On the R-way to hell

An introduction to the marvelous world of R

Julien Martin

Do what you think is interesting,
do something that you think is fun and worthwhile,
because otherwise you won't do it well anyway.

—Brian W. Kernighan

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Preface

The aim of this book

The aim of this book is to introduce you to R, a powerful and flexible interactive environment for statistical computing and research. R in itself is not difficult to learn, but as with learning any new language (spoken or computer) the initial learning curve can be steep and somewhat daunting. It is not intended to cover everything but simply to help you climb the initial learning curve (potentially faster) and provide you with the basic skills (and confidence!) needed to start your own journey with R.

Multilingual book

The book is provided as a multilingual book breaking that language barrier and potentially allow to facilitate the learn of R and its mainly english-speaking environment. We are always looking for volunteers to help developed the book further and add more languages to the growing list. Please contact us if you want to help

On the web version of the book, use  in the navigation bar to switch from one language to another. After switching to your preferred language, you can of course also download the pdf and epub versions in this language if you want to using .

List of languages:

- english (publish but need polishing)
- french (in development, waiting for english to be polished)
- spanish (in development, waiting for english to be polished)

How to use this book

For the best experience we recommend that you read the web version of this book which you can find https://biostats-uottawa.github.io/R.

The web version includes a navbar at the top of the page where you can toggle the sidebars on and off, search through the book, change the page color and suggest revisions if you spot a typo or mistake. You can also download a pdf and epub versions of the book.

We use a few typographical conventions throughout this book.

R code and the resulting output are presented in code blocks in our book.

```
2 + 2
```

```
[1] 4
```

Functions in the text are shown with brackets at the end using code font, i.e. `mean()` or `sd()` etc.

Objects are shown using code font without the round brackets, i.e. `obj1`, `obj2` etc.

R packages in the text are shown using code font and followed by the 📦 icon, i.e. `tidyverse` 📦.

A series of actions required to access menu commands in RStudio or VSCode are identified as `File -> New File -> R Script` which translates to 'click on the File menu, then click on New File and then select R Script'.

When we refer to **IDE** (**I**ntegrated **D**evelopment **E**nvironment software) later in the text we mean either RStudio of VScode.

When we refer to **.[Rq]md**, we mean either R markdown (.Rmd) or Quarto (.qmd) documents and would generally talk of R markdown documents when referring to either `.Rmd` or `.qmd` files.

The manual tries to highlight some part of the text using the following boxes and icons.

> **Exercises**
>
> Stuff for you to do

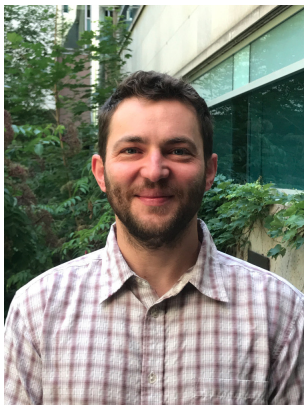
> **Solutions**
>
> R code and explanations

> **Warning**
>
> warnings

> **Important**
>
> important points

> **Note**
>
> notes

Who are we ?



Julien Martin is a Professor at the University of Ottawa working on Evolutionary Ecology and has discovered R with version 1.8.1 and teaches R since v2.4.0.

- : uOttawa https://www.uottawa.ca/faculty-science/professors/julien-martin/, lab page https://juliengamartin.github.io
- : https://twitter.com/jgamartin
- : https://github.com/juliengamartin

Thanks

This book started as a fork on github from the excellent An introduction to R book by Douglas, Roos, Mancini, Couto and Lusseau (Douglas 2023). It was forked on April 23rd, 2023 from Alexd106 github repository then modified and updated following my own needs and teaching perspective of R. This also a part of a multilingual R book project to improve equity and diversity. It started with a french translation and was/will be extended to many more languages.

License

Figure 1.: License Creative Commons

If you teach R, feel free to use some or all of the content in this book to help support your own students. The only thing I ask is that you acknowledge the original source and authors. If you find this book useful or have any comments or suggestions I would love to hear from you (contact info).

Citing the book

Julien Martin. (2024). On the R-way to hell. A multilingual introduction to R book (v0.5.0). Zenodo. https://doi.org/10.5281/zenodo.10929586

Chapter 1

Getting started

Although R is not new, its popularity has increased rapidly over the last 10 years or so (see here for some interesting data). It was originally created and developed by Ross Ihaka and Robert Gentleman during the 1990's with the first stable version released in 2000. Nowadays R is maintained by the R Development Core Team. So, why has R become so popular and why should you learn how to use it? Some reasons include:

- R is open source and freely available.
- R is available for Windows, Mac and Linux operating systems.
- R has an extensive and coherent set of tools for statistical analysis.
- R has an extensive and highly flexible graphical facility capable of producing publication quality figures.
- R has an expanding set of freely available 'packages' 📦 to extend R's capabilities.
- R has an extensive support network with numerous online and freely available documents.

All of the reasons above are great reasons to use R. However, in our opinion, the single biggest reason to use R is that it facilitates robust and reproducible research practices. In contrast to more traditional 'point and click' software, writing code ensures you have a permanent and accurate record of all the methods you used (and decisions you made) for your data analysis. You are then able to share this code (and your data) with other researchers / colleagues / journal reviewers who will be able to reproduce your analysis exactly. This is one of the tenets of open science. We will cover other topics to facilitate open science throughout this book, including creating reproducible reports and version control.

In this Chapter we'll cover:

- how to download and install R and and an IDE on your computer
- give you a brief orientation of the 2 most common IDEs used with R
- installing and working with R packages to extend R's capabilities

- some good habits to get into when working on projects
- and finally some advice on documenting your workflow and writing nice readable R code.

Some R pointers

- Use R often and use it regularly. This will help build and maintain all important momentum.
- Learning R is not a memory test. One of advantage of a scripting language is that you will always have your (well annotated) code to refer back to when you forget how to do something.
- You don't need to know everything about R to be productive.
- If you get stuck, search online, it's not cheating and writing a good search query is a skill in itself.
- If you find yourself staring at code for hours trying to figure out why it's not working then walk away for a few minutes.
- In R there are many ways to tackle a particular problem. If your code does what you want it to do in a reasonable time and robustly then don't worry about it.
- R is just a tool to help you answer your interesting questions. Don't lose sight of what's important - your research question(s) and your data. No amount of skill using R will help if your data collection is fundamentally flawed or your question vague.
- Recognize that there will be times when things will get a little tough or frustrating. Try to accept these periods as part of the natural process of learning a new skill (we've all been there) and remember, the time and energy you invest now will be more than payed back in the not too distant future.

Good luck and don't forget to have fun.

1.1. Installation

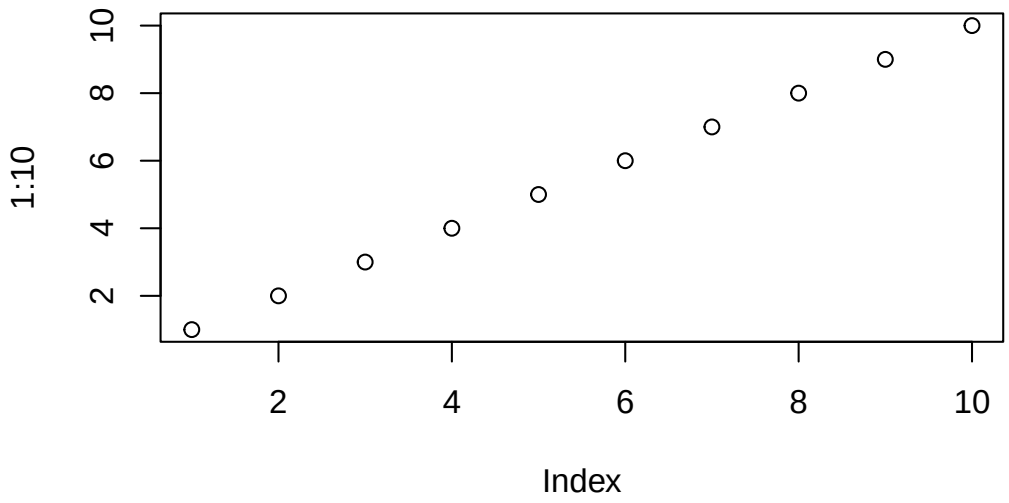
1.1.1. Installing R

To get up and running the first thing you need to do is install R. R is freely available for Windows, Mac and Linux operating systems from the Comprehensive R Archive Network (CRAN) website. For Windows and Mac users we suggest you download and install the pre-compiled binary versions. There are reasonably comprehensive instruction to install R for each OS (Windows,Mac or linux).

Whichever operating system you're using, once you have installed R you need to check its working properly. The easiest way to do this is to start R by double clicking on the R icon (Windows or Mac) or by typing `R` into the Console

(Linux). You should see the R Console and you should be able to type R commands into the Console after the command prompt >. Try typing the following R code and then press enter:

```
plot(1:10)
```



A plot of the numbers 1 to 10 on both the x and y axes should appear. If you see this, you're good to go. If not then we suggest you make a note of any errors produced and then use Google to troubleshoot.

1.1.2. Installing an IDE

We strongly recommend to use an **I**ntegrated **D**evelopment **E**nvironment (IDE) software to work with R. One simple and extremely popular IDE is RStudio. An alternative to RStudio is Visual Studio Code, or VSCode. An IDE can be thought of as an add-on to R which provides a more user-friendly interface, incorporating the R Console, a script editor and other useful functionality (like R markdown and Git Hub integration).

> **Caution**
>
> You must install R before you install an IDE (see previous section for details).

> **Note**
>
> When we refer to **IDE** later in the text we mean either RStudio of VScode

RStudio

RStudio is freely available for Windows, Mac and Linux operating systems and can be downloaded from the RStudio site. You should select the 'RStudio Desktop' version.

VSCode

VSCode is freely available for Windows, Mac and Linux operating systems and can be downloaded from the VS Code site.

In addition you need to install the R extension to VSCode. To make VSCode a true powerhouse for working with R we strongly recommend you to also install:

- radian: A modern R console that corrects many limitations of the official R terminal and supports many features such as syntax highlighting and auto-completion.
- VSCode-R-Debugger: A VS Code extension to support R debugging capabilities.
- httpgd: An R package 📦 to provide a graphics device that asynchronously serves SVG graphics via HTTP and WebSockets.

Alternatives to RStudio and VSCode

Rather than using an 'all in one' IDE many people choose to use R and a separate script editor to write and execute R code. If you're not familiar with what a script editor is, you can think of it as a bit like a word processor but specifically designed for writing code. Happily, there are many script editors freely available so feel free to download and experiment until you find one you like. Some script editors are only available for certain operating systems and not all are specific to R. Suggestions for script editors are provided below. Which one you choose is up to you: one of the great things about R is that *YOU* get to choose how you want to use R.

Advanced text editors A light yet efficient way to work with R is using advanced text editors such as:

- Atom (all operating systems)
- BBedit (Mac OS)
- gedit (Linux; comes with most Linux distributions)
- MacVim (Mac OS)
- Nano (Linux)
- Notepad++ (Windows)
- Sublime Text (all operating systems)
- vim and its extension NVim-R (Linux)

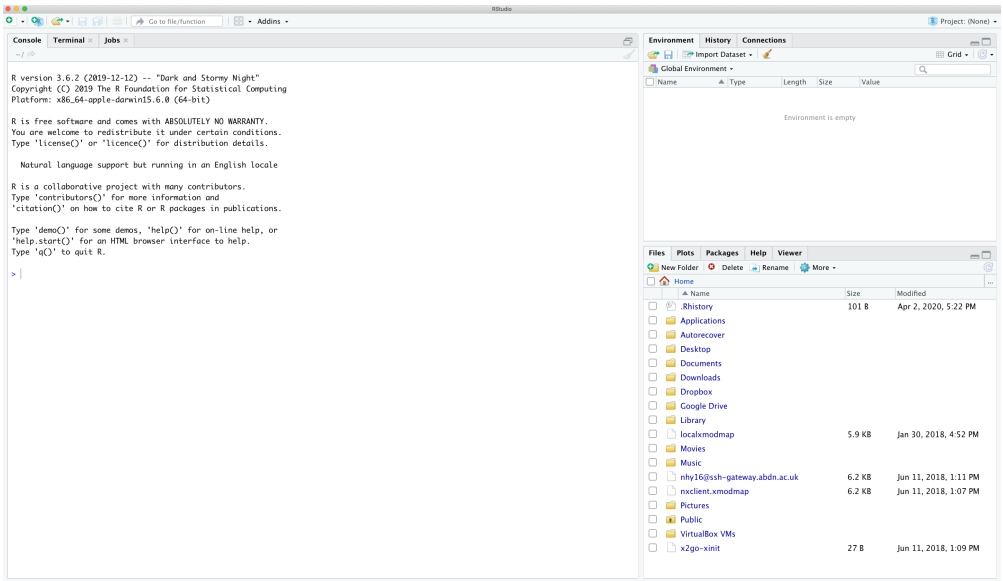
Integrated development environments These environments are more powerful than simple text editors, and are similar to RStudio:

- Emacs and its extension Emacs Speaks Statistics (all operating systems)
- RKWard (Linux)
- Tinn-R (Windows)

1.2. IDE orientation

1.2.1. RStudio

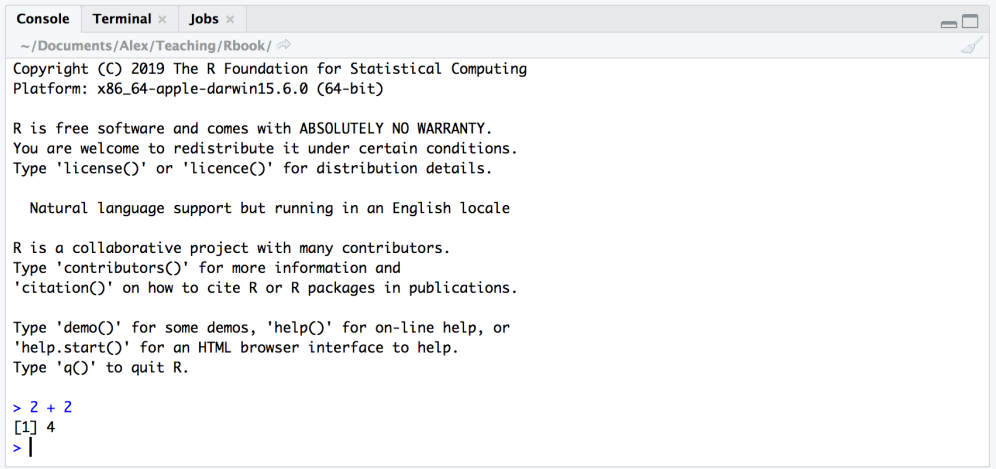
When you open R studio for the first time you should see the following layout (it might look slightly different on a Windows computer).



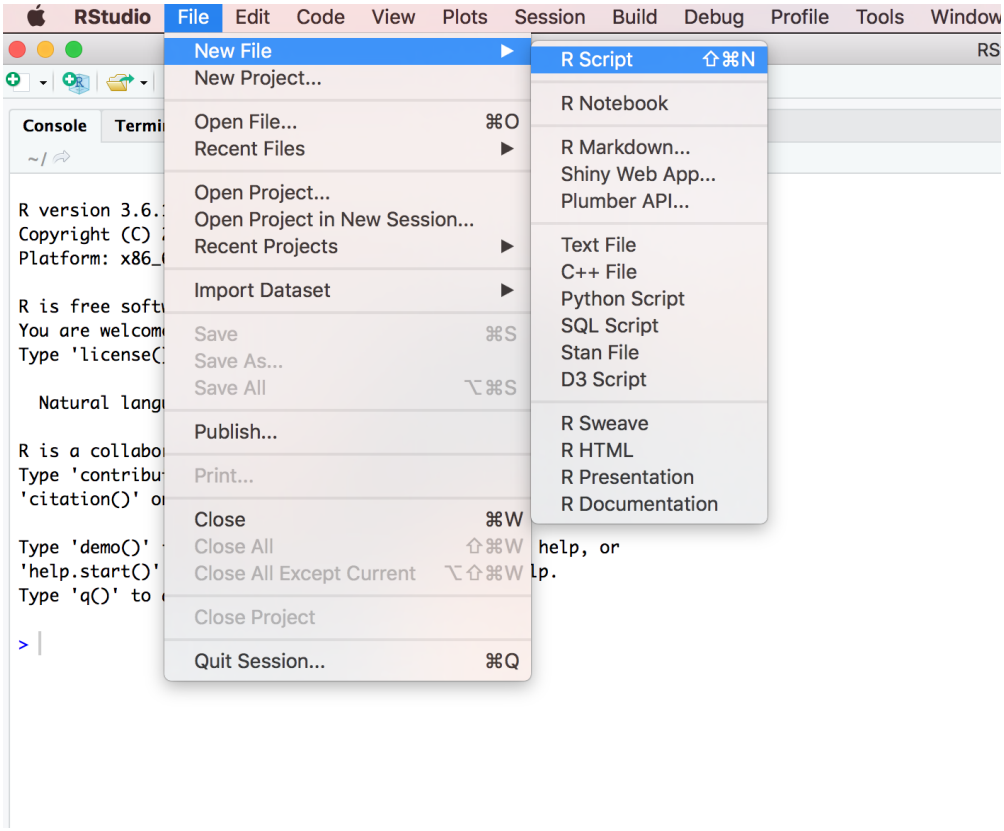
The large window (aka pane) on the left is the **Console** window. The window on the top right is the **Environment / History / Connections** pane and the bottom right window is the **Files / Plots / Packages / Help / Viewer** window. We will discuss each of these panes in turn below. You can customise the location of each pane by clicking on the 'Tools' menu then selecting Global Options –> Pane Layout. You can resize the panes by clicking and dragging the middle of the window borders in the direction you want. There are a plethora of other ways to customise RStudio.

Console

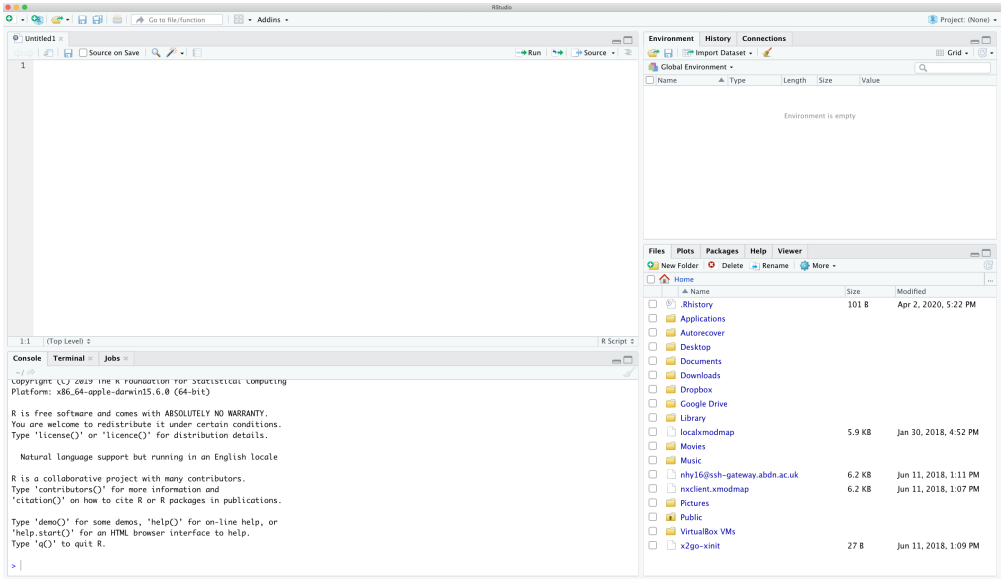
The Console is the workhorse of R. This is where R evaluates all the code you write. You can type R code directly into the Console at the command line prompt, `>`. For example, if you type `2 + 2` into the Console you should obtain the answer `4` (reassuringly). Don't worry about the `[1]` at the start of the line for now.



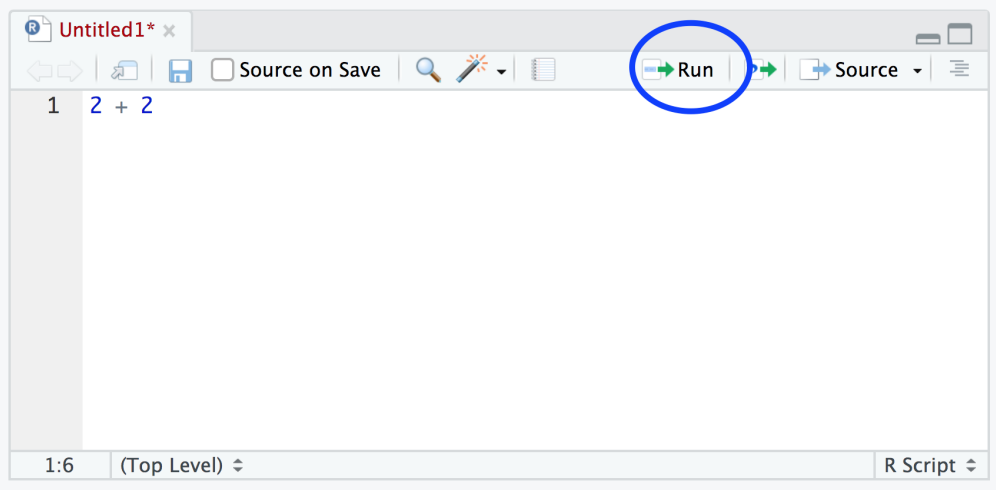
However, once you start writing more R code this becomes rather cumbersome. Instead of typing R code directly into the Console a better approach is to create an R script. An R script is just a plain text file with a `.R` file extension which contains your lines of R code. These lines of code are then sourced into the R Console line by line. To create a new R script click on the 'File' menu then select New File –> R Script.



Notice that you have a new window (called the Source pane) in the top left of RStudio and the Console is now in the bottom left position. The new window is a script editor and where you will write your code.



To source your code from your script editor to the Console simply place your cursor on the line of code and then click on the 'Run' button in the top right of the script editor pane.



You should see the result in the Console window. If clicking on the 'Run' button starts to become tiresome you can use the keyboard shortcut 'ctrl + enter' (on Windows and Linux) or 'cmd + enter' (on Mac). You can save your R scripts as a `.R` file by selecting the 'File' menu and clicking on save. Notice that the file name in the tab will turn red to remind you that you have unsaved changes. To open your R script in RStudio select the 'File' menu and then 'Open File…'. Finally, its worth noting that although R scripts are saved with a `.R` extension they are actually just plain text files which can be opened with any text editor.

Environment/History/Connections

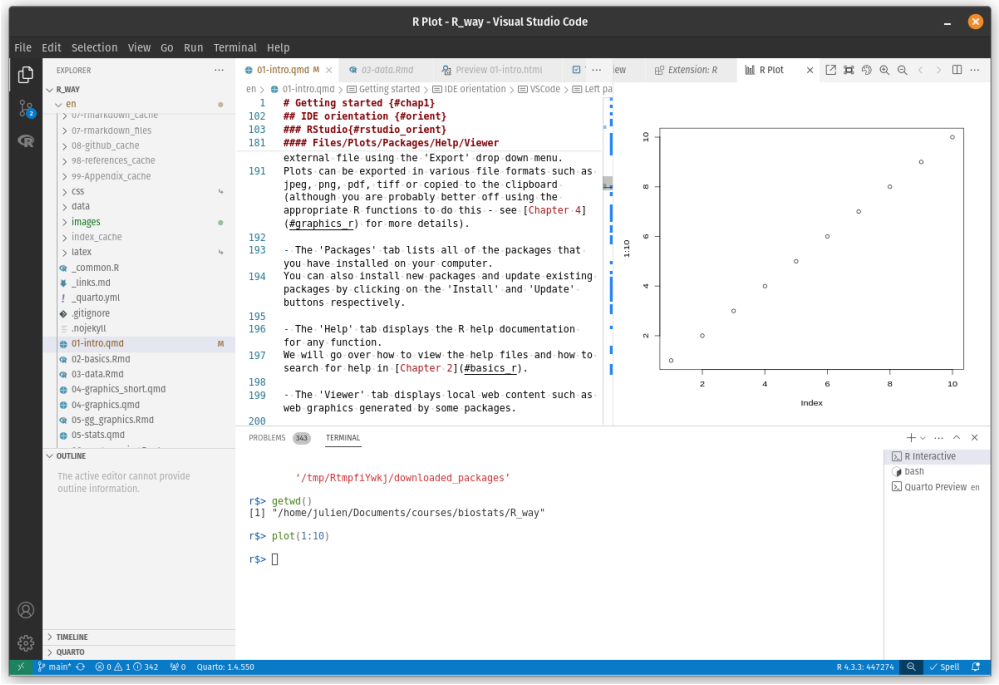
The Environment / History / Connections window shows you lots of useful information. You can access each component by clicking on the appropriate tab in the pane.

- The 'Environment' tab displays all the objects you have created in the current (global) environment. These objects can be things like data you have imported or functions you have written. Objects can be displayed as a List or in Grid format by selecting your choice from the drop down button on the top right of the window. If you're in the Grid format you can remove objects from the environment by placing a tick in the empty box next to the object name and then click on the broom icon. There's also an 'Import Dataset' button which will import data saved in a variety of file formats. However, we would suggest that you don't use this approach to import your data as it's not reproducible and therefore not robust (see Chapter 3 for more details).
- The 'History' tab contains a list of all the commands you have entered into the R Console. You can search back through your history for the line of code you have forgotten, send selected code back to the Console or Source window. We usually never use this as we always refer back to our R script.
- The 'Connections' tab allows you to connect to various data sources such as external databases.

Files/Plots/Packages/Help/Viewer

- The 'Files' tab lists all external files and directories in the current working directory on your computer. It works like file explorer (Windows) or Finder (Mac). You can open, copy, rename, move and delete files listed in the window.
- The 'Plots' tab is where all the plots you create in R are displayed (unless you tell R otherwise). You can 'zoom' into the plots to make them larger using the magnifying glass button, and scroll back through previously created plots using the arrow buttons. There is also the option of exporting plots to an external file using the 'Export' drop down menu. Plots can be exported in various file formats such as jpeg, png, pdf, tiff or copied to the clipboard (although you are probably better off using the appropriate R functions to do this - see Chapter 4 for more details).
- The 'Packages' tab lists all of the packages that you have installed on your computer. You can also install new packages and update existing packages by clicking on the 'Install' and 'Update' buttons respectively.
- The 'Help' tab displays the R help documentation for any function. We will go over how to view the help files and how to search for help in Chapter 2.
- The 'Viewer' tab displays local web content such as web graphics generated by some packages.

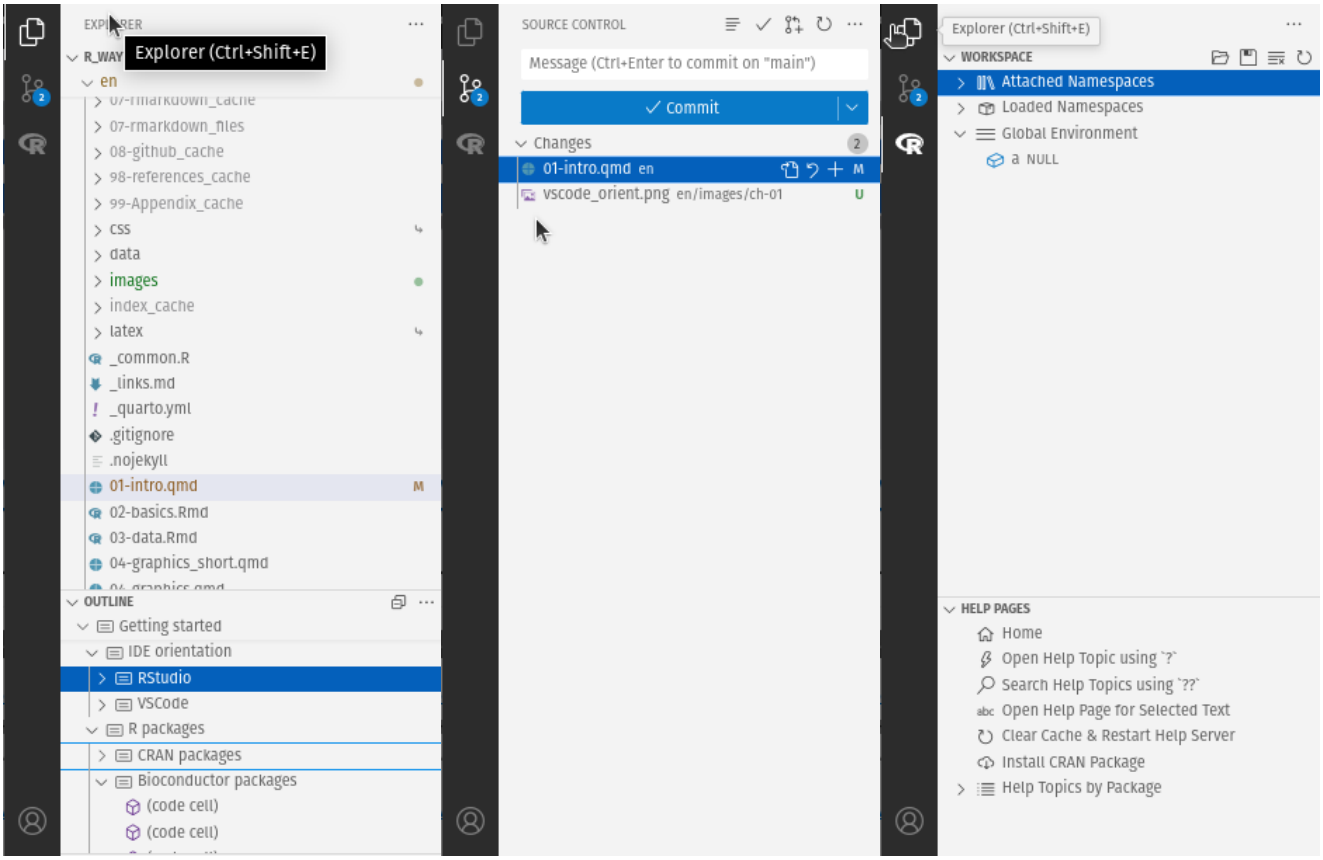
1.2.2. VSCode



Left panel

Contains :

- File manager and file outline
- R support including R environment/ R search / R help / install packages
- Github interaction



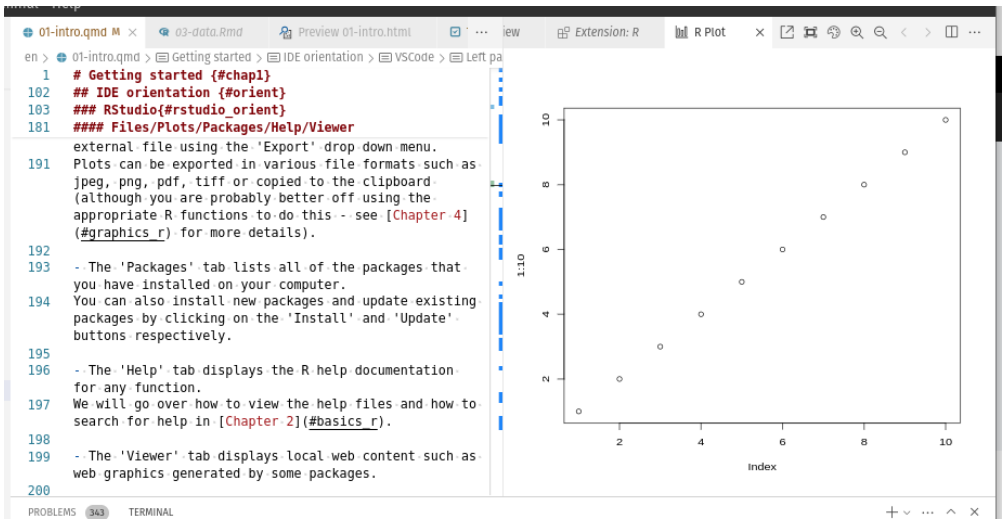
(a) file (b) git (c) r-ext

Figure 1.1.: VS Code left panel

Editor tabs

Includes:

- plot panel (with history and navigation)
- edition of scripts
- preview panels



Terminal window

Contains:

- the terminal allowing to have an R session or any other type of terminals needed (bash/tmux/). It can be split and run multiple sessions at the same time
- a problems pane highlighting both grammar and coding problems

1.3. R packages

The base installation of R comes with many useful packages as standard. These packages will contain many of the functions you will use on a daily basis. However, as you start using R for more diverse projects (and as your own use of R evolves) you will find that there comes a time when you will need to extend R's capabilities. Happily, many thousands of R users have developed useful code and shared this code as installable packages. You can think of a package as a collection of functions, data and help files collated into a well defined standard structure which you can

download and install in R. These packages can be downloaded from a variety of sources but the most popular are CRAN, Bioconductor and GitHub. Currently, CRAN hosts over 15000 packages and is the official repository for user contributed R packages. Bioconductor provides open source software oriented towards bioinformatics and hosts over 1800 R packages. GitHub is a website that hosts git repositories for all sorts of software and projects (not just R). Often, cutting edge development versions of R packages are hosted on GitHub so if you need all the new bells and whistles then this may be an option. However, a potential downside of using the development version of an R package is that it might not be as stable as the version hosted on CRAN (it's in development!) and updating packages won't be automatic.

1.3.1. CRAN packages

To install a package from CRAN you can use the `install.packages()` function. For example if you want to install the `remotes` package enter the following code into the Console window of RStudio (note: you will need a working internet connection to do this)

```
install.packages("remotes", dependencies = TRUE)
```

You may be asked to select a CRAN mirror, just select '0-cloud' or a mirror near to your location. The `dependencies = TRUE` argument ensures that additional packages that are required will also be installed.

It's good practice to regularly update your previously installed packages to get access to new functionality and bug fixes. To update CRAN packages you can use the `update.packages()` function (you will need a working internet connection for this)

```
update.packages(ask = FALSE)
```

The `ask = FALSE` argument avoids having to confirm every package download which can be a pain if you have many packages installed.

1.3.2. Bioconductor packages

To install packages from Bioconductor the process is a little different. You first need to install the `BiocManager` 📦 package. You only need to do this once unless you subsequently reinstall or upgrade R

```
install.packages("BiocManager", dependencies = TRUE)
```

Once the `BiocManager` 📦 package has been installed you can either install all of the 'core' Bioconductor packages with

```
BiocManager::install()
```

or install specific packages such as the `GenomicRanges` 📦 and `edgeR` 📦 packages

```
BiocManager::install(c("GenomicRanges", "edgeR"))
```

To update Bioconductor packages just use the `BiocManager::install()` function again

```
BiocManager::install(ask = FALSE)
```

Again, you can use the `ask = FALSE` argument to avoid having to confirm every package download.

1.3.3. GitHub packages

There are multiple options for installing packages hosted on GitHub. Perhaps the most efficient method is to use the `install_github()` function from the `remotes` 📦 package (you installed this package previously). Before you use the function you will need to know the GitHub username of the repository owner and also the name of the repository. For example, the development version of `dplyr` 📦 from Hadley Wickham is hosted on the tidyverse GitHub account and has the repository name 'dplyr' (just Google 'github dplyr'). To install this version from GitHub use

```
remotes::install_github("tidyverse/dplyr")
```

The safest way (that we know of) to update a package installed from GitHub is to just reinstall it using the above command.

1.3.4. Using packages

Once you have installed a package onto your computer it is not immediately available for you to use. To use a package you first need to load the package by using the `library()` function. For example, to load the `remotes` 📦 package you previously installed

```
library(remotes)
```

The `library()` function will also load any additional packages required and may print out additional package information. It is important to realize that every time you start a new R session (or restore a previously saved session) you need to load the packages you will be using. We tend to put all our `library()` statements required for our analysis near the top of our R scripts to make them easily accessible and easy to add to as our code develops. If you try to use a function without first loading the relevant R package you will receive an error message that R could not find the function. For example, if you try to use the `install_github()` function without loading the `remotes` 📦 package first you will receive the following error

```
install_github("tidyverse/dplyr")


# Error in install_github("tidyverse/dplyr") :
#  could not find function "install_github"
```

Sometimes it can be useful to use a function without first using the `library()` function. If, for example, you will only be using one or two functions in your script and don't want to load all of the other functions in a package then you can access the function directly by specifying the package name followed by two colons and then the function name

```
remotes::install_github("tidyverse/dplyr")
```

This is how we were able to use the `install()` and `install_github()` functions above without first loading the packages `BiocManager` 📦 and `remotes` 📦 . Most of the time we recommend using the `library()` function.

1.4. Working directories

The working directory is the default location where R will look for files you want to load and where it will put any files you save. One of the great things about using RStudio Projects is that when you open a project it will

automatically set your working directory to the appropriate location. You can check the file path of your working directory by using either `getwd()` or `here()` functions.

```
getwd()
```

```
[1] "/home/julien/Documents/courses/biostats/R_way"
```

In the example above, the working directory is a folder called 'R_way' which is a subfolder of "biostats' in the 'courses' folder which in turn is in a 'Documents' folder located in the 'julien' folder which itself is in the 'home' folder. On a Windows based computer our working directory would also include a drive letter (i.e. `C:\home\julien\Documents\courses\biostats\R_way`).

If you weren't using an IDE then you would have to set your working directory using the `setwd()` function at the start of every R script (something we did for many years).

```
setwd("/home/julien/Documents/courses/biostats/R_way/")
```

However, the problem with `setwd()` is that it uses an *absolute* file path which is specific to the computer you are working on. If you want to send your script to someone else (or if you're working on a different computer) this absolute file path is not going to work on your friend/colleagues computer as their directory configuration will be different (you are unlikely to have a directory structure `/home/julien/Documents/courses/biostats/` on your computer). This results in a project that is not self-contained and not easily portable. IDEs solves this problem by allowing you to use *relative* file paths which are relative to the *Root* project directory. The Root project directory is just the directory that contains the `.Rproj` file in Rstudio (`first_project.Rproj` in our case) or the base folder of your workspace in VScode. If you want to share your analysis with someone else, all you need to do is copy the entire project directory and send to your to your collaborator. They would then just need to open the project file and any R scripts that contain references to relative file paths will just work. For example, let's say that you've created a subdirectory called `data` in your Root project directory that contains a csv delimited datile called `mydata.csv` (we will cover directory structures below). To import this datile in an RStudio project using the `read.csv()` function (don't worry about this now, we will cover this in much more detail in Chapter 3) all you need to include in your R script is

```
dat <- read.csv("data/mydata.csv")
```

Because the file path `data/mydata.csv` is relative to the project directory it doesn't matter where you collaborator saves the project directory on their computer it will still work.

If you weren't using an RStudio project or VScode workspace then you would need to either set the working directory providing the full path to your directory or specify the full path of the data file. Neither option would be reproducible on other computers.

```
setwd("/home/julien/Documents/courses/biostats/R_way")


dat <- read.csv("data/mydata.csv")
```

or

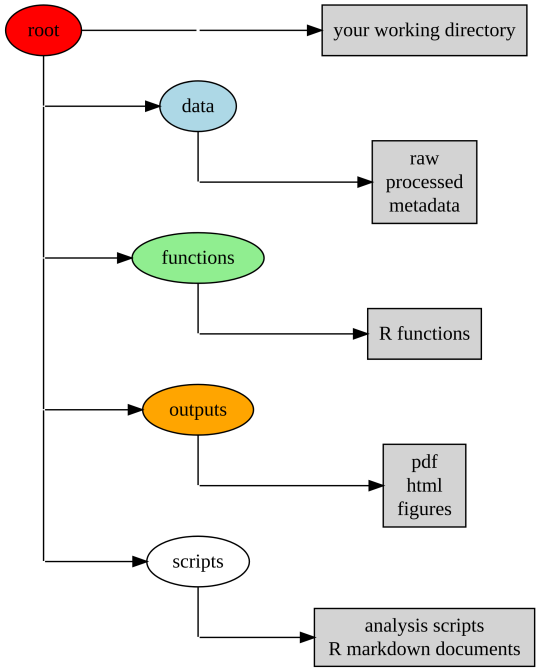
```
dat <- read.csv("/home/julien/Documents/courses/biostats/R_way/data/mydata.csv")
```

For those of you who want to take the notion of relative file paths a step further, take a look at the `here()` function in the `here` package. The `here()` function allows you to build file paths for any file relative to the project root directory that are also operating system agnostic (works on a Mac, Windows or Linux machine). For example, to import our `mydata.csv` file from the `data` directory just use:

```
library(here) # you may need to install the here package first
dat <- read.csv(here("data", "mydata.csv"))
```

1.5. Directory structure

In addition to using RStudio Projects, it's also really good practice to structure your working directory in a consistent and logical way to help both you and your collaborators. We frequently use the following directory structure in our R based projects.



In our working directory we have the following directories:

- **Root** - This is your project directory containing your `.Rproj` file. We tend to keep all the R scripts or [Rq]md document necessary for the analysis / report in this root folder or in the scripts folder when there are too many.
- **data** - We store all our data in this directory. The subdirectory called `data` contains raw data files and only raw data files. These files should be treated as **read only** and should not be changed in any way. If you need to process/clean/modify your data do this in R (not MS Excel) as you can document (and justify) any changes made. Any processed data should be saved to a separate file and stored in the `processed_data` subdirectory. Information about data collection methods, details of data download and any other useful metadata should be saved in a text document (see README text files below) in the `metadata` subdirectory.
- **functions** - This is an optional directory where we save all of the custom R functions we've written for the current analysis. These can then be sourced into R using the `source()` function.
- **scripts** - An optional directory where we save our R markdown documents and/or the main R scripts we have written for the current project are saved here if not in the root folder.
- **output** - Outputs from our R scripts such as plots, HTML files and data summaries are saved in this directory. This helps us and our collaborators distinguish what files are outputs and which are source files.

