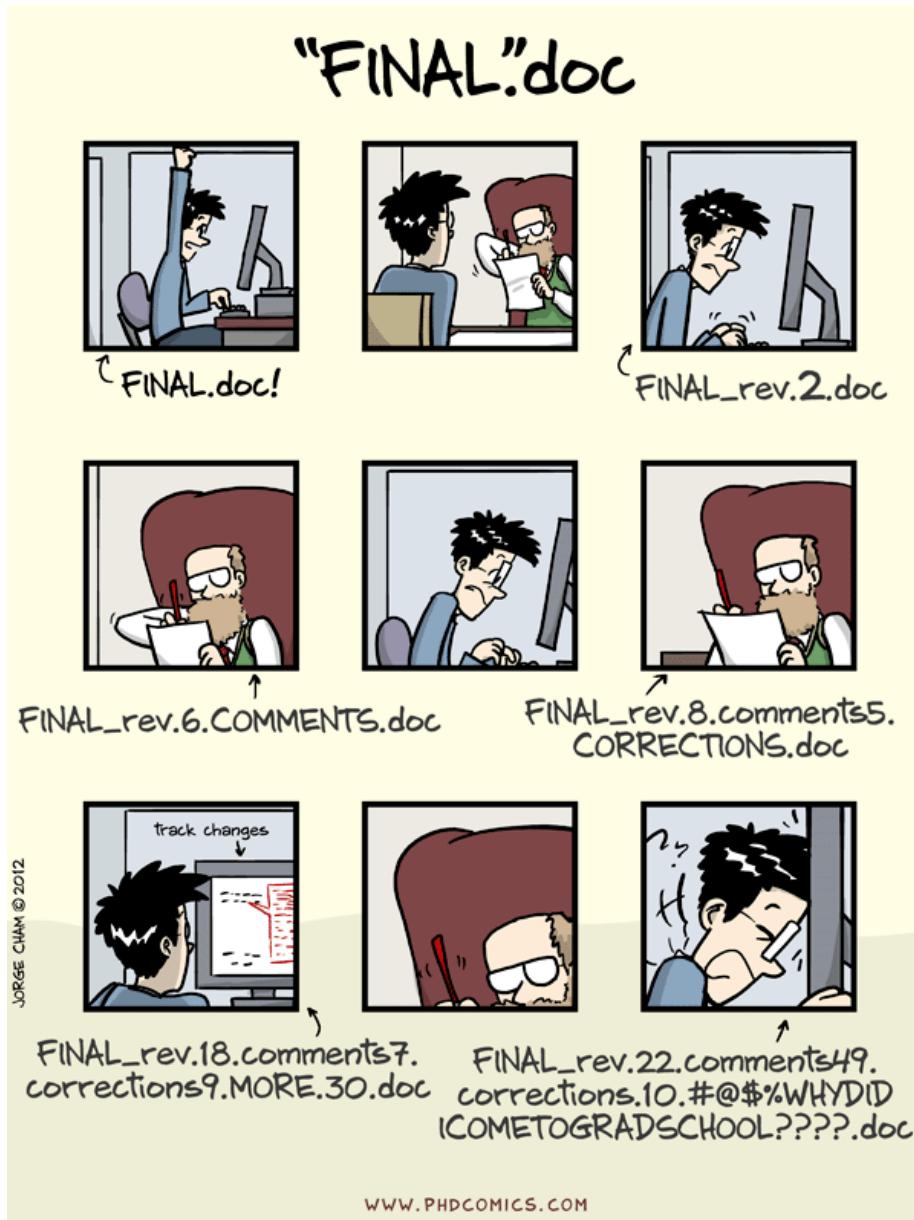
# **Git**

Perhaps the below is familiar to you...



PROTIP: NEVER LOOK IN SOMEONE ELSE'S DOCUMENTS FOLDER.

Or this...



## There is a better way

Version control systems (VCS) are software tools meant to help programmers collaborate, maintain source code, document changes, and generally keep track of their files. Instead of reading, sit back and watch this video.

Having a working knowledge of a version control system will allow you to better organize and track your own files, as well as collaborate on teams. Though there are lots of different systems out there, the most popular version control system is “git”. Let’s dive in (next chapter).

## What is git?

Git is a software for “version control”: ie, tracking changes to sets of files. It is a very commonly used tool in programming, computer science, data science, and software development in general. For anyone working in data science, knowing git is a must.

But *what is it*, exactly? Git is a system for tracking, organizing, sharing, and reviewing changes to software. It’s very flexible, and very powerful. And learning it can sometimes feel a bit overwhelming, because it has so many features and capabilities. But the Pareto principle (ie, the 80/20 rule) applies here: most of what you need to know to competently handle git, you can do in very little time.

## Why?

Why use git? Why not just save files with meaningful names, make changes to them, overwrite the old changes, etc.? Why not just treat code the same way we treat a MS Word document, or write code collaboratively using interactive, auto-saving tools like Google Docs?

There are a number reasons:

- First, writing code is not like writing a paper. If you make a mistake in the introduction of a term paper, it doesn’t “break” your conclusion. But with code, minor changes to one line of code can have a very large impact on how other parts of that code work. Therefore, tracking minor changes is essential to recovering from errors and managing complex, interdependent software components.
- Second, collaborating on code is more complex than collaborating on a term paper. To combine (merge) one person’s work with another often requires very careful review. Git optimizes for this.
- Third, code is rarely “done”. It’s usually a work in progress. Git takes this into account, and is set up for very structured checkpoints (commits), change suggestions (pull requests), etc.
- Finally, git is the “lingua franca” of version control. Employers often request to see a prospective employee’s github profile, and expect that programmers and developers of all types (including data scientists) be proficient in git.

## Get ready for git

It's time to "git" started. Rather than diving into too much theory, let's skip right to the practice. Like this:

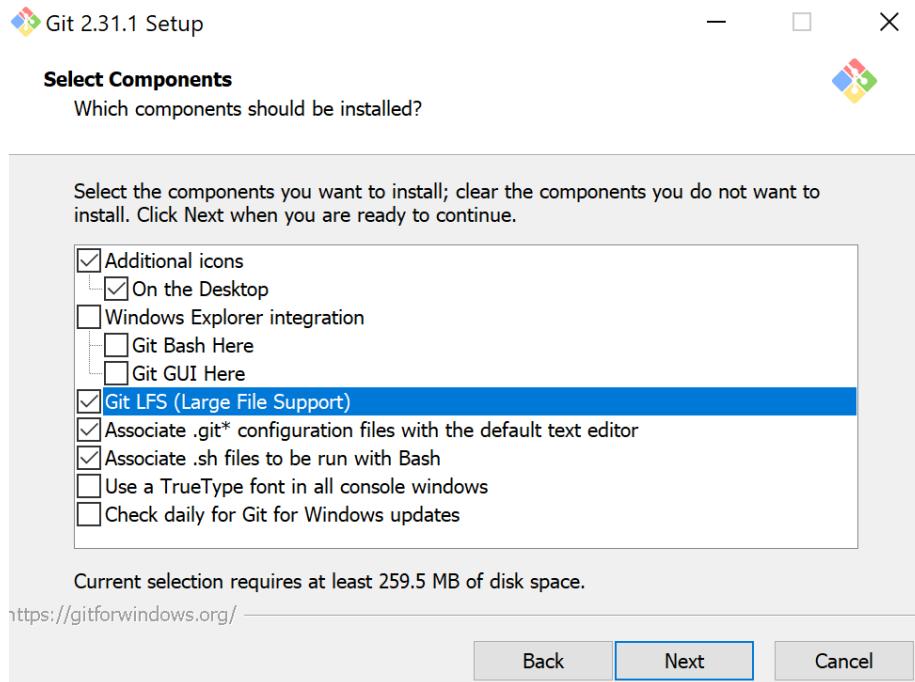


## Installation

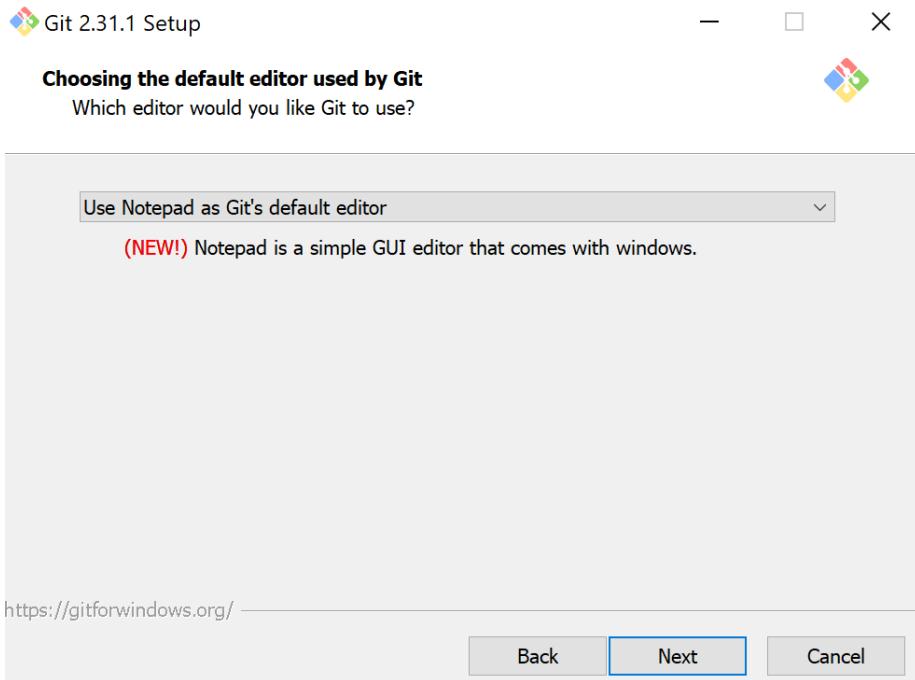
We'll start by installing git. Go here and follow the instructions for your operating system.

### Windows

On windows, once you've downloaded, you'll want to select the below parameters:

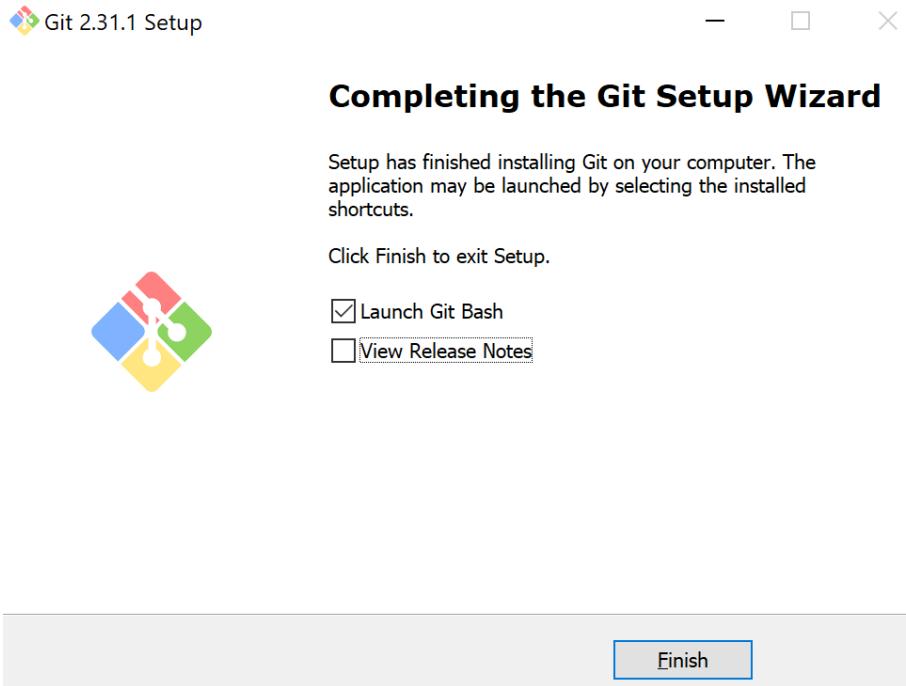


The program will prompt you to pick a text editor. Select notepad.

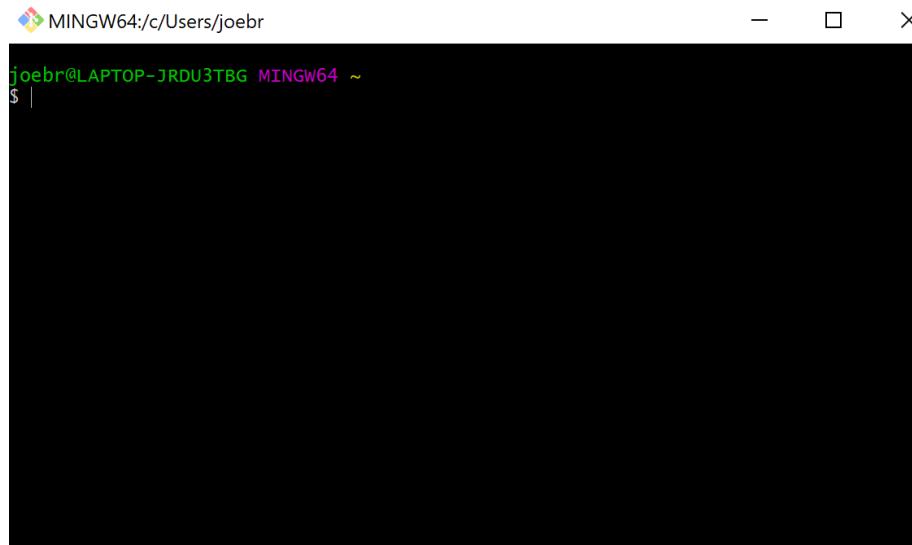


For all other options, leave settings as default and click “next”. The program will now install.

After installation, there is an option to “Launch Git Bash”. Click it.



This will open a “terminal” window:

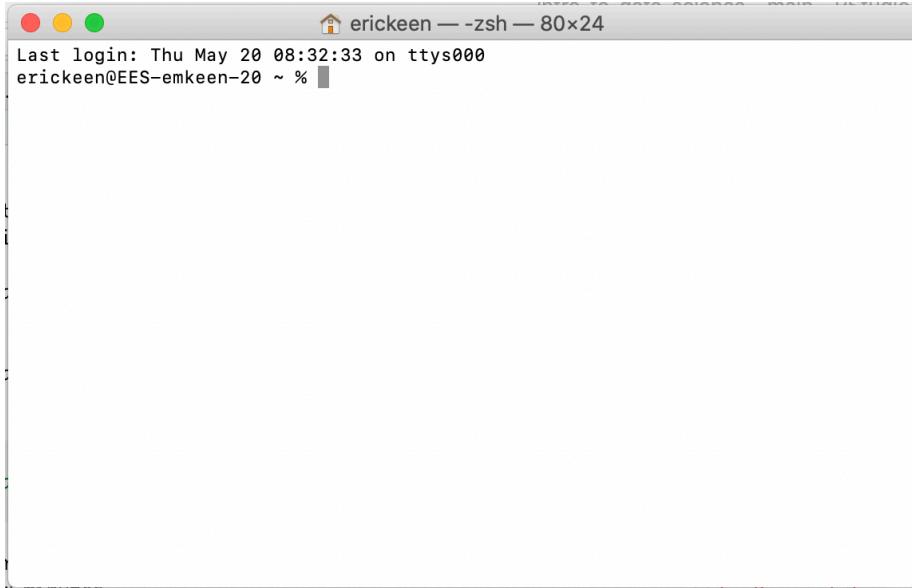


## Mac

To get Git on your Mac, you will be typing commands into your computer’s Terminal. “Terminal” is the Mac word for the “Git Bash” window you will be

using in the next section.

1. To open Terminal, open the Mac Search (Command + Spacebar) and search “Terminal”. Press **Enter**. A Terminal “shell” window will appear:



2. Next we need to download and install a software management tool called Homebrew. Copy and paste the following command into your Terminal, and press **Enter**:

```
/bin/bash -c "$(curl -fsSL https://raw.githubusercontent.com/Homebrew/install/HEAD/install.sh)"
```

You will likely be asked for your computer password. Press **Enter** when instructed to do so. Downloading Homebrew might take a few minutes.

3. Now that Homebrew is installed, copy and paste the following command into your Terminal, and press **Enter**:

```
brew install git
```

After a minute or two, Git should be downloaded, installed and ready to go.

## Getting to know git bash

The strange little black box you’re looking at is called “Git Bash”. Bash is a command line language/interface. In other words, it’s a way to interact with your computer without pointing and clicking. You type code, and the computer does things. It’ll feel a bit unfamiliar at first, but don’t worry - there are just a few commands you need to know to work with git. We’ll use the terms “bash”,

“command line”, and “terminal” interchangeably (though in reality these are a bit different).

### **pwd**

Let’s start with **pwd**. This stands for “path to working directory”. Type it, press enter, and see what happens.

If everything went to plan, you’ll see a path (ie, a location within your computer’s file structure). “Working directory” means the folder you are “in” right now. Just like with a point-and-click program for exploring folders, you can navigate between folders using bash / terminal.

When you typed **pwd** you were asking your computer which directory (folder) you’re in. It responded. Great! Now let’s see what else is in the folder where you are.

### **ls**

Type **ls**. This stands for “list” as in ”list all the files in this directory. **ls** is commonly used to quickly see contents of a folder.

### **cd**

You now know how to (a) see where you are and (b) see what else is there. But what about navigation? Let’s say you want to “move around” (ie, go to other folders). You do this using the **cd** command, which stands for “change directory”.

After typing **cd**, you should type a space and then the name of the directory you want to navigate to. This directory can be either (a) relative or (b) full. “Relative” means relative to where you are. So, for example, if you are currently in the following folder:

```
/home/abc/folder1
```

And within that folder you have the following sub-folders:

```
foldera  
folderb  
folderc
```

You could navigate to one of them by typing the full path:

```
cd /home/abc/folder1/foldera
```

Or by typing the relative path:

```
cd foldera
```

Both of the last two commands have the same result: changing your working directory to `/home/abc/folder1/foldera`.

What about if you want to navigate “up” to the `/home/abc` folder. Again, you can do this using relative or full paths. To navigate there with the full path, simply type:

```
cd /home/abc
```

To go “up” one level using a relative path, use ... So:

```
cd ..
```

So far so good. Now you can (a) see where you are with `pwd`, (b) list folder contents with `ls` and (c) navigate with `cd`. Those 3 command will cover 80% of what you’ll need to do to use git from the command line.

## Configuration

Once you’ve installed git, you’ll likely want to configure some options and preferences. Go here and walk through the steps.

## Github

Now you’ve got git. Great! Git is often used in conjunction with a third party, web-based platform. The most popular is github. Go to [www.github.com](http://www.github.com) and create a user account.

### Creating a repository

Once you’ve created an account and logged in, let’s create a repository. What is a repository? Basically, it’s a project in the form of a folder. Having logged into git, click the “plus” icon in the upper right and then click “New repository” (or go directly [here](#)).

You can fill in the “Repository name” field with whatever you’d like. For the following examples, we’ll use the word “testrepo”.

Fill in the “Description” field with the word “My first git repository”.

Set the repo as “Public” (unless you plan on putting any secrets here!), and then click the “Add a README file” checkbox. Finally, click “Create repository”.

Cool! You’ve now created your first git repository. It’s public url is <https://github.com//testrepo>. Others can see your code there, and you can too.

### Cloning a repository

“testrepo” exists on the internet, but does not yet exist on your local machine. In order to get “testrepo” on your computer, you’ll need to do something that you’ll only do once: “clone” the repo. “Cloning” in git-speak means creating a copy of the repository locally.

To clone, you'll first open your terminal window and `cd` into a directory where you'd like to clone your repo. For example, if you want to put your `testrepo` directory into `~/Documents`, you'll type the below into terminal:

```
cd ~/Documents
```

You can confirm that you are in `~/Documents` by typing: `pwd`. There? Good.

Now, we'll write the code to "clone" `testrepo`:

```
git clone https://github.com/<USERNAME>/testrepo
```

Now, you've got a folder on your machine named `testrepo`. You can confirm this by writing `ls` in the terminal. See `testrepo` there? Great!

## Writing some code

In your local `testrepo` folder, you have a "cloned" copy of the repository at `https://github.com//testrepo`. As of now, it's a pretty uninteresting folder. The only thing in it is a file named `README.md`. A "README" file is generally an explanation of a repository's content, purpose, etc. Like all files, a README can be tracked in git.

Let's open the `README` file and make a change to it. We'll add the below line of "code":

```
This is my first git repository.
```

The save and close the `README` file.

Now, let's ask "git" if it noticed if we had made any changes. Type the below into terminal:

```
git status
```

If everything has gone well until now, git will reply by telling us that we've made a change to the file. We can ask git *what* change we made by typing:

```
git diff README.md
```

`diff` stands for "difference", as in "what is the difference between the code I had and the code I have. Git will spit back some color-coded lines showing the change you've made.

Satisfied with your change? Great, now it's time to confirm it by doing the following:

```
git add README.md
```

This tells git that we want it to notice and track the change we made to `README.md`. Then:

```
git commit -m 'my first change'
```

This tells git that we are “committing” our change, it marking a checkpoint (to which we can revert later). The `-m` flag is followed by a message in quotations which will help us to navigate this checkpoint in the future.

Almost there. Now that we’ve added and committed, we need to “push” our change to the remote repository (github), by running:

```
git push
```

You did it! Go to <https://github.com//testrepo> and open the `README.md` file. You’ll notice that your most recent changes are there. Now, if someone else wants to get your code, they can “clone” your repository, and they’ll have the code you’ve “pushed” there.

## A bit more practice

### Creating another repo

Let’s face it: `testrepo` is a pretty lame name for a repository. How about we make a repo that’s actually real and useful? We’ll make one for storing all the code we’re writing in this course.

Go to <https://github.com/>

Click the “plus” icon in the upper right and then click “New repository” (or go directly here).

Now, for “Repository name”, write “`datascience`”.

Fill in the “Description” field with the words “Code I wrote during my intro to data science course”.

Set the repo as “Public” (unless you plan on putting any secrets here!), and then click the “Add a `README` file” checkbox. Finally, click “Create repository”.

Cool! You’ve now created your first git repository. Its public url is <https://github.com//datascience>. Let’s clone it:

```
git clone https://github.com/<USERNAME>/datascience
```

Now, you’ve got a folder on your machine named `datascience`. You can confirm this by writing `ls` in the terminal. See `datascience` there? Great!

Now, let’s move *everything* you have written for this course so far into `datascience`. Do this in an organized fashion. Remember to not put anything secret there.

### The `.gitignore`

If you `cd` into `datascience`, and then type `git status`, you might note that it’s a bit “busy”. That is, there are a lot of documents there! You’re going to

want to (i) add, (ii) commit, and (iii) push these documents, but perhaps there are some kinds of documents you *don't* want to push.

For example, maybe you want to push R code files (`.R`), but not data files (`.csv`). In this case, you can explicitly tell git that you don't want it to pay any attention to `.csv` files by creating a `.gitignore` file. A `.gitignore` file is simply a text file in a git repository that indicates to git that the contents of that file should be ignored.

Let's do it. First, create an empty `.gitignore` file:

```
touch .gitignore
```

Then, open the `.gitignore` file in RStudio.

Finally, add the following line to it:

```
*.csv
```

The star is a “wildcard”, meaning that it stands in place of anything (such as `ducks.csv` or `data.csv` or `xyz.csv`).

With this in your repo, git now knows to ignore anything that ends with the extension `.csv`.

Good? Great. Push everything to your repo. Now you can share your code with others, and your future self.

## Advanced git

Branching, pull requests, blaming, and more - in a break-out session.

## **Part V**

### **Sharing research**



# Chapter 41

## Sections of a report

### Learning goals

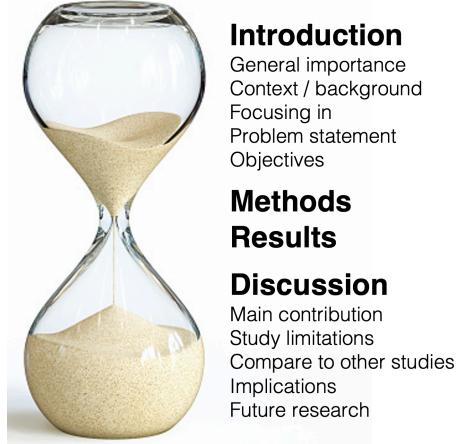
- Understand the over-arching structure and narrative flow of a research paper
- How to write each section of a paper

### Overall structure

Data reports, research papers, and scientific publications follow the same basic narrative flow:

- **Abstract:** Concise summary. This section can also be referred to as an *Overview* or *Executive Summary*.
- **Introduction:** A background section that provides context and justifies the ways that the report is important and adds value.
- **Methods:** Detailed description of what was done and how data were analyzed.
- **Results:** A concise report of what was found, drawing upon narrative prose, data tables, and figures.
- **Discussion:** Considerations and interpretations of the results' significance, limitations, and consequences for the field of study.
- **Other stuff:** Acknowledgments, literature cited (i.e., references), tables, and figures.

These sections map onto a high-level conceptual flow: a **research paper is like an hourglass**.



Your *Intro* narrows from a point of common and general interest to an articulation of a *specific* knowledge gap and a *focused* purpose. Your focus remains narrow as you cover your study's *Methods* and *Results*. Only in the *Discussion* does your paper begin expanding out again to place your findings in the context of other studies and consider your findings' implications on broader issues. Your paper ends as broadly as it began: a point of common interest and importance, this time focused on future concerns and priorities.

In this module, we will cover how to adhere to this narrative arc while meeting the standards and expectations of each individual section.

## Abstract

An *Abstract* is a concise and sharp distillation of your paper.

### Standards

A strong *Abstract* section will answer “*Hell yes!*” to all of the following questions:

- 1. Is your abstract actually a helpful overview?** That is, is your abstract a *specific summary of your paper's content*, rather than a vague overview of its organization? As a good example of what *NOT* to do, in 1951 a geologist published an opinion article, “*A Scrutiny of the Abstract*”, about how abstracts should and should not be written. He decided to make his article's abstract sarcastic:

BULLETIN OF THE AMERICAN ASSOCIATION OF PETROLEUM GEOLOGISTS  
 VOL. 35, NO. 7 (JULY, 1951), PP. 1660-1680, 10 FIGS., 1 PLATE

## GEOLOGICAL NOTES

### A SCRUTINY OF THE ABSTRACT<sup>1</sup>

KENNETH K. LANDES<sup>2</sup>  
 Ann Arbor, Michigan

#### ABSTRACT

The behavior of editors is discussed. What should be covered by an abstract is considered. The importance of the abstract is described. Dictionary definitions of "abstract" are quoted. At the conclusion a revised abstract is presented.

Avoid this style! There is a way to summarize that avoids any helpful information, and there is a way to summarize that provides an *executive summary* of your work. Aim for the latter.

At the end of the above paper, the author provided a *good* version of his abstract:

#### ABSTRACT

The abstract is of utmost importance, for it is read by 10 to 500 times more people than hear or read the entire article. It should not be a mere recital of the subjects covered. Expressions such as "is discussed" and "is described" should *never* be included! The abstract should be a condensation and concentration of the *essential information* in the paper.

2. Does your abstract adhere to the Abstract Recipe detailed below?
3. Does your abstract fit within the word limits provided by the assignment or instructions? Most *Abstract* word limits range between 250 and 300 words.