Of course, the structure described above is just what works for us most of the time and should be viewed as a starting point for your own needs. We tend to have a fairly consistent directory structure across our projects as this allows us

to quickly orientate ourselves when we return to a project after a while. Having said that, different projects will have different requirements so we happily add and remove directories as required.

You can create your directory structure using Windows Explorer (or Finder on a Mac) or within your IDE by clicking on the 'New folder' button in the 'Files' pane.

An alternative approach is to use the `dir.create()` functions in the R Console.

```
# create directory called 'data'
dir.create("data")
```

1.6. Projects organisation

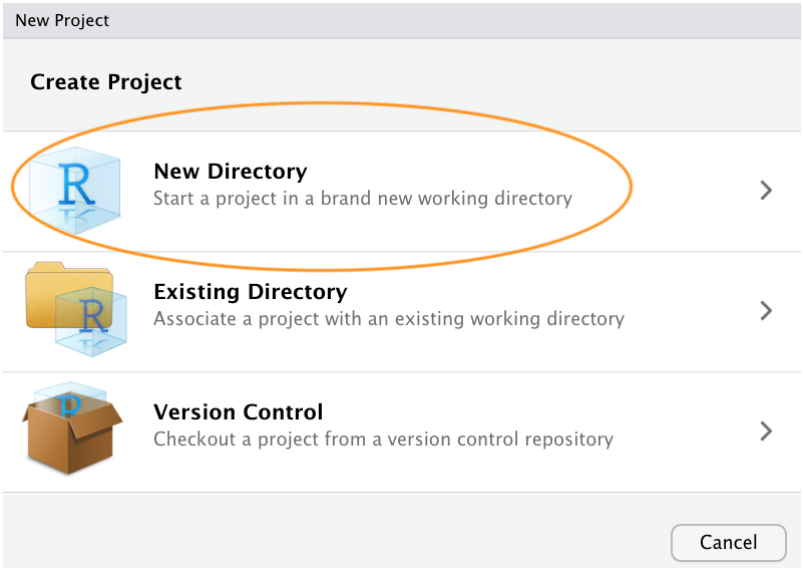
As with most things in life, when it comes to dealing with data and data analysis things are so much simpler if you're organized. Clear project organisation makes it easier for both you (especially the future you) and your collaborators to make sense of what you've done. There's nothing more frustrating than coming back to a project months (sometimes years) later and have to spend days (or weeks) figuring out where everything is, what you did and why you did it. A well documented project that has a consistent and logical structure increases the likelihood that you can pick up where you left off with minimal fuss no matter how much time has passed. In addition, it's much easier to write code to automate tasks when files are well organized and are sensibly named. This is even more relevant nowadays as it's never been easier to collect vast amounts of data which can be saved across 1000's or even 100,000's of separate data files. Lastly, having a well organized project reduces the risk of introducing bugs or errors into your workflow and if they do occur (which inevitably they will at some point), it makes it easier to track down these errors and deal with them efficiently.

There are also a few simple steps you can take right at the start of any project to help keep things shipshape.

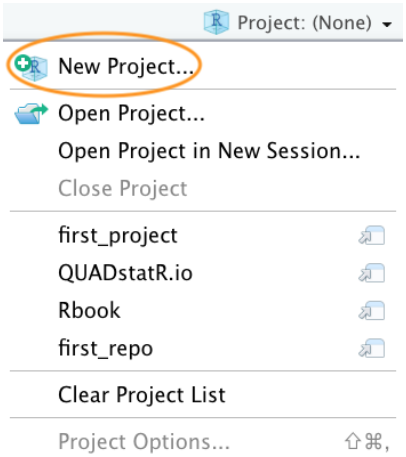
A great way of keeping things organized is to use RStudio Projects or VSCode workspaces, referred after as `project`. A `project` keeps all of your R scripts, R markdown documents, R functions and data together in one place. The nice thing about `project` is that each has its own directory, history and source documents so different analyses that you are working on are kept completely separate from each other. This means that you can very easily switch between `projects` without fear of them interfering with each other.

1.6.1. RStudio

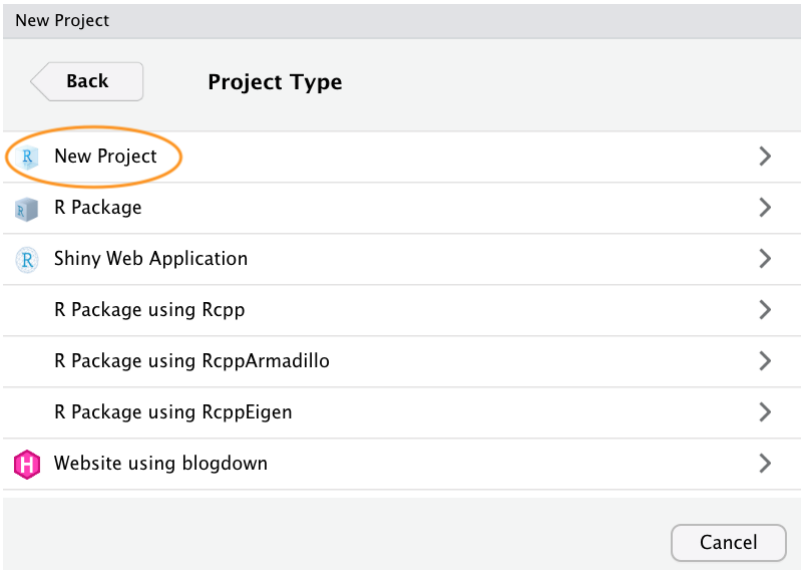
To create a project, open RStudio and select `File -> New Project...` from the menu. You can create either an entirely new project, a project from an existing directory or a version controlled project (see the GitHub Chapter for further details about this). In this Chapter we will create a project in a new directory.



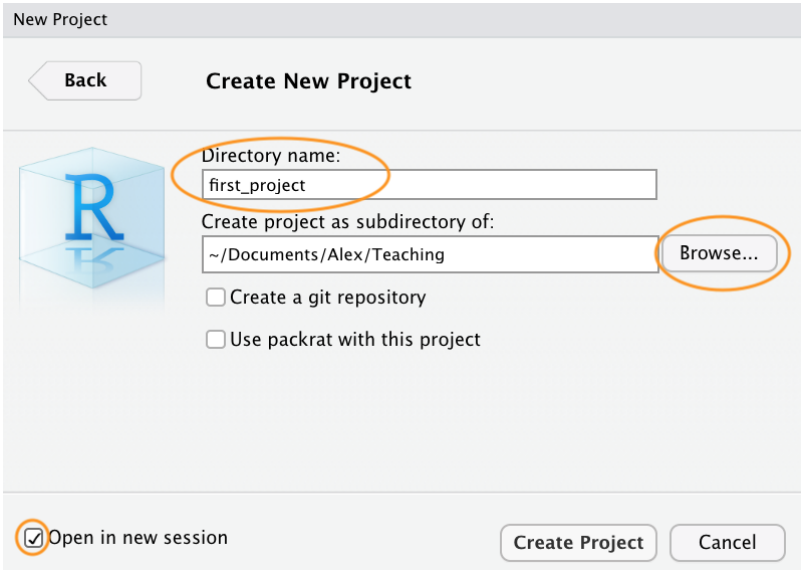
You can also create a new project by clicking on the 'Project' button in the top right of RStudio and selecting 'New Project…'



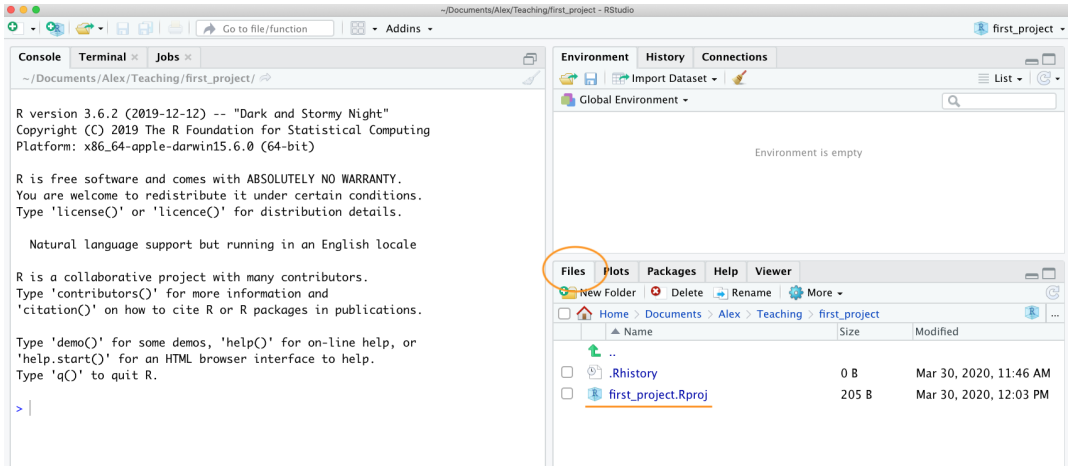
In the next window select 'New Project'.



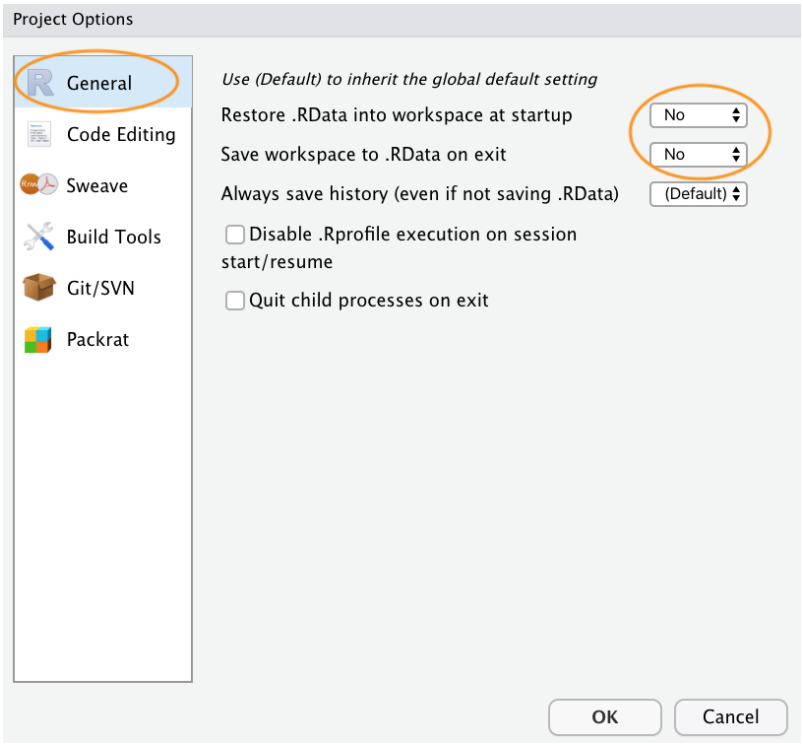
Now enter the name of the directory you want to create in the 'Directory name:' field (we'll call it `first_project` for this Chapter). If you want to change the location of the directory on your computer click the 'Browse…' button and navigate to where you would like to create the directory. We always tick the 'Open in new session' box as well. Finally, hit the 'Create Project' to create the new project.



Once your new project has been created you will now have a new folder on your computer that contains an RStudio project file called `first_project.Rproj`. This `.Rproj` file contains various project options (but you shouldn't really interact with it) and can also be used as a shortcut for opening the project directly from the file system (just double click on it). You can check this out in the 'Files' tab in RStudio (or in Finder if you're on a Mac or File Explorer in Windows).



The last thing we suggest you do is select `Tools` -> `Project Options...` from the menu. Click on the 'General' tab on the left hand side and then change the values for 'Restore .RData into workspace at startup' and 'Save workspace to .RData on exit' from 'Default' to 'No'. This ensures that every time you open your project you start with a clean R session. You don't have to do this (many people don't) but we prefer to start with a completely clean workspace whenever we open our projects to avoid any potential conflicts with things we have done in previous sessions (sometimes leading to surprising results and headaches figuring out the problem). The downside to this is that you will need to rerun your R code every time you open your project.



Now that you have an RStudio project set up you can start creating R scripts (or R markdown documents) or whatever

you need to complete you project. All of the R scripts will now be contained within the RStudio project and saved in the project folder.

1.6.2. VSCode

workspace are similar to RStudio projects. You however need to create a new folder with a R file (or text file) and save as workspace.

1.7. File names

What you call your files matters more than you might think. Naming files is also more difficult than you think. The key requirement for a 'good' file name is that it's informative whilst also being relatively short. This is not always an easy compromise and often requires some thought. Ideally you should try to avoid the following!

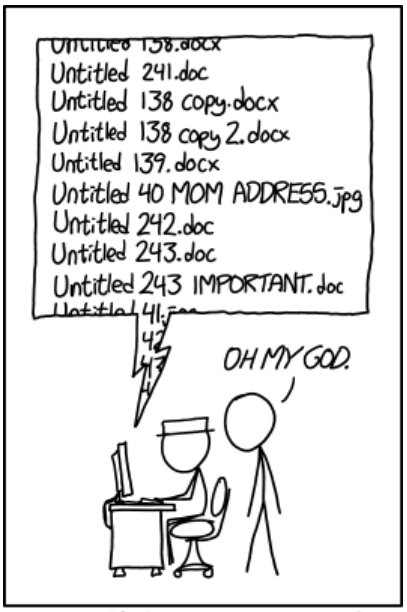


Figure 1.2.: source:https://xkcd.com/1459/

Although there's not really a recognized standard approach to naming files (actually there is, just not everyone uses it), there are a couple of things to bear in mind.

- First, avoid using spaces in file names by replacing them with underscores or even hyphens. Why does this matter? One reason is that some command line software (especially many bioinformatic tools) won't recognise a file name with a space and you'll have to go through all sorts of shenanigans using escape characters to make

sure spaces are handled correctly. Even if you don't think you will ever use command line software you may be doing so indirectly. Take R markdown for example, if you want to render an R markdown document to pdf using the `rmarkdown` 📦 package you will actually be using a command line LaTeX engine under the hood (called Pandoc). Another good reason not to use spaces in file names is that it makes searching for file names (or parts of file names) using regular expressions in R (or any other language) much more difficult.

- For the reasons given above, also avoid using special characters (i.e. @£$%^&*(:/)) in your file names.
- If you are versioning your files with sequential numbers (i.e. file1, file2, file3 …) and you have more than 9 files you should use 01, 02, 03 .. 10 as this will ensure the files are printed in the correct order (see what happens if you don't). If you have more than 99 files then use 001, 002, 003… etc.
- If your file names include dates, use the ISO 8601 format YYYY-MM-DD (or YYYYMMDD) to ensure your files are listed in proper chronological order.
- Never use the word *final* in any file name - it never is!

Whatever file naming convention you decide to use, try to adopt early, stick with it and be consistent. You'll thank us!

1.8. Script documentation

A quick note or two about writing R code and creating R scripts. Unless you're doing something really quick and dirty we suggest that you always write your R code as an R script. R scripts are what make R so useful. Not only do you have a complete record of your analysis, from data manipulation, visualisation and statistical analysis, you can also share this code (and data) with friends, colleagues and importantly when you submit and publish your research to a journal. With this in mind, make sure you include in your R script all the information required to make your work reproducible (author names, dates, sampling design etc). This information could be included as a series of comments `#` or, even better, by mixing executable code with narrative into an R markdown document. It's also good practice to include the output of the `sessionInfo()` function at the end of any script which prints the R version, details of the operating system and also loaded packages. A really good alternative is to use the `session_info()` function from the `xfun` 📦 package for a more concise summary of our session environment.

Here's an example of including meta-information at the start of an R script

```
# Title: Time series analysis of lasagna consumption

# Purpose : This script performs a time series analyses on
#           lasagna meals kids want to have each week.
#           Data consists of counts of (dreamed) lasagna meals per week
#           collected from 24 kids at the "Food-dreaming" school
#           between 2042 and 2056.

# data file: lasagna_dreams.csv

# Author: A. Stomach
# Contact details: a.stomach@food.uni.com

# Date script created: Fri Mar 29 17:06:44 2010 -----------
# Date script last modified: Thu Dec 12 16:07:12 2019 ----

# package dependencies
library(tidyverse)
library(ggplot2)

print("put your lovely R code here")

# good practice to include session information

xfun::session_info()
```

This is just one example and there are no hard and fast rules so feel free to develop a system that works for you. A really useful shortcut in RStudio is to automatically include a time and date stamp in your R script. To do this, write `ts` where you want to insert your time stamp in your R script and then press the 'shift + tab' keys. RStudio will magically convert `ts` into the current date and time and also automatically comment out this line with a `#`. Another really useful RStudio shortcut is to comment out multiple lines in your script with a # symbol. To do this, highlight the lines of text you want to comment and then press 'ctrl + shift + c' (or 'cmd + shift + c' on a mac). To uncomment the lines just use 'ctrl + shift + c' again.

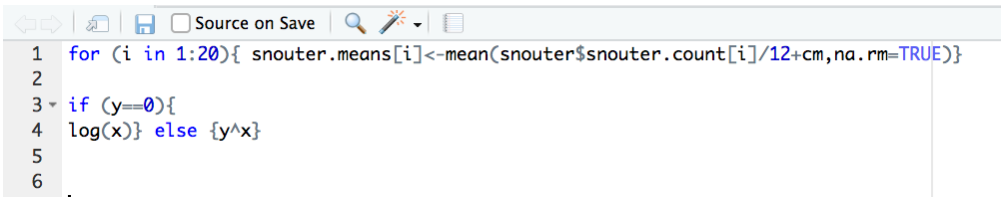
In addition to including metadata in your R scripts it's also common practice to create a separate text file to record important information. By convention these text files are named `README`. We often include a `README` file in the directory where we keep our raw data. In this file we include details about when data were collected (or downloaded), how data were collected, information about specialised equipment, preservation methods, type and version of any machines used (i.e. sequencing equipment) etc. You can create a README file for your project in RStudio by clicking on the `File -> New File -> Text File` menu.

1.9. R style guide

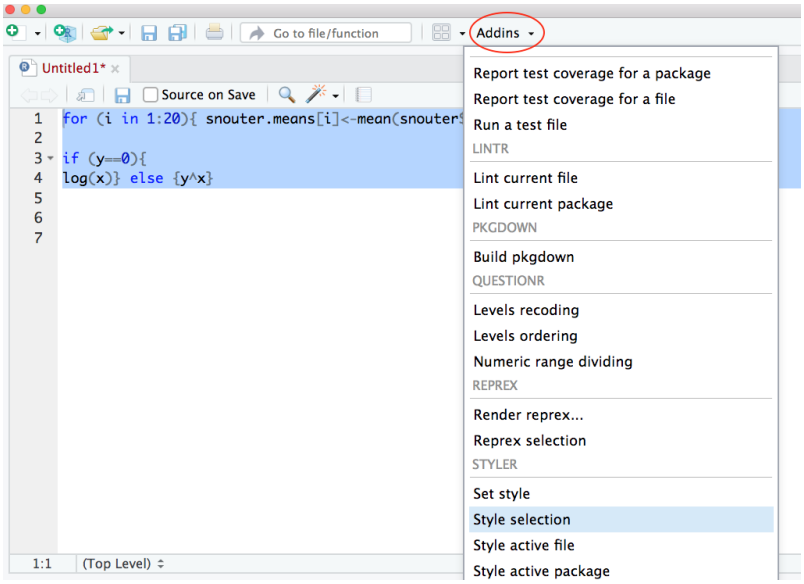
How you write your code is more or less up to you although your goal should be to make it as easy to read as possible (for you and others). Whilst there are no rules (and no code police), we encourage you to get into the habit of writing readable R code by adopting a particular style. We suggest that you follow Google's R style guide whenever possible. This style guide will help you decide where to use spaces, how to indent code and how to use square `[ ]` and curly `{ }` brackets amongst other things.

To help you with code formatting:

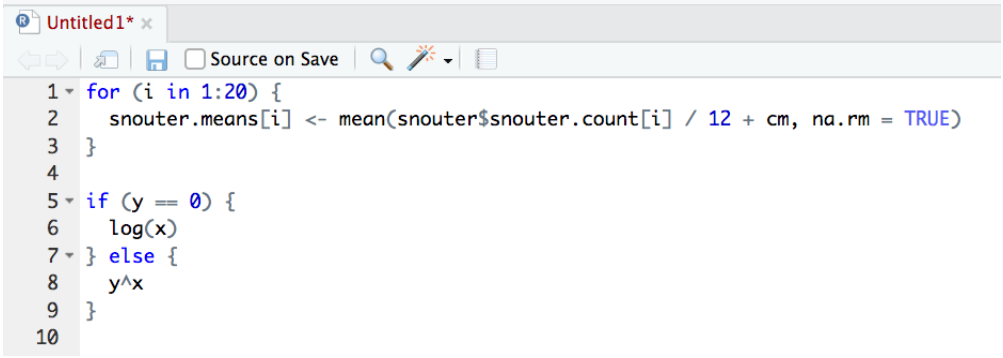
- VSCode there is an embedded formatter in the R extension for VSCode. You can just use the keyboard shortcut to reformat the code nicely and automatically.
- RStudio you can install the `styler` 📦 package which includes an RStudio add-in to allow you to automatically restyle selected code (or entire files and projects) with the click of your mouse. You can find more information about the `styler` 📦 package including how to install here. Once installed, you can highlight the code you want to restyle, click on the 'Addins' button at the top of RStudio and select the 'Style Selection' option. Here is an example of poorly formatted R code



Now highlight the code and use the `styler` 📦 package to reformat



To produce some nicely formatted code



1.10. Backing up projects

Don't be that person who loses hard won (and often expensive) data and analyses. Don't be that person who thinks it'll never happen to me - it will! Always think of the absolute worst case scenario, something that makes you wake up in a cold sweat at night, and do all you can to make sure this never happens. Just to be clear, if you're relying on copying your precious files to an external hard disk or USB stick this is **NOT** an effective backup strategy. These things go wrong all the time as you lob them into your rucksack or 'bag for life' and then lug them between your office and home. Even if you do leave them plugged into your computer what happens when the building burns down (we did say worst case!)?

Ideally, your backups should be offsite and incremental. Happily there are numerous options for backing up your files. The first place to look is in your own institute. Most (all?) Universities have some form of network based

storage that should be easily accessible and is also underpinned by a comprehensive disaster recovery plan. Other options include cloud based services such as Google Drive and Dropbox (to name but a few), but make sure you're not storing sensitive data on these services and are comfortable with the often eye watering privacy policies.

Whilst these services are pretty good at storing files, they don't really help with incremental backups. Finding previous versions of files often involves spending inordinate amounts of time trawling through multiple files named *'final.doc'*, *'final_v2.doc'* and *'final_usethisone.doc'* etc until you find the one you were looking for. The best way we know for both backing up files and managing different versions of files is to use Git and GitHub. To find out more about how you can use RStudio, Git and GitHub together see the Git and GitHub Chapter.

1.11. Citing R

Many people have invested huge amounts of time and energy making R the great piece of software you're now using. If you use R in your work (and we hope you do) please remember to give appropriate credit by citing R. To get the most up to date citation for R you can use the `citation()` function.

```
citation()
```

```
To cite R in publications use:

  R Core Team (2024). _R: A Language and Environment for Statistical
  Computing_. R Foundation for Statistical Computing, Vienna, Austria.
  <https://www.R-project.org/>.

A BibTeX entry for LaTeX users is

  @Manual{,
    title = {R: A Language and Environment for Statistical Computing},
    author = {{R Core Team}},
    organization = {R Foundation for Statistical Computing},
    address = {Vienna, Austria},
    year = {2024},
    url = {https://www.R-project.org/},
  }
```

```
We have invested a lot of time and effort in creating R, please cite it
when using it for data analysis. See also 'citation("pkgname")' for
citing R packages.
```

If you want to cite a particular package you've used for your data analysis.

```
citation(package = "here")
```

```
To cite package 'here' in publications use:

  Müller K (2020). _here: A Simpler Way to Find Your Files_. R package
  version 1.0.1, <https://CRAN.R-project.org/package=here>.

A BibTeX entry for LaTeX users is

  @Manual{,
    title = {here: A Simpler Way to Find Your Files},
    author = {Kirill Müller},
    year = {2020},
    note = {R package version 1.0.1},
    url = {https://CRAN.R-project.org/package=here},
  }
```

To cite multiple packages, the package `grateful` 📦 is extermely useful. See Table 8.1 for an example output produced with grateful.

Chapter 2

Some R basics

In this Chapter we'll introduce you to using R to perform some basic R tasks such as creating objects and assigning values to objects, exploring different types of objects and how to perform some common operations on objects. We'll also learn how to get help in R and highlight some resources to help support your R learning. Finally, we'll cover how to save your work.

We provide screenshot of RStudio but everything is really similar when using VSCode.

Before we continue, here are a few things to bear in mind as you work through this Chapter:

- R is case sensitive i.e. `A` is not the same as `a` and `anova` is not the same as `Anova`.
- Anything that follows a `#` symbol is interpreted as a comment and ignored by R. Comments should be used liberally throughout your code for both your own information and also to help your collaborators. Writing comments is a bit of an art and something that you will become more adept at as your experience grows.
- In R, commands are generally separated by a new line. You can also use a semicolon `;` to separate your commands but this is rarely used.
- If a continuation prompt `+` appears in the console after you execute your code this means that you haven't completed your code correctly. This often happens if you forget to close a bracket and is especially common when nested brackets are used (`(((some command)))`). Just finish the command on the new line and fix the typo or hit escape on your keyboard (see point below) and fix.
- In general, R is fairly tolerant of extra spaces inserted into your code, in fact using spaces is actively encouraged. However, spaces should not be inserted into operators i.e. `<-` should not read `< -` (note the space). See Google's style guide for advice on where to place spaces to make your code more readable.

- If your console 'hangs' and becomes unresponsive after running a command you can often get yourself out of trouble by pressing the escape key (esc) on your keyboard or clicking on the stop icon in the top right of your console. This will terminate most current operations.

2.1. Getting started

In Chapter 1 we learned about the R Console and creating scripts and Projects. We also saw how you write your R code in a script and then source this code into the console to get it to run (if you've forgotten how to do this, pop back to the console section to refresh your memory). Writing your code in a script means that you'll always have a permanent record of everything you've done (provided you save your script) and also allows you to make loads of comments to remind your future self what you've done. So, while you're working through this Chapter we suggest that you create a new script (or RStudio Project) to write your code as you follow along.

As we saw in the previous Chapter, at a basic level we can use R much as you would use a calculator. We can type an arithmetic expression into our script, then source it into the console and receive a result. For example, if we type the expression `2 + 2` and then source this line of code we get the answer `4` (reassuringly!)

```
2 + 2
```

```
[1] 4
```

The `[1]` in front of the result tells you that the observation number at the beginning of the line is the first observation. This is not much help in this example, but can be quite useful when printing results with multiple lines (we'll see an example below). The other obvious arithmetic operators are `-`, `*`, `/` for subtraction, multiplication and division respectively. R follows the usual mathematical convention of order of operations. For example, the expression `2 + 3 * 4` is interpreted to have the value `2 + (3 * 4) = 14`, not `(2 + 3) * 4 = 20`. There are a huge range of mathematical functions in R, some of the most useful include; `log()`, `log10()`, `exp()`, `sqrt()`.

```
log(1) # logarithm to base e
```

```
[1] 0
```

```
log10(1) # logarithm to base 10
```

```
[1] 0
```

```
exp(1) # natural antilog
```

```
[1] 2.718282
```

```
sqrt(4) # square root
```

```
[1] 2
```

```
4^2 # 4 to the power of 2
```

```
[1] 16
```

```
pi # not a function but useful
```

```
[1] 3.141593
```

It's important to realise that when you run code as we've done above, the result of the code (or **value**) is only displayed in the console. Whilst this can sometimes be useful it is usually much more practical to store the value(s) in a object.

2.2. Objects in R

At the heart of almost everything you will do (or ever likely to do) in R is the concept that everything in R is an object. These objects can be almost anything, from a single number or character string (like a word) to highly complex structures like the output of a plot, a summary of your statistical analysis or a set of R commands that perform a specific task. Understanding how you create objects and assign values to objects is key to understanding R.

2.2.1. Creating objects

To create an object we simply give the object a name. We can then assign a value to this object using the *assignment operator* `<-` (sometimes called the *gets operator*). The assignment operator is a composite symbol comprised of a 'less than' symbol `<` and a hyphen `-` .

```
my_obj <- 48
```

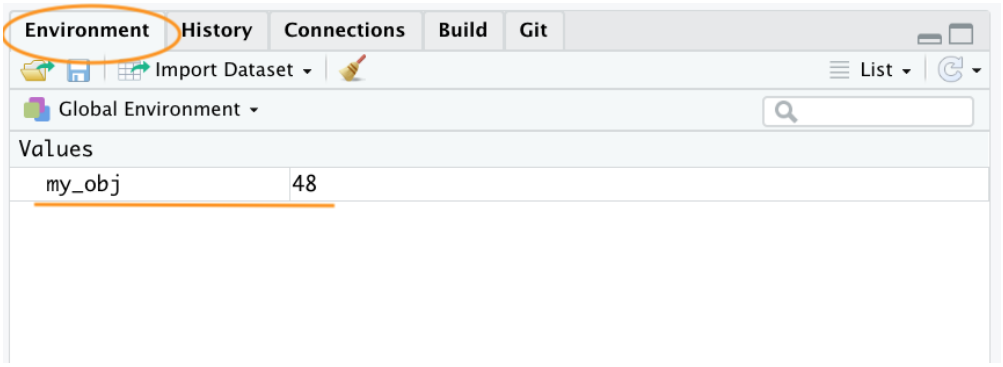
In the code above, we created an object called `my_obj` and assigned it a value of the number `48` using the assignment operator (in our head we always read this as '*my_obj gets 48*'). You can also use `=` instead of `<-` to assign values but this is considered bad practice and we would discourage you from using this notation.

To view the value of the object you simply type the name of the object

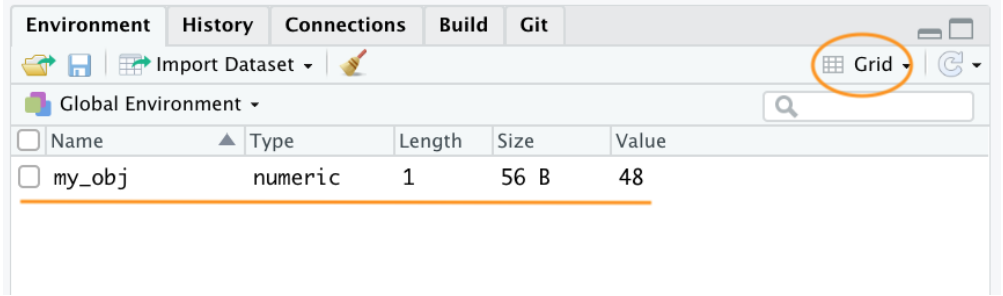
```
my_obj
```

```
[1] 48
```

Now that we've created this object, R knows all about it and will keep track of it during this current R session. All of the objects you create will be stored in the current workspace and you can view all the objects in your workspace in RStudio by clicking on the 'Environment' tab in the top right hand pane.



If you click on the down arrow on the 'List' icon in the same pane and change to 'Grid' view RStudio will show you a summary of the objects including the type (numeric - it's a number), the length (only one value in this object), its 'physical' size and its value (48 in this case).

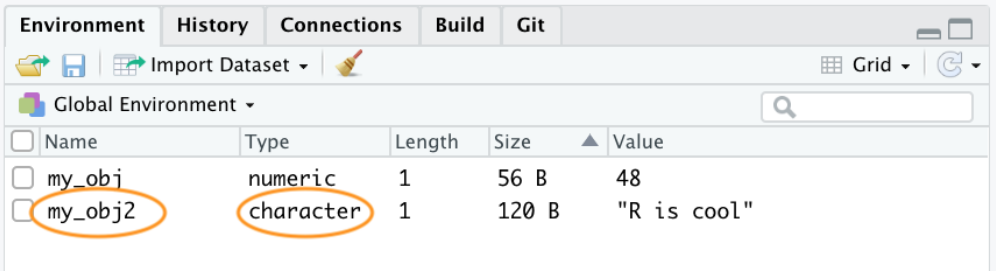


There are many different types of values that you can assign to an object. For example

```
my_obj2 <- "R is cool"
```

Here we have created an object called `my_obj2` and assigned it a value of `R is cool` which is a character string. Notice that we have enclosed the string in quotes. If you forget to use the quotes you will receive an error message.

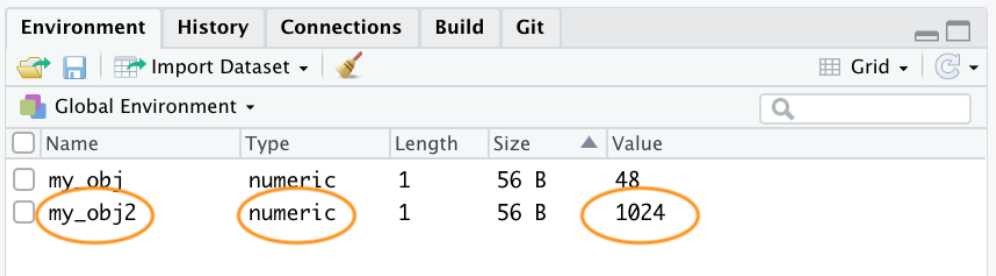
Our workspace now contains both objects we've created so far with `my_obj2` listed as type character.



To change the value of an existing object we simply reassign a new value to it. For example, to change the value of `my_obj2` from `"R is cool"` to the number `1024`

```
my_obj2 <- 1024
```

Notice that the Type has changed to numeric and the value has changed to 1024 in the environment



Once we have created a few objects, we can do stuff with our objects. For example, the following code creates a new object `my_obj3` and assigns it the value of `my_obj` added to `my_obj2` which is 1072 (48 + 1024 = 1072).

```
my_obj3 <- my_obj + my_obj2
my_obj3
```

```
[1] 1072
```

Notice that to display the value of `my_obj3` we also need to write the object's name. The above code works because the values of both `my_obj` and `my_obj2` are numeric (i.e. a number). If you try to do this with objects with character values (**character class**) you will receive an error

```
char_obj <- "hello"
char_obj2 <- "world!"
char_obj3 <- char_obj + char_obj2
# Error in char_obj+char_obj2:non-numeric argument to binary operator
```

The error message is essentially telling you that either one or both of the objects `char_obj` and `char_obj2` is not a number and therefore cannot be added together.

When you first start learning R, dealing with errors and warnings can be frustrating as they're often difficult to understand (what's an *argument*? what's a *binary operator*?). One way to find out more information about a particular error is to Google a generalised version of the error message. For the above error try Googling *'non-numeric argument to binary operator error + r'* or even *'common r error messages'*.

Another error message that you'll get quite a lot when you first start using R is `Error: object 'XXX' not found`. As an example, take a look at the code below

```
my_obj <- 48
my_obj4 <- my_obj + no_obj
# Error: object 'no_obj' not found
```

R returns an error message because we haven't created (defined) the object `no_obj` yet. Another clue that there's a problem with this code is that, if you check your environment, you'll see that object `my_obj4` has not been created.

2.2.2. Naming objects

Naming your objects is one of the most difficult things you will do in R. Ideally your object names should be kept both short and informative which is not always easy. If you need to create objects with multiple words in their name then use either an underscore or a dot between words or capitalise the different words. We prefer the underscore format and never include uppercases in names (called *snake case*)

```
output_summary <- "my analysis" # recommended#
output.summary <- "my analysis"
outputSummary <- "my analysis"
```

There are also a few limitations when it come to giving objects names. An object name cannot start with a number or a dot followed by a number (i.e. `2my_variable` or `.2my_variable`). You should also avoid using non-alphanumeric characters in your object names (i.e. &, ^, /, ! etc). In addition, make sure you don't name your objects with reserved words (i.e. `TRUE`, `NA`) and it's never a good idea to give your object the same name as a built-in function. One that crops up more times than we can remember is

```
data <- read.table("mydatafile", header = TRUE) # data is a
# function!
```

2.3. Using functions in R

Up until now we've been creating simple objects by directly assigning a single value to an object. It's very likely that you'll soon want to progress to creating more complicated objects as your R experience grows and the complexity of your tasks increase. Happily, R has a multitude of functions to help you do this. You can think of a function as an object which contains a series of instructions to perform a specific task. The base installation of R comes with many functions already defined or you can increase the power of R by installing one of the 10000's of packages now available. Once you get a bit more experience with using R you may want to define your own functions to perform tasks that are specific to your goals (more about this in Chapter 6).

The first function we will learn about is the `c()` function. The `c()` function is short for concatenate and we use it to join together a series of values and store them in a data structure called a **vector** (more on vectors in Chapter 3).

```
my_vec <- c(2, 3, 1, 6, 4, 3, 3, 7)
```

In the code above we've created an object called `my_vec` and assigned it a value using the function `c()`. There are a couple of really important points to note here. Firstly, when you use a function in R, the function name is **always** followed by a pair of round brackets even if there's nothing contained between the brackets. Secondly, the argument(s) of a function are placed inside the round brackets and are separated by commas. You can think of an argument as way of customising the use or behaviour of a function. In the example above, the arguments are the numbers we want to concatenate. Finally, one of the tricky things when you first start using R is to know which

function to use for a particular task and how to use it. Thankfully each function will always have a help document associated with it which will explain how to use the function (more on this later) and a quick Google search will also usually help you out.

To examine the value of our new object we can simply type out the name of the object as we did before

```
my_vec
```

```
[1] 2 3 1 6 4 3 3 7
```

Now that we've created a vector we can use other functions to do useful stuff with this object. For example, we can calculate the mean, variance, standard deviation and number of elements in our vector by using the `mean()`, `var()`, `sd()` and `length()` functions

```
mean(my_vec) # returns the mean of my_vec
```

```
[1] 3.625
```

```
var(my_vec) # returns the variance of my_vec
```

```
[1] 3.982143
```

```
sd(my_vec) # returns the standard deviation of my_vec
```

```
[1] 1.995531
```

```
length(my_vec) # returns the number of elements in my_vec
```

```
[1] 8
```

If we wanted to use any of these values later on in our analysis we can just assign the resulting value to another object

```
vec_mean <- mean(my_vec) # returns the mean of my_vec
vec_mean
```

```
[1] 3.625
```

Sometimes it can be useful to create a vector that contains a regular sequence of values in steps of one. Here we can make use of a shortcut using the : symbol.

```
my_seq <- 1:10 # create regular sequence
my_seq
```

```
 [1]  1  2  3  4  5  6  7  8  9 10
```

```
my_seq2 <- 10:1 # in decending order
my_seq2
```

```
 [1] 10  9  8  7  6  5  4  3  2  1
```

Other useful functions for generating vectors of sequences include the `seq()` and `rep()` functions. For example, to generate a sequence from 1 to 5 in steps of 0.5

```
my_seq2 <- seq(from = 1, to = 5, by = 0.5)
my_seq2
```

```
[1] 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0
```

Here we've used the arguments `from =` and `to =` to define the limits of the sequence and the `by =` argument to specify the increment of the sequence. Play around with other values for these arguments to see their effect.

The `rep()` function allows you to replicate (repeat) values a specified number of times. To repeat the value 2, 10 times

```
my_seq3 <- rep(2, times = 10) # repeats 2, 10 times
my_seq3
```

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

You can also repeat non-numeric values

```
my_seq4 <- rep("abc", times = 3) # repeats 'abc' 3 times
my_seq4
```

```
[1] "abc" "abc" "abc"
```

or each element of a series

```
my_seq5 <- rep(1:5, times = 3) # repeats the series 1 to
# 5, 3 times
my_seq5
```

```
 [1] 1 2 3 4 5 1 2 3 4 5 1 2 3 4 5
```

or elements of a series

```
my_seq6 <- rep(1:5, each = 3) # repeats each element of the
# series 3 times
my_seq6
```

```
 [1] 1 1 1 2 2 2 3 3 3 4 4 4 5 5 5
```

We can also repeat a non-sequential series

```
my_seq7 <- rep(c(3, 1, 10, 7), each = 3) # repeats each
# element of the
# series 3 times
my_seq7
```

```
 [1]  3  3  3  1  1  1 10 10 10  7  7  7
```

Note in the code above how we've used the `c()` function inside the `rep()` function. Nesting functions allows us to build quite complex commands within a single line of code and is a very common practice when using R. However, care needs to be taken as too many nested functions can make your code quite difficult for others to understand (or yourself some time in the future!). We could rewrite the code above to explicitly separate the two different steps to generate our vector. Either approach will give the same result, you just need to use your own judgement as to which is more readable.

```
in_vec <- c(3, 1, 10, 7)
my_seq7 <- rep(in_vec, each = 3) # repeats each element of
# the series 3 times
my_seq7
```

```
 [1]  3  3  3  1  1  1 10 10 10  7  7  7
```

2.4. Working with vectors

Manipulating, summarising and sorting data using R is an important skill to master but one which many people find a little confusing at first. We'll go through a few simple examples here using vectors to illustrate some important concepts but will build on this in much more detail in Chapter 3 where we will look at more complicated (and useful) data structures.

2.4.1. Extracting elements

To extract (also known as indexing or subscripting) one or more values (more generally known as elements) from a vector we use the square bracket `[ ]` notation. The general approach is to name the object you wish to extract from, then a set of square brackets with an index of the element you wish to extract contained within the square brackets. This index can be a position or the result of a logical test.

Positional index

To extract elements based on their position we simply write the position inside the `[ ]`. For example, to extract the 3rd value of `my_vec`

```
my_vec # remind ourselves what my_vec looks like
```

```
[1] 2 3 1 6 4 3 3 7
```

```
my_vec[3] # extract the 3rd value
```

```
[1] 1
```

```
# if you want to store this value in another object
val_3 <- my_vec[3]
val_3
```

```
[1] 1
```

Note that the positional index starts at 1 rather than 0 like some other other programming languages (i.e. Python).