### Strategies

There are hundreds of approaches to writing an *Abstract*. (For proof, just type "how to write an abstract" into *GoogleScholar*!) In your first few tries at writing your own abstract, we recommend the following approach.

Every single sentence serves a specific purpose, outlined in the following **Abstract Recipe**:

- **Sentence 1:** establishes broad interest and the relevance of your topic.
- **Sentence 2:** articulates your problem statement.
- **Sentence 3:** articulates your research question and study objectives.
- **Sentence 4:** summarizes your data collection methods.
- **Sentence 5:** summarizes your statistical approach.

- **Results sentences:** The next few sentences (2 - 4) summarize your most important results. This is the most important part of your *Abstract*, since it tells the reader what your study is contributing to the world, and as such it should be the longest portion of the paragraph.
- **Discussion sentences:** Use one to two sentences to explain the importance and implications of your findings.
- **Final sentence:** summarizes recommendations for future research (“Future research on this topic should focus on...”) and/or emphasizes the implications and importance of the findings.

Like a professional chef, professional academics may adjust this recipe as they see fit, but nearly all good abstracts conform to this general formula.

### Good example

Below is the abstract from a publication whose first author is an undergraduate student (Zeitler et al. 2021, *Journal of Environmental Management*). This a strong abstract that maps almost perfectly to the recipe above.

1. Broad interest & relevance	Constructed wetlands (CWs) are a potential solution for wastewater treatment due to their capacity to support native species and provide tertiary wastewater treatment.
2. Problem statement	However, CWs can expose wildlife communities to excess nutrients and harmful contaminants, affecting their development, morphology, and behavior.
3. Objectives	To examine how wastewater CWs may affect wildlife, we raised
4. Methods & analyses	Southern leopard frogs, <i>Lithobates sphenocephalus</i> , in wastewater from conventional secondary lagoon and tertiary CW treatments for comparison with pondwater along with the presence and absence of a common plant invader to these systems – common duckweed ( <i>Lemna minor</i> ) – and monitored their juvenile development for potential carryover effects into the terrestrial environment.
5. Results	The tertiary CW treatment did not change demographic or morphological outcomes relative to conventional wastewater treatment in our study. Individuals emerging from both wastewater treatments demonstrated lower terrestrial survival rates than those emerging from pondwater throughout the experiment though experiment-wide survival rates were equivalent among treatments. Individuals from wastewater treatments transformed at larger sizes relative to those in pondwater, but this advantage was minimized in the terrestrial environment. Individuals that developed with duckweed had consistent but marginally better performance in both environments. Our results suggest a potential trade-off between short-term benefits of development in treated effluent and long-term consequences on overall fitness.
6. Discussion sentences (interpretation)	Overall, we demonstrate that CWs for the purpose of wastewater treatment may not be suitable replicates for wildlife habitat and could have consequences for local population dynamics.
7. Final sentence (implications)	

## Introduction

An *Introduction* is an information-rich and persuasive *argument* for the importance of the contribution your paper will be making to the field of study.

### Standards

An *Introduction* has to do many things at once. Here are the necessary elements of a quality *Intro*:

1. **Engage & Justify.** The entire Introduction is a carefully crafted, convincing argument for the importance of your topic and the urgent need for your research.
2. **Establish context & convince readers to care.** Early into the Intro, place your topic in a broad context. Make it clear who should be interested in your topic.
3. **Invite readers in.** A good Intro is an accessible one; it should not send the message that only experts will get something out of the paper.
4. **Get everyone on the same page.** Mention and explain any concepts that will be crucial to understanding your methodology, interpreting your results, or intuiting the impact of your work.
5. **Demonstrate authoritative knowledge.** Demonstrate exhaustive knowledge of the topic, and sharp awareness of the ‘state of the science’.
6. **Demonstrate basis in previous research.** Aim for a 1:1 ratio of citations to sentences. Each sentence should end with a citation. Your Introduction is an *assemblage of previous findings* strategically arranged to identify a knowledge gap and set the stage for your own study. (*See Literature Review details below.*)
7. **Provide more than a history lesson or a list of facts.** Your Introduction is a tightly organized and persuasive argument, not a brain dump or an aimless encyclopedia entry. Your deep knowledge of the field ought to be sprinkled throughout, *interspersed within your narrowing arc*.
8. **Narrow in on a problem statement.** The entire Intro should narrow to a *problem statement* (a knowledge gap, an urgent need). Along the way, you are garnering reader buy-in (yes, this is important) which causes them to care about the gap you have identified.
9. **Follow with a motivation/objectives statement.** Your study is a response to the problem statement. “To address this knowledge gap, I developed a study based upon the following objectives...”

*Examples of problem statements & hypotheses / aims:*

In the examples below, the problem statement is in boldface & the objectives/aims statement is italicized.

- “**Although there have been several modern investigations of cladogenesis and tree shape [2], [3], the manufactory hypothesis has not, to our knowledge, been tested since Darwin...** *This paper follows Darwin by examining autocorrelation among ancestral and descendent branches of the tree at the level of subspecies through genera and we also extend the comparison to the level of families.*” (from Haskell & Adhikari 2009)

- “Few efforts explicitly quantify the consequences of including demand into conservation efforts to safeguard [Ecosystem Services] and biodiversity (Wolff et al. 2015; Verhagen et al. 2016). We aimed to quantify differences between supply and benefit within the context of conservation planning. We addressed 3 questions: How does incorporating demand shift the spatial distribution of benefits relative to supply? How much benefit is captured by conservation efforts that target supply? How do efforts targeting supply and benefit compare in terms of their biodiversity outcomes?” (from Watson et al. 2019)

There are plenty of good and bad examples of *Introductions* in scientific publications. Here are a few recommendations for excellent introductions that follow the rules above. Note how each example demonstrates how to achieve the necessary conceptual arc while maintaining a large ratio of citations to sentences (nearly every sentence has at least one citation).

- See Watson et al. 2019 for a sharp and concise *Intro*.
- See Pitman et al. 2019 for an extensive introduction with excellent writing.

### Strategies

With so much to cover in an Introduction, it can be difficult to know where to begin. There are two main steps to preparing an *Introduction*: (1) reviewing literature, and (2) writing. Begin with the literature.

**41.0.0.0.1 1. Conducting a literature review** Carrying out a literature review can be daunting, especially if you are new to a field of study.

But regardless of your level of experience, you can follow a **common basic workflow**. The overall goal is to **dive into the literature**, follow rabbit holes, and take notes until you begin to feel familiar with the canon of knowledge on your topic. That feeling of familiarity will come once you stop finding new studies in the literature cited sections of the papers you are reading, and once you start to recognize the names of the most prolific and influential scientists in your topic of interest.

**a. Find your first paper to review.** Begin your search on *GoogleScholar* scholar.google.com. You may need to search other search engines eventually (e.g., JStor, PubMed, etc.), but this is a good place to start.

The most productive starting point is looking for recent *review* articles on your topic. Reviews try to be definitive and exhaustive in their list of references. They also point to the studies that were foundationally important in the early days of your topic, as well as to the “cutting edge”: the most recent and exciting developments in the literature.

**b. Open up a scratchpad for taking notes** in *Word* or *GoogleDocs*. Type (or screenshot) the citation for your first article to the top of your scratchpad

(e.g., Keen EM and Brew JR. 2021. Ping pong: the Sport of Kings? *Table Tennis Weekly* 56(1): 343-356.)

- c. **Begin reading & taking notes.** Don't sit down to read it word for word. Read it *selectively* for the topics and details that are most relevant to your work. If your first paper is a research article (i.e., with sections on Methods and Results) instead of a review, focus on its Introduction and Discussion. Your notes should be brief. If you are copying language from the paper word for word, place it in quotes so that you can remember what needs to be paraphrased at a later time. In each note that involves a reference to a separate article, include that reference in your note (e.g., Puckette et al. 2021) so you can track it later.
- d. **Copy down all references** that are included in your notes using the literature cited section. This can be tedious but it will pay off in the long run.
- e. **Clean up your notes for this first paper.** Make sure *every single* note has a parenthetical citation attached to it, so you don't lose track of where it came from. If the note is a direct contribution from the paper you have reviewed, add the reference for that paper to your note (e.g., Keen & Brew 2021).
- f. **Select one of these references as your second paper to review.**
- g. **Repeat.** Until you begin to feel familiar with the current literature and stop being surprised by new studies.

*Once you reach a familiarity plateau (shoot for 80% expertise), pause your literature review!* For a peer-reviewed article submitted for publication, anything less than 30 reviewed papers is highly unlikely to provide a sufficient grasp of the state of your field of study (most studies cite many times this number).

**41.0.0.0.2 2. Organizing and writing your Introduction** You now know enough about the literature now to have a basic sense of what is currently known and not know about your topic.

- a. **Write your problem statement,** the *gap in knowledge* the justifies and motivates your study.
- b. **Articulate your hypotheses and/or objectives** Frame these as a way of *addressing* or *ameliorating* the problem statement.
- c. **Determine your starting point.** Choose your audience, your hook, and the initial direction of your conceptual flow. This is arguably the most difficult part of the writing process.
- d. **Outline the narrative path from your starting point to your problem statement,** with the key step in your argumentative arc must be, and therefore what the purpose of each paragraph must be.
- e. **For each paragraph, articulate the main point or key idea.** This sentence can typically serve as the first sentence of the paragraph (or in some cases the last).

- f. **Sort your notes into each paragraph.** Some notes may be useful in multiple paragraphs, in which case you can copy them rather than just moving them. This is why it is *critical* that you add a parenthetical citation for the source of each reference. Otherwise you will lose track of which content comes from which source!
- g. **Sort your notes *within* each paragraph.** Each paragraph has its own narrative flow, taking the reader from concept A to concept B using a *sequence* or *chain* of evidence-based claims. How do your notes need to be organized in order to build that chain?
- h. **Determine the *holes* in your literature review.** As you organize your notes into an argumentative sequence, you will find “holes” in your argument that require substantiation with an as-yet undiscovered reference. This will guide your *second stage* of literature review (see next steps).
- i. **Now begins an iterative process** of writing, seeking new references, and reorganizing your writing. Iterate until satisfied. Once you are satisfied, ask a colleague to review your writing, not only for grammatical errors and typos, but also with an eye toward the overall arc. Where is your argument weakest? How can it be reorganized? Incorporate their feedback and repeat.

## Methods

Your *Methods* section provides all the detail necessary to (1) understand how you collected data, (2) understand how you analyzed the data, (3) how to interpret the results, and (4) reproduce your study (at least in principle).

### Standards

A strong *Methods* section will answer “*Hell yes!*” to all of the following questions:

1. **Do your methods make sense** based upon the research question and the objectives stated in your Introduction? For example, if your goal is to understand the risks of a new drug, it would not make sense if you were measuring seismic activity near a volcano. That’s a dumb example, but you get the idea: what you *do* should actually answer your *research question*.
2. **Is your research and analysis fully reproducible**, based upon the level of detail and quality of explanation in your Methods section?
3. **Is your analytical approach appropriate** given your objectives and the limitations of your data? For example, if you are interested in the correlation between two variables, it would not make sense to use a *t-test*.
4. **Is your analytical approach properly thorough?** Are you doing everything you can with the data you have, within the confines of a your project’s

scope and objectives? Data are valuable and difficult to come by. Are you learning everything you can regarding your research question from the data you have collected? (*Note that it is possible to go too far here, i.e., to include analyses that have nothing to do with your research question. The key is to be thorough but focused.*)

**5. Is your Methods section written clearly, concisely, and with precision?** See the Module on Style for guidance.

Use the papers you found during your literature review for examples of what is included in *Methods* sections within publications related to your topic, and the style in which that material is written.

### Strategies

- Your *Methods* section will likely be the thing you write second, immediately after you develop your research question, objectives, and hypotheses. Writing your *Methods* in full and with detail will help you uncover mistakes with your sampling design and/or analyses before it is too late.
- Most *Methods* sections have a few distinct subsections: Study area, Data collection, Data analysis.
- Most *Methods* sections are written in the past tense.
- Do not hesitate to use tables or diagrams to present details of data collection.

## Results

The *Results* section is a concise narrative of your findings, *without* interpretation or commentary on the importance and consequences of your findings.

### Standards

A strong *Results* section will answer “*Hell yes!*” to all of the following questions:

1. **Are your results complete** based on the analyses you described in your *Methods* section?
2. **Is your Results section organized as a coherent narrative** that is directly related to your research question, and not just a list of seemingly random findings?
3. **Are your findings and conclusion appropriate**, given the limitations of the data and the methods you employed?
4. **Are tables and figures included where appropriate?**
5. **Are tables and figures referenced correctly** within the text of your results? See the next Module on Style for guidance.
6. **Does your Results section contain results only**, and not any methodological details that should

have been in the *Methods*, nor interpretation commentary that would be more appropriate in the *Discussion*?

**7. Is your Results section written clearly and with precision?** This is especially important with respect to the inclusion of statistical results. Again, for guidance see the next Module on Style.

Again, use the papers you found during your literature review for examples of what is included in *Results* sections within publications related to your topic, and the style in which that material is written.

### Strategies

- It is usually best to produce your tables and figures *first*, then write your *Results* narrative around those assets.
- You want your tables, figures, and narrative to be *strategically redundant*. Your tables and figures represent the detailed version of your *Results*; they are the raw numbers that answer your research question. Your *narrative* should refer constantly to the raw results presented in your tables and figures, but they should not repeat them. Your narrative *summarizes* the tables and figures and frames your findings with respect to how they address your research question. Minimize the numbers you include in your results, but be sure to include the most important ones.
- Aim for a parallel structure in your *Methods* and *Results*. Present your results in the same order in which you explain your methodological process. This makes it easy for readers to go back and forth between the two sections as they make sense of what you found.
- Most *Results* sections begin with a brief paragraph summarizing the data that were collected: dates of collection, sample size, and any other context that a reader might need to understand the analytical results that will come in the proceeding paragraphs.
- Usually, the most difficult thing about writing a *Results* section, other than writing an intelligible story instead of a list of facts, is to *keep your Discussion out of your Results*. The results section is a straightforward report of what you found, without commentary on the importance or implications of those findings.
- That said, you will still have to make some editorial decisions in your *Results* section. Which findings will you emphasize with narrative prose, and which will you simply refer to using a table or figure? Which findings are misleading if the reader fails to keep certain aspects of your methodology in mind, and how can you frame those findings to avoid misinterpretation?

## Discussion

The *Discussion* is where you interpret your results, discuss the limitations of your study, place your findings within the context of the literature, highlight the contributions and implications of your findings, and identify future directions of research.

### Standards

The *Discussion* is probably the most variable and unstructured section of a report, and can therefore be the most difficult to write. For your first few attempts at writing a *Discussion*, we recommend adhering to the recipe we outline below. A strong *Discussion* section will have the following components or subsections:

**The opening paragraph** is a brief summary of your most important results that highlights the findings that make your study important. Think of this paragraph as a ‘hook’ that convinces readers they should read the rest of your *Discussion*.

**Subsection on Study Limitations.** This subsection allows you to (1) place boundaries on how you are able to interpret your results given the limitations or unexpected issues that arose from your methods, and (2) identify areas in which your study could be improved if it were reproduced in the future.

**Subsection on Interpretation of Results.** Use this subsection as an area to highlight and explore your findings, what they mean, and what the important takeaways are.

**Subsection on Comparison to Previous Studies.** Use this subsection to place your findings within the context of other research. Are your results in line with previous findings? Are they surprising? If so, why might that be? If it is difficult to compare your study to others, explain why. This is a chance for you to control the conversation in the event that others try to compare your study to other literature.

**Subsection on Study Implications.** Use this subsection to articulate how your findings relate to your study objectives, address your research question, and are important in a broad sense. Why do your results matter? What implications do they have for the issues, places, and people you are focused on in this project? How might your findings influence future policies, technological innovations, or other changes?

**Subsection on Suggestions for Future Research** with a concluding statement that reinforces the importance and contribution of your project.

Usually, strong *Discussions* refer regularly to the concepts introduced in the *Introduction*. This makes sense, since your *Discussion* is exploring the ways in which your new findings have contributed to the body of knowledge and gaps in knowledge articulated in your *Intro*. If your *Discussion* is not addressing the

same issues raised in your *Intro*, you may need to restructure and reframe one or both of those sections.

Most of the papers you collect for your literature review will have their own variation on this recipe. Some sections will be more relevant and extensive than others, depending on your topic and findings. Use your literature collection to get a sense of writing style for *Discussions*.

## Other elements of a report

### Acknowledgments

A brief statement of whom you thank for their contributions and support of your project. Be sure to include any sources of funding, equipment, analytical assistance, or other resources.

### Literature Cited

- Be sure that every reference mentioned in the body of your report has a full citation in this section.
- Conversely, make sure that every full citation in this section has a corresponding reference within your report. Remove all un-referenced citations!
- See the Module on Style for details on how to format your references and citations.

### Tables

- Present and enumerate tables in the order they are referenced in your report.
- Ensure that each table has its own caption placed *above the table*.
- See the Module on Style for details on how to create and format tables.

### Figures

- Present and enumerate figures in the order they are referenced in your report.
- Ensure that each figure has its own caption placed *below the figure*.
- See the Module on Style for details on how to create and format tables.

### Other resources

“How to Write a First-class Paper”, by the editors at *Nature*

## Chapter 42

# Formatting, structure & style

### Learning goals

- Understand the principles of good research writing
- Gain practical skills in formatting the elements of a research report

There are thousands of resources available in print and online to support students who are trying to improve their scientific writing. The recommendations offered below are by no means exhaustive, and by no means are they the only way. Our aim here is to *get students started* on the right track. Our underlying premise is that good writing in research is the *same as good writing anywhere else*. The same basic standards apply.

The best single resource we know of is a 1990 article in the *American Scientist*, “The Science of Science Writing”, by George Opan and Judith Swan. Most of the concepts and examples below are distillations from that article.

### Core principles

Opan and Swan (1990) offer many fundamental principles for strong scientific writing, but they all stem from the same core idea: **Write with the reader in mind.** It is not enough to have all the correct information on the page; that information must organized and presented in ways that helps the reader understand.

To illustrate this point in a brief example, they show three different ways to present the same information:

*Option 1:*

“Our results were t(time)=15’, T(temperature)=32°, t=0’, T=25°; t=6’, T=29°; t=3’, T=27°; t=12’, T=32°; t=9’, T=31°”

*Option 2:*

time (min)	temperature(°C)
0	25
3	27
6	29
9	31
12	32
15	32

*Option 3:*

temperature(°C)	time (min)
25	0
27	3
29	6
31	9
32	12
32	15

Which of these is easiest to interpret? Why?

In short, *place information where readers expect to find it*. This applies broad organization, such as keep all methodological details within the *Methods* sections, or deciding which information to place in tables and which to write out in the narrative of your *Results* section, but it also applies to writing at the sentence-level. In every sentence readers take in, they have subconscious expectations about how coherent ideas will be structured. Shape your sentences to meet those expectations.

Opan and Swan (1990) provide a good example of really bad writing:

*“The smallest of the URF’s (URFA6L), a 207-nucleotide (nt) reading frame overlapping out of phase the NH2-terminal portion of the adenosinetriphosphatase (ATPase) subunit 6 gene has been identified as the animal equivalent of the recently discovered yeast H+-ATPase subunit 8 gene. The functional significance of the other URF’s has been, on the contrary, elusive. Recently, however, immunoprecipitation experiments with antibodies to purified, rotenone-sensitive NADH-ubiquinone oxidoreductase [hereafter referred to as respiratory chain NADH dehydrogenase or complex I] from bovine heart, as well as enzyme fractionation studies, have indicated that six human URF’s (that is, URF1, URF2, URF3, URF4, URF4L, and URF5, hereafter referred to as ND1, ND2, ND3,*

*ND4, ND4L, and ND5) encode subunits of complex I. This is a large complex that also contains many subunits synthesized in the cytoplasm."*

If you are like most readers, this paragraph is difficult to make sense of and the authors' intended meaning is completely lost.

To fix this paragraph and others like it, Opan and Swan recommend the following steps:

**Principle 1. Keep language as straightforward and clear as possible.** The more complex a sentence or paragraph becomes, the more likely that a reader will get confused or just give up. Note, however, that long sentences are not necessarily bad. If a sentence is shaped well and written clearly, there is no limit to its length.

**Principle 2. Minimize jargon,** so that people other than the world expert can understand what you are saying.

**Principle 3. Keep the subject and the verb as close together as possible.**

*Bad example:* The smallest of the URF's is URFA6L, a 207-nucleotide (nt) reading frame overlapping out of phase the NH<sub>2</sub>-terminal portion of the adenosinetriphosphatase (ATPase) subunit 6 gene; it has been identified as the animal equivalent of the recently discovered yeast H+-ATPase subunit 8 gene.

*Good example:* The smallest of the URF's (URFA6L) has been identified as the animal equivalent of the recently discovered yeast H+-ATPase subunit 8 gene.

**Principle 4. In each ‘unit of discourse’, make only a single point.** A unit of discourse is any part of your writing with a beginning and an end: a report section, a paragraph, a sentence, or a clause. Do not jam multiple main ideas into a single unit.

Building on this principle, each paragraph should have a sentence that clearly encapsulates the paragraph's main point. This usually comes at either the beginning or end of the paragraph. As an example of this, checkout this white paper from a company that studies respiratory illnesses by tracking coughs. In this paper, the main point of each paragraph is in **boldface** to help readers more easily understand the purpose of each paragraph.

**Principle 5. Make use of the ‘Stress Position’.** Readers naturally emphasize the material at the sentence's end. Arrange the emphatic information in your sentence to arrive last. In other words, save the best for last.

*Bad example:* The end of a sentence is usually where readers naturally place emphasis on material. Place the emphatic information near the end of your sentence in order to re-arrange. The last is the place for which the best should be saved.

*Good example:* See Principle 5.

**Principle 6. The ‘Topic Position’ keeps things clear.** The ‘topic position’, i.e., the material at the beginning of a sentence, establishes context and expectations for the remainder of the sentence. The first pieces of information help the reader understand what the sentence will be about. As Oppan & Swan (1990) put it, “‘Bees disperse pollen’ and ‘Pollen is dispersed by bees’ are two different but equally respectable sentences about the same facts. The first tells us something about bees; the second tells us something about pollen.” If you are writing a paragraph about pollen, then the second is superior. Even though it utilizes passive voice, it correctly reinforces who the main character is.

**Principle 7. Use Topic Positions and Stress Positions to link ideas in a paragraph.** In a clear-flowing paragraph, the Topic Position of each sentence is linked to the Stress Position of the previous. In other words, the topic position provides both context (looking ahead) and linkage (looking back). Try to get into the pattern of placing ‘old information’, i.e., material you have already introduced, in the Topic Position and ‘new information’ in the Stress Position. Maintaining this pattern consistently is an enormous aid to reader comprehension.

This stress-topic linkage is particularly important in persuasive writing, such as a report’s *Introduction*. Those sections are really evidence-based arguments that build on top of one another, connecting ideas in a chain. They are not lists of facts. In a strong argument, sentences are connected in a chain.

*Bad example:* “A is something interesting. B is something interesting. C is ...”

*Good:* “A is related to B. B is related to C. C is related D...”

Oppan and Swan (1990) provide the following examples:

*Bad example:*

*Large earthquakes along a given fault segment do not occur at random intervals because it takes time to accumulate the strain energy for the rupture. The rates at which tectonic plates move and accumulate strain at their boundaries are approximately uniform. Therefore, in first approximation, one may expect that large ruptures of the same fault segment will occur at approximately constant time intervals. If subsequent main shocks have different amounts of slip across the fault, then the recurrence time may vary, and the basic idea of periodic mainshocks must be modified. For great plate boundary ruptures the length and slip often vary by a factor of 2. Along the southern segment of the San Andreas fault the recurrence interval is 145 years with variations of several decades. The smaller the standard deviation of the average recurrence interval, the more specific could be the long term prediction of a future mainshock.*

*Good example:*

*Large earthquakes along a given fault segment do not occur at random intervals because it takes time to accumulate the strain energy for the rupture. The rates at which tectonic plates move and accumulate strain at their boundaries are roughly*

*uniform. Therefore, nearly constant time intervals (at first approximation) would be expected between large ruptures of the same fault segment. However, the recurrence time may vary; the basic idea of periodic mainshocks may need to be modified if subsequent mainshocks have different amounts of slip across the fault. Indeed, the length and slip of great plate boundary ruptures often vary by a factor of 2. For example, the recurrence intervals along the southern segment of the San Andreas fault is 145 years with variations of several decades. The smaller the standard deviation of the average recurrence interval, the more specific could be the long term prediction of a future mainshock.*

Oppan and Swan (1990) conclude this recommendation by stating that, “*In our experience, the misplacement of old and new information turns out to be the No. 1 problem in American professional writing today.*”

**Principle 8. Anticipate and avoid logical gaps.** When a new sentence contains no reference whatsoever to ‘old information’ in previous sentences, the readers will make their own logical leaps, and those leaps will almost always be wrong.

Opan & Swan (199) conclude that writers who do not take the trouble to adhere to these principles “*are attending more to their own need for unburdening themselves of their information than to the reader’s need for receiving the material.*”

So, in short, be kind to your reader, and do your share of the work.

## Further considerations

### Sharp & precise writing

In good writing, the goal is to present information as succinctly and clearly as possible. In other words, you want to say *precisely what you mean* with *as few words as possible*.

Put another way: Cut your word count without losing any content.

Sharp writing with fewer words is a good end in itself, but it also forces you to be thoughtful about your organization, since a well-organized paragraphs helps you say what you want with fewer words.

Below are three strategies we’ve found useful for improving precision and concision:

**(1) The ‘Director’s Cut’:** It can help to first write a “director’s cut” of your writing that is *exactly* how you like it. Then make a copy of your writing. Now use that copy to reduce and re-write it to fit within the confines of the assignment. This two-stage process makes it easier to delete and re-work paragraphs that you are attached to; it allows for more objective and dispassionate deci-

sions, and it allows you to focus on the reader's experience rather than your own.

**(2) Iterative line reduction:** In each paragraph, try to figure out a way to reduce it by one line of text without cutting any content. Ask yourself: *How can I convey the same point with fewer words?* After you achieve this, do it again: cut another line without losing content. Then, for relatively long paragraphs (more than 8 lines), cut it by *another* line.

**(3) Iterative reading aloud:** As a general rule, never write something that would be strange to say aloud. So read your essay out loud and see if it flows naturally. Then have a friend you trust listen to you do it, and see if they can identify any areas that seem repetitive or unrelated to your conceptual flow. Next, ask a different friend (whom you also trust) to read it aloud *for you*, and see where they trip up and accidentally apply an incorrect tone or emphasis. This will show you where you need to streamline and re-work your language to make your conceptual flow more obvious to someone who is not inside your own headspace.

### Use of passive voice and first-person

Most beginners are told that the use of first-person language within a research report is inappropriate, but that is simply not true. It certain *is* true that it is possible to *misuse* first-person structure, but it is also true that first person structure can occasionally improve the flow of a paragraph and, counterintuitively, it can help keep the reader's focus on your objectives and methods.