We can also extract more than one value by using the `c()` function inside the square brackets. Here we extract the 1st, 5th, 6th and 8th element from the `my_vec` object

```
my_vec[c(1, 5, 6, 8)]
```

```
[1] 2 4 3 7
```

Or we can extract a range of values using the `:` notation. To extract the values from the 3rd to the 8th elements

```
my_vec[3:8]
```

```
[1] 1 6 4 3 3 7
```

Logical index

Another really useful way to extract data from a vector is to use a logical expression as an index. For example, to extract all elements with a value greater than 4 in the vector `my_vec`

```
my_vec[my_vec > 4]
```

```
[1] 6 7
```

Here, the logical expression is `my_vec > 4` and R will only extract those elements that satisfy this logical condition. So how does this actually work? If we look at the output of just the logical expression without the square brackets you can see that R returns a vector containing either `TRUE` or `FALSE` which correspond to whether the logical condition is satisfied for each element. In this case only the 4^{th} and 8^{th} elements return a `TRUE` as their value is greater than 4.

```
my_vec > 4
```

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

So what R is actually doing under the hood is equivalent to

```
my_vec[c(FALSE, FALSE, FALSE, TRUE, FALSE, FALSE, FALSE, TRUE)]
```

```
[1] 6 7
```

and only those element that are `TRUE` will be extracted.

In addition to the `<` and `>` operators you can also use composite operators to increase the complexity of your expressions. For example the expression for 'greater or equal to' is `>=`. To test whether a value is equal to a value we need to use a double equals symbol `==` and for 'not equal to' we use `!=` (the `!` symbol means 'not').

```
my_vec[my_vec >= 4] # values greater or equal to 4
```

```
[1] 6 4 7
```

```
my_vec[my_vec < 4] # values less than 4
```

```
[1] 2 3 1 3 3
```

```
my_vec[my_vec <= 4] # values less than or equal to 4
```

```
[1] 2 3 1 4 3 3
```

```
my_vec[my_vec == 4] # values equal to 4
```

```
[1] 4
```

```
my_vec[my_vec != 4] # values not equal to 4
```

```
[1] 2 3 1 6 3 3 7
```

We can also combine multiple logical expressions using Boolean expressions. In R the `&` symbol means AND and the `|` symbol means OR. For example, to extract values in `my_vec` which are less than 6 AND greater than 2

```
val26 <- my_vec[my_vec < 6 & my_vec > 2]
val26
```

```
[1] 3 4 3 3
```

or extract values in `my_vec` that are greater than 6 OR less than 3

```
val63 <- my_vec[my_vec > 6 | my_vec < 3]
val63
```

```
[1] 2 1 7
```

2.4.2. Replacing elements

We can change the values of some elements in a vector using our `[ ]` notation in combination with the assignment operator `<-`. For example, to replace the 4^{th} value of our `my_vec` object from 6 to 500

```
my_vec[4] <- 500
my_vec
```

```
[1]   2   3   1 500   4   3   3   7
```

We can also replace more than one value or even replace values based on a logical expression

```
# replace the 6th and 7th element with 100
my_vec[c(6, 7)] <- 100
my_vec
```

```
[1]   2   3   1 500   4 100 100   7
```

```
# replace element that are less than or equal to 4 with 1000
my_vec[my_vec <= 4] <- 1000
my_vec
```

```
[1] 1000 1000 1000  500 1000  100  100    7
```

2.4.3. Ordering elements

In addition to extracting particular elements from a vector we can also order the values contained in a vector. To sort the values from lowest to highest value we can use the `sort()` function

```
vec_sort <- sort(my_vec)
vec_sort
```

```
[1]    7  100  100  500 1000 1000 1000 1000
```

To reverse the sort, from highest to lowest, we can either include the `decreasing = TRUE` argument when using the `sort()` function

```
vec_sort2 <- sort(my_vec, decreasing = TRUE)
vec_sort2
```

```
[1] 1000 1000 1000 1000  500  100  100    7
```

or first sort the vector using the `sort()` function and then reverse the sorted vector using the `rev()` function. This is another example of nesting one function inside another function.

```
vec_sort3 <- rev(sort(my_vec))
vec_sort3
```

```
[1] 1000 1000 1000 1000  500  100  100    7
```

Whilst sorting a single vector is fun, perhaps a more useful task would be to sort one vector according to the values of another vector. To do this we should use the `order()` function in combination with `[ ]`. To demonstrate this let's create a vector called `height` containing the height of 5 different people and another vector called `p.names` containing the names of these people (so Joanna is 180 cm, Charlotte is 155 cm etc)

```
height <- c(180, 155, 160, 167, 181)
height
```

```
[1] 180 155 160 167 181
```

```
p.names <- c("Joanna", "Charlotte", "Helen", "Karen", "Amy")
p.names
```

```
[1] "Joanna"    "Charlotte" "Helen"     "Karen"     "Amy"
```

Our goal is to order the people in `p.names` in ascending order of their `height`. The first thing we'll do is use the `order()` function with the `height` variable to create a vector called `height_ord`

```
height_ord <- order(height)
height_ord
```

```
[1] 2 3 4 1 5
```

OK, what's going on here? The first value, 2, (remember ignore `[1]`) should be read as 'the smallest value of `height` is the second element of the `height` vector'. If we check this by looking at the `height` vector above, you can see that element 2 has a value of 155, which is the smallest value. The second smallest value in `height` is the 3rd element of `height`, which when we check is 160 and so on. The largest value of `height` is element 5 which is 181. Now that

we have a vector of the positional indices of heights in ascending order (`height_ord`), we can extract these values from our `p.names` vector in this order

```
names_ord <- p.names[height_ord]
names_ord
```

```
[1] "Charlotte" "Helen"     "Karen"     "Joanna"    "Amy"
```

You're probably thinking 'what's the use of this?' Well, imagine you have a dataset which contains two columns of data and you want to sort each column. If you just use `sort()` to sort each column separately, the values of each column will become uncoupled from each other. By using the 'order()' on one column, a vector of positional indices is created of the values of the column in ascending order This vector can be used on the second column, as the index of elements which will return a vector of values based on the first column.

2.4.4. Vectorisation

One of the great things about R functions is that most of them are vectorised. This means that the function will operate on all elements of a vector without needing to apply the function on each element separately. For example, to multiple each element of a vector by 5 we can simply use

```
# create a vector
my_vec2 <- c(3, 5, 7, 1, 9, 20)


# multiply each element by 5
my_vec2 * 5
```

```
[1]  15  25  35   5  45 100
```

Or we can add the elements of two or more vectors

```
# create a second vector
my_vec3 <- c(17, 15, 13, 19, 11, 0)


# add both vectors
my_vec2 + my_vec3
```

```
[1] 20 20 20 20 20 20
```

```
# multiply both vectors
my_vec2 * my_vec3
```

```
[1] 51 75 91 19 99  0
```

However, you must be careful when using vectorisation with vectors of different lengths as R will quietly recycle the elements in the shorter vector rather than throw a wobbly (error).

```
# create a third vector
my_vec4 <- c(1, 2)


# add both vectors - quiet recycling!
my_vec2 + my_vec4
```

```
[1]  4  7  8  3 10 22
```

2.4.5. Missing data

In R, missing data is usually represented by an `NA` symbol meaning 'Not Available'. Data may be missing for a whole bunch of reasons, maybe your machine broke down, maybe you broke down, maybe the weather was too bad to collect data on a particular day etc etc. Missing data can be a pain in the proverbial both from an R perspective and also a statistical perspective. From an R perspective missing data can be problematic as different functions deal with missing data in different ways. For example, let's say we collected air temperature readings over 10 days, but our thermometer broke on day 2 and again on day 9 so we have no data for those days

```
temp <- c(7.2, NA, 7.1, 6.9, 6.5, 5.8, 5.8, 5.5, NA, 5.5)
temp
```

```
 [1] 7.2  NA 7.1 6.9 6.5 5.8 5.8 5.5  NA 5.5
```

We now want to calculate the mean temperature over these days using the `mean()` function

```
mean_temp <- mean(temp)
mean_temp
```

```
[1] NA
```

Flippin heck, what's happened here? Why does the `mean()` function return an `NA`? Actually, R is doing something very sensible (at least in our opinion!). If a vector has a missing value then the only possible value to return when calculating a mean is `NA`. R doesn't know that you perhaps want to ignore the `NA` values (R can't read your mind - yet!). Happily, if we look at the help file (use `help("mean")` - see the next section for more details) associated with the `mean()` function we can see there is an argument `na.rm =` which is set to `FALSE` by default.

> na.rm - a logical value indicating whether NA values should be stripped before the computation proceeds.

If we change this argument to `na.rm = TRUE` when we use the `mean()` function this will allow us to ignore the `NA` values when calculating the mean

```
mean_temp <- mean(temp, na.rm = TRUE)
mean_temp
```

```
[1] 6.2875
```

It's important to note that the `NA` values have not been removed from our `temp` object (that would be bad practice), rather the `mean()` function has just ignored them. The point of the above is to highlight how we can change the default behaviour of a function using an appropriate argument. The problem is that not all functions will have an `na.rm =` argument, they might deal with `NA` values differently. However, the good news is that every help file associated with any function will **always** tell you how missing data are handled by default.

2.5. Getting help

This book is intended as a relatively brief introduction to R and as such you will soon be using functions and packages that go beyond this scope of this introductory text. Fortunately, one of the strengths of R is its comprehensive and easily accessible help system and wealth of online resources where you can obtain further information.

2.5.1. R help

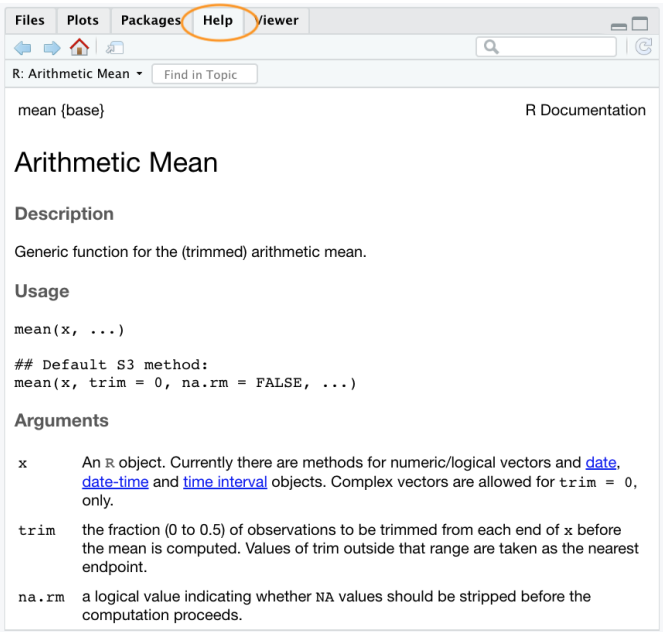
To access R's built-in help facility to get information on any function simply use the `help()` function. For example, to open the help page for our friend the `mean()` function.

```
help("mean")
```

or you can use the equivalent shortcut

```
?mean
```

the help page is displayed in the 'Help' tab in the Files pane (usually in the bottom right of RStudio)



Admittedly the help files can seem anything but helpful when you first start using R. This is probably because they're written in a very concise manner and the language used is often quite technical and full of jargon. Having said that, you do get used to this and will over time even come to appreciate a certain beauty in their brevity (honest!). One of the great things about the help files is that they all have a very similar structure regardless of the function. This makes it easy to navigate through the file to find exactly what you need.

The first line of the help document contains information such as the name of the function and the package where the function can be found. There are also other headings that provide more specific information such as

- **Description:** gives a brief description of the function and what it does.

- **Usage:** gives the name of the arguments associated with the function and possible default values.
- **Arguments:** provides more detail regarding each argument and what they do.
- **Details:** gives further details of the function if required.
- **Value:** if applicable, gives the type and structure of the object returned by the function or the operator.
- **See Also:** provides information on other help pages with similar or related content.
- **Examples:** gives some examples of using the function. These are really helpful, all you need to do is copy and paste them into the console to see what happens. You can also access examples at any time by using the `example()` function (i.e. `example("mean")`)

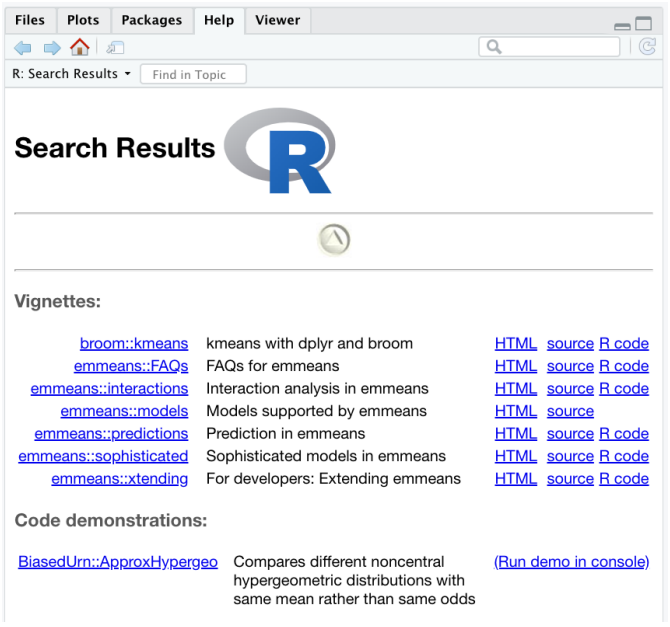
The `help()` function is useful if you know the name of the function. If you're not sure of the name, but can remember a key word then you can search R's help system using the `help.search()` function.

```
help.search("mean")
```

or you can use the equivalent shortcut

```
??mean
```

The results of the search will be displayed in RStudio under the 'Help' tab as before. The `help.search()` function searches through the help documentation, code demonstrations and package vignettes and displays the results as clickable links for further exploration.



Another useful function is `apropos()`. This function can be used to list all functions containing a specified character string. For example, to find all functions with `mean` in their name

```
apropos("mean")
```

```
 [1] ".colMeans"     ".rowMeans"     "colMeans"      "kmeans"
 [5] "mean"          "mean_temp"     "mean.Date"     "mean.default"
 [9] "mean.difftime" "mean.POSIXct"  "mean.POSIXlt"  "rowMeans"
[13] "vec_mean"      "weighted.mean"
```

You can then bring up the help file for the relevant function.

```
help("kmeans")
```

An extremely useful function is `RSiteSearch()` which enables you to search for keywords and phrases in function help pages and vignettes for all CRAN packages, and in CRAN task views. This function allows you to access the https://www.r-project.org/search.html search engine directly from the Console with the results displayed in your web browser

```
RSiteSearch("regression")
```

2.5.2. Other sources of help

There really has never been a better time to start learning R. There are a plethora of freely available online resources ranging from whole courses to subject specific tutorials and mailing lists. There are also plenty of paid for options if that's your thing but unless you've money to burn there really is no need to part with your hard earned cash. Some resources we have found helpful are listed below.

General R resources

- R-Project: User contributed documentation
- The R Journal: Journal of the R project for statistical computing
- Swirl: An R package that teaches you R from within R
- RStudio's printable cheatsheets
- Rseek A custom Google search for R-related sites

Getting help

- Google it!: Try Googling any error messages you get. It's not cheating and everyone does it! You'll be surprised how many other people have probably had the same problem and solved it.
- Stack Overflow: There are many thousands of questions relevant to R on Stack Overflow. Here are the most popular ones, ranked by vote. Make sure you search for similar questions before asking your own, and make sure you include a reproducible example to get the most useful advice. A reproducible example is a minimal example that lets others who are trying to help you to see the error themselves.

R markdown resources

- Basic markdown and R markdown reference
- A good markdown reference
- A good 10-minute markdown tutorial
- RStudio's R markdown cheatsheet
- R markdown reference sheet
- The R markdown documentation including a getting started guide, a gallery of demos, and several articles for more advanced usage.
- The knitr website has lots of useful reference material about how knitr works.

Git and GitHub resources

- Happy Git: Great resource for using Git and GitHub
- Version control with RStudio: RStudio document for using version control
- Using Git from RStudio: Good 10 minute guide
- The R Class: In depth guide to using Git and GitHub with RStudio

R programming

- R Programming for Data Science: In depth guide to R programming
- R for Data Science: Fantastic book, tidyverse orientated

2.6. Saving stuff in R

Your approach to saving work in R and RStudio depends on what you want to save. Most of the time the only thing you will need to save is the R code in your script(s). Remember your script is a reproducible record of everything

you've done so all you need to do is open up your script in a new RStudio session and source it into the R Console and you're back to where you left off.

Unless you've followed our suggestion about changing the default settings for RStudio Projects you will be asked whether you want to save your workspace image every time you exit RStudio. We suggest that 99.9% of the time that you don't want do this. By starting with a clean RStudio session each time we come back to our analysis we can be sure to avoid any potential conflicts with things we've done in previous sessions.

There are, however, some occasions when saving objects you've created in R is useful. For example, let's say you're creating an object that takes hours (even days) of computational time to generate. It would be extremely inconvenient to have to wait all this time each time you come back to your analysis (although we would suggest exporting this to an external file is a better solution). In this case we can save this object as an external `.RData` file which we can load back into RStudio the next time we want to use it. To save an object to an `.RData` file you can use the `save()` function (notice we don't need to use the assignment operator here)

```
save(nameOfObject, file = "name_of_file.RData")
```

or if you want to save all of the objects in your workspace into a single `.RData` file use the `save.image()` function

```
save.image(file = "name_of_file.RData")
```

To load your `.RData` file back into RStudio use the `load()` function

```
load(file = "name_of_file.RData")
```

Chapter 3

Data in R

Until now, you've created fairly simple data in R and stored it as a vector. However, most (if not all) of you will have much more complicated datasets from your various experiments and surveys that go well beyond what a vector can handle. Learning how R deals with different types of data and data structures, how to import your data into R and how to manipulate and summarize your data are some of the most important skills you will need to master.

In this Chapter we'll go over the main data types in R and focus on some of the most common data structures. We will also cover how to import data into R from an external file, how to manipulate (wrangle) and summarize data and finally how to export data from R to an external file.

3.1. Data types

Understanding the different types of data and how R deals with these data is important. The temptation is to glaze over and skip these technical details, but beware, this can come back to bite you somewhere unpleasant if you don't pay attention. We've already seen an example of this when we tried (and failed) to add two character objects together using the + operator.

R has six basic types of data; numeric, integer, logical, complex and character. The keen eyed among you will notice we've only listed five data types here, the final data type is raw which we won't cover as it's not useful 99.99% of the time. We also won't cover complex numbers as we don't have the imagination!

- **Numeric** data are numbers that contain a decimal. Actually they can also be whole numbers but we'll gloss over that.

- **Integers** are whole numbers (those numbers without a decimal point).
- **Logical** data take on the value of either `TRUE` or `FALSE`. There's also another special type of logical called `NA` to represent missing values.
- **Character** data are used to represent string values. You can think of character strings as something like a word (or multiple words). A special type of character string is a *factor*, which is a string but with additional attributes (like levels or an order). We'll cover factors later.

R is (usually) able to automatically distinguish between different classes of data by their nature and the context in which they're used although you should bear in mind that R can't actually read your mind and you may have to explicitly tell R how you want to treat a data type. You can find out the type (or class) of any object using the `class()` function.

```
num <- 2.2
class(num)
```

```
[1] "numeric"
```

```
char <- "hello"
class(char)
```

```
[1] "character"
```

```
logi <- TRUE
class(logi)
```

```
[1] "logical"
```

Alternatively, you can ask if an object is a specific class using using a logical test. The `is.[classOfData]()` family of functions will return either a `TRUE` or a `FALSE`.

```
is.numeric(num)
```

```
[1] TRUE
```

```
is.character(num)
```

```
[1] FALSE
```

```
is.character(char)
```

```
[1] TRUE
```

```
is.logical(logi)
```

```
[1] TRUE
```

It can sometimes be useful to be able to change the class of a variable using the `as.[className]()` family of coercion functions, although you need to be careful when doing this as you might receive some unexpected results (see what happens below when we try to convert a character string to a numeric).

```
# coerce numeric to character
class(num)
```

```
[1] "numeric"
```

```
num_char <- as.character(num)
num_char
```

```
[1] "2.2"
```

```
class(num_char)
```

```
[1] "character"
```

```
# coerce character to numeric!
class(char)
```

```
[1] "character"
```

```
char_num <- as.numeric(char)
```

```
Warning: NAs introduced by coercion
```

Here's a summary table of some of the logical test and coercion functions available to you.

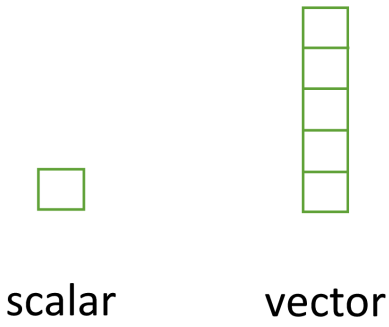
Type	Logical test	Coercing
Character	`is.character`	`as.character`
Numeric	`is.numeric`	`as.numeric`
Logical	`is.logical`	`as.logical`
Factor	`is.factor`	`as.factor`
Complex	`is.complex`	`as.complex`

3.2. Data structures

Now that you've been introduced to some of the most important classes of data in R, let's have a look at some of main structures that we have for storing these data.

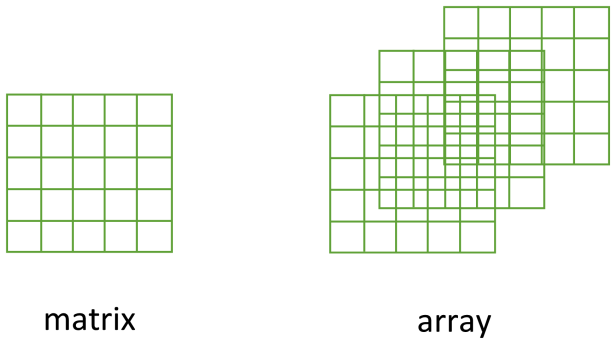
3.2.1. Scalars and vectors

Perhaps the simplest type of data structure is the vector. You've already been introduced to vectors in Chapter 2 although some of the vectors you created only contained a single value. Vectors that have a single value (length 1) are called scalars. Vectors can contain numbers, characters, factors or logicals, but the key thing to remember is that all the elements inside a vector must be of the same class. In other words, vectors can contain either numbers, characters or logicals but not mixtures of these types of data. There is one important exception to this, you can include `NA` (remember this is special type of logical) to denote missing data in vectors with other data types.



3.2.2. Matrices and arrays

Another useful data structure used in many disciplines such as population ecology, theoretical and applied statistics is the matrix. A matrix is simply a vector that has additional attributes called dimensions. Arrays are just multidimensional matrices. Again, matrices and arrays must contain elements all of the same data class.



A convenient way to create a matrix or an array is to use the `matrix()` and `array()` functions respectively. Below, we will create a matrix from a sequence 1 to 16 in four rows (`nrow = 4`) and fill the matrix row-wise (`byrow = TRUE`) rather than the default column-wise. When using the `array()` function we define the dimensions using the `dim =` argument, in our case 2 rows, 4 columns in 2 different matrices.

```r
my_mat <- matrix(1:16, nrow = 4, byrow = TRUE)
my_mat
```

```
     [,1] [,2] [,3] [,4]
[1,]    1    2    3    4
[2,]    5    6    7    8
[3,]    9   10   11   12
[4,]   13   14   15   16
```

```r
my_array <- array(1:16, dim = c(2, 4, 2))
my_array
```

```
, , 1

     [,1] [,2] [,3] [,4]
[1,]    1    3    5    7
[2,]    2    4    6    8

, , 2

     [,1] [,2] [,3] [,4]
[1,]    9   11   13   15
[2,]   10   12   14   16
```

Sometimes it's also useful to define row and column names for your matrix but this is not a requirement. To do this use the `rownames()` and `colnames()` functions.

```r
rownames(my_mat) <- c("A", "B", "C", "D")
colnames(my_mat) <- c("a", "b", "c", "d")
my_mat
```

```
  a b c d
A 1 2 3 4
B 5 6 7 8
```

```
C  9 10 11 12
D 13 14 15 16
```

Once you've created your matrices you can do useful stuff with them and as you'd expect, R has numerous built in functions to perform matrix operations. Some of the most common are given below. For example, to transpose a matrix we use the transposition function `t()`

```
my_mat_t <- t(my_mat)
my_mat_t
```

```
  A B  C  D
a 1 5  9 13
b 2 6 10 14
c 3 7 11 15
d 4 8 12 16
```

To extract the diagonal elements of a matrix and store them as a vector we can use the `diag()` function

```
my_mat_diag <- diag(my_mat)
my_mat_diag
```

```
[1]  1  6 11 16
```

The usual matrix addition, multiplication etc can be performed. Note the use of the %*% operator to perform matrix multiplication.

```
mat.1 <- matrix(c(2, 0, 1, 1), nrow = 2)    # notice that the matrix has been filled
mat.1                                       # column-wise by default
```

```
     [,1] [,2]
[1,]    2    1
[2,]    0    1
```

```
mat.2 <- matrix(c(1, 1, 0, 2), nrow = 2)
mat.2
```

```
     [,1] [,2]
[1,]    1    0
[2,]    1    2
```

```
mat.1 + mat.2           # matrix addition
```

```
     [,1] [,2]
[1,]    3    1
[2,]    1    3
```

```
mat.1 * mat.2           # element by element products
```

```
     [,1] [,2]
[1,]    2    0
[2,]    0    2
```

```
mat.1 %*% mat.2         # matrix multiplication
```

```
     [,1] [,2]
[1,]    3    2
[2,]    1    2
```

3.2.3. Lists

The next data structure we will quickly take a look at is a list. Whilst vectors and matrices are constrained to contain data of the same type, lists are able to store mixtures of data types. In fact we can even store other data structures such as vectors and arrays within a list or even have a list of a list. This makes for a very flexible data structure which is ideal for storing irregular or non-rectangular data (see Chapter 7 for an example).

To create a list we can use the `list()` function. Note how each of the three list elements are of different classes (character, logical, and numeric) and are of different lengths.

```
list_1 <- list(c("black", "yellow", "orange"),
               c(TRUE, TRUE, FALSE, TRUE, FALSE, FALSE),
               matrix(1:6, nrow = 3))
list_1
```

```
[[1]]
[1] "black"  "yellow" "orange"

[[2]]
[1]  TRUE  TRUE FALSE  TRUE FALSE FALSE

[[3]]
     [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6
```

Elements of the list can be named during the construction of the list

```
list_2 <- list(colours = c("black", "yellow", "orange"),
               evaluation = c(TRUE, TRUE, FALSE, TRUE, FALSE, FALSE),
               time = matrix(1:6, nrow = 3))
list_2
```

```
$colours
[1] "black"  "yellow" "orange"

$evaluation
[1]  TRUE  TRUE FALSE  TRUE FALSE FALSE

$time
     [,1] [,2]
[1,]    1    4
[2,]    2    5
```

```
[3,]    3    6
```

or after the list has been created using the `names()` function

```
names(list_1) <- c("colours", "evaluation", "time")
list_1
```

```
$colours
[1] "black"  "yellow" "orange"

$evaluation
[1]  TRUE  TRUE FALSE  TRUE FALSE FALSE

$time
     [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6
```

3.2.4. Data frames

By far the most commonly used data structure to store data in is the data frame. A data frame is a powerful two-dimensional object made up of rows and columns which looks superficially very similar to a matrix. However, whilst matrices are restricted to containing data all of the same type, data frames can contain a mixture of different types of data. Typically, in a data frame each row corresponds to an individual observation and each column corresponds to a different measured or recorded variable. This setup may be familiar to those of you who use LibreOffice Calc or Microsoft Excel to manage and store your data. Perhaps a useful way to think about data frames is that they are essentially made up of a bunch of vectors (columns) with each vector containing its own data type but the data type can be different between vectors.

As an example, the data frame below contains the results of an experiment to determine the effect of removing the tip of petunia plants (*Petunia sp.*) grown at 3 levels of nitrogen on various measures of growth (note: data shown below are a subset of the full dataset). The data frame has 8 variables (columns) and each row represents an individual plant. The variables `treat` and `nitrogen` are factors (categorical variables). The `treat` variable has 2 levels (`tip` and `notip`) and the `nitrogen` level variable has 3 levels (`low`, `medium` and `high`). The variables `height`, `weight`,

treat	nitrogen	block	height	weight	leafarea	shootarea	flowers
tip	medium	1	7.5	7.62	11.7	31.9	1
tip	medium	1	10.7	12.14	14.1	46.0	10
tip	medium	1	11.2	12.76	7.1	66.7	10
tip	medium	1	10.4	8.78	11.9	20.3	1
tip	medium	1	10.4	13.58	14.5	26.9	4
tip	medium	1	9.8	10.08	12.2	72.7	9
notip	low	2	3.7	8.10	10.5	60.5	6
notip	low	2	3.2	7.45	14.1	38.1	4
notip	low	2	3.9	9.19	12.4	52.6	9
notip	low	2	3.3	8.92	11.6	55.2	6
notip	low	2	5.5	8.44	13.5	77.6	9
notip	low	2	4.4	10.60	16.2	63.3	6

`leafarea` and `shootarea` are numeric and the variable `flowers` is an integer representing the number of flowers. Although the variable `block` has numeric values, these do not really have any order and could also be treated as a factor (i.e. they could also have been called A and B).

There are a couple of important things to bear in mind about data frames. These types of objects are known as rectangular data (or tidy data) as each column must have the same number of observations. Also, any missing data should be recorded as an `NA` just as we did with our vectors.

We can construct a data frame from existing data objects such as vectors using the `data.frame()` function. As an example, let's create three vectors `p.height`, `p.weight` and `p.names` and include all of these vectors in a data frame object called `dataf`.

```
p.height <- c(180, 155, 160, 167, 181)
p.weight <- c(65, 50, 52, 58, 70)
p.names <- c("Joanna", "Charlotte", "Helen", "Karen", "Amy")

dataf <- data.frame(height = p.height, weight = p.weight, names = p.names)
dataf
```

```
  height weight     names
1    180     65    Joanna
2    155     50 Charlotte
```

```
3    160     52     Helen
4    167     58     Karen
5    181     70       Amy
```

You'll notice that each of the columns are named with variable name we supplied when we used the `data.frame()` function. It also looks like the first column of the data frame is a series of numbers from one to five. Actually, this is not really a column but the name of each row. We can check this out by getting R to return the dimensions of the `dataf` object using the `dim()` function. We see that there are 5 rows and 3 columns.

```
dim(dataf)   # 5 rows and 3 columns
```

```
[1] 5 3
```

Another really useful function which we use all the time is `str()` which will return a compact summary of the structure of the data frame object (or any object for that matter).

```
str(dataf)
```

```
'data.frame':   5 obs. of  3 variables:
 $ height: num  180 155 160 167 181
 $ weight: num  65 50 52 58 70
 $ names : chr  "Joanna" "Charlotte" "Helen" "Karen" ...
```

The `str()` function gives us the data frame dimensions and also reminds us that `dataf` is a `data.frame` type object. It also lists all of the variables (columns) contained in the data frame, tells us what type of data the variables contain and prints out the first five values. We often copy this summary and place it in our R scripts with comments at the beginning of each line so we can easily refer back to it whilst writing our code. We showed you how to comment blocks in RStudio here.

Also notice that R has automatically decided that our `p.names` variable should be a character (`chr`) class variable when we first created the data frame. Whether this is a good idea or not will depend on how you want to use this variable in later analysis. If we decide that this wasn't such a good idea we can change the default behaviour of the `data.frame()` function by including the argument `stringsAsFactors = TRUE`. Now our strings are automatically converted to factors.

```
p.height <- c(180, 155, 160, 167, 181)
p.weight <- c(65, 50, 52, 58, 70)
p.names <- c("Joanna", "Charlotte", "Helen", "Karen", "Amy")

dataf <- data.frame(height = p.height, weight = p.weight, names = p.names,
                                          stringsAsFactors = TRUE)
str(dataf)
```

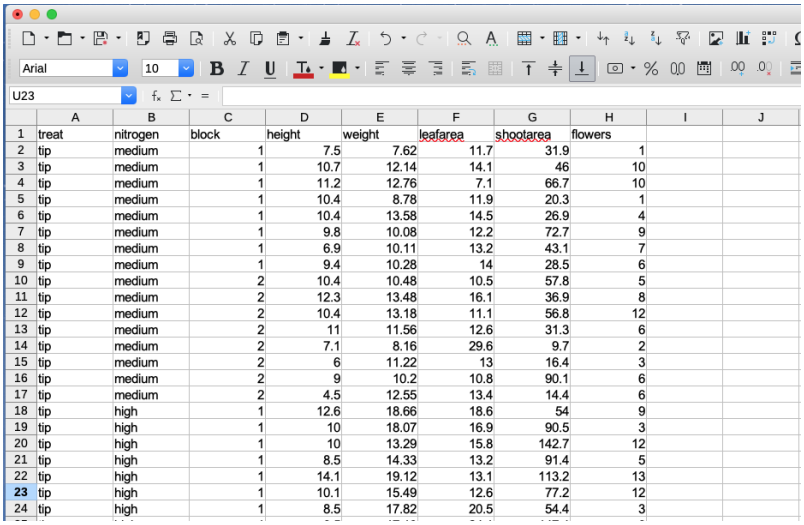
```
'data.frame':   5 obs. of  3 variables:
 $ height: num  180 155 160 167 181
 $ weight: num  65 50 52 58 70
 $ names : Factor w/ 5 levels "Amy","Charlotte",..: 4 2 3 5 1
```

3.3. Importing data

Although creating data frames from existing data structures is extremely useful, by far the most common approach is to create a data frame by importing data from an external file. To do this, you'll need to have your data correctly formatted and saved in a file format that R is able to recognise. Fortunately for us, R is able to recognise a wide variety of file formats, although in reality you'll probably end up only using two or three regularly.

3.3.1. Saving files to import

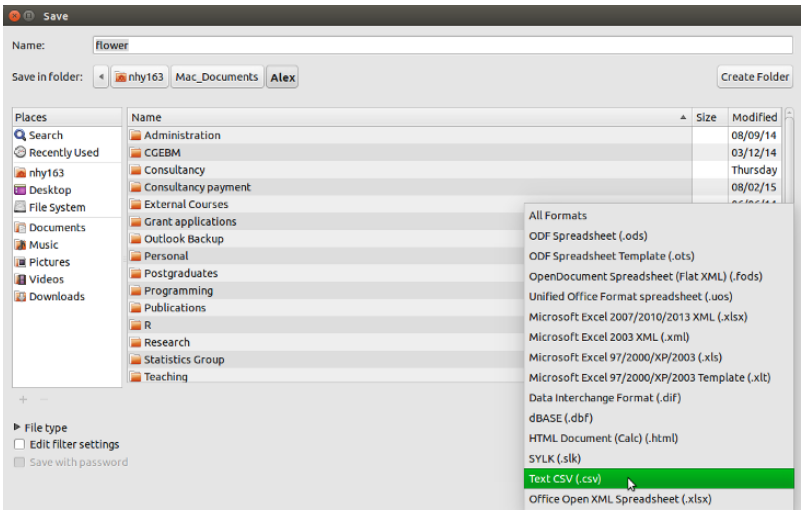
The easiest method of creating a data file to import into R is to enter your data into a spreadsheet using either Microsoft Excel or LibreOffice Calc and save the spreadsheet as a tab delimited file. We prefer LibreOffice Calc as it's open source, platform independent and free but MS Excel is OK too (but see here for some gotchas). Here's the data from the petunia experiment we dicussed previously displayed in LibreOffice. If you want to follow along you can download the data file (*'flower.xls'*) from the companion website here.



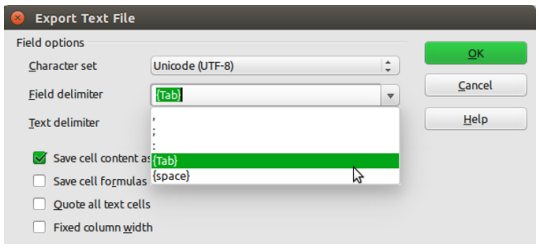
	A	B	C	D	E	F	G	H	I	J
1	treat	nitrogen	block	height	weight	leafarea	shootarea	flowers		
2	tip	medium	1	7.5	7.62	11.7	31.9	1		
3	tip	medium	1	10.7	12.14	14.1	46	10		
4	tip	medium	1	11.2	12.76	7.1	66.7	10		
5	tip	medium	1	10.4	8.78	11.9	20.3	1		
6	tip	medium	1	10.4	13.58	14.5	26.9	4		
7	tip	medium	1	9.8	10.08	12.2	72.7	9		
8	tip	medium	1	6.9	10.11	13.2	43.1	7		
9	tip	medium	1	9.4	10.28	14	28.5	6		
10	tip	medium	2	10.4	10.48	10.5	57.8	5		
11	tip	medium	2	12.3	13.48	16.1	36.9	8		
12	tip	medium	2	10.4	13.18	11.1	56.8	12		
13	tip	medium	2	11	11.56	12.6	31.3	6		
14	tip	medium	2	7.1	8.16	29.6	9.7	2		
15	tip	medium	2	6	11.22	13	16.4	3		
16	tip	medium	2	9	10.2	10.8	90.1	6		
17	tip	medium	2	4.5	12.55	13.4	14.4	6		
18	tip	high	1	12.6	18.66	18.6	54	9		
19	tip	high	1	10	18.07	16.9	90.5	3		
20	tip	high	1	10	13.29	15.8	142.7	12		
21	tip	high	1	8.5	14.33	13.2	91.4	5		
22	tip	high	1	14.1	19.12	13.1	113.2	13		
23	tip	high	1	10.1	15.49	12.6	77.2	12		
24	tip	high	1	8.5	17.82	20.5	54.4	3		

For those of you unfamiliar with the tab delimited file format it simply means that data in different columns are separated with a 'tab' character (yes, the same one as on your keyboard) and is usually saved as a file with a '.txt' extension (you might also see `.tsv` which is short for tab separated values).

To save a spreadsheet as a tab delimited file in LibreOffice Calc select `File` -> `Save as ...` from the main menu. You will need to specify the location you want to save your file in the 'Save in folder' option and the name of the file in the 'Name' option. In the drop down menu located above the 'Save' button change the default 'All formats' to 'Text CSV (.csv)'.

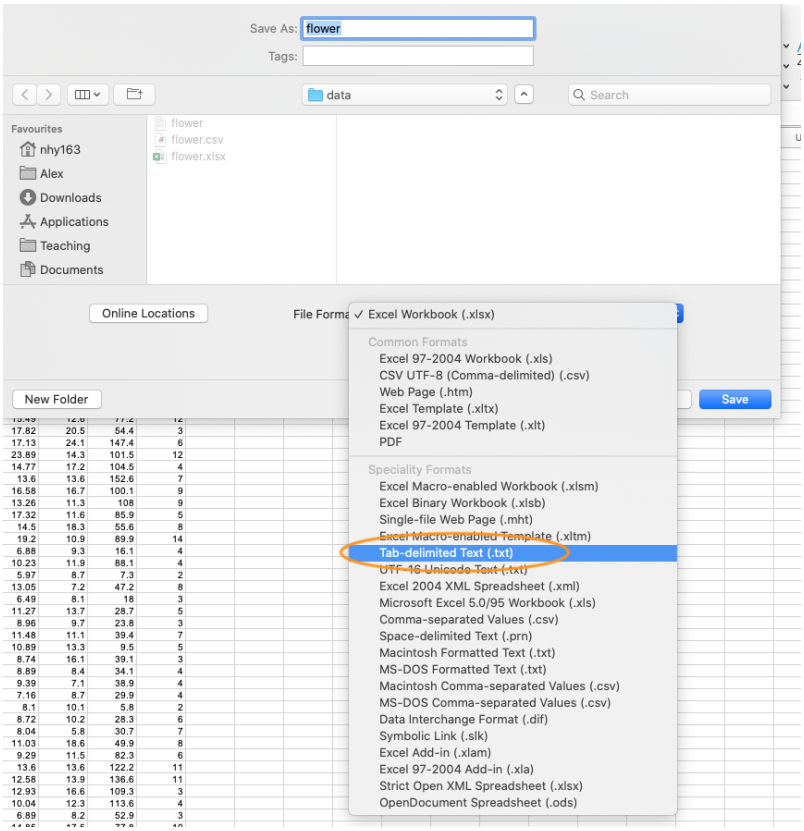


Click the Save button and then select the 'Use Text CSV Format' option. In the next pop-up window select `{Tab}` from the drop down menu in the 'Field delimiter' option. Click on OK to save the file.



The resulting file will annoyingly have a '.csv' extension even though we've saved it as a tab delimited file. Either live with it or rename the file with a '.txt' extension instead.

In MS Excel, select `File -> Save as ...` from the main menu and navigate to the folder where you want to save the file. Enter the file name (keep it fairly short, no spaces!) in the 'Save as:' dialogue box. In the 'File format:' dialogue box click on the down arrow to open the drop down menu and select 'Text (Tab delimited)' as your file type. Select OK to save the file.



There are a couple of things to bear in mind when saving files to import into R which will make your life easier in the long run. Keep your column headings (if you have them) short and informative. Also avoid spaces in your column headings by replacing them with an underscore or a dot (i.e. replace `shoot height` with `shoot_height` or `shoot.height`) and avoid using special characters (i.e. `leaf area (mm^2)`). Remember, if you have missing data in your data frame (empty cells) you should use an `NA` to represent these missing values. This will keep the data frame tidy.