Examples of appropriate use of first-person:

- “*We aimed to quantify differences between supply and benefit within the context of conservation planning. We addressed 3 questions...*” (from Watson et al. 2019)
- “*Because wetland invasion by common duckweed often accompanies eutrophication, we also assessed whether the presence of Lemna minor could impact anuran development. We tracked population- and individual-level responses to development in the three water treatments with and without duckweed...*” (from Zeitler et al. 2021)

Examples of inappropriate use:

- “*In this part of the Introduction, I will ...*”
- “*No Discussion would be complete without ...*”
- “*In this complicated analysis, I was able to ...*”
- “*I really did not enjoy that day of fieldwork.*”

In general, avoid self-aware commentary about what is happening in your report, and avoid self-centered commentary about how difficult or impressive something

was. *Always* avoid “I was able to...” statements.

## Logistics of scientific writing

### Writing about results

In general, a results statement needs to address the following elements of content and design:

1. Describe the pattern in your data
2. Include units with all numbers / metrics you provide
3. Round numbers to an appropriate number of significant digits (usually two decimal places is best)
4. Refer to the figure number that portrays the data, typically using a parenthetical at the end of a sentence (e.g., “(Fig. 1).”)
5. Name the statistical test you used
6. Report all necessary statistical metrics in parentheses: sample size, p-value, and any other details (e.g., regressions also need to have their regression coefficients reported.)
7. State whether or not the pattern you see supported by your significance test?
8. State whether or not the results support your hypothesis, if applicable.

Results needs to be written as concisely as possible in order to be intelligible to a reader. Treat this like a puzzle: how can you report all the necessary information in as few words as possible while maximizing the logical flow of your sentences?

#### **Bad example:**

*“The sample size was 25 clams for both non-predated and predicated clams. We did a t-test comparing the lengths of these two clams. With a p-value of 0.023, this t-test indicated that the results were statistically significant, since the p-value was below 0.05. This therefore proves our hypothesis that predicated clams are different than non-predated clams. These findings are also presented in Figure 1.”*

#### **Good example:**

*“The length of predicated clams (mean= 27.1 cm; n=25) was significantly different from that of non-predated clams (mean= 36.3 cm; n=25) (t-test, p = 0.02), supporting our hypothesis that predation state determines clam length (Fig. 1).”*

Note that the *Bad example* above is bad due to more than just its writing. You should never say that a statistical test *proves* a hypothesis correct or incorrect. A test can only fail to reject the null hypothesis.

### Captions for tables and figures

In general, a caption must provide all the information necessary to interpret the table or graph with which it is associated.

The following details must be included:

1. Brief statement of what is shown or what was measured. Summarize the content.
2. Explain any metrics that are provided. Do the bars on your graph represent Standard Error or 95% confidence intervals?
3. Include sample sizes if not included in the asset, e.g., “(n=15)”.
4. Units for all measurements, if not displayed.
5. Sampling location, date, and time.
6. Any other details required to interpret the data.

#### Bad examples:

- “*Figure 1: Clam length.*” [missing tons of information!]
- “*Figure 1. This figure is comparing two categories of data: predicated clams and non-predicated clams...*” [way too wordy!]
- “*Figure 1. Showing mean lengths of predicated and non-predicated clams...*” [too wordy! Never say “showing...” or “this figure...”]

#### Good examples:

- “*Figure 1: Mean and standard error of the heights of white oak and chestnut oak (n=8 trees per species) measured at Green’s View, Sewanee, 23rd July 2006.*”
- “*Figure 2: Height (cm) and width (kg) of students (n=15, with linear trendline) in Biology 130 class. Data collected 27 August, 2017.*”

### Referencing tables & figures

Tables and figures (collectively known as report *assets*) should be referenced throughout the *Results* and *Discussion* using parenthetical references, e.g., “(Table 1, Fig 4)”. These asset references typically come at the end of a sentence, but can sometimes be used in the middle of a complex sentence.

Try to avoid sentences that explain what tables or figures contain (e.g., “*Measurements can be found in Table 1.*”). Instead, summarize a pattern then ref-

erence the asset (e.g., “*The mean measurement was 32 (standard deviation = 4.3; Table 1)*”).

## Citing references

Literature should be cited within the body of your report using parenthetical citations, e.g., “(Keen & Brew 2021)”.

Like in-line references to tables and figures, these parentheticals typically come at the end of a sentence, but can sometimes be used in the middle of a complex sentence to make it clear which concept is connected to the reference.

The exact formatting of that parenthetical depends on the citation style you use. See the next section.

## Formatting *Literature Cited*

All in-line references and full citations within your *Literature Cited* section need to have consistent formatting. The precise formatting of your references depends on the style system you are using. Many styles are in widespread use.

If you have your choice of the kind of style you are allowed to use, we recommend the *Scientific Style* maintained by the Council of Science Editors.

Common use cases are provided below:

### In-line citations

*For a single author:*

“We don’t know ANYTHING about what’s down there! (Ezell 2021)”

*Two authors:* (Hofman and Rick 2018).

*Three or more authors:* (Smart et al. 2003).

### Bibliographic entry

This is how full references are to be written in the Literature Cited section.

*Basic layout:* Author(s). Date. Article title. Journal title. Volume(issue):location.

*For a single author:*

Laskowski DA. 2002. Physical and chemical properties of pyrethroids. Rev Environ Contam Toxicol. 174(1):49–170.

*Two authors:* Mazan MR, Hoffman AM. 2001. Effects of aerosolized albuterol on physiologic responses to exercise in standardbreds. Am J Vet Res. 62(11):1812–1817.

*Three or more authors:* Smart N, Fang ZY, Marwick TH. 2003. A practical guide to exercise training for heart failure patients. J Card Fail. 9(1):49–58.

*Ten or more authors:*

Pizzi C, Caraglia M, Cianciulli M, Fabbrocini A, Libroia A, Matano E, Contegiacomo A, Del Prete S, Abbruzzese A, Martignetti A, et al. 2002. Low-dose recombinant IL-2 induces psychological changes: monitoring by Minnesota Multiphasic Personality Inventory (MMPI). *Anticancer Res.* 22(2A):727–732.

## Formatting tables

Tables need to be tightly organized, with as few horizontal lines as possible, and with no vertical lines whatsoever. Make strategic use of lines of different thickness and boldface type to visually organize the table's content.

Microsoft *Word* and Google *Docs* will automatically generate tables that are poorly formatted:

Category	Trait	Individual network position metric			
		Degree centrality	Betweenness centrality	Closeness centrality	Contacts
Behavior / Biology	Known bubble netter	0.000	0.000	0.000	0.000
	Bubble net rate	0.000	0.003	0.000	0.000
	Feeding rate	1.000	0.901	1.000	1.000
	Social rate	0.964	0.117	0.492	0.808
	Resting rate	0.990	0.714	0.991	0.892
	Known mother	0.214	0.441	0.771	0.030
Habitat use	Mean fjord position	0.000	0.392	0.002	0.027
	SD fjord position	0.189	0.004	0.131	0.093
Site fidelity	Years seen	0.000	0.001	0.000	0.000
	SSFI	0.009	0.111	0.005	0.033
	Average arrival date	0.984	0.138	0.594	0.956
	Minimum stay	0.003	0.409	0.239	0.001

Adjust the table formatting to turn the default into something digestible:

Category	Trait	Individual network position metric			
		Degree centrality	Betweenness centrality	Closeness centrality	Contacts
Behavior / Biology	Known bubble netter	0.000	0.000	0.000	0.000
	Bubble net rate	0.000	0.003	0.000	0.000
	Feeding rate	1.000	0.901	1.000	1.000
	Social rate	0.964	0.117	0.492	0.808
	Resting rate	0.990	0.714	0.991	0.892
	Known mother	0.214	0.441	0.771	0.030
Habitat use	Mean fjord position	0.000	0.392	0.002	0.027
	SD fjord position	0.189	0.004	0.131	0.093
Site fidelity	Years seen	0.000	0.001	0.000	0.000
	SSFI	0.009	0.111	0.005	0.033
	Average arrival date	0.984	0.138	0.594	0.956
	Minimum stay	0.003	0.409	0.239	0.001

For more tips on table styles, refer to the Module on Summarizing Datasets

## Formatting figures

## Plots

Refer to the Module on Visualizing Data for the theory of effective data visualizations.

In addition to the principles outlined there, make sure that each plot meets the following standards:

1. The figure has a good caption (see above), including a figure number.
2. All text on the figure is clear and legible.
3. Each axis has a label, and the label is helpful to the reader.
4. The axis labels include units of measure, if applicable.
5. Red and green colors are avoided, since some people are color-blind to them.

## Maps

Maps should also adhere to the fundamental principles of good data visualization..

In addition to those principles, be sure that your map meets the following standards:

1. The map has a scale
2. The map has some reference to a coordinate system.
3. The map has a north arrow.
4. The map has includes some form of context (e.g., an inset map showing where the main map is located in the world.)
5. The map's caption includes information on the source of the spatial data used to build up the map.

## Diagrams

Diagrams, such as schematics that demonstrate a sampling design, should also adhere to the fundamental principles of good data visualization..



# Chapter 43

## Presentations

Just as good writing in science is no different from good writing anywhere else, good research talks should be a good talk by any standard. The only difference should be the *target audience*. Far too often, data scientists are given a pass for poor presentations and boring delivery. We believe that should change.

Research talks are typically given to colleagues who share some level of familiarity with your study topic; but those colleagues are still humans and they deserve to listen to an enjoyable talk that allows them to connect to the speaker.

As a data scientist, you will have to be adept at preparing two types of presentations: (1) talks for colleagues and (2) talks for the public.

Below we first provide standards that should apply to *any* talk for *any* audience. Second, we specify which additional standards to consider, depending on your audience.

### Standards for all presentations

#### Content & substance

##### 43.0.0.0.1 First moments

- The first seconds of your talk are an excellent, engaging, and relevant attention getter,
- the tone of which matches and sets the stage for the remainder of the talk.

##### 43.0.0.0.2 Early audience orientation

- Sound orientation to topic and clear thesis delivered early in talk.

- Introductory moments includes preview of main points.
- Credibility is firmly established, but only after the audience is invested in the topic.

#### **43.0.0.0.3 Research & evidence**

- Reason & evidence are used as part of case being made.
- Facts, numbers, and statistics are used effectively.
- Includes only the absolutely essential details regarding research sources, methods, and analyses.
- Evidence is not oversold as truth. The uncertainty and ignorance inherent to science is not ignored.

#### **43.0.0.0.4 Story & narrative**

- The organization of the talk takes the form of a story, taking the audience on a shared journey.
- Within this framework, anecdotes and stories are used as a medium for connecting the audience to facts, evidence, and emotional components of your case.

#### **43.0.0.0.5 Relevance & Importance**

- A compelling case for the importance of the topic to the audience's lives and/or their shared interests.
- The connection between the audience's shared interests and the topic is pointed to clearly and consistently.

#### **43.0.0.0.6 Pre- & Misconceptions**

- Content & delivery demonstrate anticipation of preconceptions regarding the topic and the presenter.
- Content demonstrates understanding of common misconceptions regarding the topic.
- These pre- and misconceptions are addressed and moved beyond deftly and thoroughly.
- No elephants in the room go unmentioned.

#### **43.0.0.0.7 Final moments**

- Provides a clear and memorable summary of points and refers back to thesis/big picture.
- Ends with strong call to action, or at least a vision for next steps, solidly grounded in data presented.

#### **43.0.0.0.8 Organization overall**

- Organization of the content amounts to a strategic and persuasive case, in which rational, emotional, and narrative components are woven together with deliberate care.
- This organization is made clear to the audience: throughout the talk, the audience is given transitions and signposts and reminders that allow them to readily reconstruct the case being made.
- The communication of this order is obvious without being condescending or ineffectually repetitive.
- The talk is delivered within the allocated time window, reflecting appropriate organization and respect for others' time.

#### **Delivery & style**

#### **43.0.0.0.9 Preparation**

- The speaker is clearly well-prepared, and this is evident in the timing of the talk, familiarity with visual aids and what will be said next, and little to no reliance upon notes.

#### **43.0.0.0.10 Speech**

- Vocal expression (projection and volume) is natural and authentic;
- Excellent use of variation in vocal intensity, tone, and expression.
- Pace of speech is always easy to follow.
- Tone is conversational and sincere.
- Each thought is brought to completion without trailing off or rambling.
- Lack of vocal fillers (e.g., ummm, so.....).
- Impactful use of pauses and silence.

**43.0.0.0.11 Language**

- Speaker is able to articulate what she means clearly through eloquent word choice and premeditated sentences.
- Language level is considerate of audience's current knowledge, particularly in science.
- Jargon, abbreviations, and acronyms are avoided; any that must be used is explained.
- Comparisons and analogies are used effectively without further complicating a concept.

**43.0.0.0.12 Explanation**

- Any word that may not be universally understood is explained, either explicitly or within abundant context.
- Any concept that may not be universally understood is explained carefully.
- These explanations occur at a level appropriate to audience.

**43.0.0.0.13 Non-verbal delivery: The “Second Conversation”**

- Attire & composure reflects the utmost sincerity and professionalism, without sacrificing authenticity.
- The speaker is expressive and compelling through eye contact and facial expressions.
- Body language (posture, gestures, and movements) exude poise and earnest engagement.
- Body language effectively augments the spoken word, in both timing and affect.
- Eyes, movements and gestures are not distracting and do not disclose anxiety or discomfort.

**43.0.0.0.14 Mistakes**

- Any mistakes are handled in a graceful and self-forgiving manner, and recovery is quick.
- The speaker demonstrates resilience and endurance; multiple mistakes do not lead to a decline in composure or energy level.

#### **43.0.0.0.15 Attentive, responsive, & adaptive**

- The speaker actively maintains audience attention throughout, rather than just assuming attention is there or not responding accordingly if it clearly isn't.
- The speaker establishes an active dialogue between themselves and the audience, either directly (through responses or questions), or indirectly (through sharing moments of laughter, joy, pain, anger, disgust, etc.).
- Speaker reiterates, clarifies, and changes course adaptively in response to their read of the audience.
- Speaker knowledgeably and concisely answers appropriate questions, if any.
- Evidence that the speaker researched and anticipated common questions, as appropriate.

#### **Rapport & Relating**

##### **43.0.0.0.16 Energetic & credible**

- Professional but enjoyable
- Enthusiastic but genuine and believable
- Excited but not overbearing

##### **43.0.0.0.17 Human & relatable**

- Poise without intimidation
- Confidence without arrogance
- Comfort & ease without apathy or indifference
- Vulnerability without fragility or volatility

##### **43.0.0.0.18 Inclusive & welcoming**

- When appropriate, uses inclusive language (“we” and “our” instead of “I” and “my”; non-gendered pronouns, politically tolerant language, etc.)
- Creates common ground by strongly emphasizing common goals, values and/or experiences.

### Visual aids

#### 43.0.0.0.19 Strategic use

- Visual aids complement the spoken word. Redundancy (if any) between what is spoken and what is displayed is strategic, not used as a crutch for presenting.
- Visual aids are not *over-used*, and do not obstruct the audience's ability to listen to and follow the narrative thread of the talk.
- Visual aids are not *under-used* if spoken concepts are too complicated. For instance, if a list of numbers absolutely must be shared, it is best to provide them visually in addition to saying them.

#### 43.0.0.0.20 Design & display

- Visual aids are of professional quality, not sloppy or thrown together.
- Visual aids prioritize simplicity, clarity, and good principles of design.
- Color palettes are sensitive to color-blind audiences.

#### 43.0.0.0.21 Visualizing information

- Use of text is minimized.
- Text is an appropriate size and font.
- Complicated figures are avoided.
- Any data visualization has been reduced to the simplest possible form.

### Talking to the public

When speaking as a researcher to the public, some of these standards need to be prioritized above others. The public is a much more diverse audience than your colleagues are. They do not necessarily know you, nor do they necessarily trust you or agree with you. To help them engage with you successfully and actually listen to what you have to say, we recommend the following adjustments:

- A public-facing talk must have **a clear and simple message** – a *single* idea worth spreading.
- To convince the public of that idea, you must **dial down the research and replace it with stories, emotion, and empathy**. Your case needs to rely heavily upon appeals to the heart and gut of the audience. By end

of talk, you want the audience to be emotionally invested in seeing the call to action come to fruition.

- That said, make sure that those **emotional appeals are made with nuance and discretion**, without exploiting victims or the voiceless. Do not be condescending toward your audience or anyone unlikely to be in your audience.

- **Minimize the number of facts, numbers, and statistics.** If you *must* use them, *never* use them in isolation from the emotional aspects of your talk. Do not simply hurl facts at your audience. Within an empathic storytelling framework, anecdotes and stories are used as the primary medium for connecting the audience to facts, evidence, and emotional components of your case. Don't shy away from your data, but use it very carefully. Ultimately, the talk is a persuasive case for elevating the importance of research in our lives.

- **End with strong call to action,** solidly grounded in the data and stories you have presented. Make sure that call to action is related to your talk in obvious and intuitive ways. Make sure it is a meaningful action by which audience members are actually able to make a difference. Finally, make sure that this call to action is expressed succinctly and memorably, as an effective and simple slogan.

This is a pretty good example of a scientifically oriented talk to the public:



# Creating websites



## **Part VI**

### **Advanced skills**



## **Chapter 44**

# **Mapping**



## Chapter 45

# Geographic computing & GIS



## Chapter 46

# Statistical modeling



## Chapter 47

### Apply family



## Chapter 48

# Randomization statistics

### Learning goals

- Understand what randomization analyses are, and why they are awesome.
- Use randomization to determine if an outcome is significantly unexpected.
- Use randomization to compare two distributions.
- Use randomization to ask whether two variables are correlated
- Use randomization to determine the chances that a correlation is declining or increasing.

### Basic idea

Classic significance statistics (i.e., p-values) are based on the frequentist framework in which you *estimate* the probability of an *observed* outcome based upon what would be *expected* if a null hypothesis were true. In a t-test, for example, you are asking, “What are the chances of observing what I have if these two sample sets were not meaningfully different?”

The key word in that first sentence is *estimate*. When frequentist theory was originally developed, statisticians did not have computers capable of generating vast amounts of random numbers. So they had to *estimate* p-values by developing strict rules and expectations about the way data are distributed. These rules had the result of (1) placing a lot of constraints on the way statistics could be done, (2) forcing the development of increasingly specific tests for each novel sampling scenario, (3) confusing students trying to learn statistics, and (4) requiring the use of simplistic conventions, such as the 0.05 significance threshold, in order to make statistical results somewhat intelligible.

But in the age of R, null distributions no longer need to be theoretical, nor do p-values need to be hypothetical. We can actually *calculate* p-values based on *real* null distributions, thanks to the random number generators built into

coding languages such as R. The practice of generating real null distributions based on your own specific dataset is known as **randomization**.

In a randomization routine, you shuffle the variables in your dataset to generate a distribution of outcomes that would be possible according to a null hypothesis. Most null hypotheses reduce to an expectation of *no meaningful difference* between two (or more) samples, which is to say that any differences between those samples are merely the product of random chance. Such randomly generated variability can be simulated easily in R.

Randomization may seem daunting at first, and it does indeed draw upon some of the higher-order skills in your R toolbag (such as custom functions, `for` loops, and sometimes even the `apply()` functions), but once you become oriented you will see how intuitive and simple these analyses can be.

The real advantages of randomization, however, are not for the programmer but for the reader. Randomization results are *much* easier to interpret and more information-rich than frequentist p-values. The advantages are many:

1. Rather than trusting a black box statistical test with obscure requirements about data distributions, you are performing the test yourself and building the test using your own data. You have more control and accountability, and no more risk of choosing the wrong statistical test. Because you are using your own data to produce the null distribution, you are able to retain the quirks of your own particular dataset; the limitations and inconsistencies in your sampling will be safely propagated into the statistic and properly reflected in the uncertainty of your results.
2. The interpretation of your p-value will be more intuitive. Rather than saying that some result is or is not significant based upon an arbitrary threshold such as 0.05, you can speak about the *chances* of meaningful results: “There is a 89% chance that these two sample sets are meaningfully different.” “There is a 92% chance that this trend is increasing.” These kinds of results are easier to interpret, and it avoids the need to make sense of p-values.
3. Finally, your statistical test returns much more than a p-value; it returns the null distribution too, which can be of enormous value in more complicated statistical analyses.

## Generalized randomization workflow

1. Define your **research question**.
2. Define the **null model** that you wish to compare your observations against. This involves determining which variable you will need to shuffle.
3. **Create a function** that calculates the value of interest.
4. Use that function to determine the **observed value** of interest.

5. Use a **for** loop to **build a null distribution** by shuffling your observations with R's random number generators.
6. **Visualize** your results to sanity-check what you are finding.
7. Calculate your **p-value**, by asking what proportion of the null distribution falls below the observed value.

The examples below will show you how to apply this generalized workflow. Note that we are purposefully applying randomization to scenarios in which classic statistical tests, such as t-tests and linear models, could also be used. We do so because those scenarios are relatively simple, they demonstrate the comparability of randomization to approaches you may already be familiar with, and they hint at the advantages of randomization over those other approaches. But the true value of randomization lies in its ability to carry out statistics when all other conventional tests fail; we hint at that value in the final use case.

## Common use cases

### 1. Is outcome X significantly unexpected?

To practice this use case, let's use the dataset : 15 years of sightings of humpback whales within a fjord system in northern British Columbia, Canada ([www.bcwildlife.org](http://www.bcwildlife.org)).

```
# Use dataset
hw <- read.csv("./data/humpback-whales.csv")
```

Each individual whale in this dataset was identified using unique patterns on its tail, so each whale has an ID number.

```
nrow(hw)
[1] 4436
head(hw)
  year      sit bhvr id
1 2004 2004070701   BNF 42
2 2004 2004071401   BNF 42
3 2004 2004071401   BNF 59
4 2004 2004080301   BNF 30
5 2004 2004080401 MI-FE 106
6 2004 2004080401 MI-FE 114
```

Each row shows a whale (column **id**) identified during a single sighting (column **sit**). Some sightings were of a single solo individual, but others were of groups of two or more individuals.

Our interest here is in these whales' social behavior: do they have "friendships", i.e., certain individuals that they prefer to associate with over others, or are they just randomly swimming around and bumping into one another?

Let's tackle this one step at a time.

**Step 1:** Our **research question** is, *Do any pairs of whales occur together an unexpectedly persistent social bonds?* Since in science we are always limited by how well we sample the population of interest, a more precise version of our research question would be this: *Based on this dataset, can we conclude whether or not any pairs of whales occur together an unexpectedly large number of times?*

**Step 2:** The **null model** for this question is simple random mixing: there is no pattern to which whales occur in which group. So the variable that we will need to shuffle is the `id` column. With this approach, we be able to preserve the number of times each individual is seen and the total number of observations. So the limitations and inconsistencies in our sampling of each individual will be safely propagated into our statistics and properly reflected in the uncertainty of our results.

**Step 3:** So we need a **function** that returns the number of times two whales are associated. We will call this function `association_tally()`.

```
association_tally <- function(hw,A,B){
  siti <- hw$sit[hw$id==A]
  sitj <- hw$sit[hw$id==B]

  common_sits <- which(siti %in% sitj)
  X <- length(common_sits)

  return(X)
}
```

**Step 4:** For our **observed** association tally, we will focus in on a single pair of humpback whales: IDs 59 and 11.

```
obs <- association_tally(hw,A="59",B="11")
obs
[1] 71
```

That's a lot of associations! Let's see if that observation is statistically significant:

**Step 5:** The **for loop** for our null distribution will look like this:

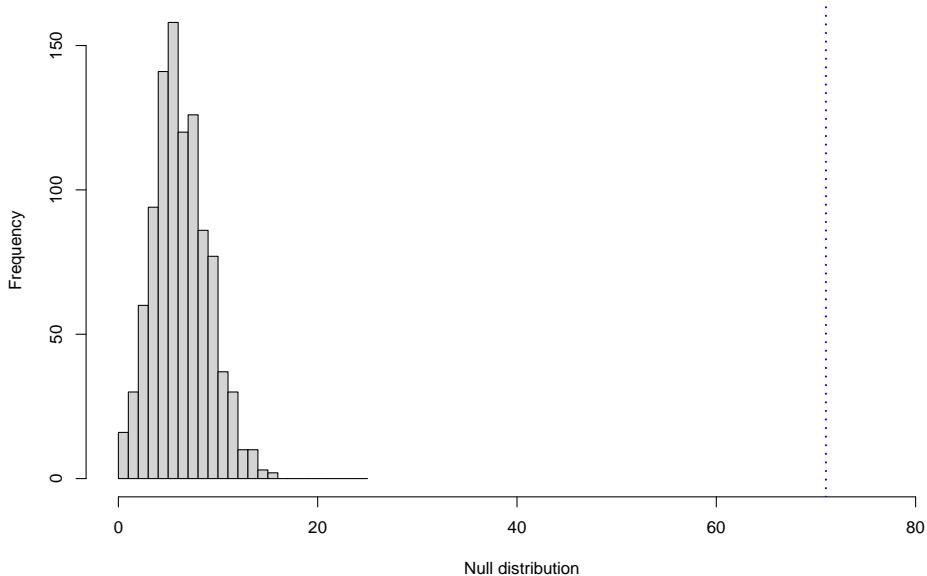
```
nulls <- c()
for(i in 1:1000){
  hw_null <- hw # save a safe copy of the data
  hw_null$id <- sample(hw_null$id,size=nrow(hw_null),replace=FALSE) # shuffle the null
  nulli <- association_tally(hw_null,A="59",B="11") # determine null rate for this iteration
  nulls[i] <- nulli # save result
}
```

*Note!* Here we only iterate our `for` loop 1,000 times, but most published ran-

domizations are run for 5,000 to 10,000 iterations, just to ensure that the null distribution is adequately unbiased.

**Step 6:** To visualize these results, use a histogram:

```
par(mar=c(4.2,4.2,1,1))
hist(nulls, breaks=seq(0,25,by=1), xlim=c(0,(obs+10)), main=NULL, xlab="Null distribution")
abline(v=obs, lwd=2, lty=3, col="blue")
```



**Step 7:** Finally, we calculate our p-value:

```
p_value <- length(which(nulls >= obs)) / length(nulls)
p_value
[1] 0
```

Let's do this again with a different humpback pair, IDs 16 and 118, who were seen together only 9 times. Is their association rate statistically significant?

```
# Individual IDs
A <- "58"
B <- "133"

# Observed association rate
obs <- association_tally(hw, A=A, B=B)
obs
[1] 9

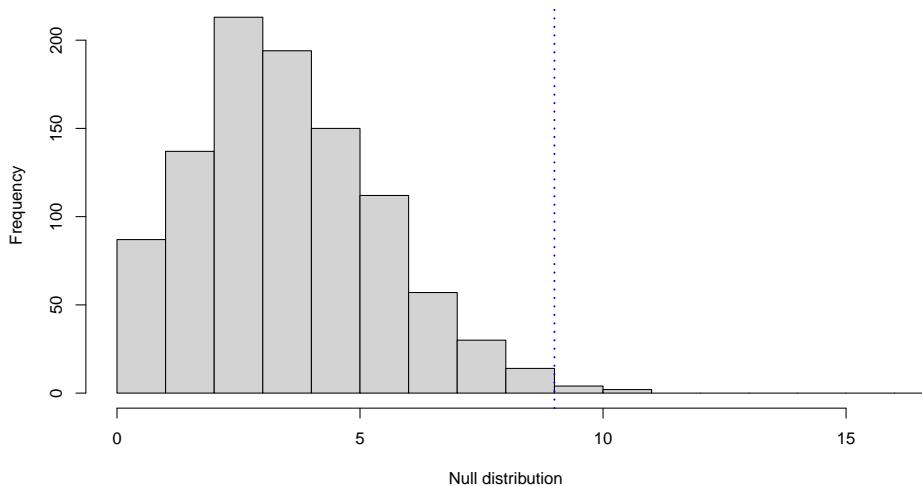
# Generate null model
nulls <- c()
```

```

for(i in 1:1000){
  hw_null <- hw
  hw_null$id <- sample(hw_null$id, size=nrow(hw_null), replace=FALSE)
  nulli <- association_tally(hw_null, A=A, B=B)
  nulls[i] <- nulli
}

# Visualize
hist(nulls, breaks=seq(0,20,by=1), xlim=c(0,(obs+7)), main=NULL, xlab="Null distribution")
abline(v=obs, lwd=2, lty=3, col="blue")

```



```

# Calculate p-value
p_value <- length(which(nulls >= obs)) / length(nulls)
p_value
[1] 0.02

```

In this case, the observed association rate is still statistically significant at the conventional 0.05 level, but there is still an off chance that this is merely the result of random mixing.