3.3.2. Import functions

Once you've saved your data file in a suitable format we can now read this file into R. The workhorse function for importing data into R is the `read.table()` function (we discuss some alternatives later in the chapter). The `read.table()` function is a very flexible function with a shed load of arguments (see `?read.table`) but it's quite simple to use. Let's import a tab delimited file called `flower.txt` which contains the data we saw previously in this Chapter and assign it to an object called `flowers`. The file is located in a `data` directory which itself is located in our root directory. The first row of the data contains the variable (column) names. To use the `read.table()` function to import this file

```
flowers <- read.table(file = 'data/flower.txt', header = TRUE, sep = "\t",
                      stringsAsFactors = TRUE)
```

There are a few things to note about the above command. First, the file path and the filename (including the file extension) needs to be enclosed in either single or double quotes (i.e. the `data/flower.txt` bit) as the `read.table()` function expects this to be a character string. If your working directory is already set to the directory which contains the file, you don't need to include the entire file path just the filename. In the example above, the file path is separated with a single forward slash `/`. This will work regardless of the operating system you are using and we recommend you stick with this. However, Windows users may be more familiar with the single backslash notation and if you want to keep using this you will need to include them as double backslashes. Note though that the double backslash notation will **not** work on computers using Mac OSX or Linux operating systems.

```
flowers <- read.table(file = 'C:\\Documents\\Prog1\\data\\flower.txt',
                      header = TRUE, sep = "\t", stringsAsFactors = TRUE)
```

The `header = TRUE` argument specifies that the first row of your data contains the variable names (i.e. `nitrogen`, `block` etc). If this is not the case you can specify `header = FALSE` (actually, this is the default value so you can omit this argument entirely). The `sep = "\t"` argument tells R that the file delimiter is a tab (`\t`).

After importing our data into R it doesn't appear that R has done much, at least nothing appears in the R Console! To see the contents of the data frame we could just type the name of the object as we have done previously. **BUT** before you do that, think about why you're doing this. If your data frame is anything other than tiny, all you're going to do is fill up your Console with data. It's not like you can easily check whether there are any errors or that your data has been imported correctly. A much better solution is to use our old friend the `str()` function to return a compact and informative summary of your data frame.

```
str(flowers)
```

```
'data.frame':   96 obs. of  8 variables:
 $ treat    : Factor w/ 2 levels "notip","tip": 2 2 2 2 2 2 2 2 2 2 ...
 $ nitrogen : Factor w/ 3 levels "high","low","medium": 3 3 3 3 3 3 3 3 3 3 ...
 $ block    : int  1 1 1 1 1 1 1 1 2 2 ...
 $ height   : num  7.5 10.7 11.2 10.4 10.4 9.8 6.9 9.4 10.4 12.3 ...
 $ weight   : num  7.62 12.14 12.76 8.78 13.58 ...
 $ leafarea : num  11.7 14.1 7.1 11.9 14.5 12.2 13.2 14 10.5 16.1 ...
```

```
 $ shootarea: num  31.9 46 66.7 20.3 26.9 72.7 43.1 28.5 57.8 36.9 ...
 $ flowers  : int  1 10 10 1 4 9 7 6 5 8 ...
```

Here we see that `flowers` is a 'data.frame' object which contains 96 rows and 8 variables (columns). Each of the variables are listed along with their data class and the first 10 values. As we mentioned previously in this Chapter, it can be quite convenient to copy and paste this into your R script as a comment block for later reference.

Notice also that your character string variables (`treat` and `nitrogen`) have been imported as factors because we used the argument `stringsAsFactors = TRUE`. If this is not what you want you can prevent this by using the `stringsAsFactors = FALSE` or from R version 4.0.0 you can just leave out this argument as `stringsAsFactors = FALSE` is the default.

```
flowers <- read.table(file = 'data/flower.txt', header = TRUE,
                      sep = "\t", stringsAsFactors = FALSE)
str(flowers)
```

```
'data.frame':   96 obs. of  8 variables:
 $ treat    : chr  "tip" "tip" "tip" "tip" ...
 $ nitrogen : chr  "medium" "medium" "medium" "medium" ...
 $ block    : int  1 1 1 1 1 1 1 2 2 ...
 $ height   : num  7.5 10.7 11.2 10.4 10.4 9.8 6.9 9.4 10.4 12.3 ...
 $ weight   : num  7.62 12.14 12.76 8.78 13.58 ...
 $ leafarea : num  11.7 14.1 7.1 11.9 14.5 12.2 13.2 14 10.5 16.1 ...
 $ shootarea: num  31.9 46 66.7 20.3 26.9 72.7 43.1 28.5 57.8 36.9 ...
 $ flowers  : int  1 10 10 1 4 9 7 6 5 8 ...
```

Other useful arguments include `dec =` and `na.strings =`. The `dec =` argument allows you to change the default character (`.`) used for a decimal point. This is useful if you're in a country where decimal places are usually represented by a comma (i.e. `dec = ","`). The `na.strings =` argument allows you to import data where missing values are represented with a symbol other than `NA`. This can be quite common if you are importing data from other statistical software such as Minitab which represents missing values as a `*` (`na.strings = "*"`).

If we just wanted to see the names of our variables (columns) in the data frame we can use the `names()` function which will return a character vector of the variable names.

```
names(flowers)
```

```
[1] "treat"     "nitrogen"  "block"     "height"    "weight"    "leafarea"
[7] "shootarea" "flowers"
```

R has a number of variants of the `read.table()` function that you can use to import a variety of file formats. Actually, these variants just use the `read.table()` function but include different combinations of arguments by default to help import different file types. The most useful of these are the `read.csv()`, `read.csv2()` and `read.delim()` functions. The `read.csv()` function is used to import comma separated value (.csv) files and assumes that the data in columns are separated by a comma (it sets `sep = ","` by default). It also assumes that the first row of the data contains the variable names by default (it sets `header = TRUE` by default). The `read.csv2()` function assumes data are separated by semicolons and that a comma is used instead of a decimal point (as in many European countries). The `read.delim()` function is used to import tab delimited data and also assumes that the first row of the data contains the variable names by default.

```
# import .csv file
flowers <- read.csv(file = 'data/flower.csv')


# import .csv file with dec = "," and sep = ";"
flowers <- read.csv2(file = 'data/flower.csv')


# import tab delim file with sep = "\t"
flowers <- read.delim(file = 'data/flower.txt')
```

You can even import spreadsheet files from MS Excel or other statistics software directly into R but our advice is that this should generally be avoided if possible as it just adds a layer of uncertainty between you and your data. In our opinion it's almost always better to export your spreadsheets as tab or comma delimited files and then import them into R using the `read.table()` function. If you're hell bent on directly importing data from other software you will need to install the `foreign` package which has functions for importing Minitab, SPSS, Stata and SAS files or the `xlsx` package to import Excel spreadsheets.

3.3.3. Common import frustrations

It's quite common to get a bunch of really frustrating error messages when you first start importing data into R. Perhaps the most common is

```
Error in file(file, "rt") : cannot open the connection
In addition: Warning message:
In file(file, "rt") :
  cannot open file 'flower.txt': No such file or directory
```

This error message is telling you that R cannot find the file you are trying to import. It usually rears its head for one of a couple of reasons (or all of them!). The first is that you've made a mistake in the spelling of either the filename or file path. Another common mistake is that you have forgotten to include the file extension in the filename (i.e. `.txt`). Lastly, the file is not where you say it is or you've used an incorrect file path. Using RStudio Projects and having a logical directory structure goes a long way to avoiding these types of errors.

Another really common mistake is to forget to include the `header = TRUE` argument when the first row of the data contains variable names. For example, if we omit this argument when we import our `flowers.txt` file everything looks OK at first (no error message at least)

```
flowers_bad <- read.table(file = 'data/flower.txt', sep = "\t")
```

but when we take a look at our data frame using `str()`

```
str(flowers_bad)
```

```
'data.frame':   97 obs. of  8 variables:
 $ V1: chr  "treat" "tip" "tip" "tip" ...
 $ V2: chr  "nitrogen" "medium" "medium" "medium" ...
 $ V3: chr  "block" "1" "1" "1" ...
 $ V4: chr  "height" "7.5" "10.7" "11.2" ...
 $ V5: chr  "weight" "7.62" "12.14" "12.76" ...
 $ V6: chr  "leafarea" "11.7" "14.1" "7.1" ...
 $ V7: chr  "shootarea" "31.9" "46" "66.7" ...
 $ V8: chr  "flowers" "1" "10" "10" ...
```

We can see an obvious problem, all of our variables have been imported as factors and our variables are named `V1`, `V2`, `V3` … `V8`. The problem happens because we haven't told the `read.table()` function that the first row contains the variable names and so it treats them as data. As soon as we have a single character string in any of our data vectors, R treats the vectors as character type data (remember all elements in a vector must contain the same type of data).

3.3.4. Other import options

There are numerous other functions to import data from a variety of sources and formats. Most of these functions are contained in packages that you will need to install before using them. We list a couple of the more useful packages and functions below.

The `fread()` function from the `read.table` package is great for importing large data files quickly and efficiently (much faster than the `read.table()` function). One of the great things about the `fread()` function is that it will automatically detect many of the arguments you would normally need to specify (like `sep =` etc). One of the things you will need to consider though is that the `fread()` function will return a `data.table` object not a `data.frame` as would be the case with the `read.table()` function. This is usually not a problem as you can pass a `data.table` object to any function that only accepts `data.frame` objects. To learn more about the differences between `data.table` and `data.frame` objects see here.

```
library(read.table)
all_data <- fread(file = 'data/flower.txt')
```

Various functions from the `readr` package are also very efficient at reading in large data files. The `readr` package is part of the 'tidyverse' collection of packages and provides many equivalent functions to base R for importing data. The `readr` functions are used in a similar way to the `read.table()` or `read.csv()` functions and many of the arguments are the same (see `?readr::read_table` for more details). There are however some differences. For example, when using the `read_table()` function the `header = TRUE` argument is replaced by `col_names = TRUE` and the function returns a `tibble` class object which is the tidyverse equivalent of a `data.frame` object (see here for differences).

```
library(readr)
# import white space delimited files
all_data <- read_table(file = 'data/flower.txt', col_names = TRUE)


# import comma delimited files
all_data <- read_csv(file = 'data/flower.txt')


# import tab delimited files
all_data <- read_delim(file = 'data/flower.txt', delim = "\t")
```

```
# or use
all_data <- read_tsv(file = 'data/flower.txt')
```

If your data file is ginormous, then the `ff` and `bigmemory` packages may be useful as they both contain import functions that are able to store large data in a memory efficient manner. You can find out more about these functions here and here.

3.4. Wrangling data frames

Now that you're able to successfully import your data from an external file into R our next task is to do something useful with our data. Working with data is a fundamental skill which you'll need to develop and get comfortable with as you'll likely do a lot of it during any project. The good news is that R is especially good at manipulating, summarising and visualising data. Manipulating data (often known as data wrangling or munging) in R can at first seem a little daunting for the new user but if you follow a few simple logical rules then you'll quickly get the hang of it, especially with some practice.

Let's remind ourselves of the structure of the `flowers` data frame we imported in the previous section.

```
flowers <- read.table(file = 'data/flower.txt', header = TRUE, sep = "\t")
str(flowers)
```

```
'data.frame':   96 obs. of  8 variables:
 $ treat    : chr  "tip" "tip" "tip" "tip" ...
 $ nitrogen : chr  "medium" "medium" "medium" "medium" ...
 $ block    : int  1 1 1 1 1 1 1 2 2 ...
 $ height   : num  7.5 10.7 11.2 10.4 10.4 9.8 6.9 9.4 10.4 12.3 ...
 $ weight   : num  7.62 12.14 12.76 8.78 13.58 ...
 $ leafarea : num  11.7 14.1 7.1 11.9 14.5 12.2 13.2 14 10.5 16.1 ...
 $ shootarea: num  31.9 46 66.7 20.3 26.9 72.7 43.1 28.5 57.8 36.9 ...
 $ flowers  : int  1 10 10 1 4 9 7 6 5 8 ...
```

To access the data in any of the variables (columns) in our data frame we can use the `$` notation. For example, to access the `height` variable in our `flowers` data frame we can use `flowers$height`. This tells R that the `height` variable is contained within the data frame `flowers`.

```
flowers$height
```

```
 [1]  7.5 10.7 11.2 10.4 10.4  9.8  6.9  9.4 10.4 12.3 10.4 11.0  7.1  6.0  9.0
[16]  4.5 12.6 10.0 10.0  8.5 14.1 10.1  8.5  6.5 11.5  7.7  6.4  8.8  9.2  6.2
[31]  6.3 17.2  8.0  8.0  6.4  7.6  9.7 12.3  9.1  8.9  7.4  3.1  7.9  8.8  8.5
[46]  5.6 11.5  5.8  5.6  5.3  7.5  4.1  3.5  8.5  4.9  2.5  5.4  3.9  5.8  4.5
[61]  8.0  1.8  2.2  3.9  8.5  8.5  6.4  1.2  2.6 10.9  7.2  2.1  4.7  5.0  6.5
[76]  2.6  6.0  9.3  4.6  5.2  3.9  2.3  5.2  2.2  4.5  1.8  3.0  3.7  2.4  5.7
[91]  3.7  3.2  3.9  3.3  5.5  4.4
```

This will return a vector of the `height` data. If we want we can assign this vector to another object and do stuff with it, like calculate a mean or get a summary of the variable using the `summary()` function.

```
f_height <- flowers$height
mean(f_height)
```

```
[1] 6.839583
```

```
summary(f_height)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  1.200   4.475   6.450   6.840   9.025  17.200
```

Or if we don't want to create an additional object we can use functions 'on-the-fly' to only display the value in the console.

```
mean(flowers$height)
```

```
[1] 6.839583
```

```
summary(flowers$height)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  1.200   4.475   6.450   6.840   9.025  17.200
```

Just as we did with vectors, we also can access data in data frames using the square bracket `[ ]` notation. However, instead of just using a single index, we now need to use two indexes, one to specify the rows and one for the columns. To do this, we can use the notation `my_data[rows, columns]` where `rows` and `columns` are indexes and `my_data` is the name of the data frame. Again, just like with our vectors our indexes can be positional or the result of a logical test.

3.4.1. Positional indexes

To use positional indexes we simple have to write the position of the rows and columns we want to extract inside the `[ ]`. For example, if for some reason we wanted to extract the first value (1st row) of the `height` variable (4th column)

```
flowers[1, 4]
```

```
[1] 7.5
```

```
# this would give you the same
flowers$height[1]
```

```
[1] 7.5
```

We can also extract values from multiple rows or columns by specifying these indexes as vectors inside the `[ ]`. To extract the first 10 rows and the first 4 columns we simple supply a vector containing a sequence from 1 to 10 for the rows index (`1:10`) and a vector from 1 to 4 for the column index (`1:4`).

```
flowers[1:10, 1:4]
```

```
   treat nitrogen block height
1    tip   medium     1    7.5
2    tip   medium     1   10.7
3    tip   medium     1   11.2
4    tip   medium     1   10.4
5    tip   medium     1   10.4
6    tip   medium     1    9.8
```

```
7    tip   medium     1    6.9
8    tip   medium     1    9.4
9    tip   medium     2   10.4
10   tip   medium     2   12.3
```

Or for non sequential rows and columns then we can supply vectors of positions using the `c()` function. To extract the 1st, 5th, 12th, 30th rows from the 1st, 3rd, 6th and 8th columns

```
flowers[c(1, 5, 12, 30), c(1, 3, 6, 8)]
```

```
   treat block leafarea flowers
1    tip     1     11.7       1
5    tip     1     14.5       4
12   tip     2     12.6       6
30   tip     2     11.6       5
```

All we are doing in the two examples above is creating vectors of positions for the rows and columns that we want to extract. We have done this by using the skills we developed in Chapter 2 when we generated vectors using the `c()` function or using the `:` notation.

But what if we want to extract either all of the rows or all of the columns? It would be extremely tedious to have to generate vectors for all rows or for all columns. Thankfully R has a shortcut. If you don't specify either a row or column index in the `[ ]` then R interprets it to mean you want all rows or all columns. For example, to extract the first 8 rows and all of the columns in the `flower` data frame

```
flowers[1:8, ]
```

```
  treat nitrogen block height weight leafarea shootarea flowers
1   tip   medium     1    7.5   7.62     11.7      31.9       1
2   tip   medium     1   10.7  12.14     14.1      46.0      10
3   tip   medium     1   11.2  12.76      7.1      66.7      10
4   tip   medium     1   10.4   8.78     11.9      20.3       1
5   tip   medium     1   10.4  13.58     14.5      26.9       4
6   tip   medium     1    9.8  10.08     12.2      72.7       9
7   tip   medium     1    6.9  10.11     13.2      43.1       7
8   tip   medium     1    9.4  10.28     14.0      28.5       6
```

or all of the rows and the first 3 columns. If you're reading the web version of this book scroll down in output panel to see all of the data. Note, if you're reading the pdf version of the book some of the output has been truncated to save some space.

```
flowers[, 1:3]
```

```
   treat nitrogen block
1    tip   medium     1
2    tip   medium     1
3    tip   medium     1
4    tip   medium     1
5    tip   medium     1
6    tip   medium     1
7    tip   medium     1
8    tip   medium     1
9    tip   medium     2
10   tip   medium     2
87 notip      low     1
88 notip      low     1
89 notip      low     2
90 notip      low     2
91 notip      low     2
92 notip      low     2
93 notip      low     2
94 notip      low     2
95 notip      low     2
96 notip      low     2
```

We can even use negative positional indexes to exclude certain rows and columns. As an example, lets extract all of the rows except the first 85 rows and all columns except the 4^{th}, 7^{th} and 8^{th} columns. Notice we need to use `-()` when we generate our row positional vectors. If we had just used `-1:85` this would actually generate a regular sequence from -1 to 85 which is not what we want (we can of course use `-1:-85`).

```
flowers[-(1:85), -c(4, 7, 8)]
```

```
   treat nitrogen block weight leafarea
86 notip      low     1   6.01     17.6
87 notip      low     1   9.93     12.0
88 notip      low     1   7.03      7.9
89 notip      low     2   9.10     14.5
90 notip      low     2   9.05      9.6
91 notip      low     2   8.10     10.5
92 notip      low     2   7.45     14.1
93 notip      low     2   9.19     12.4
94 notip      low     2   8.92     11.6
95 notip      low     2   8.44     13.5
96 notip      low     2  10.60     16.2
```

In addition to using a positional index for extracting particular columns (variables) we can also name the variables directly when using the square bracket `[ ]` notation. For example, let's extract the first 5 rows and the variables `treat`, `nitrogen` and `leafarea`. Instead of using `flowers[1:5, c(1, 2, 6)]` we can instead use

```
flowers[1:5, c("treat", "nitrogen", "leafarea")]
```

```
  treat nitrogen leafarea
1   tip   medium     11.7
2   tip   medium     14.1
3   tip   medium      7.1
4   tip   medium     11.9
5   tip   medium     14.5
```

We often use this method in preference to the positional index for selecting columns as it will still give us what we want even if we've changed the order of the columns in our data frame for some reason.

3.4.2. Logical indexes

Just as we did with vectors, we can also extract data from our data frame based on a logical test. We can use all of the logical operators that we used for our vector examples so if these have slipped your mind maybe pop back

and refresh your memory. Let's extract all rows where `height` is greater than 12 and extract all columns by default (remember, if you don't include a column index after the comma it means all columns).

```
big_flowers <- flowers[flowers$height > 12, ]
big_flowers
```

```
   treat nitrogen block height weight leafarea shootarea flowers
10   tip   medium     2   12.3  13.48     16.1      36.9       8
17   tip     high     1   12.6  18.66     18.6      54.0       9
21   tip     high     1   14.1  19.12     13.1     113.2      13
32   tip     high     2   17.2  19.20     10.9      89.9      14
38   tip      low     1   12.3  11.27     13.7      28.7       5
```

Notice in the code above that we need to use the `flowers$height` notation for the logical test. If we just named the `height` variable without the name of the data frame we would receive an error telling us R couldn't find the variable `height`. The reason for this is that the `height` variable only exists inside the `flowers` data frame so you need to tell R exactly where it is.

```
big_flowers <- flowers[height > 12, ]
Error in `[.data.frame`(flowers, height > 12, ) :
  object 'height' not found
```

So how does this work? The logical test is `flowers$height > 12` and R will only extract those rows that satisfy this logical condition. If we look at the output of just the logical condition you can see this returns a vector containing `TRUE` if `height` is greater than 12 and `FALSE` if `height` is not greater than 12.

```
flowers$height > 12
```

```
 [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE FALSE FALSE
[13] FALSE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE
[25] FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE
[37] FALSE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[49] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[61] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[73] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[85] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

So our row index is a vector containing either `TRUE` or `FALSE` values and only those rows that are `TRUE` are selected.

Other commonly used operators are shown below

```
flowers[flowers$height >= 6, ]        # values greater or equal to 6

flowers[flowers$height <= 6, ]          # values less than or equal to 6

flowers[flowers$height == 8, ]         # values  equal to 8

flowers[flowers$height != 8, ]         # values  not equal to 8
```

We can also extract rows based on the value of a character string or factor level. Let's extract all rows where the `nitrogen` level is equal to `high` (again we will output all columns). Notice that the double equals `==` sign must be used for a logical test and that the character string must be enclosed in either single or double quotes (i.e. `"high"`).

```
nit_high <- flowers[flowers$nitrogen == "high", ]
nit_high
```

```
   treat nitrogen block height weight leafarea shootarea flowers
17   tip     high     1   12.6  18.66     18.6      54.0       9
18   tip     high     1   10.0  18.07     16.9      90.5       3
19   tip     high     1   10.0  13.29     15.8     142.7      12
20   tip     high     1    8.5  14.33     13.2      91.4       5
21   tip     high     1   14.1  19.12     13.1     113.2      13
22   tip     high     1   10.1  15.49     12.6      77.2      12
23   tip     high     1    8.5  17.82     20.5      54.4       3
24   tip     high     1    6.5  17.13     24.1     147.4       6
25   tip     high     2   11.5  23.89     14.3     101.5      12
26   tip     high     2    7.7  14.77     17.2     104.5       4
71 notip     high     1    7.2  15.21     15.9     135.0      14
72 notip     high     1    2.1  19.15     15.6     176.7       6
73 notip     high     2    4.7  13.42     19.8     124.7       5
74 notip     high     2    5.0  16.82     17.3     182.5      15
75 notip     high     2    6.5  14.00     10.1     126.5       7
```

```
76 notip     high     2    2.6  18.88     16.4     181.5      14
77 notip     high     2    6.0  13.68     16.2     133.7       2
78 notip     high     2    9.3  18.75     18.4     181.1      16
79 notip     high     2    4.6  14.65     16.7      91.7      11
80 notip     high     2    5.2  17.70     19.1     181.1       8
```

Or we can extract all rows where `nitrogen` level is not equal to `medium` (using `!=`) and only return columns 1 to 4.

```
nit_not_medium <- flowers[flowers$nitrogen != "medium", 1:4]
nit_not_medium
```

```
   treat nitrogen block height
17   tip     high     1   12.6
18   tip     high     1   10.0
19   tip     high     1   10.0
20   tip     high     1    8.5
21   tip     high     1   14.1
22   tip     high     1   10.1
23   tip     high     1    8.5
24   tip     high     1    6.5
25   tip     high     2   11.5
26   tip     high     2    7.7
87 notip      low     1    3.0
88 notip      low     1    3.7
89 notip      low     2    2.4
90 notip      low     2    5.7
91 notip      low     2    3.7
92 notip      low     2    3.2
93 notip      low     2    3.9
94 notip      low     2    3.3
95 notip      low     2    5.5
96 notip      low     2    4.4
```

We can increase the complexity of our logical tests by combining them with Boolean expressions just as we did for vector objects. For example, to extract all rows where `height` is greater or equal to 6 AND `nitrogen` is equal to `medium` AND `treat` is equal to `notip` we combine a series of logical expressions with the `&` symbol.

```
low_notip_heigh6 <- flowers[flowers$height >= 6 & flowers$nitrogen == "medium" &
                            flowers$treat == "notip", ]
low_notip_heigh6
```

```
   treat nitrogen block height weight leafarea shootarea flowers
51 notip   medium     1    7.5  13.60     13.6     122.2      11
54 notip   medium     1    8.5  10.04     12.3     113.6       4
61 notip   medium     2    8.0  11.43     12.6      43.2      14
```

To extract rows based on an 'OR' Boolean expression we can use the `|` symbol. Let's extract all rows where `height` is greater than 12.3 OR less than 2.2.

```
height2.2_12.3 <- flowers[flowers$height > 12.3 | flowers$height < 2.2, ]
height2.2_12.3
```

```
   treat nitrogen block height weight leafarea shootarea flowers
17   tip     high     1   12.6  18.66     18.6      54.0       9
21   tip     high     1   14.1  19.12     13.1     113.2      13
32   tip     high     2   17.2  19.20     10.9      89.9      14
62 notip   medium     2    1.8  10.47     11.8     120.8       9
68 notip     high     1    1.2  18.24     16.6     148.1       7
72 notip     high     1    2.1  19.15     15.6     176.7       6
86 notip      low     1    1.8   6.01     17.6      46.2       4
```

An alternative method of selecting parts of a data frame based on a logical expression is to use the `subset()` function instead of the `[ ]`. The advantage of using `subset()` is that you no longer need to use the `$` notation when specifying variables inside the data frame as the first argument to the function is the name of the data frame to be subsetted. The disadvantage is that `subset()` is less flexible than the `[ ]` notation.

```
tip_med_2 <- subset(flowers, treat == "tip" & nitrogen == "medium" & block == 2)
tip_med_2
```

```
   treat nitrogen block height weight leafarea shootarea flowers
9    tip   medium     2   10.4  10.48     10.5      57.8       5
10   tip   medium     2   12.3  13.48     16.1      36.9       8
11   tip   medium     2   10.4  13.18     11.1      56.8      12
12   tip   medium     2   11.0  11.56     12.6      31.3       6
13   tip   medium     2    7.1   8.16     29.6       9.7       2
14   tip   medium     2    6.0  11.22     13.0      16.4       3
15   tip   medium     2    9.0  10.20     10.8      90.1       6
16   tip   medium     2    4.5  12.55     13.4      14.4       6
```

And if you only want certain columns you can use the `select =` argument.

```
tipplants <- subset(flowers, treat == "tip" & nitrogen == "medium" & block == 2,
                            select = c("treat", "nitrogen", "leafarea"))
tipplants
```

```
   treat nitrogen leafarea
9    tip   medium     10.5
10   tip   medium     16.1
11   tip   medium     11.1
12   tip   medium     12.6
13   tip   medium     29.6
14   tip   medium     13.0
15   tip   medium     10.8
16   tip   medium     13.4
```

3.4.3. Ordering data frames

Remember when we used the function `order()` to order one vector based on the order of another vector (way back in Chapter 2). This comes in very handy if you want to reorder rows in your data frame. For example, if we want all of the rows in the data frame `flowers` to be ordered in ascending value of `height` and output all columns by

default. If you're reading this section of the book on the web you can scroll down in the output panels to see the entire ordered data frame. If you're reading the pdf version of the book, note that some of the output from the code chunks has been truncated to save some space.

```
height_ord <- flowers[order(flowers$height), ]
height_ord
```

```
   treat nitrogen block height weight leafarea shootarea flowers
68 notip     high     1    1.2  18.24     16.6     148.1       7
62 notip   medium     2    1.8  10.47     11.8     120.8       9
86 notip      low     1    1.8   6.01     17.6      46.2       4
72 notip     high     1    2.1  19.15     15.6     176.7       6
63 notip   medium     2    2.2  10.70     15.3      97.1       7
84 notip      low     1    2.2   9.97      9.6      63.1       2
82 notip      low     1    2.3   7.28     13.8      32.8       6
89 notip      low     2    2.4   9.10     14.5      78.7       8
56 notip   medium     1    2.5  14.85     17.5      77.8      10
69 notip     high     1    2.6  16.57     17.1     141.1       3
76 notip     high     2    2.6  18.88     16.4     181.5      14
87 notip      low     1    3.0   9.93     12.0      56.6       6
42   tip      low     2    3.1   8.74     16.1      39.1       3
92 notip      low     2    3.2   7.45     14.1      38.1       4
94 notip      low     2    3.3   8.92     11.6      55.2       6
```

We can also order by descending order of a variable (i.e. `leafarea`) using the `decreasing = TRUE` argument.

```
leafarea_ord <- flowers[order(flowers$leafarea, decreasing = TRUE), ]
leafarea_ord
```

```
   treat nitrogen block height weight leafarea shootarea flowers
70 notip     high     1   10.9  17.22     49.2     189.6      17
13   tip   medium     2    7.1   8.16     29.6       9.7       2
24   tip     high     1    6.5  17.13     24.1     147.4       6
65 notip     high     1    8.5  22.53     20.8     166.9      16
```

```
23   tip     high     1    8.5  17.82     20.5      54.4       3
66 notip     high     1    8.5  17.33     19.8     184.4      12
73 notip     high     2    4.7  13.42     19.8     124.7       5
80 notip     high     2    5.2  17.70     19.1     181.1       8
17   tip     high     1   12.6  18.66     18.6      54.0       9
49 notip   medium     1    5.6  11.03     18.6      49.9       8
78 notip     high     2    9.3  18.75     18.4     181.1      16
31   tip     high     2    6.3  14.50     18.3      55.6       8
57 notip   medium     2    5.4  11.36     17.8     104.6      12
86 notip      low     1    1.8   6.01     17.6      46.2       4
56 notip   medium     1    2.5  14.85     17.5      77.8      10
```

We can even order data frames based on multiple variables. For example, to order the data frame `flowers` in ascending order of both `block` and `height`.

```
block_height_ord <- flowers[order(flowers$block, flowers$height), ]
block_height_ord
```

```
   treat nitrogen block height weight leafarea shootarea flowers
68 notip     high     1    1.2  18.24     16.6     148.1       7
86 notip      low     1    1.8   6.01     17.6      46.2       4
72 notip     high     1    2.1  19.15     15.6     176.7       6
84 notip      low     1    2.2   9.97      9.6      63.1       2
82 notip      low     1    2.3   7.28     13.8      32.8       6
56 notip   medium     1    2.5  14.85     17.5      77.8      10
69 notip     high     1    2.6  16.57     17.1     141.1       3
87 notip      low     1    3.0   9.93     12.0      56.6       6
53 notip   medium     1    3.5  12.93     16.6     109.3       3
88 notip      low     1    3.7   7.03      7.9      36.7       5
81 notip      low     1    3.9   7.17     13.5      52.8       6
52 notip   medium     1    4.1  12.58     13.9     136.6      11
85 notip      low     1    4.5   8.60      9.4     113.5       7
55 notip   medium     1    4.9   6.89      8.2      52.9       3
83 notip      low     1    5.2   5.79     11.0      67.4       5
```

```
50 notip   medium     1    5.3   9.29     11.5      82.3       6
49 notip   medium     1    5.6  11.03     18.6      49.9       8
35   tip      low     1    6.4   5.97      8.7       7.3       2
67 notip     high     1    6.4  11.52     12.1     140.5       7
24   tip     high     1    6.5  17.13     24.1     147.4       6
```

What if we wanted to order `flowers` by ascending order of `block` but descending order of `height`? We can use a simple trick by adding a `-` symbol before the `flowers$height` variable when we use the `order()` function. This will essentially turn all of the `height` values negative which will result in reversing the order. Note, that this trick will only work with numeric variables.

```
block_revheight_ord <- flowers[order(flowers$block, -flowers$height), ]
block_revheight_ord
```

```
   treat nitrogen block height weight leafarea shootarea flowers
21   tip     high     1   14.1  19.12     13.1     113.2      13
17   tip     high     1   12.6  18.66     18.6      54.0       9
38   tip      low     1   12.3  11.27     13.7      28.7       5
3    tip   medium     1   11.2  12.76      7.1      66.7      10
70 notip     high     1   10.9  17.22     49.2     189.6      17
2    tip   medium     1   10.7  12.14     14.1      46.0      10
4    tip   medium     1   10.4   8.78     11.9      20.3       1
5    tip   medium     1   10.4  13.58     14.5      26.9       4
22   tip     high     1   10.1  15.49     12.6      77.2      12
18   tip     high     1   10.0  18.07     16.9      90.5       3
19   tip     high     1   10.0  13.29     15.8     142.7      12
6    tip   medium     1    9.8  10.08     12.2      72.7       9
37   tip      low     1    9.7   6.49      8.1      18.0       3
8    tip   medium     1    9.4  10.28     14.0      28.5       6
39   tip      low     1    9.1   8.96      9.7      23.8       3
79 notip     high     2    4.6  14.65     16.7      91.7      11
16   tip   medium     2    4.5  12.55     13.4      14.4       6
60 notip   medium     2    4.5  13.68     14.8     125.5       9
96 notip      low     2    4.4  10.60     16.2      63.3       6
```

```
58 notip   medium     2    3.9   9.07      9.6      90.4       7
64 notip   medium     2    3.9  12.97     17.0      97.5       5
93 notip      low     2    3.9   9.19     12.4      52.6       9
91 notip      low     2    3.7   8.10     10.5      60.5       6
94 notip      low     2    3.3   8.92     11.6      55.2       6
92 notip      low     2    3.2   7.45     14.1      38.1       4
42   tip      low     2    3.1   8.74     16.1      39.1       3
76 notip     high     2    2.6  18.88     16.4     181.5      14
89 notip      low     2    2.4   9.10     14.5      78.7       8
63 notip   medium     2    2.2  10.70     15.3      97.1       7
62 notip   medium     2    1.8  10.47     11.8     120.8       9
```

If we wanted to do the same thing with a factor (or character) variable like `nitrogen` we would need to use the function `xtfrm()` for this variable inside our `order()` function.

```
block_revheight_ord <- flowers[order(-xtfrm(flowers$nitrogen), flowers$height), ]
block_revheight_ord
```

```
   treat nitrogen block height weight leafarea shootarea flowers
62 notip   medium     2    1.8  10.47     11.8     120.8       9
63 notip   medium     2    2.2  10.70     15.3      97.1       7
56 notip   medium     1    2.5  14.85     17.5      77.8      10
53 notip   medium     1    3.5  12.93     16.6     109.3       3
58 notip   medium     2    3.9   9.07      9.6      90.4       7
64 notip   medium     2    3.9  12.97     17.0      97.5       5
52 notip   medium     1    4.1  12.58     13.9     136.6      11
16   tip   medium     2    4.5  12.55     13.4      14.4       6
60 notip   medium     2    4.5  13.68     14.8     125.5       9
55 notip   medium     1    4.9   6.89      8.2      52.9       3
50 notip   medium     1    5.3   9.29     11.5      82.3       6
57 notip   medium     2    5.4  11.36     17.8     104.6      12
49 notip   medium     1    5.6  11.03     18.6      49.9       8
59 notip   medium     2    5.8  10.18     15.7      88.8       6
14   tip   medium     2    6.0  11.22     13.0      16.4       3
```

```
20   tip     high     1    8.5  14.33     13.2      91.4       5
23   tip     high     1    8.5  17.82     20.5      54.4       3
65 notip     high     1    8.5  22.53     20.8     166.9      16
66 notip     high     1    8.5  17.33     19.8     184.4      12
28   tip     high     2    8.8  16.58     16.7     100.1       9
29   tip     high     2    9.2  13.26     11.3     108.0       9
78 notip     high     2    9.3  18.75     18.4     181.1      16
18   tip     high     1   10.0  18.07     16.9      90.5       3
19   tip     high     1   10.0  13.29     15.8     142.7      12
22   tip     high     1   10.1  15.49     12.6      77.2      12
70 notip     high     1   10.9  17.22     49.2     189.6      17
25   tip     high     2   11.5  23.89     14.3     101.5      12
17   tip     high     1   12.6  18.66     18.6      54.0       9
21   tip     high     1   14.1  19.12     13.1     113.2      13
32   tip     high     2   17.2  19.20     10.9      89.9      14
```

Notice that the `nitrogen` variable has been reverse ordered alphabetically and `height` has been ordered by increasing values within each level of `nitrogen`.

If we wanted to order the data frame by `nitrogen` but this time order it from `low` -> `medium` -> `high` instead of the default alphabetically (`high`, `low`, `medium`), we need to first change the order of our levels of the `nitrogen` factor in our data frame using the `factor()` function. Once we've done this we can then use the `order()` function as usual. Note, if you're reading the pdf version of this book, the output has been truncated to save space.

```
flowers$nitrogen <- factor(flowers$nitrogen,
                           levels = c("low", "medium", "high"))
nit_ord <- flowers[order(flowers$nitrogen),]
nit_ord
```

```
   treat nitrogen block height weight leafarea shootarea flowers
33   tip      low     1    8.0   6.88      9.3      16.1       4
34   tip      low     1    8.0  10.23     11.9      88.1       4
35   tip      low     1    6.4   5.97      8.7       7.3       2
36   tip      low     1    7.6  13.05      7.2      47.2       8
37   tip      low     1    9.7   6.49      8.1      18.0       3
```

```
38   tip      low     1   12.3  11.27     13.7      28.7       5
39   tip      low     1    9.1   8.96      9.7      23.8       3
40   tip      low     1    8.9  11.48     11.1      39.4       7
41   tip      low     2    7.4  10.89     13.3       9.5       5
42   tip      low     2    3.1   8.74     16.1      39.1       3
43   tip      low     2    7.9   8.89      8.4      34.1       4
44   tip      low     2    8.8   9.39      7.1      38.9       4
45   tip      low     2    8.5   7.16      8.7      29.9       4
46   tip      low     2    5.6   8.10     10.1       5.8       2
47   tip      low     2   11.5   8.72     10.2      28.3       6
66 notip     high     1    8.5  17.33     19.8     184.4      12
67 notip     high     1    6.4  11.52     12.1     140.5       7
68 notip     high     1    1.2  18.24     16.6     148.1       7
69 notip     high     1    2.6  16.57     17.1     141.1       3
70 notip     high     1   10.9  17.22     49.2     189.6      17
71 notip     high     1    7.2  15.21     15.9     135.0      14
72 notip     high     1    2.1  19.15     15.6     176.7       6
73 notip     high     2    4.7  13.42     19.8     124.7       5
74 notip     high     2    5.0  16.82     17.3     182.5      15
75 notip     high     2    6.5  14.00     10.1     126.5       7
76 notip     high     2    2.6  18.88     16.4     181.5      14
77 notip     high     2    6.0  13.68     16.2     133.7       2
78 notip     high     2    9.3  18.75     18.4     181.1      16
79 notip     high     2    4.6  14.65     16.7      91.7      11
80 notip     high     2    5.2  17.70     19.1     181.1       8
```

3.4.4. Adding columns and rows

Sometimes it's useful to be able to add extra rows and columns of data to our data frames. There are multiple ways to achieve this (as there always is in R!) depending on your circumstances. To simply append additional rows to an existing data frame we can use the `rbind()` function and to append columns the `cbind()` function. Let's create a couple of test data frames to see this in action using our old friend the `data.frame()` function.

```r
# rbind for rows
df1 <- data.frame(id = 1:4, height = c(120, 150, 132, 122),
                          weight = c(44, 56, 49, 45))
df1
```

```
  id height weight
1  1    120     44
2  2    150     56
3  3    132     49
4  4    122     45
```

```r
df2 <- data.frame(id = 5:6, height = c(119, 110),
                          weight = c(39, 35))
df2
```

```
  id height weight
1  5    119     39
2  6    110     35
```

```r
df3 <- data.frame(id = 1:4, height = c(120, 150, 132, 122),
                          weight = c(44, 56, 49, 45))
df3
```

```
  id height weight
1  1    120     44
2  2    150     56
3  3    132     49
4  4    122     45
```

```r
df4 <- data.frame(location = c("UK", "CZ", "CZ", "UK"))
df4
```

```
  location
1       UK
```

```
2       CZ
3       CZ
4       UK
```

We can use the `rbind()` function to append the rows of data in `df2` to the rows in `df1` and assign the new data frame to `df_rcomb`.

```
df_rcomb <- rbind(df1, df2)
df_rcomb
```

```
  id height weight
1  1    120     44
2  2    150     56
3  3    132     49
4  4    122     45
5  5    119     39
6  6    110     35
```

And `cbind` to append the column in `df4` to the `df3` data frame and assign to df_ccomb‘.

```
df_ccomb <- cbind(df3, df4)
df_ccomb
```

```
  id height weight location
1  1    120     44       UK
2  2    150     56       CZ
3  3    132     49       CZ
4  4    122     45       UK
```

Another situation when adding a new column to a data frame is useful is when you want to perform some kind of transformation on an existing variable. For example, say we wanted to apply a $\log_{10}$ transformation on the height variable in the `df_rcomb` data frame we created above. We could just create a separate variable to contains these values but it's good practice to create this variable as a new column inside our existing data frame so we keep all of our data together. Let's call this new variable `height_log10`.

```
# log10 transformation
df_rcomb$height_log10 <- log10(df_rcomb$height)
df_rcomb
```

```
  id height weight height_log10
1  1    120     44     2.079181
2  2    150     56     2.176091
3  3    132     49     2.120574
4  4    122     45     2.086360
5  5    119     39     2.075547
6  6    110     35     2.041393
```

This situation also crops up when we want to convert an existing variable in a data frame from one data class to another data class. For example, the `id` variable in the `df_rcomb` data frame is numeric type data (use the `str()` or `class()` functions to check for yourself). If we wanted to convert the `id` variable to a factor to use later in our analysis we can create a new variable called `Fid` in our data frame and use the `factor()` function to convert the `id` variable.