## 2. Are two sample sets significantly different?

*Building off of the whale scenario:* Some of these whales have learned how to practice bubble-net feeding, a remarkable feeding strategy that requires group cooperation and special techniques for catching schooling fish such as herring. Other individuals have never been seen bubble net feeding. Are there any differences how often these two populations – the bubble netters and the “others” – use the study area?

First, let’s see how many of these individuals are known to bubble net feed:

```
[1] 108
```

So, out of 132 individuals, 108 are known to practice bubble netting.

Let's go through the steps:

**1. Research question:** Is there any difference in the number of years in which bubble-netters are seen compared to other whales?

**2. Null model:** In this case, the null model will be a *distribution of average differences* in the number of years in which individuals from the two populations are seen. This null distribution will be centered around zero. The variable we will shuffle is which individuals are known bubble netters, keeping the size of the two populations constant in each iteration.

**3. Function:**

```
annual_difference <- function(hw, bnf_ids){

  bnf <- hw[hw$id %in% bnf_ids,] # Sightings of known BNFers
  other <- hw[! hw$id %in% bnf_ids,] # Sightings of other whales

  # Get distribution of years seen for individuals within each population
  counts <- table(bnf$id, bnf$year) # sightings of each whale (rows) in each year (columns)
  n_bnf <- apply(counts, 1, function(x){length(which(x>0))}) # years seen for each individual

  counts <- table(other$id, other$year) # sightings of each whale (rows) in each year (columns)
  n_other <- apply(counts, 1, function(x){length(which(x>0))}) # years seen for each individual

  # Now get average difference between two distributions
  mean_diff <- mean(n_bnf, na.rm=TRUE) - mean(n_other, na.rm=TRUE)

  return(mean_diff)
}
```

**4. Observed value:**

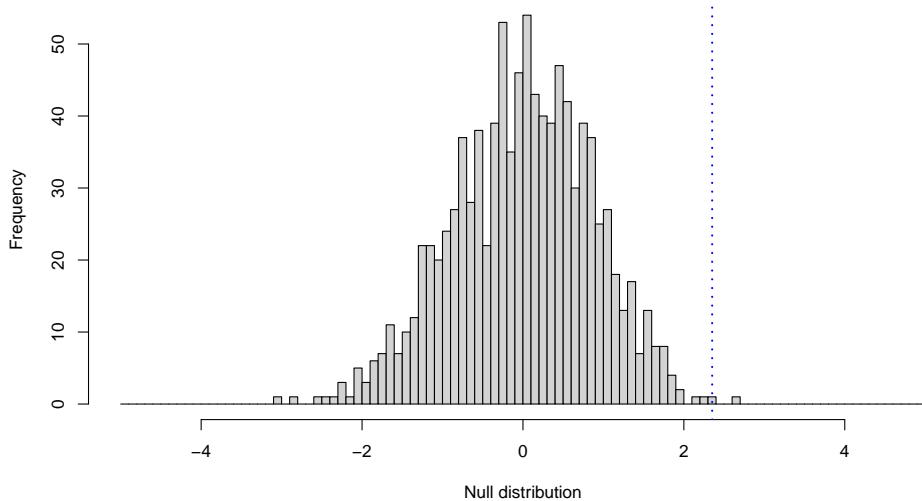
```
obs <- annual_difference(hw, bnf_ids=bnf_ids)
obs
[1] 2.351852
```

**5. Build null distribution:**

```
nulls <- c()
for(i in 1:1000){
  bnf_null <- sample(unique(hw$id), size=length(bnf_ids), replace=FALSE)
  nulli <- annual_difference(hw, bnf_ids=bnf_null)
  nulls[i] <- nulli
}
```

**6. Visualize:**

```
hist(nulls, breaks=seq(-5,5,by=.1), xlim=c(-5,5), main=NULL, xlab="Null distribution")
abline(v=obs, lwd=2, lty=3, col="blue")
```



### 7. p-value:

```
p_value <- length(which(nulls >= obs)) / length(nulls)
p_value
[1] 0.001
```

So there is indeed a significant difference in the annual site fidelity in the two populations! Bubble net feeders practice higher annual return rates than other whales ( $p = 0.001$ ).

### 3. Are two variables correlated?

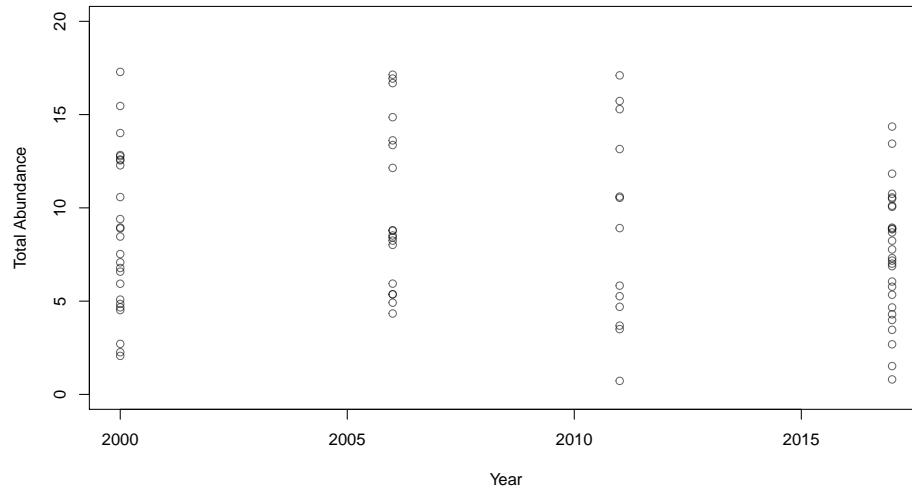
To perform a correlation analysis with randomization, let's use a classic scenario from marine conservation: We have abundance estimates for a critically endangered porpoise from four years across two decades of research. This species only has a handful of individuals left in the wild. ()

```
df <- read.csv("./data/porpoise-survey.csv")
head(df)
  year      N
1 2000 12.547943
2 2000  5.932797
3 2000 17.291144
4 2000  2.707317
5 2000 12.279161
6 2000  8.945810
```

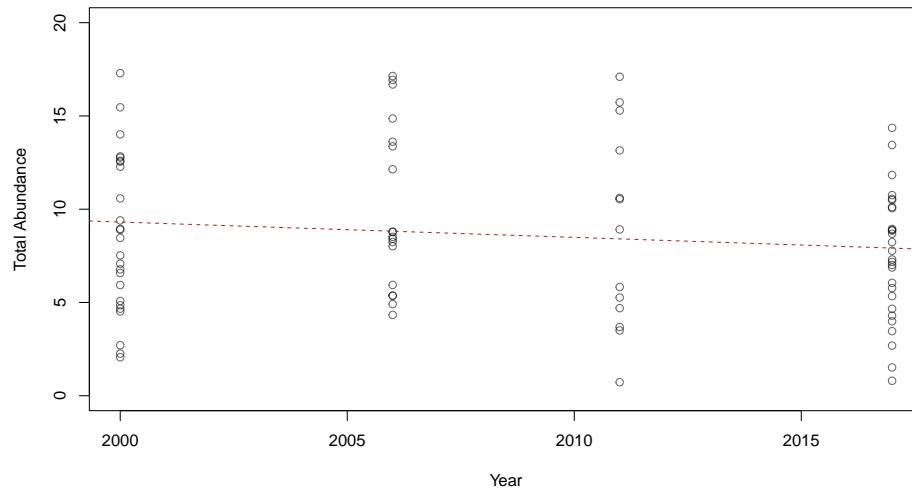
Each row of this dataset is an abundance estimate from a survey that occurred

within the vaquita's range during a certain year.

```
plot(df$N ~ df$year, ylim=c(0,20),
      xlab="Year",
      ylab="Total Abundance",
      col=adjustcolor("black", alpha.f=.6))
```



Performing a simple linear regression with this dataset yields the following results:



The slope appears to be negative, but the regression has a non-significant p-value ( $p=0.22$ ) and a very small correlation coefficient:

```
summary(df_lm)
```

```
Call:
```

```

lm(formula = df$N ~ df$year)

Residuals:
    Min      1Q  Median      3Q     Max 
-7.6841 -3.3981 -0.3879  3.0338  8.6945 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 173.63645 133.70824   1.299   0.198    
df$year      -0.08216    0.06657  -1.234   0.221    
                                                        
Residual standard error: 4.221 on 82 degrees of freedom
Multiple R-squared:  0.01824, Adjusted R-squared:  0.006268 
F-statistic: 1.523 on 1 and 82 DF, p-value: 0.2206

```

These results may compel some conservation skeptics to stop worrying about the porpoise. “Yes, the population is small, but it appears stable, and there is no evidence that it is decreasing.” This is a situation in which using a randomization regression analysis could give us more information and help us speak more precisely about the risks to which this population is exposed.

Let’s go through the steps:

- 1. Research question:** Is there a trend in porpoise abundance over time?
- 2. Null model:** There is no trend; the abundance estimates might as well come from any given year and the trendline would look the same.
- 3. Function:** Get the slope estimate for the time series.

```

df_lm <- function(df){
  lmi <- lm(df$N ~ df$year)
  slopi <- summary(lmi)$coefficients[2,1]
  rsqu <- summary(lmi)$r.squared

  return(c("slope"=slopi, "r"=rsqu))
}

```

- 4. Observed value:**

```

obs <- df_lm(df)
obs
      slope          r
-0.08216195  0.01824031

```

- 5. Build null distribution:**

```

nulls <- data.frame()
for(i in 1:1000){

```

```

df_null <- df
df_null$year <- sample(df_null$year, size=nrow(df_null), replace=FALSE)
nulli <- df_lm(df_null)
nulli <- data.frame(slope=nulli[1], r=nulli[2])
nulls <- rbind(nulls, nulli)
}

```

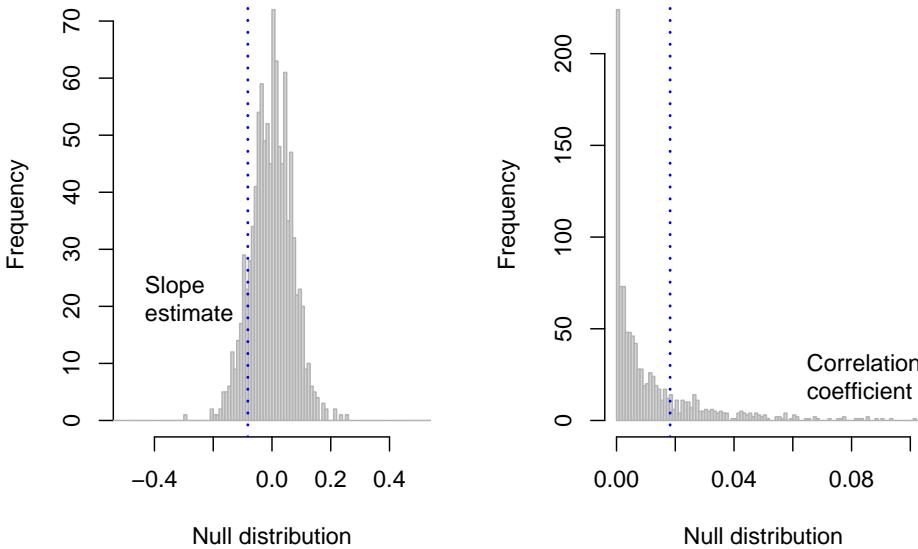
#### 6. Visualize:

```

par(mfrow=c(1,2))
hist(nulls$slope, breaks=seq(-1,1,by=.01), xlim=c(-.5,.5), main=NULL, xlab="Null distribution", border="black")
text(-.48, 20, "Slope \nestimate", pos=4)
abline(v=obs[1], lwd=2, lty=3, col="blue")

hist(nulls$r, breaks=seq(0,1,by=.001), xlim=c(0,.1), main=NULL, xlab="Null distribution", border="grey")
text(.06, 20, "Correlation \ncoefficient", pos=4)
abline(v=obs[2], lwd=2, lty=3, col="blue")

```



#### 7. p-value:

Significance of slope:

```

p_value <- length(which(nulls$slope >= obs[1])) / nrow(nulls)
p_value
[1] 0.879

```

This indicates that the chance that the slope is lower than the null expectation is 87.9%.

Significance of correlation coefficient:

```
p_value <- length(which(nulls$r >= obs[2])) / nrow(nulls)
p_value
[1] 0.221
```

This indicates that the observed regression is better than 77.9% of scenarios that might be expected under the null expectation.