```
# convert to a factor
df_rcomb$Fid <- factor(df_rcomb$id)
df_rcomb
```

```
  id height weight height_log10 Fid
1  1    120     44     2.079181   1
2  2    150     56     2.176091   2
3  3    132     49     2.120574   3
4  4    122     45     2.086360   4
5  5    119     39     2.075547   5
6  6    110     35     2.041393   6
```

```
str(df_rcomb)
```

```
'data.frame':   6 obs. of  5 variables:
 $ id          : int  1 2 3 4 5 6
```

```
 $ height      : num  120 150 132 122 119 110
 $ weight      : num  44 56 49 45 39 35
 $ height_log10: num  2.08 2.18 2.12 2.09 2.08 ...
 $ Fid         : Factor w/ 6 levels "1","2","3","4",..: 1 2 3 4 5 6
```

3.4.5. Merging data frames

Instead of just appending either rows or columns to a data frame we can also merge two data frames together. Let's say we have one data frame that contains taxonomic information on some common UK rocky shore invertebrates (called `taxa`) and another data frame that contains information on where they are usually found on the rocky shore (called `zone`). We can merge these two data frames together to produce a single data frame with both taxonomic and location information. Let's first create both of these data frames (in reality you would probably just import your different datasets).

```
taxa <- data.frame(GENUS = c("Patella", "Littorina", "Halichondria", "Semibalanus"),
         species = c("vulgata", "littoria", "panacea", "balanoides"),
         family = c("patellidae", "Littorinidae", "Halichondriidae", "Archaeobalanidae"))
taxa
```

```
         GENUS    species           family
1      Patella    vulgata       patellidae
2    Littorina   littoria     Littorinidae
3 Halichondria    panacea  Halichondriidae
4  Semibalanus balanoides Archaeobalanidae
```

```
zone <- data.frame(genus = c("Laminaria", "Halichondria", "Xanthoria", "Littorina",
                             "Semibalanus", "Fucus"),
                   species = c("digitata", "panacea", "parietina", "littoria",
                               "balanoides", "serratus"),
                   zone = c( "v_low", "low", "v_high", "low_mid", "high", "low_mid"))
zone
```

```
         genus    species    zone
1    Laminaria   digitata   v_low
```

```
2 Halichondria    panacea     low
3    Xanthoria  parietina  v_high
4    Littorina   littoria low_mid
5  Semibalanus balanoides    high
6        Fucus   serratus low_mid
```

Because both of our data frames contains at least one variable in common (`species` in our case) we can simply use the `merge()` function to create a new data frame called `taxa_zone`.

```
taxa_zone <- merge(x = taxa, y = zone)
taxa_zone
```

```
     species        GENUS           family        genus    zone
1 balanoides  Semibalanus Archaeobalanidae  Semibalanus    high
2   littoria    Littorina     Littorinidae    Littorina low_mid
3    panacea Halichondria  Halichondriidae Halichondria     low
```

Notice that the merged data frame contains only the rows that have `species` information in **both** data frames. There are also two columns called `GENUS` and `genus` because the `merge()` function treats these as two different variables that originate from the two data frames.

If we want to include all data from both data frames then we will need to use the `all = TRUE` argument. The missing values will be included as `NA`.

```
taxa_zone <- merge(x = taxa, y = zone, all = TRUE)
taxa_zone
```

```
     species        GENUS           family        genus    zone
1 balanoides  Semibalanus Archaeobalanidae  Semibalanus    high
2   digitata         <NA>             <NA>    Laminaria   v_low
3   littoria    Littorina     Littorinidae    Littorina low_mid
4    panacea Halichondria  Halichondriidae Halichondria     low
5  parietina         <NA>             <NA>    Xanthoria  v_high
6   serratus         <NA>             <NA>        Fucus low_mid
7    vulgata      Patella       patellidae         <NA>    <NA>
```

If the variable names that you want to base the merge on are different in each data frame (for example `GENUS` and `genus`) you can specify the names in the first data frame (known as `x`) and the second data frame (known as `y`) using the `by.x =` and `by.y =` arguments.

```
taxa_zone <- merge(x = taxa, y = zone, by.x = "GENUS", by.y = "genus", all = TRUE)
taxa_zone
```

```
         GENUS  species.x           family  species.y    zone
1        Fucus       <NA>             <NA>   serratus low_mid
2 Halichondria    panacea  Halichondriidae    panacea     low
3    Laminaria       <NA>             <NA>   digitata   v_low
4    Littorina   littoria     Littorinidae   littoria low_mid
5      Patella    vulgata       patellidae       <NA>    <NA>
6  Semibalanus balanoides Archaeobalanidae balanoides    high
7    Xanthoria       <NA>             <NA>  parietina  v_high
```

Or using multiple variable names.

```
taxa_zone <- merge(x = taxa, y = zone, by.x = c("species", "GENUS"),
                   by.y = c("species", "genus"), all = TRUE)
taxa_zone
```

```
     species        GENUS           family    zone
1 balanoides  Semibalanus Archaeobalanidae    high
2   digitata    Laminaria             <NA>   v_low
3   littoria    Littorina     Littorinidae low_mid
4    panacea Halichondria  Halichondriidae     low
5  parietina    Xanthoria             <NA>  v_high
6   serratus        Fucus             <NA> low_mid
7    vulgata      Patella       patellidae    <NA>
```

3.4.6. Reshaping data frames

Reshaping data into different formats is a common task. With rectangular type data (data frames have the same number of rows in each column) there are two main data frame shapes that you will come across: the 'long' format

(sometimes called stacked) and the 'wide' format. An example of a long format data frame is given below. We can see that each row is a single observation from an individual subject and each subject can have multiple rows. This results in a single column of our `measurement`.

```
long_data <- data.frame(
             subject = rep(c("A", "B", "C", "D"), each = 3),
             sex = rep(c("M", "F", "F", "M"), each =3),
             condition = rep(c("control", "cond1", "cond2"), times = 4),
             measurement = c(12.9, 14.2, 8.7, 5.2, 12.6, 10.1, 8.9,
                             12.1, 14.2, 10.5, 12.9, 11.9))
long_data
```

```
   subject sex condition measurement
1        A   M   control        12.9
2        A   M     cond1        14.2
3        A   M     cond2         8.7
4        B   F   control         5.2
5        B   F     cond1        12.6
6        B   F     cond2        10.1
7        C   F   control         8.9
8        C   F     cond1        12.1
9        C   F     cond2        14.2
10       D   M   control        10.5
11       D   M     cond1        12.9
12       D   M     cond2        11.9
```

We can also format the same data in the wide format as shown below. In this format we have multiple observations from each subject in a single row with measurements in different columns (`control`, `cond1` and `cond2`). This is a common format when you have repeated measurements from sampling units.

```
wide_data <- data.frame(subject = c("A", "B", "C", "D"),
               sex = c("M", "F", "F", "M"),
               control = c(12.9, 5.2, 8.9, 10.5),
```

```
                cond1 = c(14.2, 12.6, 12.1, 12.9),
                cond2 = c(8.7, 10.1, 14.2, 11.9))
wide_data
```

```
  subject sex control cond1 cond2
1       A   M    12.9  14.2   8.7
2       B   F     5.2  12.6  10.1
3       C   F     8.9  12.1  14.2
4       D   M    10.5  12.9  11.9
```

Whilst there's no inherent problem with either of these formats we will sometimes need to convert between the two because some functions will require a specific format for them to work. The most common format is the long format.

There are many ways to convert between these two formats but we'll use the `melt()` and `dcast()` functions from the `reshape2` package (you will need to install this package first). The `melt()` function is used to convert from wide to long formats. The first argument for the `melt()` function is the data frame we want to melt (in our case `wide_data`). The `id.vars = c("subject", "sex")` argument is a vector of the variables you want to stack, the `measured.vars = c("control", "cond1", "cond2")` argument identifies the columns of the measurements in different conditions, the `variable.name = "condition"` argument specifies what you want to call the stacked column of your different conditions in your output data frame and `value.name = "measurement"` is the name of the column of your stacked measurements in your output data frame.

```
library(reshape2)
wide_data    # remind ourselves what the wide format looks like
```

```
  subject sex control cond1 cond2
1       A   M    12.9  14.2   8.7
2       B   F     5.2  12.6  10.1
3       C   F     8.9  12.1  14.2
4       D   M    10.5  12.9  11.9
```

```
# convert wide to long
my_long_df <- melt(data = wide_data, id.vars = c("subject", "sex"),
                   measured.vars = c("control", "cond1", "cond2"),
                   variable.name = "condition", value.name = "measurement")
my_long_df
```

```
   subject sex condition measurement
1        A   M   control        12.9
2        B   F   control         5.2
3        C   F   control         8.9
4        D   M   control        10.5
5        A   M     cond1        14.2
6        B   F     cond1        12.6
7        C   F     cond1        12.1
8        D   M     cond1        12.9
9        A   M     cond2         8.7
10       B   F     cond2        10.1
11       C   F     cond2        14.2
12       D   M     cond2        11.9
```

The `dcast()` function is used to convert from a long format data frame to a wide format data frame. The first argument is again is the data frame we want to cast (`long_data` for this example). The second argument is in formula syntax. The `subject + sex` bit of the formula means that we want to keep these columns separate, and the `~ condition` part is the column that contains the labels that we want to split into new columns in our new data frame. The `value.var = "measurement"` argument is the column that contains the measured data.

```
long_data   # remind ourselves what the long format look like
```

```
   subject sex condition measurement
1        A   M   control        12.9
2        A   M     cond1        14.2
3        A   M     cond2         8.7
4        B   F   control         5.2
5        B   F     cond1        12.6
```

```
6        B   F     cond2        10.1
7        C   F   control         8.9
8        C   F     cond1        12.1
9        C   F     cond2        14.2
10       D   M   control        10.5
11       D   M     cond1        12.9
12       D   M     cond2        11.9
```

```
# convert long to wide
my_wide_df <- dcast(data = long_data, subject + sex ~ condition,
                    value.var = "measurement")
my_wide_df
```

```
  subject sex cond1 cond2 control
1       A   M  14.2   8.7    12.9
2       B   F  12.6  10.1     5.2
3       C   F  12.1  14.2     8.9
4       D   M  12.9  11.9    10.5
```

3.5. Introduction to the `tidyverse`

it seems it is not super tidy in here and we need to improve that

3.6. Summarising data frames

Now that we're able to manipulate and extract data from our data frames our next task is to start exploring and getting to know our data. In this section we'll start producing tables of useful summary statistics of the variables in our data frame and in the next two Chapters we'll cover visualising our data with base R graphics and using the `ggplot2` package.

A really useful starting point is to produce some simple summary statistics of all of the variables in our `flowers` data frame using the `summary()` function.

```
summary(flowers)
```

```
   treat             nitrogen      block         height           weight
 Length:96          low   :32   Min.   :1.0   Min.   : 1.200   Min.   : 5.790
 Class :character   medium:32   1st Qu.:1.0   1st Qu.: 4.475   1st Qu.: 9.027
 Mode  :character   high  :32   Median :1.5   Median : 6.450   Median :11.395
                                Mean   :1.5   Mean   : 6.840   Mean   :12.155
                                3rd Qu.:2.0   3rd Qu.: 9.025   3rd Qu.:14.537
                                Max.   :2.0   Max.   :17.200   Max.   :23.890
   leafarea       shootarea         flowers
 Min.   : 5.80   Min.   :  5.80   Min.   : 1.000
 1st Qu.:11.07   1st Qu.: 39.05   1st Qu.: 4.000
 Median :13.45   Median : 70.05   Median : 6.000
 Mean   :14.05   Mean   : 79.78   Mean   : 7.062
 3rd Qu.:16.45   3rd Qu.:113.28   3rd Qu.: 9.000
 Max.   :49.20   Max.   :189.60   Max.   :17.000
```

For numeric variables (i.e. `height`, `weight` etc) the mean, minimum, maximum, median, first (lower) quartile and third (upper) quartile are presented. For factor variables (i.e. `treat` and `nitrogen`) the number of observations in each of the factor levels is given. If a variable contains missing data then the number of `NA` values is also reported.

If we wanted to summarise a smaller subset of variables in our data frame we can use our indexing skills in combination with the `summary()` function. For example, to summarise only the `height`, `weight`, `leafarea` and `shootarea` variables we can include the appropriate column indexes when using the `[ ]`. Notice we include all rows by not specifying a row index.

```
summary(flowers[, 4:7])
```

```
     height           weight          leafarea       shootarea
 Min.   : 1.200   Min.   : 5.790   Min.   : 5.80   Min.   :  5.80
 1st Qu.: 4.475   1st Qu.: 9.027   1st Qu.:11.07   1st Qu.: 39.05
 Median : 6.450   Median :11.395   Median :13.45   Median : 70.05
 Mean   : 6.840   Mean   :12.155   Mean   :14.05   Mean   : 79.78
 3rd Qu.: 9.025   3rd Qu.:14.537   3rd Qu.:16.45   3rd Qu.:113.28
 Max.   :17.200   Max.   :23.890   Max.   :49.20   Max.   :189.60
```

```
# or equivalently
# summary(flowers[, c("height", "weight", "leafarea", "shootarea")])
```

And to summarise a single variable.

```
summary(flowers$leafarea)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   5.80   11.07   13.45   14.05   16.45   49.20
```

```
# or equivalently
# summary(flowers[, 6])
```

As you've seen above, the `summary()` function reports the number of observations in each level of our factor variables. Another useful function for generating tables of counts is the `table()` function. The `table()` function can be used to build contingency tables of different combinations of factor levels. For example, to count the number of observations for each level of `nitrogen`

```
table(flowers$nitrogen)
```

```
   low medium   high
    32     32     32
```

We can extend this further by producing a table of counts for each combination of `nitrogen` and `treat` factor levels.

```
table(flowers$nitrogen, flowers$treat)
```

```
        notip tip
  low       16  16
  medium    16  16
  high      16  16
```

A more flexible version of the `table()` function is the `xtabs()` function. The `xtabs()` function uses a formula notation (`~`) to build contingency tables with the cross-classifying variables separated by a `+` symbol on the right hand side of the formula. `xtabs()` also has a useful `data =` argument so you don't have to include the data frame name when specifying each variable.

```
xtabs(~ nitrogen + treat, data = flowers)
```

```
        treat
nitrogen notip tip
  low       16  16
  medium    16  16
  high      16  16
```

We can even build more complicated contingency tables using more variables. Note, in the example below the `xtabs()` function has quietly coerced our `block` variable to a factor.

```
xtabs(~ nitrogen + treat + block, data = flowers)
```

```
, , block = 1

        treat
nitrogen notip tip
  low        8   8
  medium     8   8
  high       8   8

, , block = 2

        treat
nitrogen notip tip
  low        8   8
  medium     8   8
  high       8   8
```

And for a nicer formatted table we can nest the `xtabs()` function inside the `ftable()` function to 'flatten' the table.

```
ftable(xtabs(~ nitrogen + treat + block, data = flowers))
```

```
               block 1 2
nitrogen treat
low      notip       8 8
         tip         8 8
medium   notip       8 8
         tip         8 8
high     notip       8 8
         tip         8 8
```

We can also summarise our data for each level of a factor variable. Let's say we want to calculate the mean value of `height` for each of our `low`, `meadium` and `high` levels of `nitrogen`. To do this we will use the `mean()` function and apply this to the `height` variable for each level of `nitrogen` using the `tapply()` function.

```
tapply(flowers$height, flowers$nitrogen, mean)
```

```
     low   medium     high
5.853125 7.012500 7.653125
```

The `tapply()` function is not just restricted to calculating mean values, you can use it to apply many of the functions that come with R or even functions you've written yourself (see Chapter 7 for more details). For example, we can apply the `sd()` function to calculate the standard deviation for each level of `nitrogen` or even the `summary()` function.

```
tapply(flowers$height, flowers$nitrogen, sd)
```

```
     low   medium     high
2.828425 3.005345 3.483323
```

```
tapply(flowers$height, flowers$nitrogen, summary)
```

```
$low
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  1.800   3.600   5.550   5.853   8.000  12.300

$medium
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  1.800   4.500   7.000   7.013   9.950  12.300

$high
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  1.200   5.800   7.450   7.653   9.475  17.200
```

Note, if the variable you want to summarise contains missing values (`NA`) you will also need to include an argument specifying how you want the function to deal with the `NA` values. We saw an example if this in Chapter 2 where the `mean()` function returned an `NA` when we had missing data. To include the `na.rm = TRUE` argument we simply add this as another argument when using `tapply()`.

```
tapply(flowers$height, flowers$nitrogen, mean, na.rm = TRUE)
```

```
     low   medium     high
5.853125 7.012500 7.653125
```

We can also use `tapply()` to apply functions to more than one factor. The only thing to remember is that the factors need to be supplied to the `tapply()` function in the form of a list using the `list()` function. To calculate the mean `height` for each combination of `nitrogen` and `treat` factor levels we can use the `list(flowers$nitrogen, flowers$treat)` notation.

```
tapply(flowers$height, list(flowers$nitrogen, flowers$treat), mean)
```

```
         notip    tip
low    3.66875 8.0375
medium 4.83750 9.1875
high   5.70625 9.6000
```

And if you get a little fed up with having to write `flowers$` for every variable you can nest the `tapply()` function inside the `with()` function. The `with()` function allows R to evaluate an R expression with respect to a named data object (in this case `flowers`).

```
with(flowers, tapply(height, list(nitrogen, treat), mean))
```

```
         notip    tip
low    3.66875 8.0375
medium 4.83750 9.1875
high   5.70625 9.6000
```

The `with()` function also works with many other functions and can save you alot of typing!

Another really useful function for summarising data is the `aggregate()` function. The `aggregate()` function works in a very similar way to `tapply()` but is a bit more flexible.

For example, to calculate the mean of the variables `height`, `weight`, `leafarea` and `shootarea` for each level of `nitrogen`.

```
aggregate(flowers[, 4:7], by = list(nitrogen = flowers$nitrogen), FUN = mean)
```

```
  nitrogen   height    weight leafarea shootarea
1      low 5.853125  8.652812 11.14375   45.1000
2   medium 7.012500 11.164062 13.83125   67.5625
3     high 7.653125 16.646875 17.18125  126.6875
```

In the code above we have indexed the columns we want to summarise in the `flowers` data frame using `flowers[, 4:7]`. The `by =` argument specifies a list of factors (`list(nitrogen = flowers$nitrogen)`) and the `FUN =` argument names the function to apply (`mean` in this example).

Similar to the `tapply()` function we can include more than one factor to apply a function to. Here we calculate the mean values for each combination of `nitrogen` and `treat`

```
aggregate(flowers[, 4:7], by = list(nitrogen = flowers$nitrogen,
                                    treat = flowers$treat), FUN = mean)
```

```
  nitrogen treat  height    weight leafarea shootarea
1      low notip 3.66875  8.289375 12.32500  59.89375
2   medium notip 4.83750 11.316875 14.17500  94.53125
3     high notip 5.70625 16.604375 18.81875 155.31875
4      low   tip 8.03750  9.016250  9.96250  30.30625
5   medium   tip 9.18750 11.011250 13.48750  40.59375
6     high   tip 9.60000 16.689375 15.54375  98.05625
```

We can also use the `aggregate()` function in a different way by using the formula method (as we did with `xtabs()`). On the left hand side of the formula (`~`) we specify the variable we want to apply the mean function on and to the right hand side our factors separated by a `+` symbol. The formula method also allows you to use the `data =` argument for convenience.

```
aggregate(height ~ nitrogen + treat, FUN = mean, data = flowers)
```

```
  nitrogen treat  height
1      low notip 3.66875
2   medium notip 4.83750
3     high notip 5.70625
4      low   tip 8.03750
5   medium   tip 9.18750
6     high   tip 9.60000
```

One advantage of using the formula method is that we can also use the `subset =` argument to apply the function to subsets of the original data. For example, to calculate the mean `height` for each combination of the `nitrogen` and `treat` levels but only for those plants that have less than 7 `flowers`.

```
aggregate(height ~ nitrogen + treat, FUN = mean, subset = flowers < 7, data = flowers)
```

```
  nitrogen treat   height
1      low notip 3.533333
2   medium notip 5.316667
3     high notip 3.850000
4      low   tip 8.176923
```

```
5   medium   tip 8.570000
6     high   tip 7.900000
```

Or for only those plants in `block` 1.

```
aggregate(height ~ nitrogen + treat, FUN = mean, subset = block == "1", data = flowers)
```

```
  nitrogen treat  height
1      low notip  3.3250
2   medium notip  5.2375
3     high notip  5.9250
4      low   tip  8.7500
5   medium   tip  9.5375
6     high   tip 10.0375
```

3.7. Exporting data

By now we hope you're getting a feel for how powerful and useful R is for manipulating and summarising data (and we've only really scratched the surface). One of the great benefits of doing all your data wrangling in R is that you have a permanent record of all the things you've done to your data. Gone are the days of making undocumented changes in Excel or Calc! By treating your data as 'read only' and documenting all of your decisions in R you will have made great strides towards making your analysis more reproducible and transparent to others. It's important to realise, however, that any changes you've made to your data frame in R will not change the original data file you imported into R (and that's a good thing). Happily it's straightforward to export data frames to external files in a wide variety of formats.

3.7.1. Export functions

The main workhorse function for exporting data frames is the `write.table()` function. As with the `read.table()` function, the `write.table()` function is very flexible with lots of arguments to help customise it's behaviour. As an example, let's take our original `flowers` data frame, do some useful stuff to it and then export these changes to an external file.

Let's order the rows in the data frame in ascending order of `height` within each level `nitrogen`. We will also apply a square root transformation on the number of flowers variable (`flowers`) and a $\log_{10}$ transformation on the `height` variable and save these as additional columns in our data frame (hopefully this will be somewhat familiar to you!).

```
flowers_df2 <- flowers[order(flowers$nitrogen, flowers$height), ]
flowers_df2$flowers_sqrt <- sqrt(flowers_df2$flowers)
flowers_df2$log10_height <- log10(flowers_df2$height)
str(flowers_df2)
```

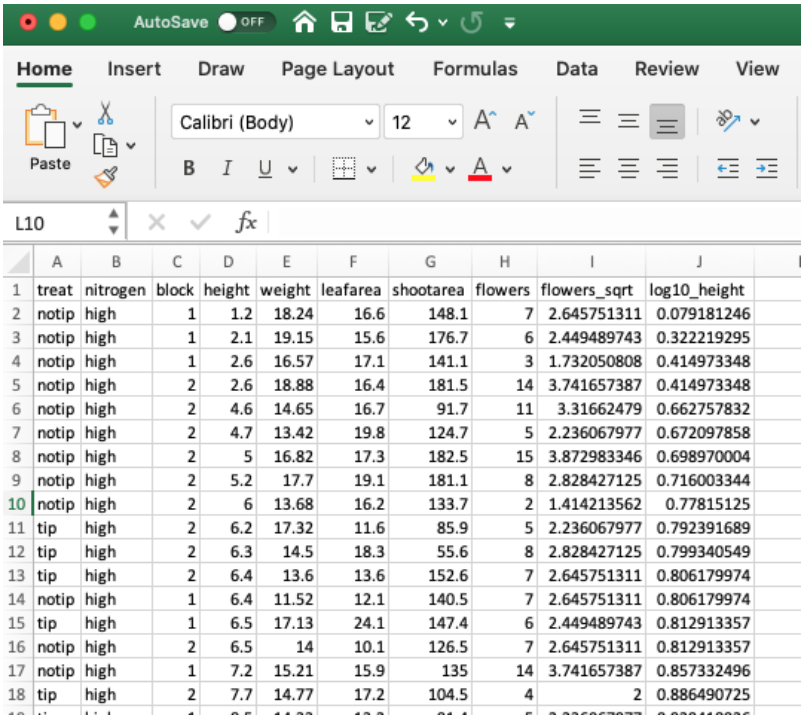
```
'data.frame':   96 obs. of  10 variables:
 $ treat       : chr  "notip" "notip" "notip" "notip" ...
 $ nitrogen    : Factor w/ 3 levels "low","medium",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ block       : int  1 1 1 2 1 2 2 2 1 2 ...
 $ height      : num  1.8 2.2 2.3 2.4 3 3.1 3.2 3.3 3.7 3.7 ...
 $ weight      : num  6.01 9.97 7.28 9.1 9.93 8.74 7.45 8.92 7.03 8.1 ...
 $ leafarea    : num  17.6 9.6 13.8 14.5 12 16.1 14.1 11.6 7.9 10.5 ...
 $ shootarea   : num  46.2 63.1 32.8 78.7 56.6 39.1 38.1 55.2 36.7 60.5 ...
 $ flowers     : int  4 2 6 8 6 3 4 6 5 6 ...
 $ flowers_sqrt: num  2 1.41 2.45 2.83 2.45 ...
 $ log10_height: num  0.255 0.342 0.362 0.38 0.477 ...
```

Now we can export our new data frame `flowers_df2` using the `write.table()` function. The first argument is the data frame you want to export (`flowers_df2` in our example). We then give the filename (with file extension) and the file path in either single or double quotes using the `file =` argument. In this example we're exporting the data frame to a file called `flowers_04_12.txt` in the `data` directory. The `col.names = TRUE` argument indicates that the variable names should be written in the first row of the file and the `row.names = FALSE` argument stops R from including the row names in the first column of the file. Finally, the `sep = "\t"` argument indicates that a Tab should be used as the delimiter in the exported file.

```
write.table(flowers_df2, file = 'data/flowers_04_12.txt', col.names = TRUE,
            row.names = FALSE, sep = "\t")
```

As we saved the file as a tab delimited text file we could open this file in any text editor. Perhaps a more familiar option would be to open the file in Excel. First start Excel and then select `File` -> `Open ..` in the main menu and

then select our `flowers_04_12.txt` file to open. Next. choose the 'Tab' option to set the delimiter and then click on the 'Finish' button.



	A	B	C	D	E	F	G	H	I	J
1	treat	nitrogen	block	height	weight	leafarea	shootarea	flowers	flowers_sqrt	log10_height
2	notip	high	1	1.2	18.24	16.6	148.1	7	2.645751311	0.079181246
3	notip	high	1	2.1	19.15	15.6	176.7	6	2.449489743	0.322219295
4	notip	high	1	2.6	16.57	17.1	141.1	3	1.732050808	0.414973348
5	notip	high	2	2.6	18.88	16.4	181.5	14	3.741657387	0.414973348
6	notip	high	2	4.6	14.65	16.7	91.7	11	3.31662479	0.662757832
7	notip	high	2	4.7	13.42	19.8	124.7	5	2.236067977	0.672097858
8	notip	high	2	5	16.82	17.3	182.5	15	3.872983346	0.698970004
9	notip	high	2	5.2	17.7	19.1	181.1	8	2.828427125	0.716003344
10	notip	high	2	6	13.68	16.2	133.7	2	1.414213562	0.77815125
11	tip	high	2	6.2	17.32	11.6	85.9	5	2.236067977	0.792391689
12	tip	high	2	6.3	14.5	18.3	55.6	8	2.828427125	0.799340549
13	tip	high	2	6.4	13.6	13.6	152.6	7	2.645751311	0.806179974
14	notip	high	1	6.4	11.52	12.1	140.5	7	2.645751311	0.806179974
15	tip	high	1	6.5	17.13	24.1	147.4	6	2.449489743	0.812913357
16	notip	high	2	6.5	14	10.1	126.5	7	2.645751311	0.812913357
17	notip	high	1	7.2	15.21	15.9	135	14	3.741657387	0.857332496
18	tip	high	2	7.7	14.77	17.2	104.5	4	2	0.886490725

We can of course export our files in a variety of other formats. Another popular option is to export files in csv (comma separated values) format. We can do this using the `write.table()` function by setting the separator argument to `sep = ","`.

```
write.table(flowers_df2, file = 'data/flowers_04_12.csv', col.names = TRUE,
            row.names = FALSE, sep = ",")
```

Or alternatively by using the convenience function `write.csv()`. Notice that we don't need to set the `sep = ","` or `col.names = TRUE` arguments as these are the defaults when using the `read.csv()` function.

```
write.csv(flowers_df2, file = 'data/flowers_04_12.csv', row.names = FALSE)
```

3.7.2. Other export functions

As with importing data files into R, there are also many alternative functions for exporting data to external files beyond the `write.table()` function. If you followed the 'Other import functions' section of this Chapter you will already have the required packages installed.

The `fwrite()` function from the `read.table` package is very efficient at exporting large data objects and is much faster than the `write.table()` function. It's also quite simple to use as it has most of the same arguments as `write.table()`. To export a tab delimited text file we just need to specify the data frame name, the output file name and file path and the separator between columns.

```
library(read.table)
fwrite(flowers_df2, file = 'data/flowers_04_12.txt', sep = "\t")
```

To export a csv delimited file it's even easier as we don't even need to include the `sep =` argument.

```
library(read.table)
fwrite(flowers_df2, file = 'data/flowers_04_12.csv')
```

The `readr` package also comes with two useful functions for quickly writing data to external files: the `write_tsv()` function for writing tab delimited files and the `write_csv()` function for saving comma separated values (csv) files.

```
library(readr)
write_tsv(flowers_df2, path = 'data/flowers_04_12.txt')


write_csv(flowers_df2, path = 'data/flowers_04_12.csv')
```

Chapter 4

Graphics with R

Summarising your data, either numerically or graphically, is an important (if often overlooked) component of any data analysis. Fortunately, R has excellent graphics capabilities and can be used whether you want to produce plots for initial data exploration, model validation or highly complex publication quality figures. There are three main systems for producing graphics in R; base R graphics, lattice graphics and ggplot2.

The base R graphics system is the original plotting system that's been around (and has evolved) since the first days of R. When creating plots with base R we tend to use high level functions (like the `plot()` function) to first create our plot and then use one or more low level functions (like `lines()` and `text()` etc) to add additional information to these plots. This can seem a little weird (and time consuming) when you first start creating fancy plots in R, but it does allow you to customise almost every aspect of your plot and build complexity up in layers. The flip side to this flexibility is that you'll often need to make many decisions about how you want your plot to look rather than rely on the software to make these decisions for you. Having said that, it's generally very quick and easy to generate simple exploratory plots with base R graphics.

The lattice system is implemented in the `lattice()` package that comes pre-installed with the standard installation of R. However, it won't be loaded by default so you'll first need to use `library(lattice)` to access all the plotting functions. Unlike base R graphics, lattice plots are mostly generated all in one go using a single function so there's no need to use high and low level plotting functions to customise the look of a plot. This can be a real advantage as things like margin sizes and plot spacing are adjusted automatically. Lattice plots also make a few more decisions for you about how the plots will look but this comes with a slight cost as customising lattice plots to get them to look exactly how you want can become quite involved. Where lattice plots really shine is plotting complex multi-dimensional data using panel plots (also called trellis plots). We'll see a couple of examples of these types of plots later in the Chapter.

ggplot2 was based on a book called *Grammar of Graphics* by Wilkinson (2005). For an interesting summary of Wilkinson's book here. The *Grammar of Graphics* approach breaks figures down into their various components (e.g. the underlying statistics, the geometric arrangement, the theme, see Figure 4.2). Users are thus able to manipulate each of these components (i.e. layers) and produce a tailor-made figure fit for their specific needs.

Each of these systems have their strengths and weaknesses and we often use them interchangeably. In this Chapter we'll introduce you to the both base R plotting function and theggplot2 package. It's important to note that ggplot2 is not **required** to make "fancy" and informative figures in R. If you prefer using base R graphics then feel free to continue as almost all ggplot2 type figures can be created using base R (we often use either approach depending on what we're doing). The difference betweenggplot2 and base R is how you *get* to the end product rather than any substantial differences in the end product itself. This is, never-the-less, a common belief probably due to the fact that making a moderately attractive figure is (in our opinion at least), easier to do with ggplot2 as many aesthetic decisions are made for the user, without you necessarily even knowing that a decision was ever made!

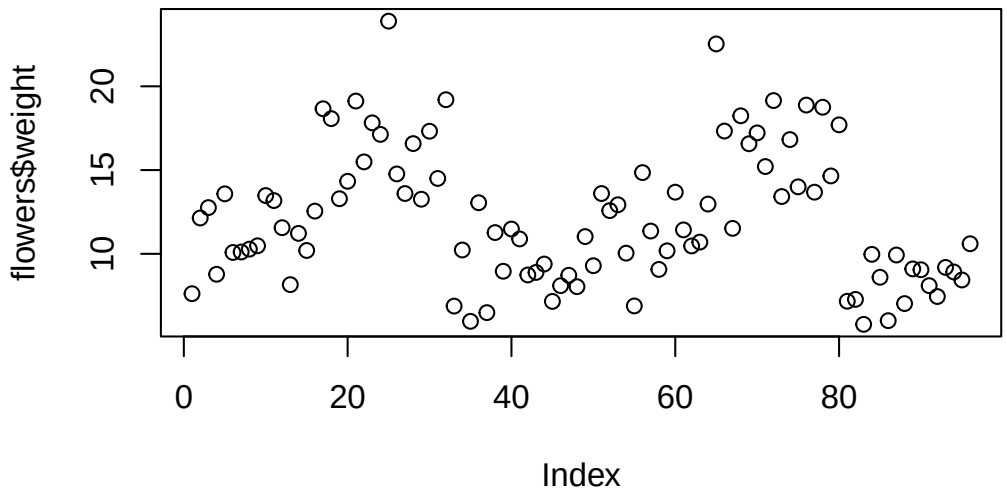
With that in mind, let's get started making some figures.

4.1. Simple base R plots

There are many functions in R to produce plots ranging from the very basic to the highly complex. It's impossible to cover every aspect of producing graphics in R in this book so we'll introduce you to most of the common methods of graphing data and describe how to customise your graphs later on in this Chapter.

The most common high level function used to produce plots in R is (rather unsurprisingly) the `plot()` function. For example, let's plot the `weight` of petunia plants from our `flowers` data frame which we imported in Chapter 3.

```
flowers <- read.csv(file = "data/flower.csv")


plot(flowers$weight)
```



R has plotted the values of `weight` (on the y axis) against an index since we are only plotting one variable to plot. The index is just the order of the `weight` values in the data frame (1 first in the data frame and 97 last). The `weight` variable name has been automatically included as a y axis label and the axes scales have been automatically set.

If we'd only included the variable `weight` rather than `flowers$weight`, the `plot()` function will display an error as the variable `weight` only exists in the `flowers` data frame object.

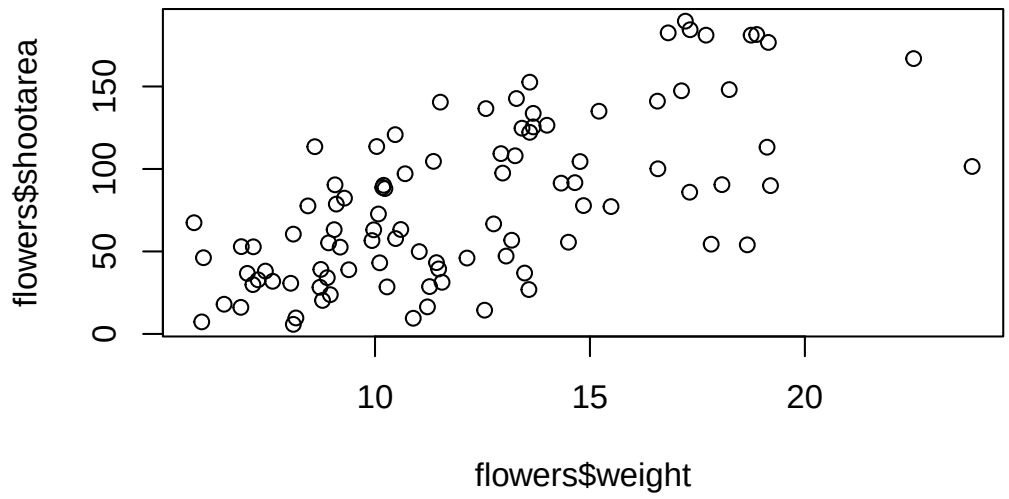
```
plot(weight)
## Error in plot(weight) : object 'weight' not found
```

As many of the base R plotting functions don't have a `data =` argument to specify the data frame name directly we can use the `with()` function in combination with `plot()` as a shortcut.

```
with(flowers, plot(weight))
```

To plot a scatterplot of one numeric variable against another numeric variable we just need to include both variables as arguments when using the `plot()` function. For example to plot `shootarea` on the y axis and `weight` of the x axis.

```
plot(x = flowers$weight, y = flowers$shootarea)
```



There is an equivalent approach for these types of plots which often causes some confusion at first. You can also use the formula notation when using the `plot()` function. However, in contrast to the previous method the formula method requires you to specify the y axis variable first, then a ~ and then our x axis variable.

```
plot(shootarea ~ weight, data = flowers)
```

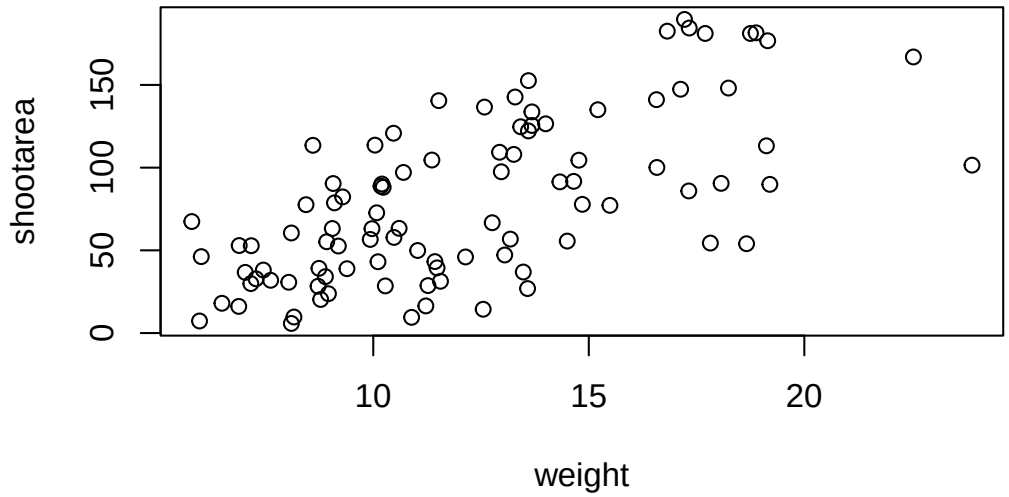


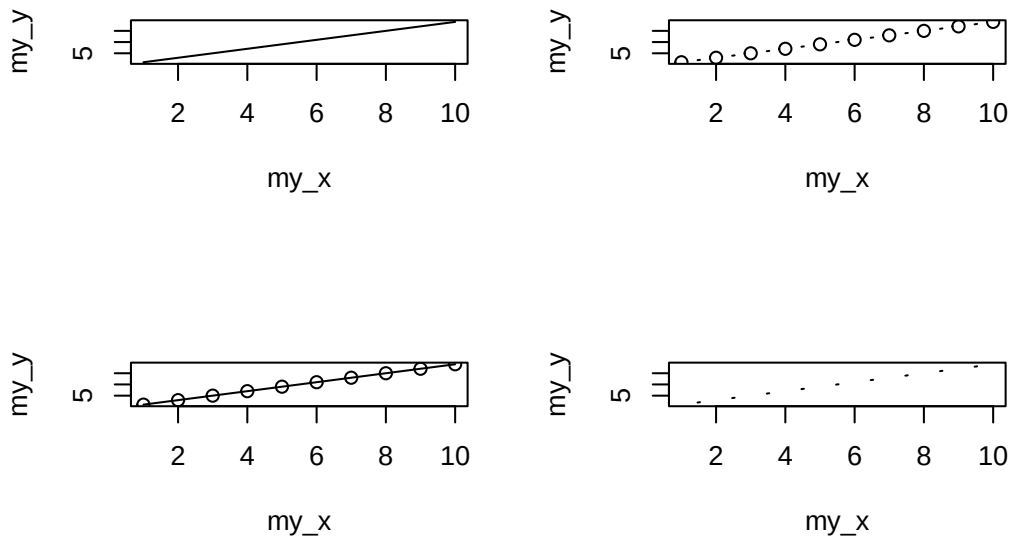
Figure 4.1.

Both of these two approaches are equivalent so we suggest that you just choose the one you prefer and go with it.

You can also specify the type of graph you wish to plot using the argument `type =`. You can plot just the points (`type = "p"`, this is the default), just lines (`type = "l"`), both points and lines connected (`type = "b"`), both points and lines with the lines running through the points (`type = "o"`) and empty points joined by lines (`type = "c"`). For example, let's use our skills from Chapter 2 to generate two vectors of numbers (`my_x` and `my_y`) and then plot one against the other using different `type =` values to see what type of plots are produced. Don't worry about

the `par(mfrow = c(2, 2))` line of code yet. We're just using this to split the plotting device so we can fit all four plots on the same device to save some space. See later in the Chapter for more details about this. The top left plot is `type = "l"`, the top right `type = "b"`, bottom left `type = "o"` and bottom right is `type = "c"`.

```
my_x <- 1:10
my_y <- seq(from = 1, to = 20, by = 2)

par(mfrow = c(2, 2))
plot(my_x, my_y, type = "l")
plot(my_x, my_y, type = "b")
plot(my_x, my_y, type = "o")
plot(my_x, my_y, type = "c")
```



Admittedly the plots we've produced so far don't look anything particularly special. However, the `plot()` function is incredibly versatile and can generate a large range of plots which you can customise to your own taste. We'll cover how to customise plots later in the Chapter. As a quick aside, the `plot()` function is also what's known as a generic function which means it can change its default behaviour depending on the type of object used as an argument. You will see an example of this in Chapter 5 where we use the `plot()` function to generate diagnostic plots of residuals from a linear model object (bet you can't wait!).

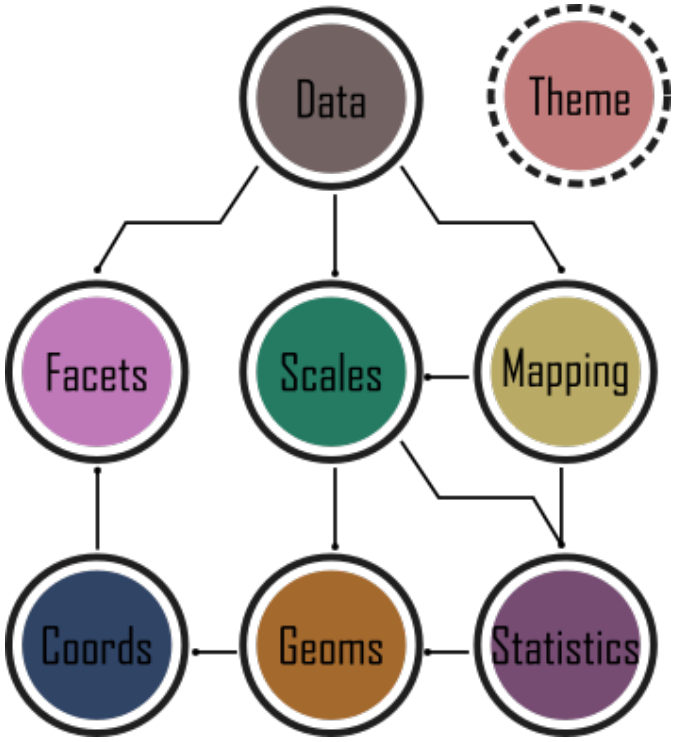


Figure 4.2.: Structure of graphics with ggplot2

4.2. ggplot2

As mentionned earlier `ggplot` grammar requires several elements to produce a graphic and a minimum of 3 are required:

- a data frame
- a mapping system defining x and y
- a geometry layer

The data and mapping are provided within the called to the `ggplot()` function with the `data` and `mapping` arguments. The geometry layer is added using specific functions.

To redo the Figure 4.1, that contain only a scatterplot of point we can use the `geom_point()` function.

```
ggplot(
  data = flowers,
  mapping = aes(x = weight, y = shootarea)
) +
  geom_point()
```

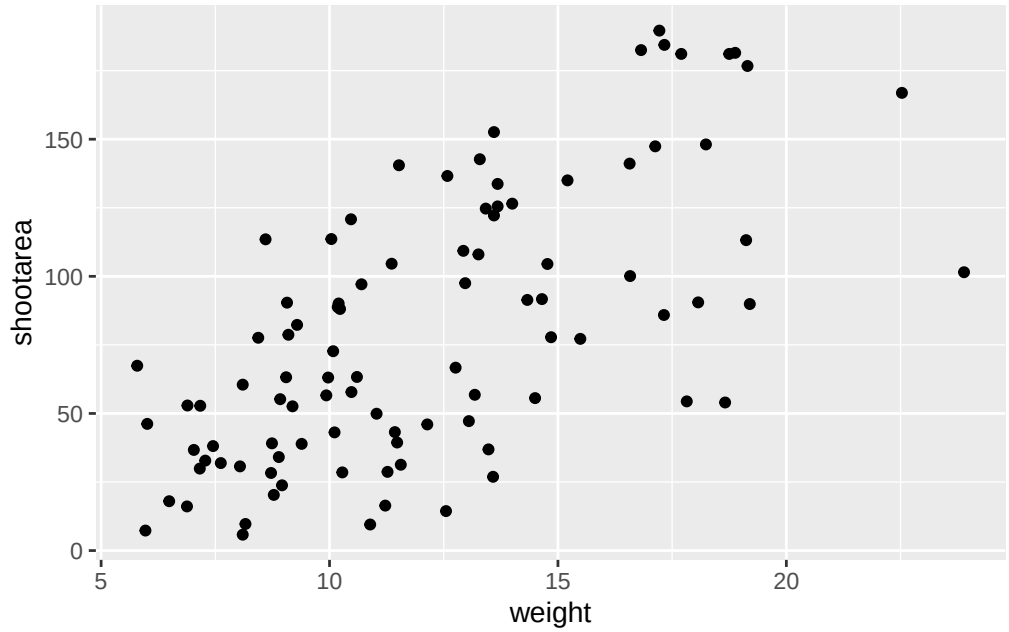


Figure 4.3.

Now that we have basic understanding of `ggplot`we can explore some graphics using both base R and ggplot code

4.3. Simple plots

4.3.1. Scatterplots

Simple type of plots really useful to have a look at the relation between 2 variables for example. Here are the code to do it using base R (Figure 4.1)

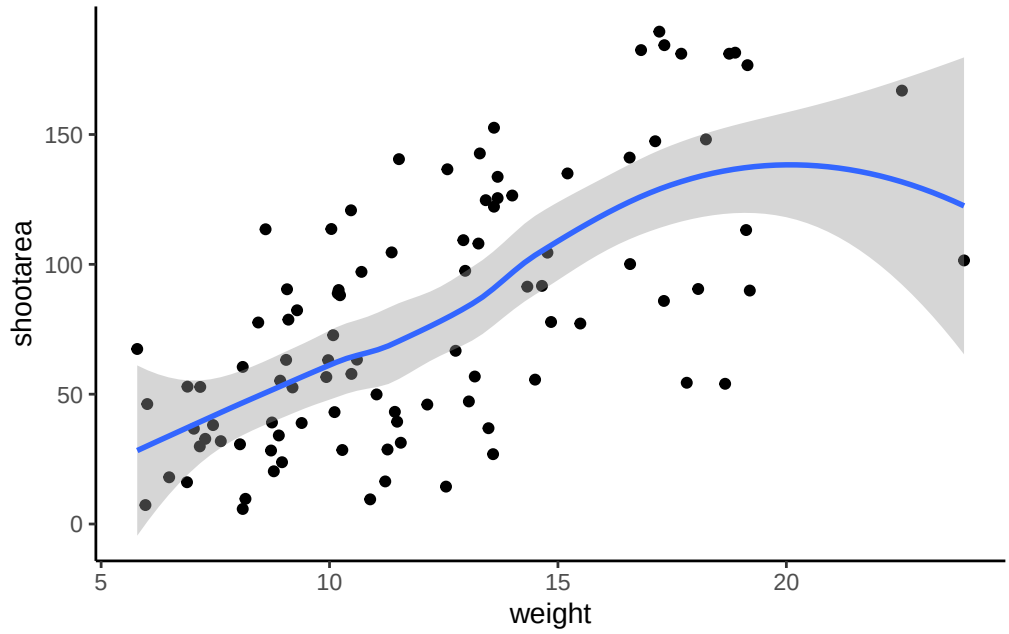
```
plot(shootarea ~ weight, data = flowers)
```

or ggplot (Figure 4.3)

```
ggplot(
  data = flowers,
  mapping = aes(x = weight, y = shootarea)
) +
  geom_point()
```

One gig advantage of `ggplot` for simple scatterplot is the ease with which we can add a regression, smoother (loes or gam) line to the plot using `stat_smooth()`function to add a statistic layer to the plot.

```
ggplot(
  data = flowers,
  mapping = aes(x = weight, y = shootarea)
) +
  geom_point() +
  stat_smooth()
```

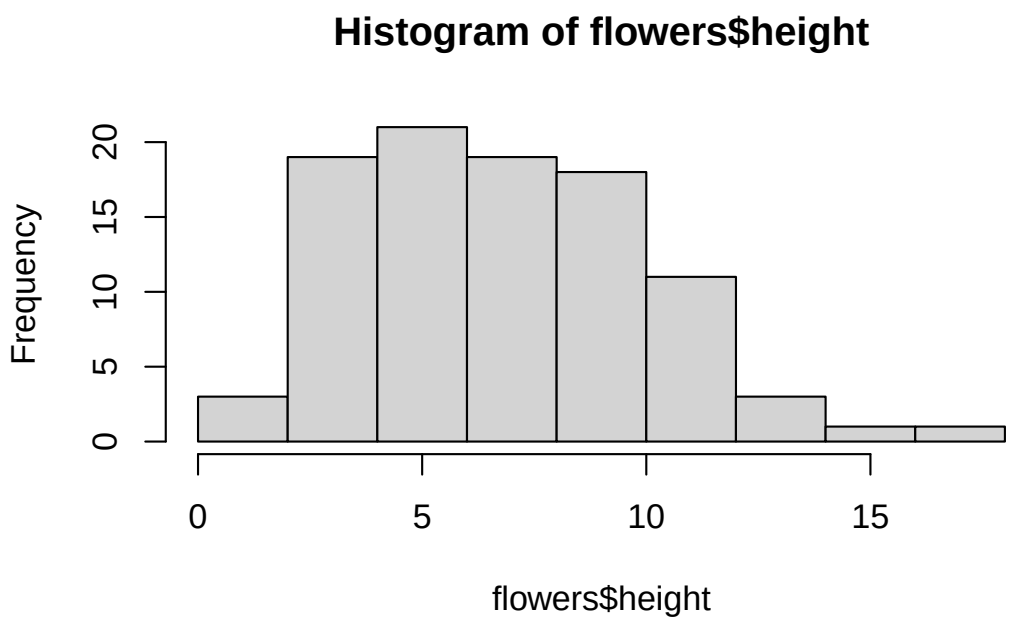


4.3.2. Histograms

Frequency histograms are useful when you want to get an idea about the distribution of values in a numeric variable. Using base R, the `hist()` function takes a numeric vector as its main argument. In ggplot, we need to use `geom_histogram()`. Let's generate a histogram of the `height` values.

With base R

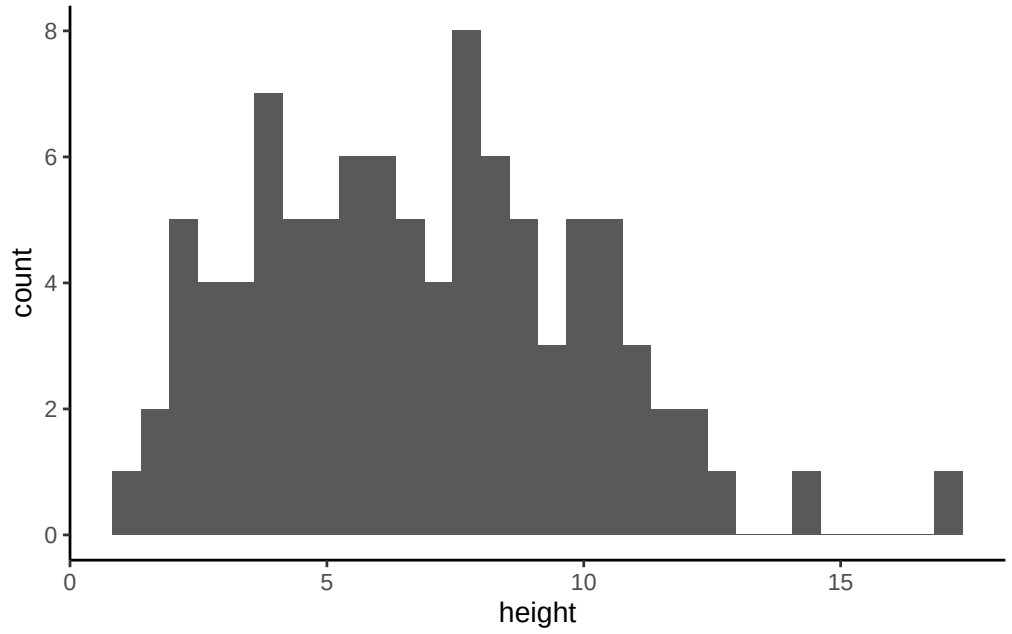
```
hist(flowers$height)
```



with ggplot2

```
ggplot(flowers, aes(x = height)) +
  geom_histogram()
```

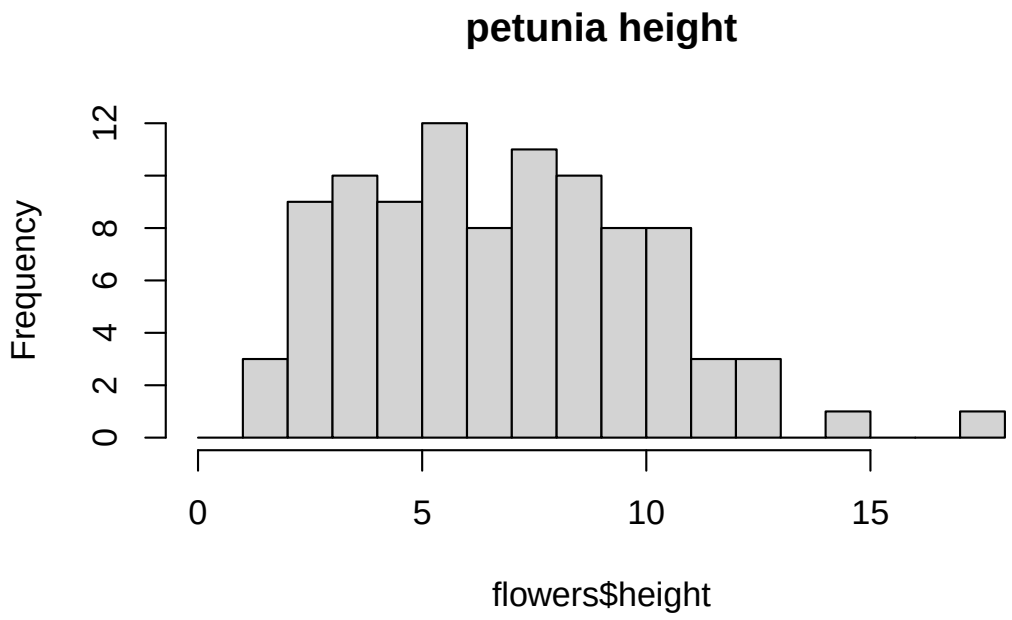
```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



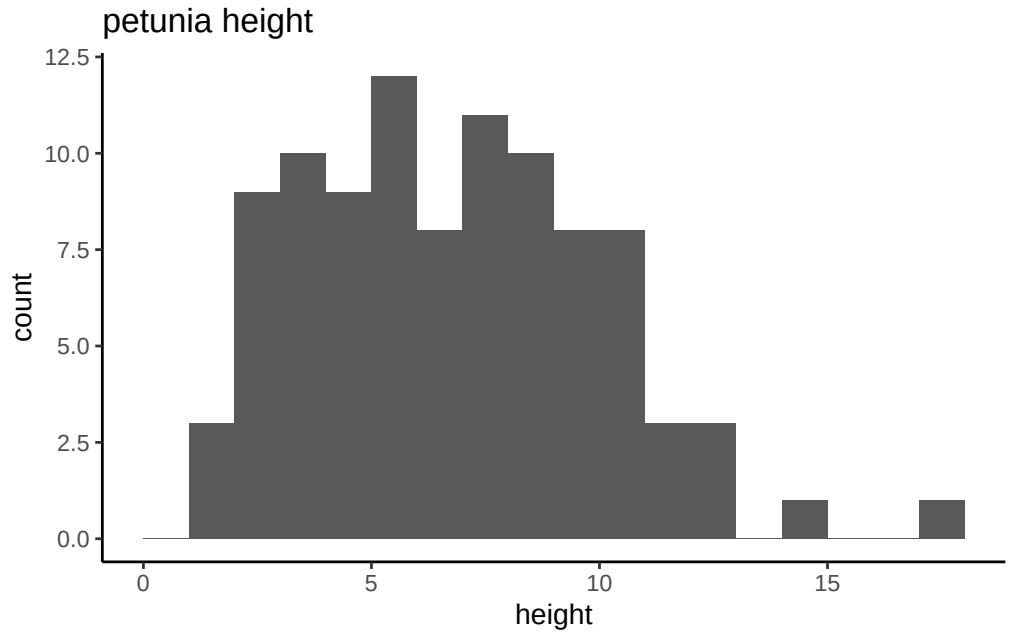
The `hist()` and `geom_histogram()` function automatically creates the breakpoints (or bins) in the histogram unless you specify otherwise by using the `breaks =` argument. For example, let's say we want to plot our histogram

with breakpoints every 1 cm flower height. We first generate a sequence from zero to the maximum value of `height` (18 rounded up) in steps of 1 using the `seq()` function. We can then use this sequence with the `breaks =` argument. While we're at it, let's also replace the ugly title for something a little better using the `main =` argument

```
brk <- seq(from = 0, to = 18, by = 1)
hist(flowers$height, breaks = brk, main = "petunia height")
```




```
brk <- seq(from = 0, to = 18, by = 1)
ggplot(flowers, aes(x = height)) +
  geom_histogram(breaks = brk) +
  ggtitle("petunia height")
```

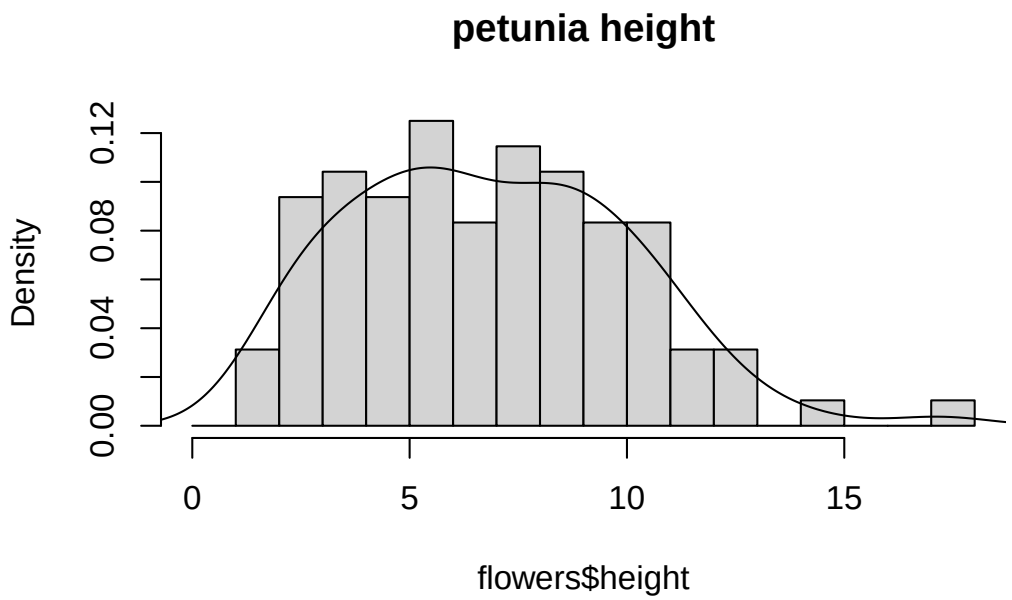


You can also display the histogram as a proportion rather than a frequency by using the `freq = FALSE` argument to `hist()` or indicating `aes(y = after_stat(density))` in `geom_histogram()`.

```
brk <- seq(from = 0, to = 18, by = 1)
hist(flowers$height,
  breaks = brk, main = "petunia height",
  freq = FALSE
)
ggplot(flowers, aes(x = height)) +
  geom_histogram(aes(y = after_stat(density)), breaks = brk) +
  ggtitle("petunia height")
```

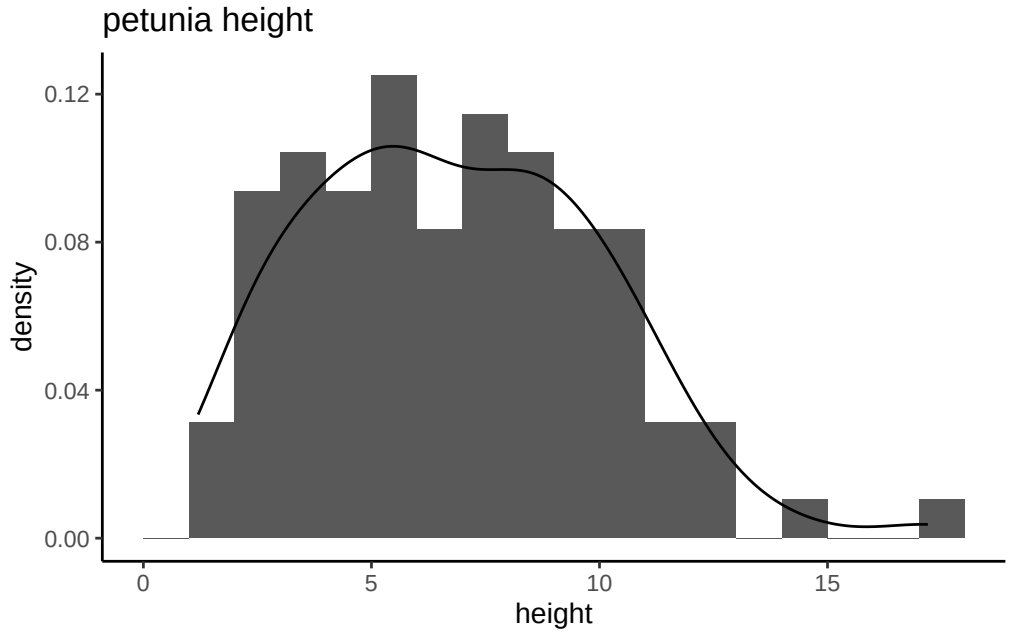
An alternative to plotting just a straight up histogram is to add a kernel density curve to the plot. In base R, you first need to compute the kernel density estimates using the `density()` and then ad the estimates to plot as a line using the `lines()` function.

```
dens <- density(flowers$height)
hist(flowers$height,
  breaks = brk, main = "petunia height",
  freq = FALSE
)
lines(dens)
```



With ggplot, you can simply add the `geom_density()` layer to the plot

```
ggplot(flowers, aes(x = height)) +
  geom_histogram(aes(y = after_stat(density)), breaks = brk) +
  geom_density() +
  ggtitle("petunia height")
```

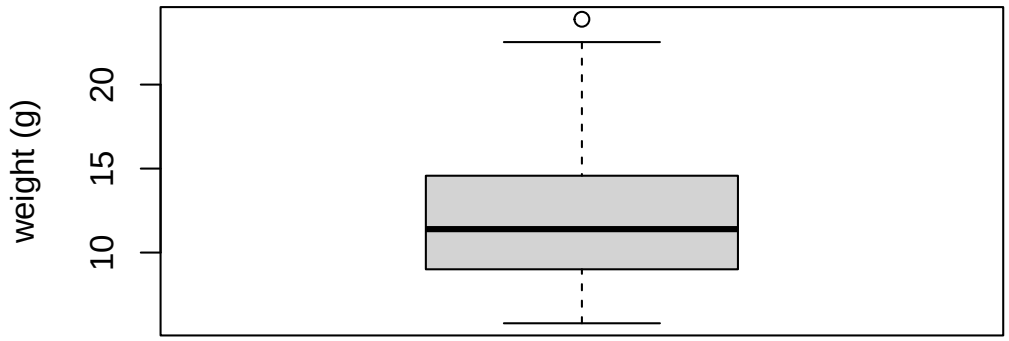


4.3.3. Box plots

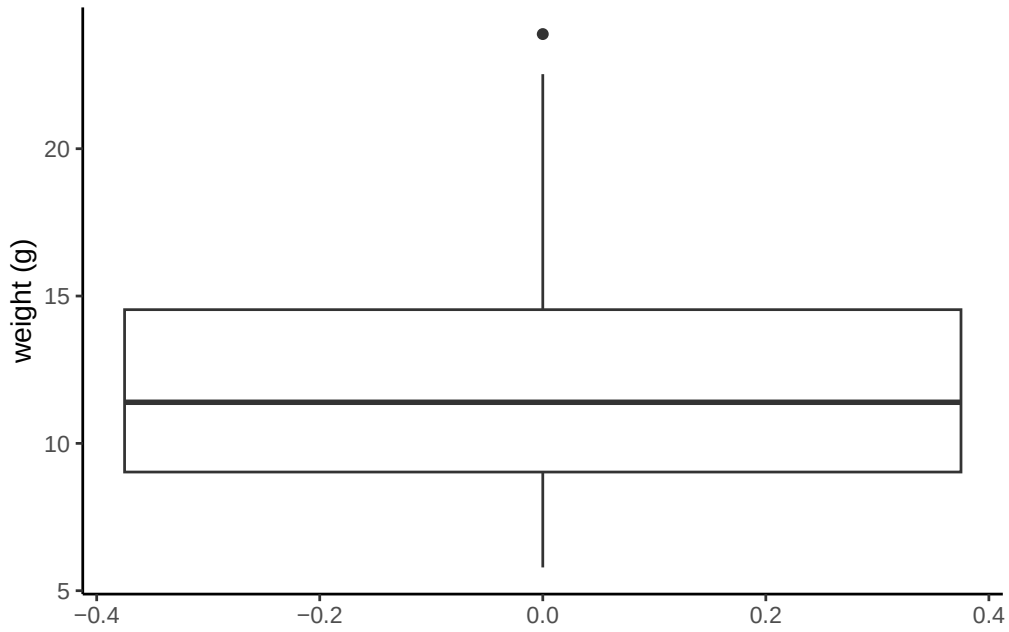
OK, we'll just come and out and say it, we love boxplots and their close relation the violin plot. Boxplots (or box-and-whisker plots to give them their full name) are very useful when you want to graphically summarise the distribution of a variable, identify potential unusual values and compare distributions between different groups. The reason we love them is their ease of interpretation, transparency and relatively high data-to-ink ratio (i.e. they convey lots of information efficiently). We suggest that you try to use boxplots as much as possible when exploring your data and avoid the temptation to use the more ubiquitous bar plot (even with standard error or 95% confidence intervals bars). The problem with bar plots (aka dynamite plots) is that they hide important information from the reader such as the distribution of the data and assume that the error bars (or confidence intervals) are symmetric around the mean. Of course, it's up to you what you do but if you're tempted to use bar plots just Google 'dynamite plots are evil' or see here or here for a fuller discussion.

To create a boxplot in R we use the `boxplot()` function. For example, let's create a boxplot of the variable `weight` from our `flowers` data frame. We can also include a y axis label using the `ylab =` argument.

```
boxplot(flowers$weight, ylab = "weight (g)")
```



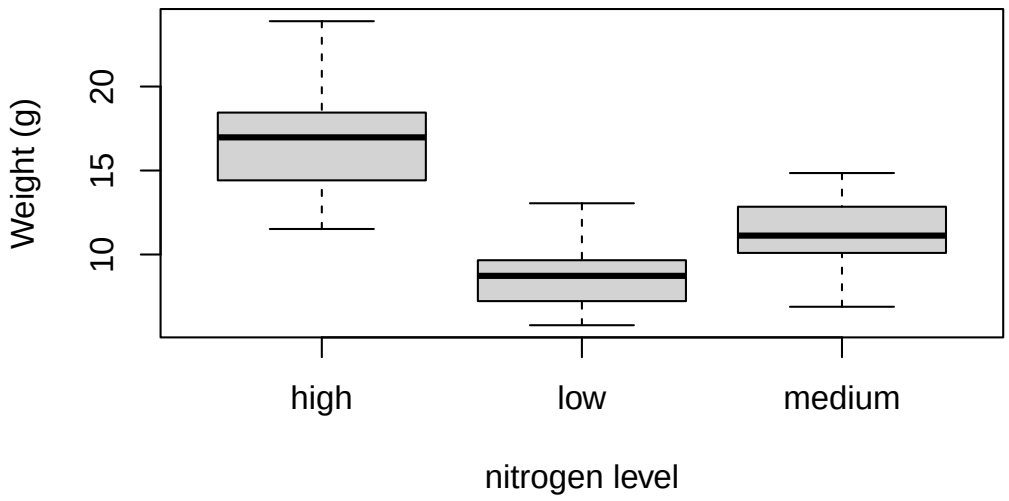

```
ggplot(flowers, aes(y = weight)) +
  geom_boxplot() +
  labs(y = "weight (g)")
```



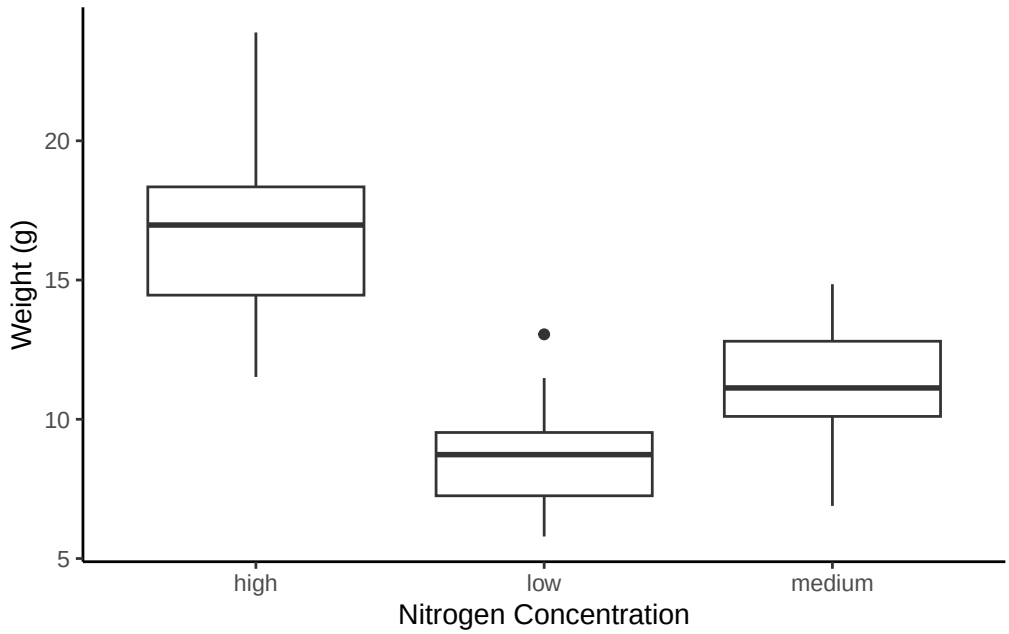
The thick horizontal line in the middle of the box is the median value of `weight` (around 11 g). The upper line of the box is the upper quartile (75th percentile) and the lower line is the lower quartile (25th percentile). The distance between the upper and lower quartiles is known as the inter quartile range and represents the values of `weight` for 50% of the data. The dotted vertical lines are called the whiskers and their length is determined as 1.5 x the inter quartile range. Data points that are plotted outside the the whiskers represent potential unusual observations. This doesn't mean they are unusual, just that they warrant a closer look. We recommend using boxplots in combination with Cleveland dotplots to identify potential unusual observations (see the next section of this Chapter for more details). The neat thing about boxplots is that they not only provide a measure of central tendency (the median value) they also give you an idea about the distribution of the data. If the median line is more or less in the middle of the box (between the upper and lower quartiles) and the whiskers are more or less the same length then you can be reasonably sure the distribution of your data is symmetrical.

If we want examine how the distribution of a variable changes between different levels of a factor we need to use the formula notation with the `boxplot()` function. For example, let's plot our `weight` variable again, but this time see how this changes with each level of `nitrogen`. When we use the formula notation with `boxplot()` we can use the `data =` argument to save some typing. We'll also introduce an x axis label using the `xlab =` argument.

```
boxplot(weight ~ nitrogen,
  data = flowers,
  ylab = "Weight (g)", xlab = "nitrogen level"
)
```

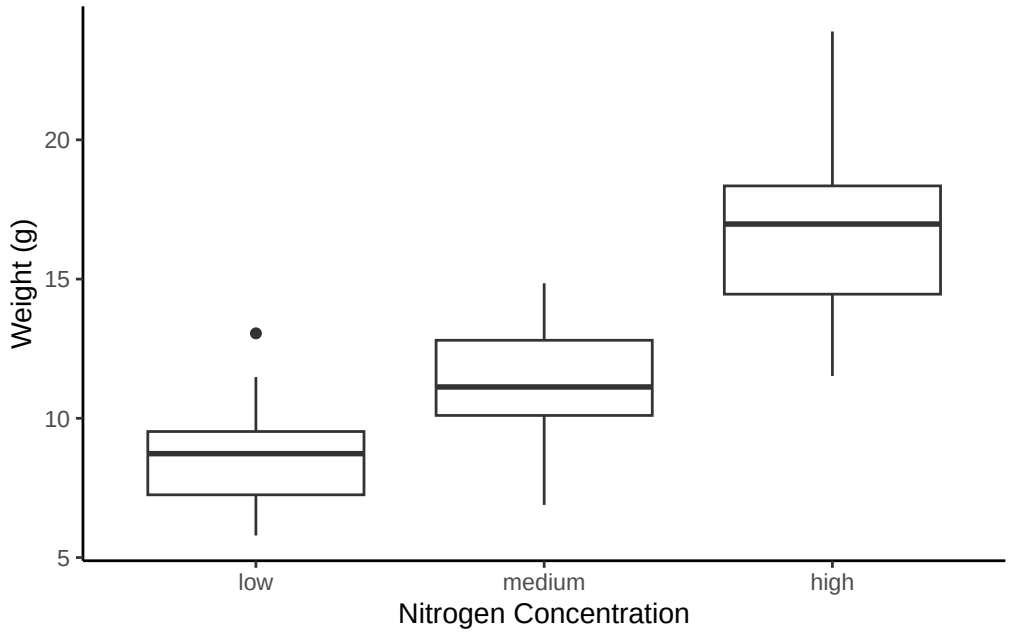



```
ggplot(flowers, aes(y = weight, x = nitrogen)) +
  geom_boxplot() +
  labs(y = "Weight (g)", x = "Nitrogen Concentration")
```



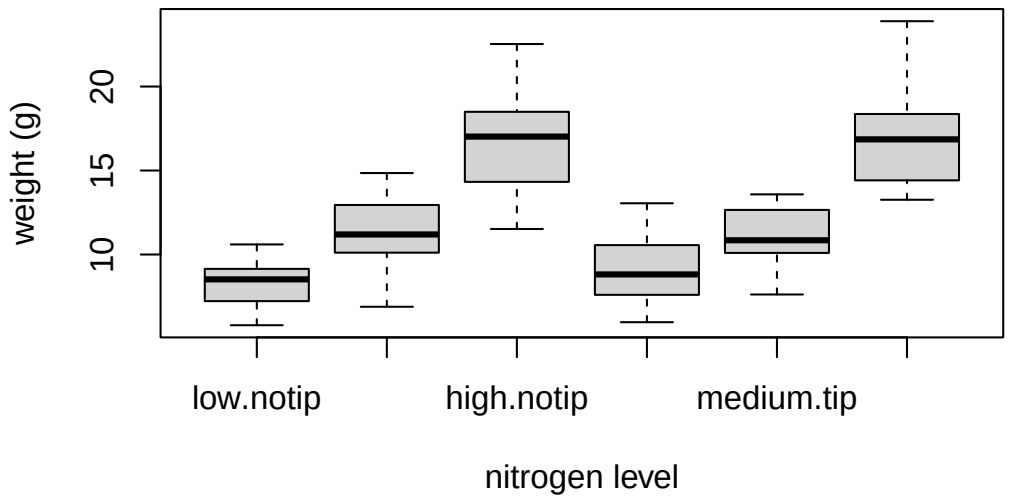
The factor levels are plotted in the same order defined by our factor variable `nitrogen` (often alphabetically). To change the order we need to change the order of our levels of the `nitrogen` factor in our data frame using the `factor()` function and then re-plot the graph. Let's plot our boxplot with our factor levels going from `low` to `high`.

```
flowers$nitrogen <- factor(flowers$nitrogen,
  levels = c("low", "medium", "high")
)
ggplot(flowers, aes(y = weight, x = nitrogen)) +
  geom_boxplot() +
  labs(y = "Weight (g)", x = "Nitrogen Concentration")
```

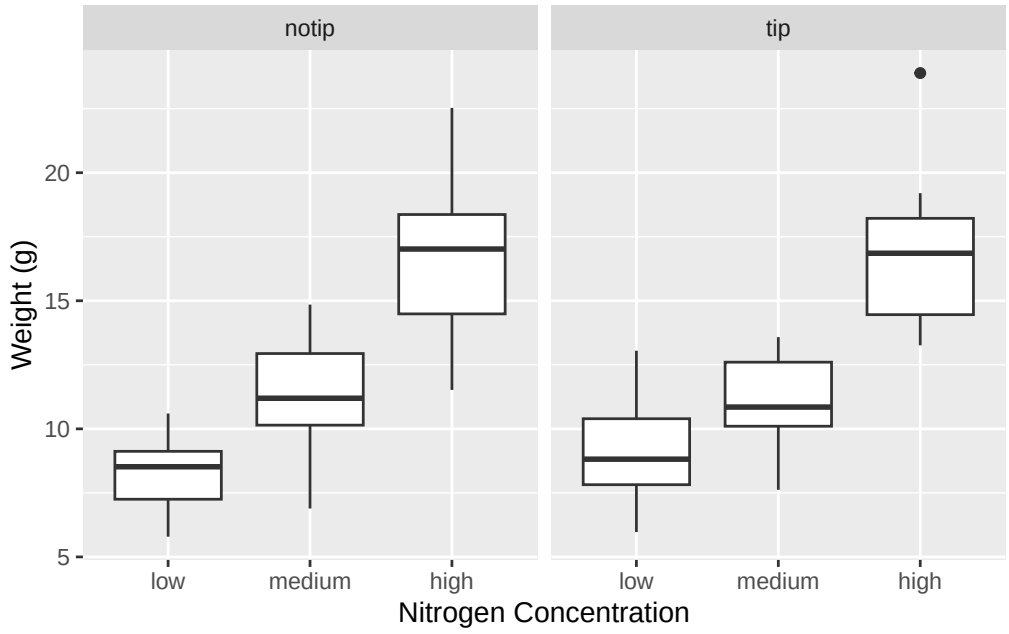


We can also group our variables by two factors in the same plot. Let's plot our `weight` variable but this time plot a separate box for each `nitrogen` and treatment (`treat`) combination.

```
boxplot(weight ~ nitrogen * treat,
  data = flowers,
  ylab = "weight (g)", xlab = "nitrogen level"
)
```




```
ggplot(flowers, aes(y = weight, x = nitrogen)) +
  geom_boxplot() +
  labs(y = "Weight (g)", x = "Nitrogen Concentration") +
  facet_grid(.
~ treat)
```

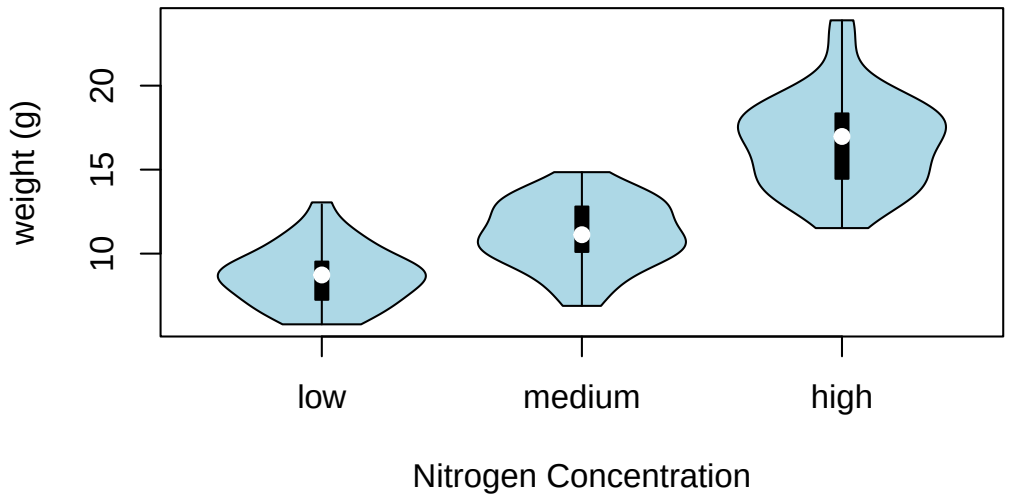


This plot looks much better in ggplot with the use of facet_grid allowing to make similar plots as a function of a third (or even fourth) variable.

4.3.4. Violin plots

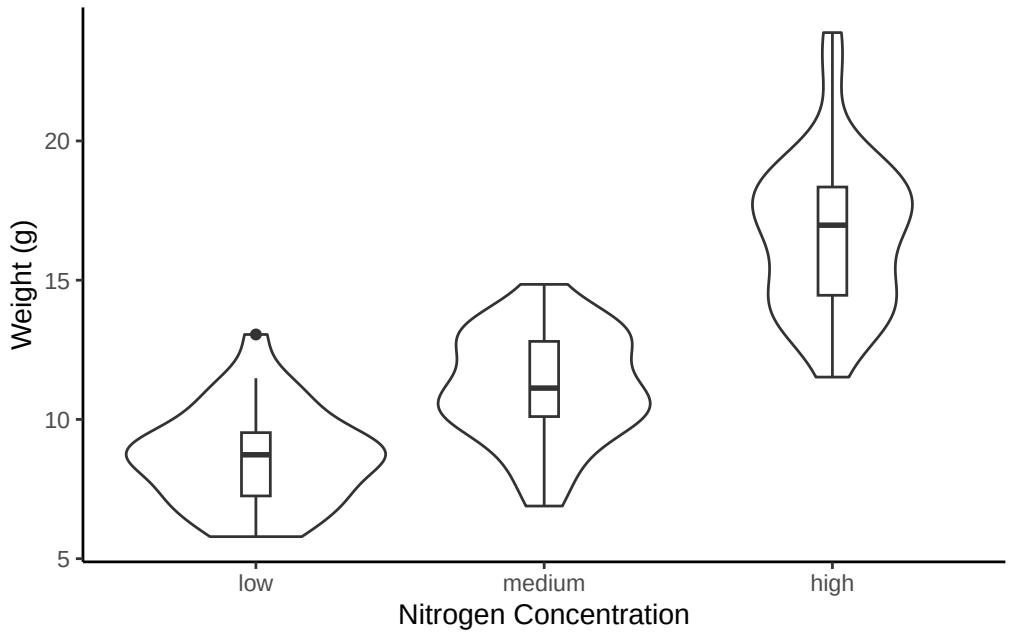
Violin plots are like a combination of a boxplot and a kernel density plot (you saw an example of a kernel density plot in the histogram section above) all rolled into one figure. We can create a violin plot in R using the `vioplot()` function from the `vioplot` package. You'll need to first install this package using `install.packages('vioplot')` function as usual. The nice thing about the `vioplot()` function is that you use it in pretty much the same way you would use the `boxplot()` function. We'll also use the argument `col = "lightblue"` to change the fill colour to light blue.

```
library(vioplot)
vioplot(weight ~ nitrogen,
  data = flowers,
  ylab = "weight (g)", xlab = "Nitrogen Concentration",
  col = "lightblue"
)
```



In the violin plot above we have our familiar boxplot for each `nitrogen` level but this time the median value is represented by a white circle. Plotted around each boxplot is the kernel density plot which represents the distribution of the data for each nitrogen level.