#### 4. Is the slope of a regression line negative?

Sometimes we have even less data about an endangered species. Let's say we go out in 2021 for another porpoise survey and come up with these estimates from the species' range:

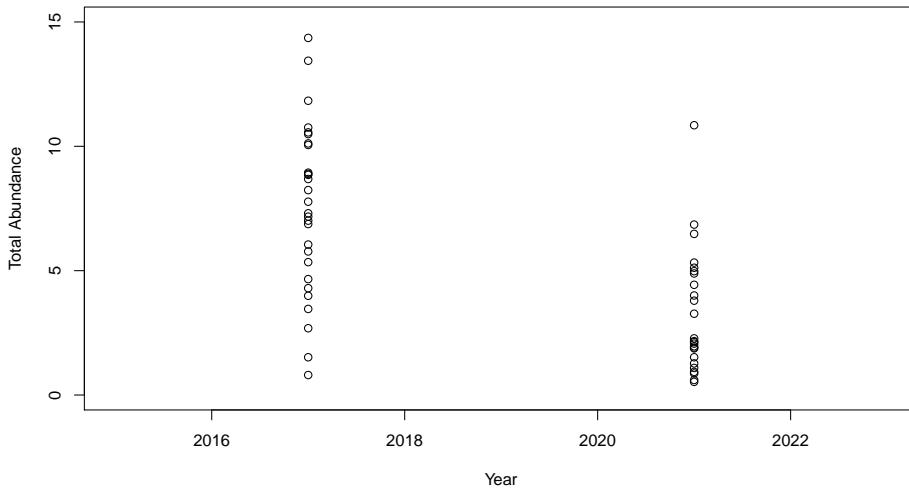
```
library(truncnorm) ; set.seed(1234)
n2021 <- rtruncnorm(n=25,a=0,mean=3.6,sd=3)
n2021
[1] 4.4322877 6.8533235 4.8873741 5.1181677 1.8757801 1.9601044
[7] 1.9066440 0.9298865 2.1684219 0.6048407 1.2712383 3.7933765
[13] 6.4784822 3.2691435 2.0669715 0.8664138 1.0884850 10.8475055
[19] 4.0022647 2.1279423 2.2783564 4.9787683 1.5188393 5.3242672
[25] 0.5290328
```

We want to know what the chances are that the population has declined between 2017 and 2021.

```
n2017 <- df$N[df$year==2017]

plot(1,type="n",ylim=c(0,15),xlim=c(2015,2023),
      xlab="Year",
      ylab="Total Abundance",
      col=adjustcolor("black",alpha.f=.6))

points(n2017 ~ rep(2017,times=length(n2017)))
points(n2021 ~ rep(2021,times=length(n2021)))
```



If this is all we have, what can we say about the status of this endangered species? With such a low sample size and so much variability, it can be really hard to produce significant or even compelling results. **Well, what are the chances that this population is in decline?** That is a question that a simple linear model cannot tell us.

In this case, our null model will be the distribution of differences of values drawn randomly from the two years' datasets.

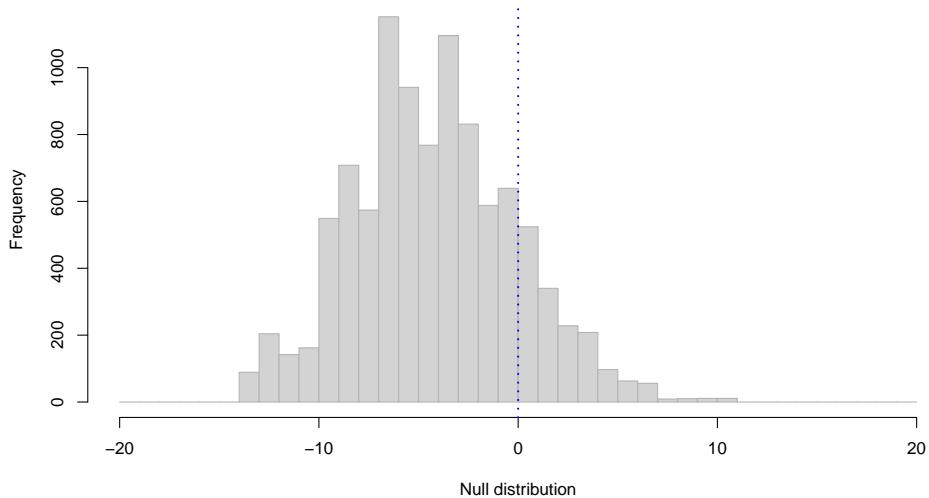
And in this randomization application, the workflow is a bit more simplified. We don't need a core function, and we don't even need a `for` loop.

```
# Randomly draw from the 2017 dataset 5,000 times
r2017 <- sample(n2017, size=10000, replace=TRUE)

# Do the same for the 2021 dataset
r2021 <- sample(n2021, size=10000, replace=TRUE)

# Get the difference of these two datasets
diffs <- r2021 - r2017

# Visualize
hist(diffs, breaks=seq(-20,20,by=1), xlim=c(-20,20), main=NULL, xlab="Null distribution", border="grey")
abline(v=0, lwd=2, lty=3, col="blue")
```



```
# Get p_value
p_value <- length(which(dirfs >= 0)) / length(dirfs)

# Convert to chances of decline
chances_of_decline <- 100*(1 - p_value)
chances_of_decline
[1] 84.43
```

The chances that this population is in decline is 84.43%.

## Review assignment

Let's return to the humpback whale scenario

### (a) Do bubble net feeders have stronger social bonds?

Above we asked whether bubble net feeders exhibit higher year-to-year site fidelity to the study area than other individuals. What about their social bonds? Do whales known to bubble net feed tend to have more stable social associations than the others?

Make sure you are working with the correct data:

```
hw <- read.csv("./data/humpback-whales.csv")

# Establish the two populations
bnf_indices <- grep("BNF", hw$bhv) # which detections are of BNFers
bnf_sits <- hw[bnf_indices,] # BNF sightings
bnf_ids <- unique(bnf_sits$id) # BNF individuals
```

```
length(bnf_ids)
[1] 108
```

**Answer key:**

```
# Internal function for determining times seen together for a single row of a dyads dataframe
social_X <- function(dyad){
  A <- dyad[1]
  B <- dyad[2]
  sitA <- hw$sit[hw$id==A]
  sitB <- hw$sit[hw$id==B]
  X <- length(which(sitA %in% sitB))
  return(X)
}

# Core function
social_difference <- function(hw, bnf_ids){

  bnf <- hw[hw$id %in% bnf_ids,] # Sightings of known BNFers
  other <- hw[! hw$id %in% bnf_ids,] # Sightings of other whales
  other_ids <- unique(other$id)

  bnfs <- expand.grid(bnf_ids, bnf_ids) # Make a dataframe of all possible dyad combinations
  bnfs$X <- apply(bnfs, 1, social_X) # Get number of times seen

  # Do same for others
  others <- expand.grid(other_ids, other_ids)
  others$X <- apply(others, 1, social_X)

  # Now get average difference between two distributions
  mean_diff <- mean(bnfs$X, na.rm=TRUE) - mean(others$X, na.rm=TRUE)

  return(mean_diff)
}

# Observed
obs <- social_difference(hw, bnf_ids)
obs

# Null distribution (only do 100 iterations for sake of time)
nulls <- c()
for(i in 1:100){
  bnf_null <- sample(unique(hw$id), size=length(bnf_ids), replace=FALSE)
  nulli <- social_difference(hw, bnf_ids=bnf_null)
  nulls[i] <- nulli
}
```

```

# Visualize
par(mar=c(4.2,4.2,1,1))
hist(nulls, breaks=seq(-6,6,by=.1), xlim=c(-3,1), main=NULL, xlab="Null distribution")
abline(v=obs, lwd=2, lty=3, col="blue")

# p-value
p_value <- length(which(nulls >= obs)) / length(nulls)
p_value

# BNFers have much more persistent bonds than other whales (p=0.00000)

```

**(b) Are bubble net feeders more closely related to each other?**

In 2019, researchers took DNA samples from 36 individuals in this dataset. They collected the samples by flying drones through the whale's spouts and harvesting DNA from their *snot!* *GROSS!!!* But also *super RAD!*

Using these genetic samples, the researchers determined the relatedness of each pair of individuals they sampled. Those results are provided in the dataset

```
kinship <- readRDS("./data/humpback-kinship.rds")
```

And providing the IDs of these 36 whales and their status as a known bubble net feeder.

```
bnf_status <- readRDS("./data/bnf-status.rds")
```

Use these datasets within a randomization routine to determine whether known bubble netters are more closely related to each other than they are to other whales.

**Answer key:**

```

# How many BNFers are in this dataset?
n_bnf <- nrow(bnf_status[bnf_status$bnf,])
n_bnf

# Core function
kinship_difference <- function(kinship, bnf_status){

  bnf_ids <- bnf_status$id[bnf_status$bnf]
  other_ids <- bnf_status$id[! bnf_status$bnf]

  bnf_rows <- which(row.names(kinship) %in% bnf_ids)
  kin_bnf <- kinship[bnf_rows, bnf_rows]
  kin_other <- kinship[-bnf_rows, -bnf_rows]
}
```

```

mean_diff <- mean(as.matrix(kin_bnf)) - mean(as.matrix(kin_other))

return(mean_diff)
}

# Observed
obs <- kinship_difference(kinship, bnf_status)
obs

# Null distribution
nulls <- c()
for(i in 1:1000){
  bnf_null <- bnf_status
  bnf_null$bnf <- sample(bnf_null$bnf, size=nrow(bnf_null), replace=FALSE)
  nulli <- kinship_difference(kinship, bnf_null)
  nulls[i] <- nulli
}

# Visualize
par(mar=c(4.2,4.2,1,1))
hist(nulls, breaks=seq(-6,6,by=.002), xlim=c(-.1,.05),
  main=NULL, xlab="Null distribution", border="grey70")
abline(v=obs, lwd=2, lty=3, col="blue")

# p-value
p_value <- length(which(nulls >= obs)) / length(nulls)
p_value

# Weak evidence for relatedness being a factor in BNF network, but >60% chance!
# A bit better than coin flip. Interesting!

```

### (c) Do social bonds relate to kinship?

Finally, let's ask whether the strength of social bonds is generally correlated to kinship. In other words, is this population assorting according to relatedness?

For your convenience, the social association rate for these 36 individuals has also been summarized in the dataset .

```
sociality <- readRDS("./data/humpback-sociality.rds")
```

**Answer key:**

```
# Core function
kin_soc <- function(kinship, sociality){
```

```

ids <- row.names(kinship) ; ids

mr <- data.frame()
i=1 ; j=10
for(i in 1:length(ids)){
  idi <- ids[i] ; idi
  kin_row <- which(row.names(kinship)==idi) ; kin_row
  soc_row <- which(row.names(sociality)==idi) ; soc_row

  for(j in 1:length(ids)){
    idj <- ids[j]; idj

    kin_col <- which(colnames(kinship)==idj) ; kin_col
    soc_col <- which(colnames(sociality)==idj) ; soc_col

    mri <- data.frame(A=idi,B=idj,
                        kinship=kinship[kin_row,kin_col],
                        sociality=sociality[soc_row,soc_col])
    mri
    mr <- rbind(mr,mri)
  }
}
mr

# remove navelgazers
navels <- which(mr$A==mr$B) ; navels
mr <- mr[-navels,]

#plot(sociality~kinship,data=mrr)
lmi <- lm(mr$sociality ~ mr$kinship)
#abline(lmi)
slopi <- summary(lmi)$coefficients[2,1]
rsqu <- summary(lmi)$r.squared

return(c("slope"=slopi,"r"=rsqu))
}

# Observed
obs <- kin_soc(kinship,sociality)
obs

# Null distribution
nulls <- data.frame()
for(i in 1:500){
  kin_null <- kinship

```

```

kin_null <- kin_null[sample(1:nrow(kin_null),size=nrow(kin_null),replace=FALSE),]
row.names(kin_null) <- row.names(kinship)
nulli <- kin_soc(kin_null,sociality)
nulli <- data.frame(slope=nulli[1],r=nulli[2])
nulls <- rbind(nulls,nulli)
}

# Visualize
par(mfrow=c(1,2))
hist(nulls$slope,breaks=seq(-1,1,by=.0005),xlim=c(-.02,.02),main=NULL,xlab="Null distribution",border="green")
text(-.48,20,"Slope \n estimate",pos=4)
abline(v=obs[1],lwd=2,lty=3,col="blue")

hist(nulls$r,breaks=seq(0,1,by=.0001),xlim=c(0,.01),main=NULL,xlab="Null distribution",border="green")
text(.06,20,"Correlation \n coefficient",pos=4)
abline(v=obs[2],lwd=2,lty=3,col="blue")

# P-value of slope
p_value <- length(which(nulls$slope >= obs[1])) / nrow(nulls)
p_value

# P-value of correlation coefficient
p_value <- length(which(nulls$r >= obs[2])) / nrow(nulls)
p_value

# How to interpret this correlation coefficient?
# Could it be said that the correlation is unexpectedly POOR?
# As in, the correlation coefficient is worse than > 95% of outcomes expected under the null distribution?
# In other words, whales of closer relatedness AVOID each other? At least a hypothesis...

```



## Chapter 49

# Iterative simulations



## Chapter 50

# Image analysis



## **Chapter 51**

# **Machine learning**



# Bibliography

Wickham, H. (2010). A layered grammar of graphics. *Journal of Computational and Graphical Statistics*, 19(1):3–28.

Wilkinson, L. (2005). *The Grammar of Graphics (Statistics and Computing)*. Springer-Verlag, Berlin, Heidelberg.