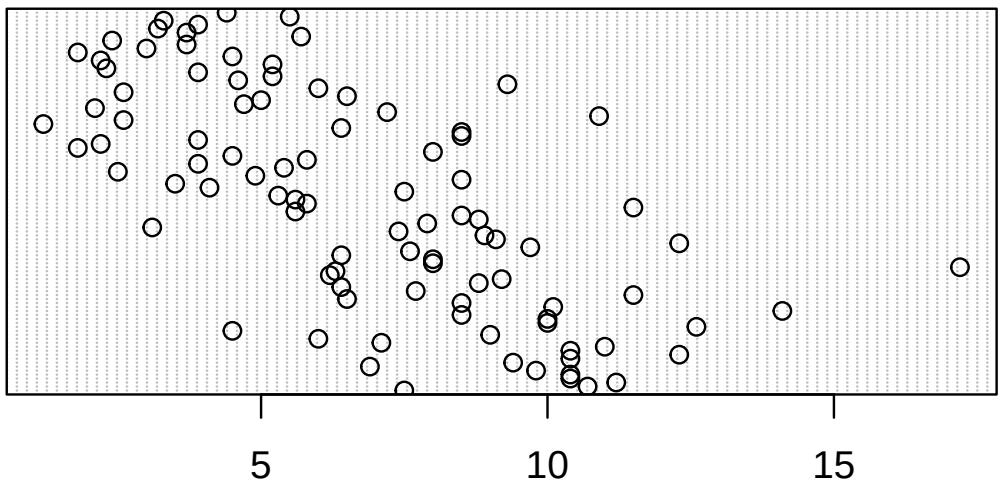
```
ggplot(flowers, aes(y = weight, x = nitrogen)) +
  geom_violin() +
  geom_boxplot(width = 0.1) +
  labs(y = "Weight (g)", x = "Nitrogen Concentration")
```



4.3.5. Dot charts

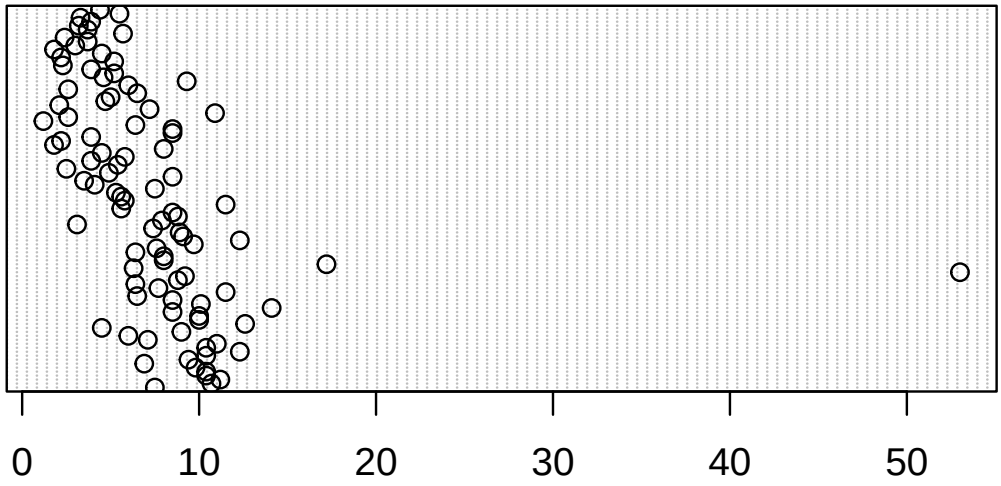
Identifying unusual observations (aka outliers) in numeric variables is extremely important as they may influence parameter estimates in your statistical model or indicate an error in your data. A really useful (if undervalued) plot to help identify outliers is the Cleveland dotplot. You can produce a dotplot in R very simply by using the `dotchart()` function.

```
dotchart(flowers$height)
```



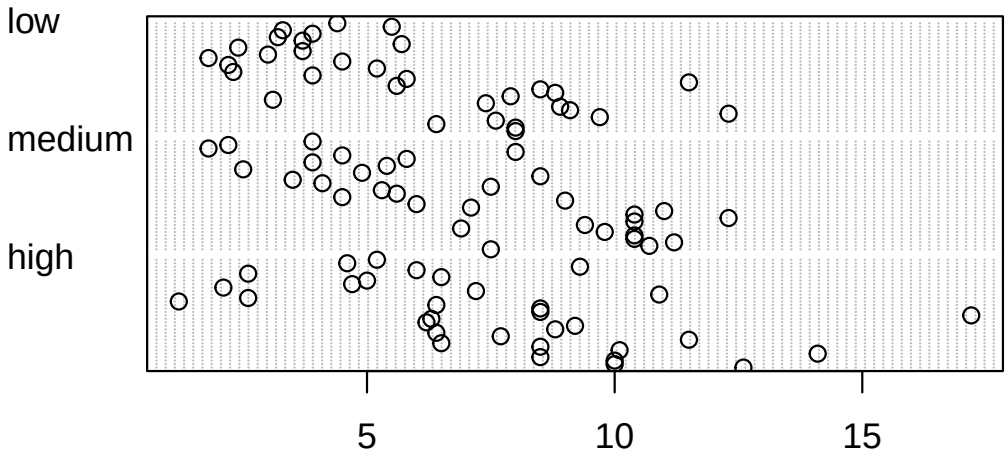
In the dotplot above the data from the `height` variable is plotted along the x axis and the data is plotted in the order it occurs in the `flowers` data frame on the y axis (values near the top of the y axis occur later in the data frame with

those lower down occurring at the beginning of the data frame). In this plot we have a single value extending to the right at about 17 cm but it doesn't appear particularly large compared to the rest. An example of a dotplot with an unusual observation is given below.

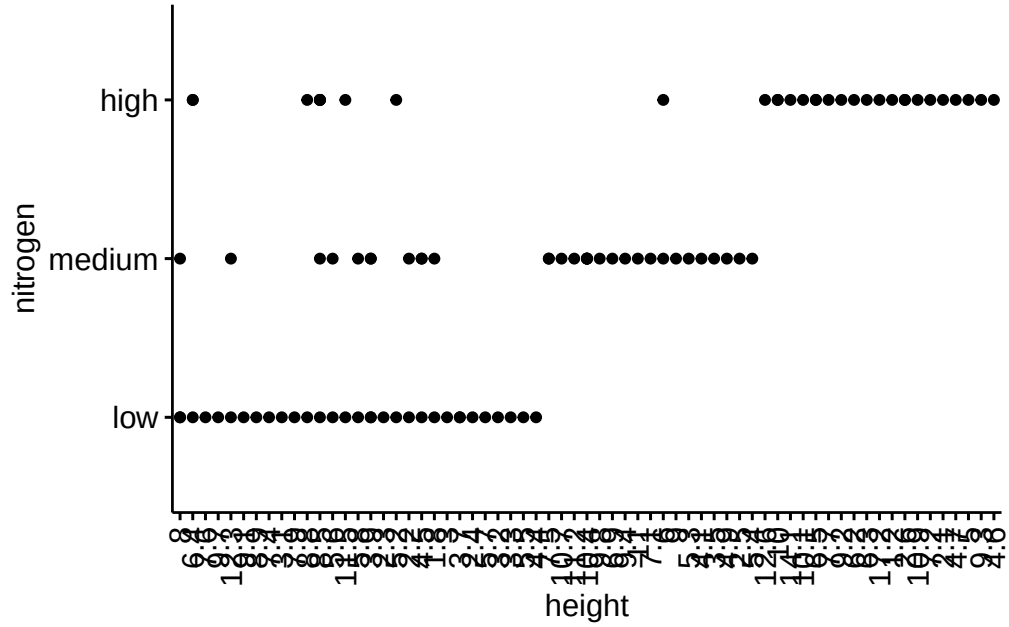


We can also group the values in our `height` variable by a factor variable such as `nitrogen` using the `groups =` argument. This is useful for identifying unusual observations within a factor level that might be obscured when looking at all the data together.

```
dotchart(flowers$height, groups = flowers$nitrogen)
```



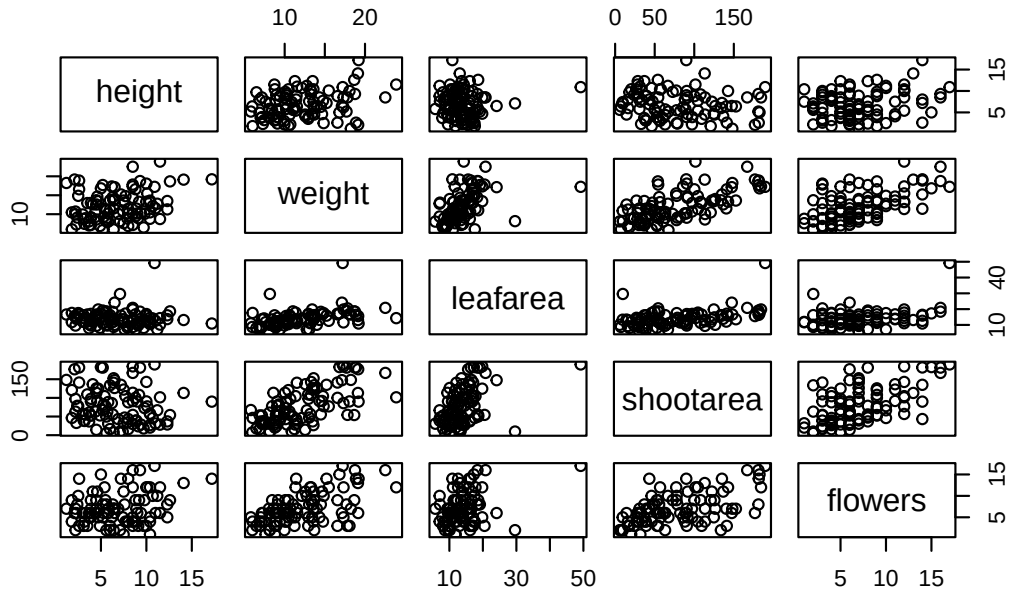

```
ggdotchart(data=flowers, x="height", y= "nitrogen")
```



4.3.6. Pairs plots

Previously in this Chapter we used the `plot()` function to create a scatterplot to explore the relationship between two numeric variables. With datasets that contain many numeric variables, it's often handy to create multiple scatterplots to visualise relationships between all these variables. We could use the `plot()` function to create each of these plot individually, but a much easier way is to use the `pairs()` function. The `pairs()` function creates a multi-panel scatterplot (sometimes called a scatterplot matrix) which plots all combinations of variables. Let's create a multi-panel scatterplot of all of the numeric variables in our `flowers` data frame. Note, you may need to click on the 'Zoom' button in RStudio to display the plot clearly.

```
pairs(flowers[, c(
  "height", "weight", "leafarea",
  "shootarea", "flowers"
)])
```

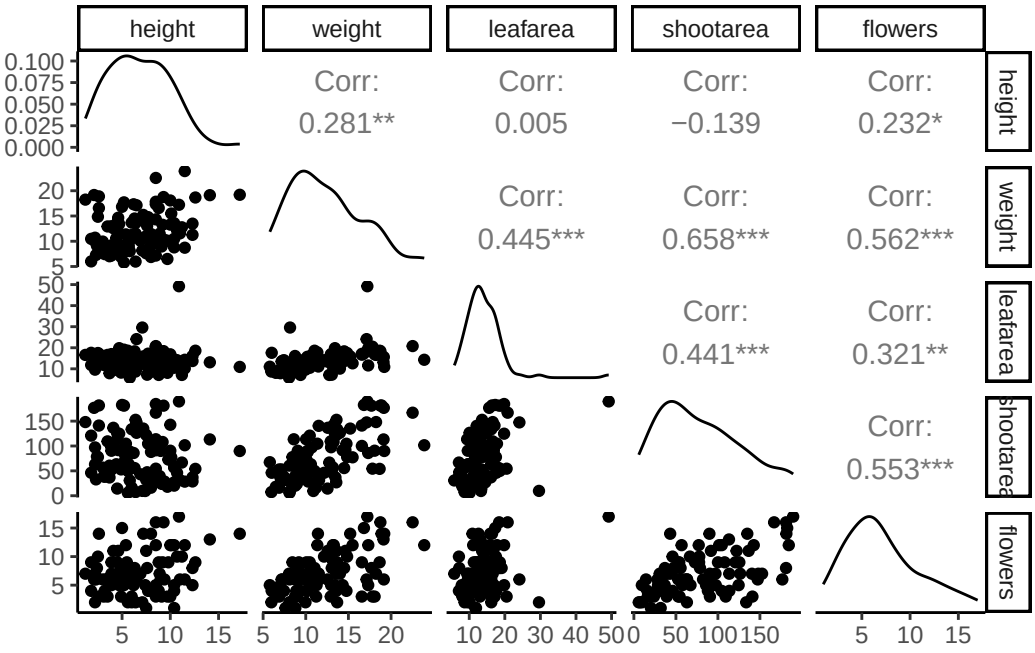



```
# or we could use the equivalent
# pairs(flowers[, 4:8])
```

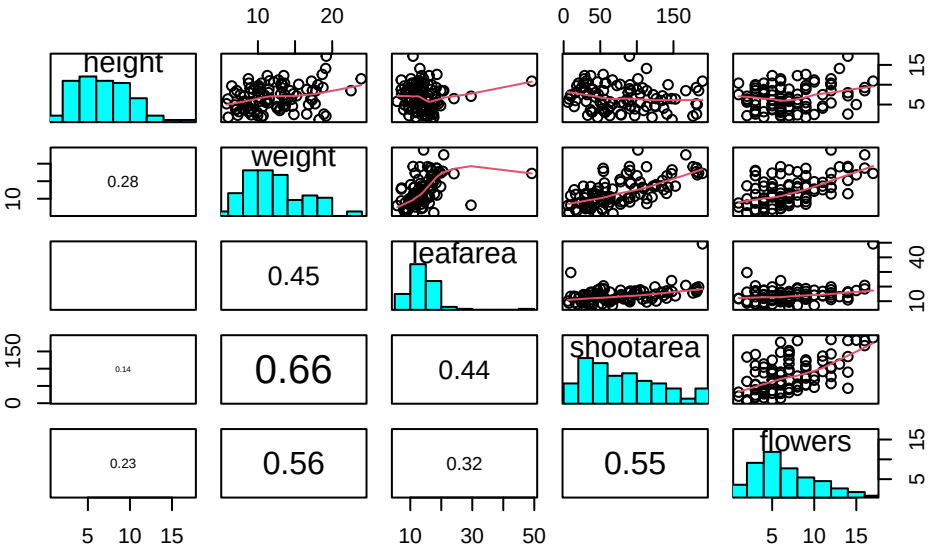
Interpretation of the pairs plot takes a bit of getting used to. The panels on the diagonal give the variable names. The first row of plots displays the `height` variable on the y axis and the variables `weight`, `leafarea`, `shootarea` and `flowers` on the x axis for each of the four plots respectively. The next row of plots have `weight` on the y axis and `height`, `leafarea`, `shootarea` and `flowers` on the x axis. We interpret the rest of the rows in the same way with the last row displaying the `flowers` variable on the y axis and the other variables on the x axis. Hopefully you'll notice that the plots below the diagonal are the same plots as those above the diagonal just with the axis reversed.

To do pairs plot with ggplot, you nee the `ggpairs()` function from `GGally` package. The output is quite similar but you have only the lower part of the matrix of plots, you get a density plot on the diagonal and the correlations on the upper part of the plot.

```
ggpairs(flowers[, c(
  "height", "weight", "leafarea",
  "shootarea", "flowers"
)])
```



The `pairs()` function can be tweak to do similar things and more but is more involved. Have a lok at the great help file for the `pairs()` function (`?pairs`)which provide all the details to do something like the plot below.

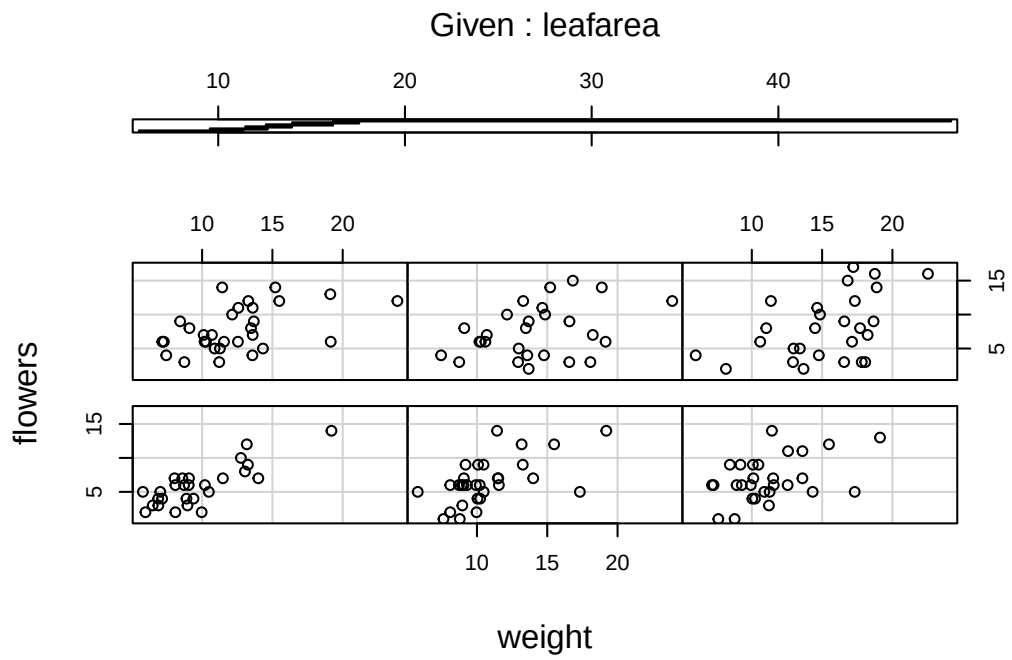


4.3.7. Coplots

When examining the relationship between two numeric variables, it is often useful to be able to determine whether a third variable is obscuring or changing any relationship. A really handy plot to use in these situations is a conditioning plot (also known as conditional scatterplot plot) which we can create in R by using the `coplot()` function. The `coplot()` function plots two variables but each plot is conditioned (`|`) by a third variable. This third variable can be either numeric or a factor. As an example, let's look at how the relationship between the number of flowers (`flowers`

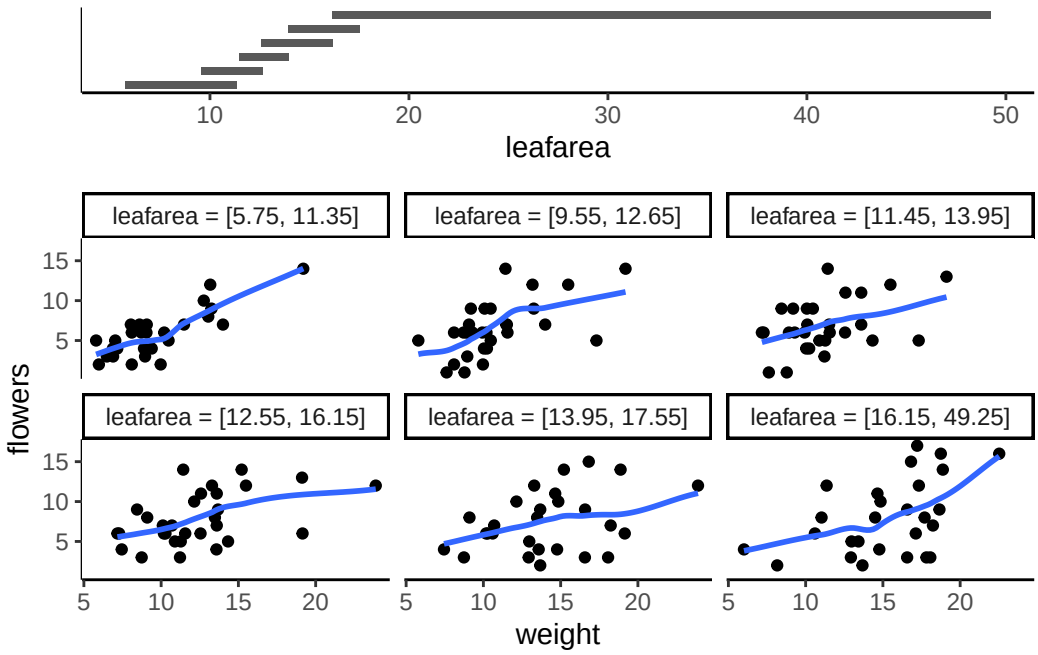
variable) and the `weight` of petunia plants changes dependent on `leafarea`. Note the `coplot()` function has a `data =` argument so no need to use the $ notation.

```
coplot(flowers ~ weight | leafarea, data = flowers)
```




```
gg_coplot(flowers,
  x = weight, y = flowers,
  faceting =leafarea)
```

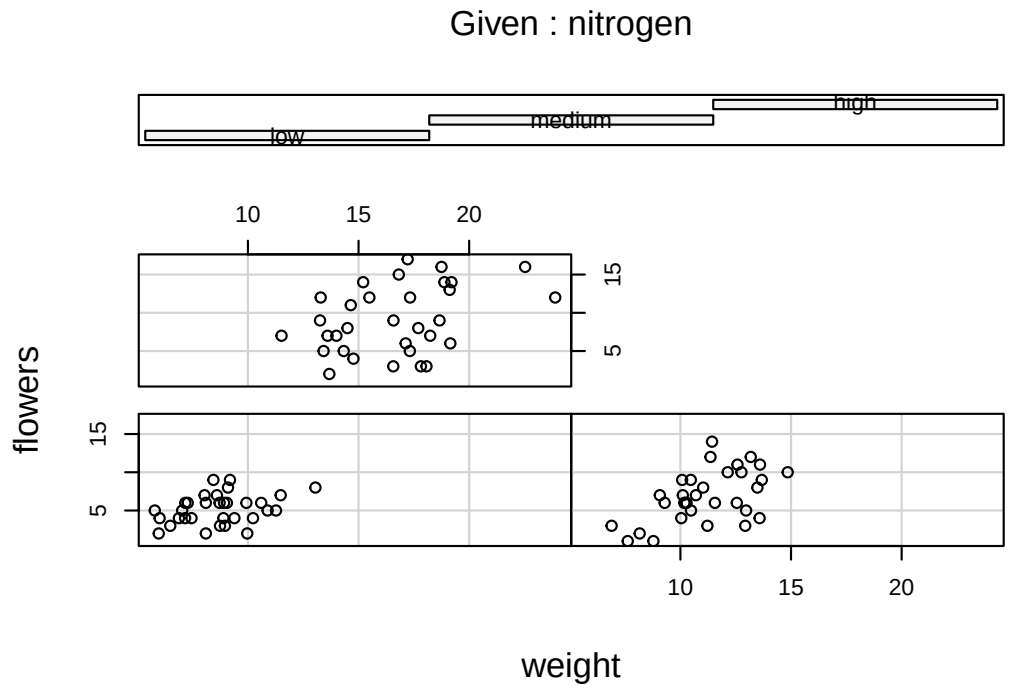
```
`geom_smooth()` using formula = 'y ~ x'
```



It takes a little practice to interpret coplots. The number of flowers is plotted on the y axis and the weight of plants on the x axis. The six plots show the relationship between these two variables for different ranges of leaf area. The bar plot at the top indicates the range of leaf area values for each of the plots. The panels are read from bottom left to top right along each row. For example, the bottom left panel shows the relationship between number of flowers and weight for plants with the lowest range of leaf area values (approximately 5 - 11 cm^2). The top right plot shows the relationship between flowers and weight for plants with a leaf area ranging from approximately 16 - 50 cm^2. Notice that the range of values for leaf area differs between panels and that the ranges overlap from panel to panel. The `coplot()` function does it's best to split the data up to ensure there are an adequate number of data points in each panel. If you don't want to produce plots with overlapping data in the panel you can set the `overlap =` argument to `overlap = 0`

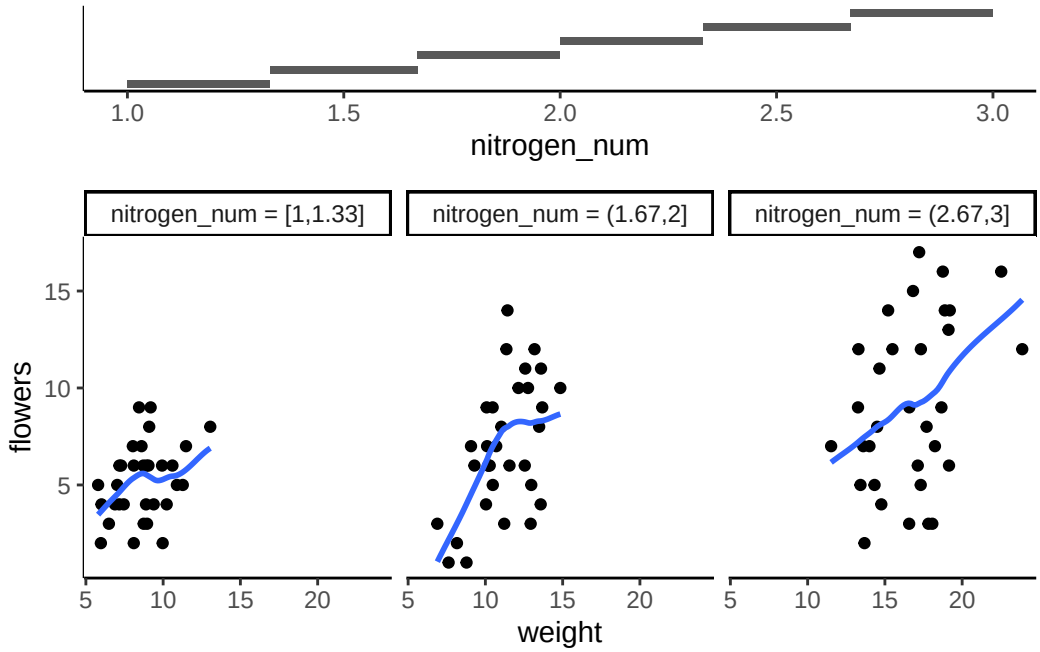
You can also use the `coplot()` function with factor conditioning variables. With `gg_coplot()` you need to first set the factor as numeric before plotting and specify `overlap=0`. For example, we can examine the relationship between `flowers` and `weight` variables conditioned on the factor `nitrogen`. The bottom left plot is the relationship between `flowers` and `weight` for those plants in the `low` nitrogen treatment. The top left plot shows the same relationship but for plants in the `high` nitrogen treatment.

```
coplot(flowers ~ weight | nitrogen, data = flowers)
```




```
flowers <- mutate(flowers, nitrogen_num = as.numeric(nitrogen))
gg_coplot(flowers,
  x = weight, y = flowers,
  faceting =nitrogen_num, overlap = 0)
```

```
`geom_smooth()` using formula = 'y ~ x'
```



4.3.8. Summary of plot function

Graph type	ggplot2	Base R function
scatterplot	`geom_point()`	`plot()`
frequency histogram	`geom_histogram()`	`hist()`
boxplot	`geom_boxplot()`	`boxplot()`
Cleveland dotplot	`ggdotchart()`	`dotchart()`
scatterplot matrix	`ggpairs()`	`pairs()`
conditioning plot	`gg_coplot()`	`coplot()`

Hopefully, you're getting the idea that we can create really informative exploratory plots quite easily using either base R or ggplot graphics. Which one you use is entirely up to you (that's the beauty of using R, you get to choose) and we happily mix and match to suit our needs. In the next section we cover how to customise your base R plots to get them to look exactly how you want.

4.4. Customising plots

Went for walk to be edited

Chapter 5

Simple Statistics in R

> ⚠ Warning
>
> To be developed (need to decide what I want in that chapter) Potentially just list a few functions since it is not at all about stats but more about r

5.1. Simple linear modelling

Linear models are one of the most widely used models in statistics and data science. They are often thought of as simple models but they're very flexible and able to model a wide variety of experimental and survey designs. Many of the statistical approaches you may have used previously (such as linear regression, *t*-test, ANOVA, ANCOVA etc) can be expressed as a linear model so the good news is that you're probably already familiar with linear models (albeit indirectly). They also form the foundation of more complicated modelling approaches and are relatively easy to extended to incorporate additional complexity. During this section we'll learn how to fit some simple linear models using R and cover some of the more common applications. We won't go into any detail of the underlying linear modelling theory but rather focus on the practicalities of model fitting and R code.

The main function for fitting linear models in R is the `lm()` function (short for linear model!). The `lm()` function has many arguments but the most important is the first argument which specifies the model you want to fit using a *model formula* which typically takes the general form:

response variable ~ explanatory variable(s)

This model formula is simply read as

> *'variation in the response variable modelled as a function (~) of the explanatory variable(s)'.*

The response variable is also commonly known as the 'dependent variable' and the explanatory variables are sometimes referred to as 'independent variables' (or less frequently as 'predictor variables'). There is also an additional term in our model formula which represents the variation in our response variable **not** explained by our explanatory variables but you don't need to specify this when using the `lm()` function.

As mentioned above, many of the statistical 'tests' you might have previously used can be expressed as a linear model. For example, if we wanted to perform a bivariate linear regression between a response variable (`y`) and a single continuous explanatory variable (`x`) our model formula would simply be

```
y ~ x
```

On the other hand, if we wanted to use an ANOVA to test whether the group means of a response variable (`y`) were different between a three level factor (`x`) our model formula would look like

```
y ~ x
```

OK, hang on, they both look identical, what gives? In addition to the model formula, the type of linear model you fit is also determined by the type of data in your explanatory variable(s) (i.e. what class of data). If your explanatory variable is continuous then you will fit a bivariate linear regression. If your explanatory variable is a factor (i.e. categorical data) you will fit an ANOVA type model.

You can also increase the complexity of your linear model by including additional explanatory variables in your model formula. For example, if we wanted to fit a two-way ANOVA both of our explanatory variables `x` and `z` would need to be factors and separated by a + symbol

```
y ~ x + z
```

If we wanted to perform a factorial ANOVA to identify an interaction between both explanatory variables we would separate our explanatory variables with a `:` symbol whilst also including our main effects in our model formula

```
y ~ x + z + x:z
```

or by using the equivalent shortcut notation

```
y ~ x * z
```

It's important that you get comfortable with using model formula (and we've only given the briefest of explanations above) when using the `lm()` function (and other functions) as it's remarkably easy to specifiy a model which is either nonsense or isn't the model you really wanted to fit. A summary table of various linear model formula and equivalent R code given below.

Traditional name	Model formula	R code
Bivariate regression	Y ~ X1 (continuous)	`lm(Y ~ X)`
One-way ANOVA	Y ~ X1 (categorical)	`lm(Y ~ X)`
Two-way ANOVA	Y ~ X1 (cat) + X2(cat)	`lm(Y ~ X1 + X2)`
ANCOVA	Y ~ X1 (cat) + X2(cont)	`lm(Y ~ X1 + X2)`
Multiple regression	Y ~ X1 (cont) + X2(cont)	`lm(Y ~ X1 + X2)`
Factorial ANOVA	Y ~ X1 (cat) * X2(cat)	`lm(Y ~ X1 * X2)` or `lm(Y ~ X1 + X2 + X1:X2)`

OK, time for an example. The data file `smoking.txt` summarises the results of a study investigating the possible relationship between mortality rate and smoking across 25 occupational groups in the UK. The variable `occupational.group` specifies the different occupational groups studied, the `risk.group` variable indicates the relative risk to lung disease for the various occupational groups and `smoking` is an index of the average number of cigarettes smoked each day (relative to the number smoked across all occupations). The variable `mortality` is an index of the death rate from lung cancer in each group (relative to the death rate across all occupational groups). In this data set, the response variable is `mortality` and the potential explanatory variables are `smoking` which is numeric and `risk.group` which is a three level factor. The first thing to do is import our data file using the `read.table()` function as usual and assign the data to an object called `smoke`. You can find a link to download these data here.

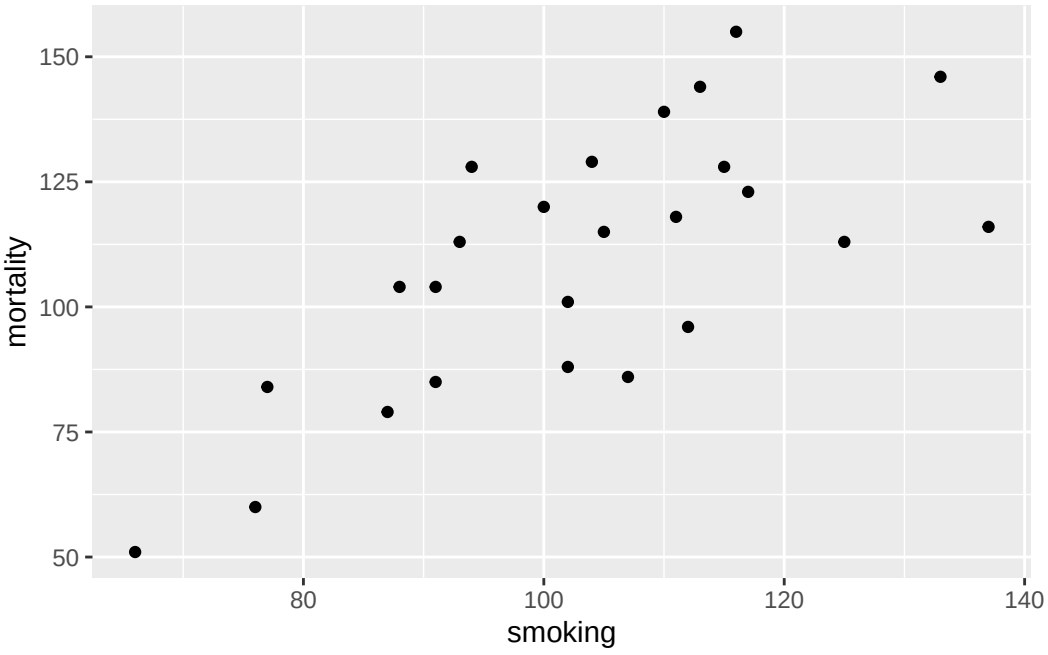
```
smoke <- read.table('data/smoking.txt', header = TRUE, sep = "\t",
                                        stringsAsFactors = TRUE)
str(smoke, vec.len = 2)
```

```
'data.frame':   25 obs. of  4 variables:
 $ occupational.group: Factor w/ 25 levels "Administrators",..: 9 14 2 11 10 ...
 $ risk.group        : Factor w/ 3 levels "high","low","medium": 2 1 1 3 1 ...
 $ smoking           : int  77 137 117 94 116 ...
 $ mortality         : int  84 116 123 128 155 ...
```

```
# vec.len argument to limited number of ' first elements' to display
```

Next, let's investigate the relationship between the `mortality` and `smoking` variables by plotting a scatter plot. We can use either the `ggplot2` package or base R graphics to do this. We'll use `ggplot2` this time and our old friend the `ggplot()` function.

```
library(ggplot2)
ggplot(mapping = aes(x = smoking, y = mortality), data = smoke) +
    geom_point()
```



The plot does suggest that there is a positive relationship between the smoking index and mortality index.

To fit a simple linear model to these data we will use the `lm()` function and include our model formula `mortality ~ smoking` and assign the results to an object called `smoke_lm`.

```
smoke_lm <- lm(mortality ~ smoking, data = smoke)
```

Notice that we have not used the `$` notation to specify the variables in our model formula, instead we've used the `data = smoke` argument. Although the `$` notation will work (i.e. `smoke$mortality ~ smoke$smoking`) it will more than likely cause you problems later on and should be avoided. In fact, we would go as far to suggest that if any function has a `data =` argument you should **always** use it. How do you know if a function has a `data =` argument? Just look in the associated help file.

Perhaps somewhat confusingly (at least at first) it appears that nothing much has happened, you don't automatically get the voluminous output that you normally get with other statistical packages. In fact, what R does, is store the output of the analysis in what is known as a `lm` class object (which we have called `smoke_lm`) from which you are able to extract exactly what you want using other functions. If you're brave, you can examine the structure of the `smoke_lm` model object using the `str()` function.

```
str(smoke_lm)
```

```
List of 12
 $ coefficients : Named num [1:2] -2.89 1.09
  ..- attr(*, "names")= chr [1:2] "(Intercept)" "smoking"
 $ residuals    : Named num [1:25] 3.15 -30.11 -1.36 28.66 31.73 ...
  ..- attr(*, "names")= chr [1:25] "1" "2" "3" "4" ...
 $ effects      : Named num [1:25] -545 -91.63 2.72 26.99 35.56 ...
  ..- attr(*, "names")= chr [1:25] "(Intercept)" "smoking" "" "" ...
 $ rank         : int 2
 $ fitted.values: Named num [1:25] 80.9 146.1 124.4 99.3 123.3 ...
  ..- attr(*, "names")= chr [1:25] "1" "2" "3" "4" ...
 $ assign       : int [1:2] 0 1
 $ qr           :List of 5
  ..$ qr   : num [1:25, 1:2] -5 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2 ...
  .. ..- attr(*, "dimnames")=List of 2
```

```
  .. .. ..$ : chr [1:25] "1" "2" "3" "4" ...
  .. .. ..$ : chr [1:2] "(Intercept)" "smoking"
  .. ..- attr(*, "assign")= int [1:2] 0 1
  ..$ qraux: num [1:2] 1.2 1.46
  ..$ pivot: int [1:2] 1 2
  ..$ tol  : num 1e-07
  ..$ rank : int 2
  ..- attr(*, "class")= chr "qr"
 $ df.residual  : int 23
 $ xlevels      : Named list()
 $ call         : language lm(formula = mortality ~ smoking, data = smoke)
 $ terms        :Classes 'terms', 'formula'  language mortality ~ smoking
  .. ..- attr(*, "variables")= language list(mortality, smoking)
  .. ..- attr(*, "factors")= int [1:2, 1] 0 1
  .. .. ..- attr(*, "dimnames")=List of 2
  .. .. .. ..$ : chr [1:2] "mortality" "smoking"
  .. .. .. ..$ : chr "smoking"
  .. ..- attr(*, "term.labels")= chr "smoking"
  .. ..- attr(*, "order")= int 1
  .. ..- attr(*, "intercept")= int 1
  .. ..- attr(*, "response")= int 1
  .. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
  .. ..- attr(*, "predvars")= language list(mortality, smoking)
  .. ..- attr(*, "dataClasses")= Named chr [1:2] "numeric" "numeric"
  .. .. ..- attr(*, "names")= chr [1:2] "mortality" "smoking"
 $ model        :'data.frame':  25 obs. of  2 variables:
  ..$ mortality: int [1:25] 84 116 123 128 155 101 118 113 104 88 ...
  ..$ smoking  : int [1:25] 77 137 117 94 116 102 111 93 88 102 ...
  ..- attr(*, "terms")=Classes 'terms', 'formula'  language mortality ~ smoking
  .. .. ..- attr(*, "variables")= language list(mortality, smoking)
  .. .. ..- attr(*, "factors")= int [1:2, 1] 0 1
  .. .. .. ..- attr(*, "dimnames")=List of 2
  .. .. .. .. ..$ : chr [1:2] "mortality" "smoking"
```

```
  .. .. .. .. ..$ : chr "smoking"
  .. .. ..- attr(*, "term.labels")= chr "smoking"
  .. .. ..- attr(*, "order")= int 1
  .. .. ..- attr(*, "intercept")= int 1
  .. .. ..- attr(*, "response")= int 1
  .. .. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
  .. .. ..- attr(*, "predvars")= language list(mortality, smoking)
  .. .. ..- attr(*, "dataClasses")= Named chr [1:2] "numeric" "numeric"
  .. .. .. ..- attr(*, "names")= chr [1:2] "mortality" "smoking"
 - attr(*, "class")= chr "lm"
```

To obtain a summary of our analysis we can use the `summary()` function on our `smoke_lm` model object.

```
summary(smoke_lm)
```

```
Call:
lm(formula = mortality ~ smoking, data = smoke)

Residuals:
    Min      1Q  Median      3Q     Max
-30.107 -17.892   3.145  14.132  31.732

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -2.8853    23.0337  -0.125    0.901
smoking       1.0875     0.2209   4.922 5.66e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 18.62 on 23 degrees of freedom
Multiple R-squared:  0.513, Adjusted R-squared:  0.4918
F-statistic: 24.23 on 1 and 23 DF,  p-value: 5.658e-05
```

This shows you everything you need to know about the parameter estimates (intercept and slope), their standard errors and associated t statistics and p values. The estimate for the Intercept suggests that when the relative smoking index is 0 the relative mortality rate is `-2.885`! The p value associated with the intercept tests the null hypothesis that the intercept is equal to zero. As the p value is large we fail to reject this null hypothesis. The `smoking` parameter estimate (`1.0875`) is the estimate of the slope and suggests that for every unit increase in the average number of cigarettes smoked each day the mortality risk index increases by 1.0875. The p value associated with the `smoking` parameter tests whether the slope of this relationship is equal to zero (i.e. no relationship). As our p value is small we reject this null hypothesis and therefore the slope is different from zero and therefore there is a significant relationship. The summary table also includes other important information such as the coefficient of determination (R^2), adjusted R^2 , F statistic, associated degrees of freedom and p value. This information is a condensed form of an ANOVA table which you can see by using the `anova()` function.

```
anova(smoke_lm)
```

```
Analysis of Variance Table

Response: mortality
          Df Sum Sq Mean Sq F value    Pr(>F)
smoking    1 8395.7  8395.7  24.228 5.658e-05 ***
Residuals 23 7970.3   346.5
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Now let's fit another linear model, but this time we will use the `risk.group` variable as our explanatory variable. Remember the `risk.group` variable is a factor and so our linear model will be equivalent to an ANOVA type analysis. We will be testing the null hypothesis that there is no difference in the mean mortality rate between the `low`, `medium` and `high` groups. We fit the model in exactly the same way as before.

```
smoke_risk_lm <- lm(mortality ~ risk.group, data = smoke)
```

Again, we can produce an ANOVA table using the `anova()` function

```
anova(smoke_risk_lm)
```

```
Analysis of Variance Table

Response: mortality
           Df  Sum Sq Mean Sq F value    Pr(>F)
risk.group  2 11514.4  5757.2  26.107 1.554e-06 ***
Residuals  22  4851.6   220.5
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The results presented in the ANOVA table suggest that we can reject the null hypothesis (very small p value) and therefore the mean mortality rate index is different between `low`, `medium` and `high` risk groups.

As we did with our first linear model we can also produce a summary of the estimated parameters using the `summary()` function.

```
summary(smoke_risk_lm)
```

```
Call:
lm(formula = mortality ~ risk.group, data = smoke)

Residuals:
   Min     1Q Median     3Q    Max
-26.17 -11.45   4.00   9.00  26.83

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)        135.00       5.25  25.713  < 2e-16 ***
risk.grouplow      -57.83       8.02  -7.211 3.16e-07 ***
risk.groupmedium   -27.55       6.90  -3.992 0.000615 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 14.85 on 22 degrees of freedom
Multiple R-squared:  0.7036,    Adjusted R-squared:  0.6766
```

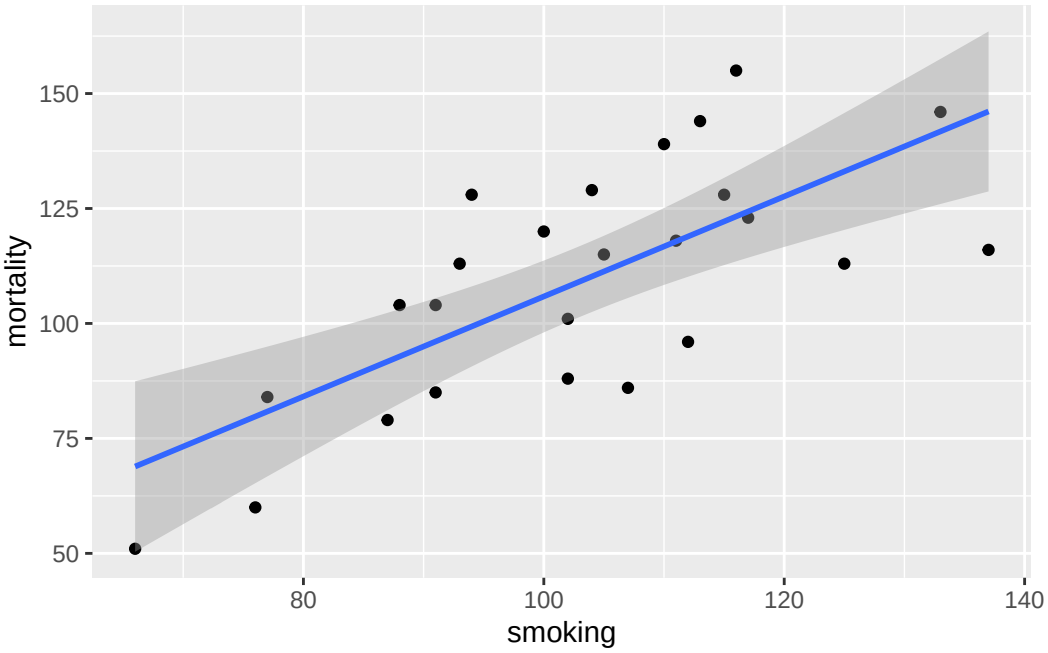
```
F-statistic: 26.11 on 2 and 22 DF,  p-value: 1.554e-06
```

In the summary table the Intercept is set to the first level of `risk.group` (`high`) as this occurs first alphabetically. Therefore, the estimated mean mortality index for `high` risk individuals is `135`. The estimates for `risk.grouplow` and `risk.groupmedium` are mean differences from the intercept (`high` group). So the mortality index for the `low` group is `135 - 57.83 = 77.17` and for the `medium` group is `135 - 27.55 = 107.45`. The *t* values and *p* values in the summary table are associated with testing specific hypotheses. The *p* value associated with the intercept tests the null hypothesis that the mean mortality index for the `high` group is equal to zero. To be honest this is not a particularly meaningful hypothesis to test but we can reject it anyway as we have a very small *p* value. The *p* value for the `risk.grouplow` parameter tests the null hypothesis that the mean difference between `high` and `low` risk groups is equal to zero (i.e. there is no difference). Again we reject this null hypothesis and conclude that the means are different between these two groups. Similarly, the *p* value for `risk.groupmedium` tests the null hypothesis that the mean difference between `high` and `medium` groups is equal to zero which we also reject.

Don't worry too much if you find the output from the `summary()` function a little confusing. Its takes a bit of practice and experience to be able to make sense of all the numbers. Remember though, the more complicated your model is, the more complicated your interpretion will be. And always remember, a model that you can't interpret is not worth fitting (most of the time!).

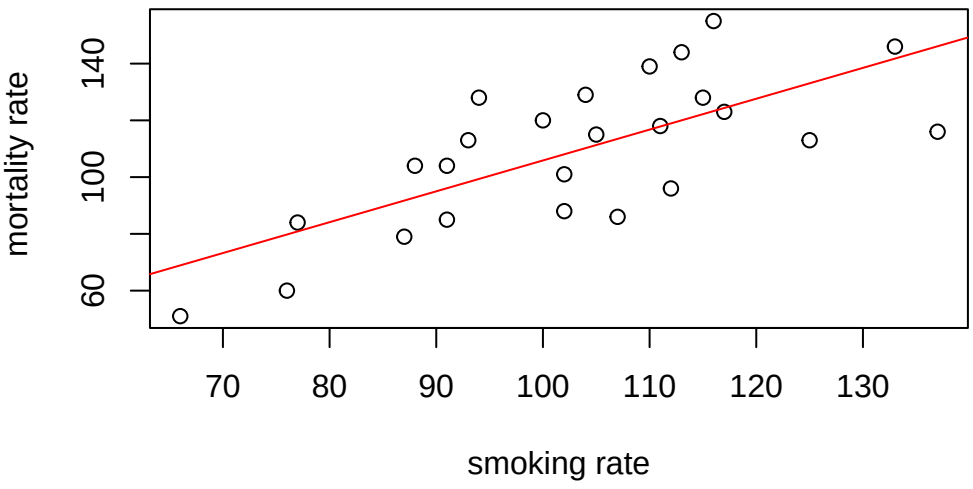
Another approach to interpreting your model output is to plot a graph of your data and then add the fitted model to this plot. Let's go back to the first linear model we fitted (`smoke_lm`). We can add the fitted line to our previous plot using the `ggplot2` package and the `geom_smooth` geom. We can easily include the standard errors by specifying the `se = TRUE` argument.

```
ggplot(mapping = aes(x = smoking, y = mortality), data = smoke) +
    geom_point() +
    geom_smooth(method = "lm", se = TRUE)
```



You can also do this with R's base graphics. Note though that the fitted line extends beyond the data which is not great practice. If you want to prevent this you can generate predicted values from the model using the `predict()` function within the range of your data and then add these values to the plot using the `lines()` function (not shown).

```
plot(smoke$smoking, smoke$mortality, xlab = "smoking rate", ylab = " mortality rate")
abline(smoke_lm, col = "red")
```

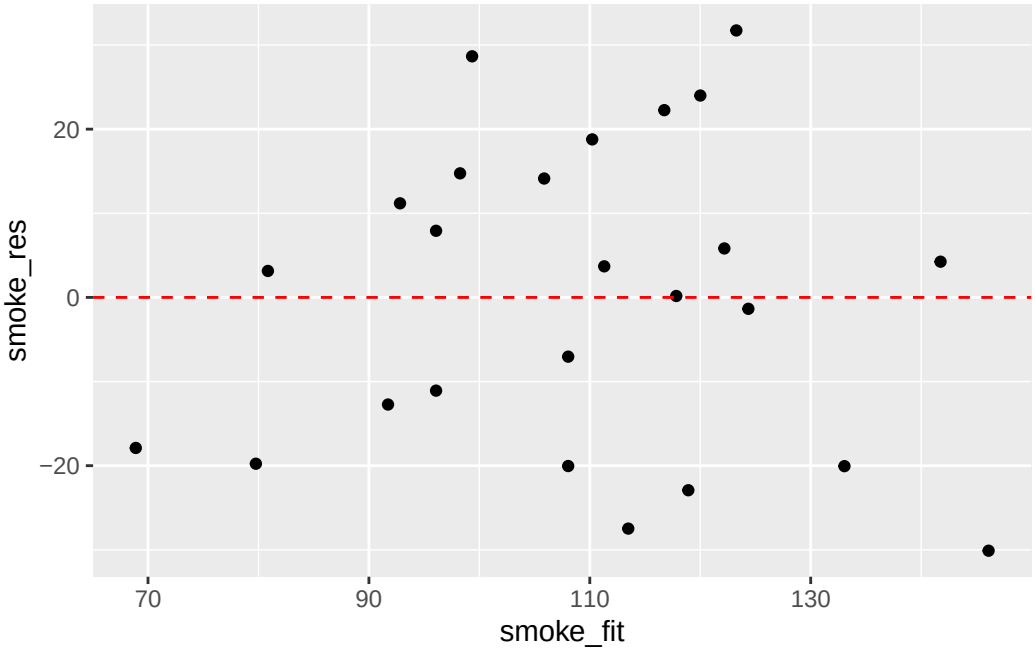


Before we sit back and relax and admire our model (or go write that high impact paper your supervisor/boss has been harassing you about) our work is not finished. It's vitally important to check the underlying assumptions of your linear model. Two of the most important assumption are equal variances (homogeneity of variance) and normality of residuals. To check for equal variances we can construct a graph of residuals versus fitted values. We can do this by first extracting the residuals and fitted values from our model object using the `resid()` and `fitted()` functions.

```
smoke_res <- resid(smoke_lm)
smoke_fit <- fitted(smoke_lm)
```

And then plot them using `ggplot` or base R graphics.

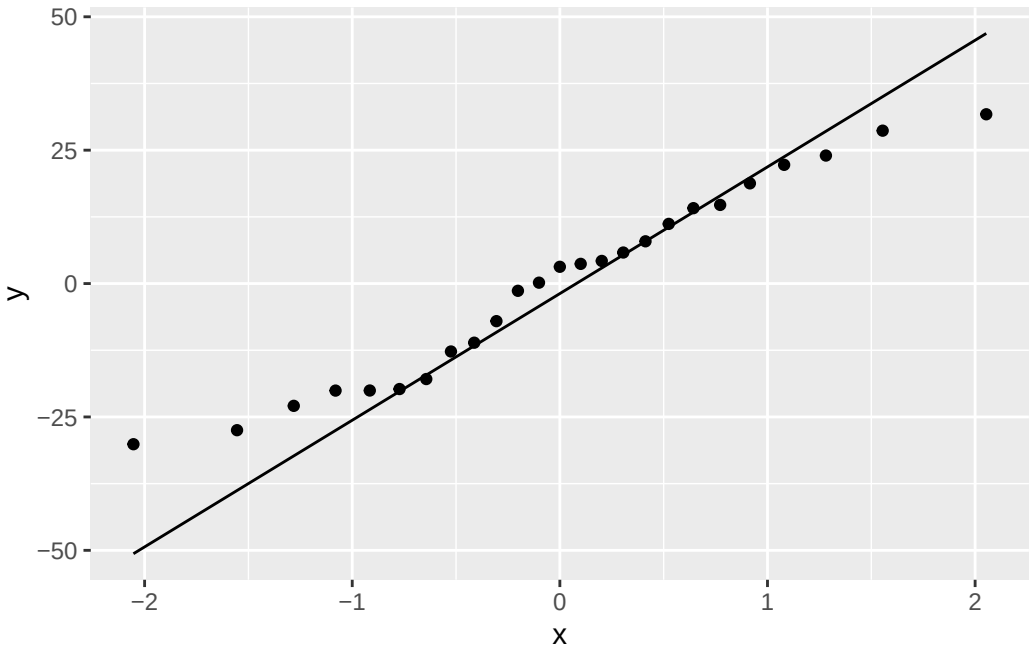
```
ggplot(mapping = aes(x = smoke_fit, y = smoke_res)) +
    geom_point() +
    geom_hline(yintercept = 0, colour = "red", linetype = "dashed")
```



It takes a little practice to interpret these types of graph, but what you are looking for is no pattern or structure in your residuals. What you definitely don't want to see is the scatter increasing around the zero line (red dashed line) as the fitted values get bigger (this has been described as looking like a trumpet, a wedge of cheese or even a slice of pizza) which would indicate unequal variances (heteroscedacity).

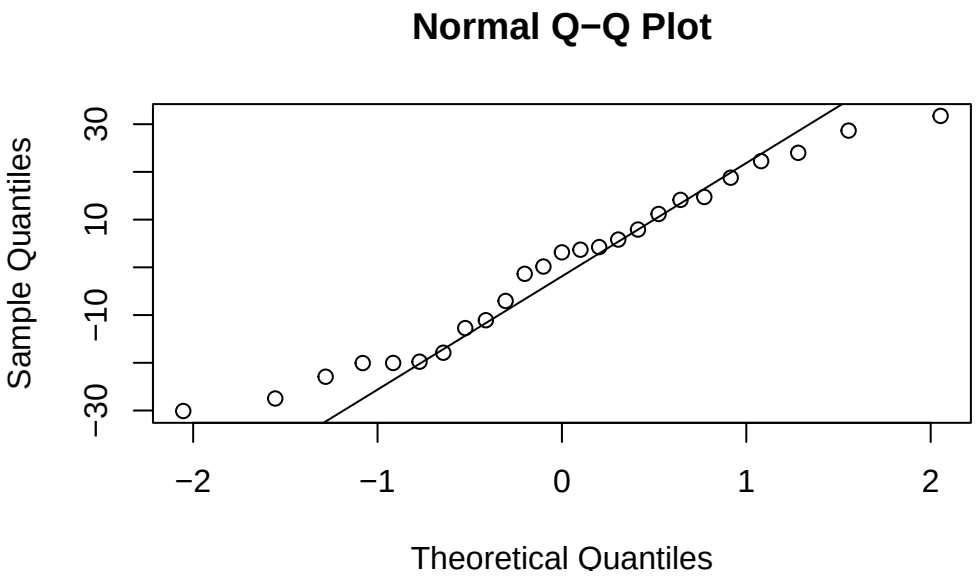
To check for normality of residuals we can use our old friend the Q-Q plot using the residuals stored in the `smoke_res` object we created earlier.

```
ggplot(mapping = aes(sample = smoke_res)) +
    stat_qq() +
    stat_qq_line()
```



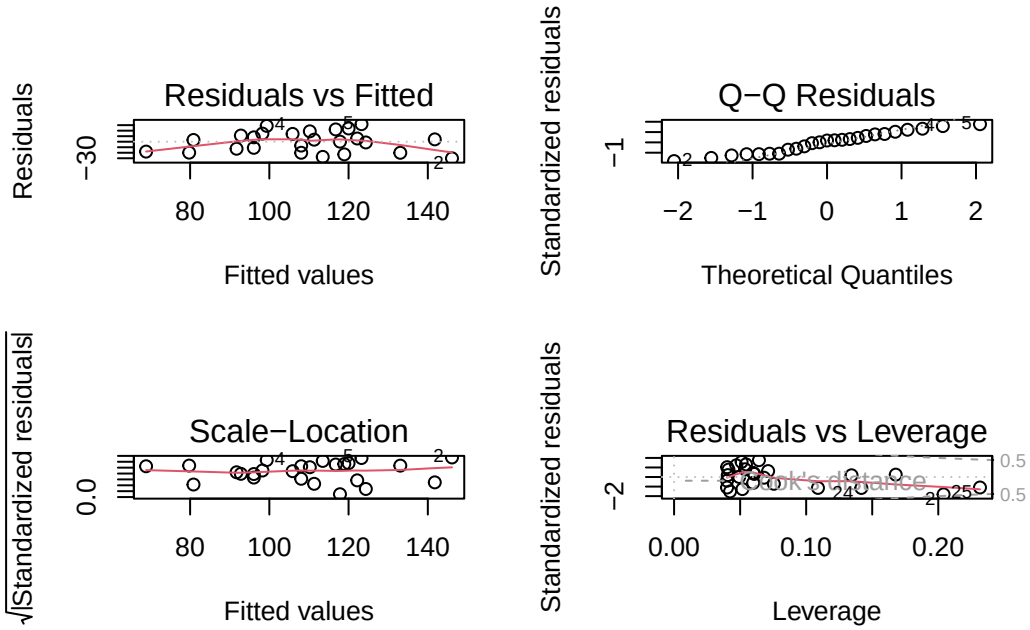
Or the same plot with base graphics.

```
qqnorm(smoke_res)
qqline(smoke_res)
```



Alternatively, you can get R to do most of the hard work by using the `plot()` function on the model object `smoke_lm`. Before we do this we should tell R that we want to plot four graphs in the same plotting window in RStudio using the `par(mfrow = c(2,2))`. This command splits the plotting window into 2 rows and 2 columns.

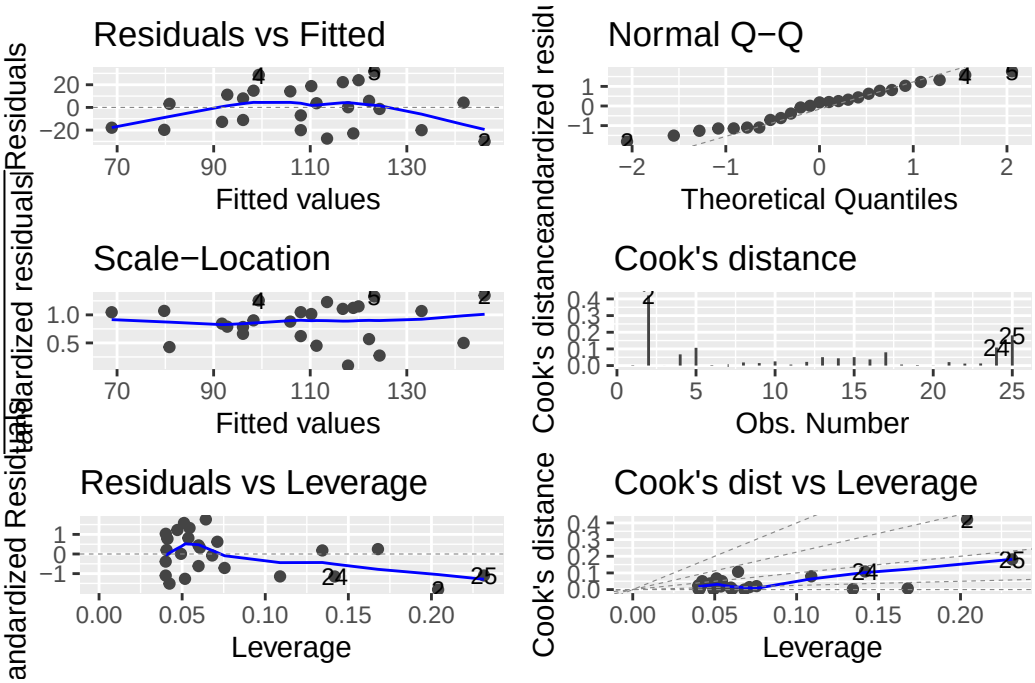
```
par(mfrow = c(2,2))
plot(smoke_lm)
```



The first two graphs (top left and top right) are the same residual versus fitted and Q-Q plots we produced before. The third graph (bottom left) is the same as the first but plotted on a different scale (the absolute value of the square root of the standardised residuals) and again you are looking for no pattern or structure in the data points. The fourth graph (bottom right) gives you an indication whether any of your observations are having a large influence (Cook's distance) on your regression coefficient estimates. Levearge identifies observations which have unusually large values in their explanatory variables.

You can also produce these diagnostic plots using `ggplot` by installing the package `ggfortify` and using the `autoplot()` function.

```
library(ggfortify)
autoplot(smoke_lm, which = 1:6, ncol = 2, label.size = 3)
```



What you do about influential data points or data points with high leverage is up to you. If you would like to examine the effect of removing one of these points on the parameter estimates you can use the `update()` function. Let's remove data point 2 (miners, mortality = 116 and smoking = 137) and store the results in a new object called `smoke_lm2`. Note, we do this to demonstrate the use of the `update()` function. You should think long and hard about removing any data point(s) and if you do you should **always** report this and justify your reasoning.

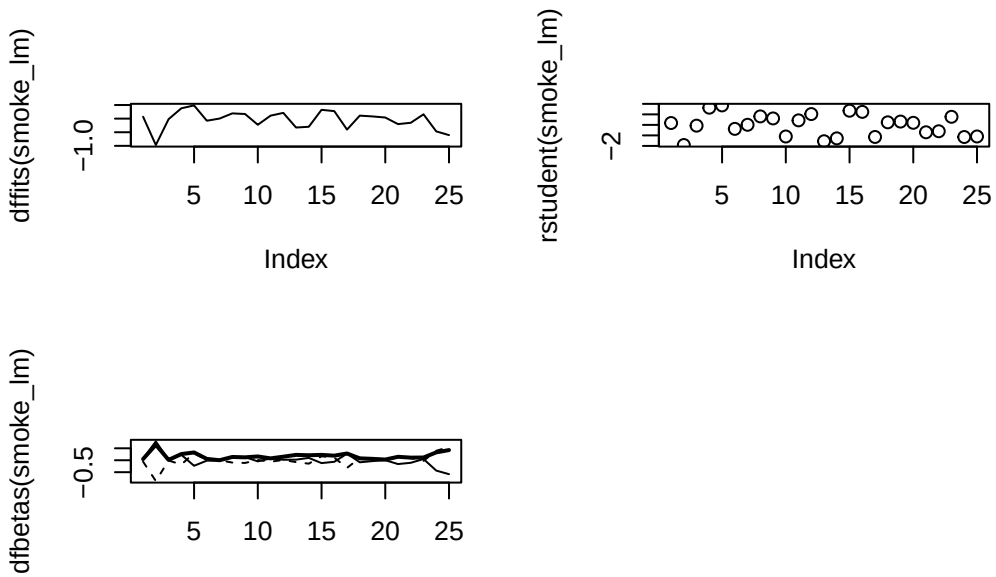
```
smoke_lm2 <- update(smoke_lm, subset = -2)
summary(smoke_lm2)
```

```
Call:
lm(formula = mortality ~ smoking, data = smoke, subset = -2)

Residuals:
     Min       1Q   Median       3Q      Max
-29.7425 -11.6920  -0.4745  13.6141  28.7587

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -20.0755    23.5798  -0.851    0.404
smoking       1.2693     0.2297   5.526 1.49e-05 ***
```

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

Residual standard error: 17.62 on 22 degrees of freedom
Multiple R-squared:  0.5813,    Adjusted R-squared:  0.5622
F-statistic: 30.54 on 1 and 22 DF,  p-value: 1.488e-05
```

There are numerous other functions which are useful for producing diagnostic plots. For example, `rstandard()` and `rstudent()` returns the standardised and studentised residuals. The function `dffits()` expresses how much an observation influences the associated fitted value and the function `dfbetas()` gives the change in the estimated parameters if an observation is excluded, relative to its standard error (intercept is the solid line and slope is the dashed line in the example below). The solid bold line in the same graph represents the Cook's distance. Examples of how to use these functions are given below.

```
par(mfrow=c(2,2))
plot(dffits(smoke_lm), type = "l")
plot(rstudent(smoke_lm))
matplot(dfbetas(smoke_lm), type = "l", col = "black")
lines(sqrt(cooks.distance(smoke_lm)), lwd = 2)
```



5.2. Other modelling approaches

As with most things R related, a complete description of the variety and flexibility of different statistical analyses you can perform is beyond the scope of this introductory text. Further information can be found in any of the excellent documents referred to in Chapter 2. A table of some of the more common statistical functions is given below to get you started.

R function	Use
`glm()`	Fit a generalised linear model with a specific error structure specified using the `family =` argument (Poisson, binomial, gamma)
`gam()`	Fit a generalised additive model. The R package `mgcv` must be loaded
`lme()` & `nlme()`	Fit linear and non-linear mixed effects models. The R package `nlme` must be loaded
`lmer()`	Fit linear and generalised linear and non-linear mixed effects models. The package `lme4` must be **installed** and loaded
`gls()`	Fit generalised least squares models. The R package `nlme` must be loaded
`kruskal.test()`	Performs a Kruskal-Wallis rank sum test
`friedman.test()`	Performs a Friedman's test

Chapter 6

Programming in R

After learning the basics, programming in R is the next big step. There are already a vast number of R packages available, surely more than enough to cover everything you could possibly want to do? Why then, would you ever need to create you own R functions? Why not just stick to the functions from a package? Well, in some cases you'll want to customise those existing functions to suit your specific needs. Or you may want to implement a new approach which means there won't be any pre-existing packages that work for you. Both of these are not particularly common. Functions are mainly used to do one thing well in a simple manner without having to type of the code necessary to do that function each time. We can see functions as a short-cut to copy-pasting. If you have to do a similar task 4 times or more, build a function for it, and simply call that function 4 times or call it in a loop .

6.1. Looking behind the curtain

A good way to start learning to program in R is to see what others have done. We can start by briefly peeking behind the curtain. In Chapter 5 we made use of the `theme_classic()` function when customising our `ggplot` figures. With many functions in R, if you want to have a quick glance at the machinery behind the scenes, we can simply write the function name but without the `()`. This is the same trick we used in Chapter 5 to alter the `theme_classic()` style of `ggplot2` to make `theme_rbook()`.

Note that to view the source code of base R packages (those that come with R) requires some additional steps which we won't cover here (see this link if you're interested), but for most other packages that you install yourself, generally entering the function name without `()` will show the source code of the function.

```
theme_classic
```

```
function (base_size = 11, base_family = "", base_line_size = base_size/22,
    base_rect_size = base_size/22)
{
    theme_bw(base_size = base_size, base_family = base_family,
        base_line_size = base_line_size, base_rect_size = base_rect_size) %+replace%
        theme(panel.border = element_blank(), panel.grid.major = element_blank(),
            panel.grid.minor = element_blank(), axis.line = element_line(colour = "black",
                linewidth = rel(1)), strip.background = element_rect(fill = "white",
                colour = "black", linewidth = rel(2)), complete = TRUE)
}
<bytecode: 0x5840a29ca028>
<environment: namespace:ggplot2>
```

What we see above is the underlying code for this particular function. As we did in Chapter 5, we could copy and paste this into our own script and make any changes we deemed necessary. This approach isn't limited to `ggplot2` functions and can be used for other functions as well, although tread carefully and test the changes you've made.

Don't worry overly if most of the code contained in functions doesn't make sense immediately. This will be especially true if you are new to R, in which case it seems incredibly intimidating. To help with that, we'll begin by making our own functions in R in the next section.

6.2. Functions in R

Functions are your loyal servants, waiting patiently to do your bidding to the best of their ability. They're made with the utmost care and attention … though sometimes may end up being something of a Frankenstein's monster - with an extra limb or two and a head put on backwards. But no matter how ugly they may be they're completely faithful to you.

They're also very stupid.

If we asked you to go to the supermarket to get us some ingredients to make *Francesinha*, even if you don't know what the heck that is, you'd be able to guess and bring at least *something* back. Or you could decide to make something else. Or you could ask a celebrity chef for help. Or you could pull out your phone and search online for what *Francesinha*

is. The point is, even if we didn't give you enough information to do the task, you're intelligent enough to, at the very least, try to find a work around.

If instead, we asked our loyal function to do the same, it would listen intently to our request, stand still for a few milliseconds, compose itself, and then start shouting `Error: 'data' must be a data frame, or other object ...`. It would then repeat this every single time we asked it to do the job. The point here, is that code and functions are not intelligent. They cannot find workarounds. It's totally reliant on you, to tell it very explicitly what it needs to do step by step.

Remember two things: the intelligence of code comes from the coder, not the computer and functions need exact instructions to work.

To prevent functions from being *too* stupid you must provide the information the function needs in order for it to function. As with the *Francesinha* example, if we'd supplied a recipe list to the function, it would have managed just fine. We call this "fulfilling an argument". The vast majority of functions require the user to fulfill at least one argument.

This can be illustrated in the pseudocode below. When we make a function we can specify what arguments the user must fulfill (e.g. `argument1` and `argument2`), as well as what to do once it has this information (`expression`):

```
nameOfFunction <- function(argument1, argument2, ...) {expression}
```

The first thing to note is that we've used the function `function()` to create a new function called `nameOfFunction`. To walk through the above code; we're creating a function called `nameOfFunction`. Within the round brackets we specify what information (i.e. arguments) the function requires to run (as many or as few as needed). These arguments are then passed to the expression part of the function. The expression can be any valid R command or set of R commands and is usually contained between a pair of braces `{ }` (if a function is only one line long you can omit the braces). Once you run the above code, you can then use your new function by typing:

```
nameOfFunction(argument1, argument2)
```

Confused? Let's work through an example to help clear things up.

First we are going to create a data frame called `city`, where columns `porto`, `aberdeen`, `nairobi`, and `genoa` are filled with 100 random values drawn from a bag (using the `rnorm()` function to draw random values from a Normal distribution with mean 0 and standard deviation of 1). We also include a "problem", for us to solve later, by including 10 `NA` values within the `nairobi` column (using `rep(NA, 10)`).

```
city <- data.frame(
  porto = rnorm(100),
  aberdeen = rnorm(100),
  nairobi = c(rep(NA, 10), rnorm(90)),
  genoa = rnorm(100)
)
```

Let's say that you want to multiply the values in the variables `Porto` and `Aberdeen` and create a new object called `porto_aberdeen`. We can do this "by hand" using:

```
porto_aberdeen <- city$porto * city$aberdeen
```

We've now created an object called `porto_aberdeen` by multiplying the vectors `city$porto` and `city$aberdeen`. Simple. If this was all we needed to do, we can stop here. R works with vectors, so doing these kinds of operations in R is actually much simpler than other programming languages, where this type of code might require loops (we say that R is a vectorised language). Something to keep in mind for later is that doing these kinds of operations with loops can be much slower compared to vectorisation.

But what if we want to repeat this multiplication many times? Let's say we wanted to multiply columns `porto` and `aberdeen`, `aberdeen` and `genoa`, and `nairobi` and `genoa`. In this case we could copy and paste the code, replacing the relevant information.

```
porto_aberdeen <- city$porto * city$aberdeen
aberdeen_genoa <- city$aberdeen * city$aberdeen
nairobi_genoa <- city$nairobi * city$genoa
```

While this approach works, it's easy to make mistakes. In fact, here we've "forgotten" to change `aberdeen` to `genoa` in the second line of code when copying and pasting. This is where writing a function comes in handy. If we were to write this as a function, there is only one source of potential error (within the function itself) instead of many copy-pasted lines of code (which we also cut down on by using a function).

In this case, we're using some fairly trivial code where it's maybe hard to make a genuine mistake. But what if we increased the complexity?

```
city$porto * city$aberdeen / city$porto + (city$porto * 10^(city$aberdeen))
                  - city$aberdeen - (city$porto * sqrt(city$aberdeen + 10))
```

Now imagine having to copy and paste this three times, and in each case having to change the `porto` and `aberdeen` variables (especially if we had to do it more than three times).

What we could do instead is generalise our code for `x` and `y` columns instead of naming specific cities. If we did this, we could recycle the `x * y` code. Whenever we wanted to multiple columns together, we assign a city to either `x` or `y`. We'll assign the multiplication to the objects `porto_aberdeen` and `aberdeen_nairobi` so we can come back to them later.

```
# Assign x and y values
x <- city$porto
y <- city$aberdeen

# Use multiplication code
porto_aberdeen <- x * y

# Assign new x and y values
x <- city$aberdeen
y <- city$nairobi

# Reuse multiplication code
aberdeen_nairobi <- x * y
```

This is essentially what a function does. OK down to business, let's call our new function `multiply_columns()` and define it with two arguments, `x` and `y`. In the function code we simply return the value of `x * y` using the `return()` function. Using the `return()` function is not strictly necessary in this example as R will automatically return the value of the last line of code in our function. We include it here to make this explicit.

```
multiply_columns <- function(x, y) {
  return(x * y)
}
```

Now that we've defined our function we can use it. Let's use the function to multiple the columns `city$porto` and `city$aberdeen` and assign the result to a new object called `porto_aberdeen_func`

```
porto_aberdeen_func <- multiply_columns(x = city$porto, y = city$aberdeen)
porto_aberdeen_func
```

```
  [1] -0.2226534692  1.1880805231  0.1814270915  0.0989020854  3.9872291132
  [6] -0.5977754686  0.5444666325  1.1996874055 -0.8343032529  0.2920254640
 [11]  0.0007133667 -0.1934707357 -0.5403180552  0.3287203437 -0.0001032719
 [16] -0.9880346135 -1.8595135151  0.1273776558  0.0249131833 -0.4446982234
 [21] -1.0627693011 -0.0219348037 -0.4157523087  1.6286201097 -1.5984824351
 [26]  0.4200883988  2.1574689907  1.5349735546 -0.9636286684  0.0014540914
 [31]  0.2322260663  0.1866718461  0.0718934802 -0.2886349138 -1.4588574414
 [36] -0.2813320401 -0.8126343133 -0.4426513050 -0.1012059885  0.7730529441
 [41] -0.2746255839 -2.1301745839  0.1265593402 -0.0256411285  0.1098799491
 [46] -0.0241617139  1.0513142030 -4.4240003942  0.0053162222 -0.8499524978
 [51] -0.0929776155  0.3308466444 -0.4727574830  0.1588052756  4.0041293844
 [56] -1.9853903599  1.3471289721 -0.5057469750  0.6251433258 -1.0253361904
 [61] -0.9409894960 -1.4980674042 -6.6943955805  1.8230059581 -0.1831085116
 [66] -1.4705061624  0.6385654600 -0.6715011665 -0.2287881593 -1.4417718700
 [71] -0.1217697828  0.1355584070 -1.1730128394  0.6642334006 -0.1055202208
 [76]  0.1853072661 -0.4816117616 -0.1242301856 -0.2122008605  0.3719609647
 [81] -0.6301360553 -0.0991322474  0.6812676223 -0.3780289254  0.1411044208
 [86]  0.3549194481  1.7646705511 -0.0065988156 -2.8174014582  0.0575420245
 [91]  0.5683463601 -0.2517295319 -0.0104356564  1.3652787622  0.2741571035
 [96]  0.4440003960  0.3358861153 -2.2791604147 -0.0563732373  0.4509992873
```

If we're only interested in multiplying `city$porto` and `city$aberdeen`, it would be overkill to create a function to do something once. However, the benefit of creating a function is that we now have that function added to our environment which we can use as often as we like. We also have the code to create the function, meaning we can use it in completely new projects, reducing the amount of code that has to be written (and retested) from scratch each time. As a rule of thumb, you should consider writing a function whenever you've copied and pasted a block of code more than twice.

To satisfy ourselves that the function has worked properly, we can compare the `porto_aberdeen` variable with our new variable `porto_aberdeen_func` using the `identical()` function. The `identical()` function tests whether

two objects are *exactly* identical and returns either a `TRUE` or `FALSE` value. Use `?identical` if you want to know more about this function.

```
identical(porto_aberdeen, porto_aberdeen_func)
```

```
[1] TRUE
```

And we confirm that the function has produced the same result as when we do the calculation manually. We recommend getting into a habit of checking that the function you've created works the way you think it has.

Now let's use our `multiply_columns()` function to multiply columns `aberdeen` and `nairobi`. Notice now that argument `x` is given the value `city$aberdeen`and `y` the value `city$nairobi`.

```
aberdeen_nairobi_func <- multiply_columns(x = city$aberdeen, y = city$nairobi)
aberdeen_nairobi_func
```

```
  [1]           NA           NA           NA           NA           NA
  [6]           NA           NA           NA           NA           NA
 [11]  0.0545634360  1.3576118854 -1.0999833175 -0.6862792586  0.0001551237
 [16] -0.7461097190  2.0969921558 -0.0194061873  0.1410558187  1.7306148008
 [21] -0.6779174706 -0.0724864784 -0.1158826365  2.2382544647 -0.4820598014
 [26]  0.2805586422  0.3663618817 -0.9503373609  0.5757721888  0.1211847607
 [31]  1.2333184366  0.2814665723  0.6232603358 -0.3954594402 -0.4814305123
 [36] -0.3763252817  1.8777569904  0.9548340500  0.1257968369 -1.7359822151
 [41]  0.1838761622  0.0595199560  0.0034114398 -0.0736841353 -0.7440389702
 [46]  0.0025158196 -0.6578604808 -0.1353340904  0.1102598078 -0.0087700111
 [51] -0.2917424090  0.2593827318  0.6109757591  0.0401056587  1.3957914012
 [56] -1.2150507745 -0.1651263862 -1.7729517482 -1.8766781615 -2.1302674515
 [61]  1.5033990188  0.7927088281  2.1836706688 -0.3061005757  0.5002538542
 [66] -0.5953826183  1.5950390561 -0.1319082236  0.1839734519  0.1827633576
 [71] -0.1948817218  0.1840029066 -0.7511408894  0.8067155851 -0.0909972235
 [76]  0.3696791485 -0.2525939688  0.0915550202 -0.1363958195 -0.4249354581
 [81]  0.5562872088 -0.3749797734 -0.4544912787  0.1101833315 -0.2659179494
 [86] -0.1068542866  0.0035725589 -0.0372862127 -1.4550406317  0.1227147745
 [91]  0.0453921853 -0.8164114865 -0.0162087442 -0.9020195666 -0.6349623851
 [96]  0.1468290842  0.1685790506 -0.2879575842  0.3751092806  1.5998959633
```

So far so good. All we've really done is wrapped the code `x * y` into a function, where we ask the user to specify what their `x` and `y` variables are.

Now let's add a little complexity. If you look at the output of `nairobi_genoa` some of the calculations have produced `NA` values. This is because of those `NA` values we included in `nairobi` when we created the `city` data frame. Despite these `NA` values, the function appeared to have worked but it gave us no indication that there might be a problem. In such cases we may prefer if it had warned us that something was wrong. How can we get the function to let us know when `NA` values are produced? Here's one way.

```
multiply_columns <- function(x, y) {
  temp_var <- x * y
  if (any(is.na(temp_var))) {
    warning("The function has produced NAs")
    return(temp_var)
  } else {
    return(temp_var)
  }
}

aberdeen_nairobi_func <- multiply_columns(city$aberdeen, city$nairobi)
```

```
Warning in multiply_columns(city$aberdeen, city$nairobi): The function has
produced NAs
```

```
porto_aberdeen_func <- multiply_columns(city$porto, city$aberdeen)
```

The core of our function is still the same. We still have `x * y`, but we've now got an extra six lines of code. Namely, we've included some conditional statements, `if` and `else`, to test whether any `NA`s have been produced and if they have we display a warning message to the user. The next section of this Chapter will explain how these work and how to use them.

6.3. Conditional statements

`x * y` does not apply any logic. It merely takes the value of `x` and multiplies it by the value of `y`. Conditional statements are how you inject some logic into your code. The most commonly used conditional statement is `if`.

Whenever you see an `if` statement, read it as *'If X is TRUE, do a thing'*. Including an `else` statement simply extends the logic to *'If X is TRUE, do a thing, or else do something different'*.

Both the `if` and `else` statements allow you to run sections of code, depending on a condition is either `TRUE` or `FALSE`. The pseudocode below shows you the general form.

```
if (condition) {
Code executed when condition is TRUE
} else {
Code executed when condition is FALSE
}
```

To delve into this a bit more, we can use an old programmer joke to set up a problem.

> A programmer's partner says: *'Please go to the store and buy a carton of milk and if they have eggs, get six.'*
>
> The programmer returned with 6 cartons of milk.
>
> When the partner sees this, and exclaims *'Why the heck did you buy six cartons of milk?'*
>
> The programmer replied *'They had eggs'*

At the risk of explaining a joke, the conditional statement here is whether or not the store had eggs. If coded as per the original request, the programmer should bring 6 cartons of milk if the store had eggs (condition = TRUE), or else bring 1 carton of milk if there weren't any eggs (condition = FALSE). In R this is coded as:

```
eggs <- TRUE # Whether there were eggs in the store


  if (eggs == TRUE) { # If there are eggs
  n.milk <- 6 # Get 6 cartons of milk
    } else { # If there are not eggs
  n.milk <- 1 # Get 1 carton of milk
  }
```

We can then check `n.milk` to see how many milk cartons they returned with.

```
n.milk
```

```
[1] 6
```

And just like the joke, our R code has missed that the condition was to determine whether or not to buy eggs, not more milk (this is actually a loose example of the Winograd Scheme, designed to test the *intelligence* of artificial intelligence by whether it can reason what the intended referent of a sentence is).

We could code the exact same egg-milk joke conditional statement using an `ifelse()` function.

```
eggs <- TRUE
n.milk <- ifelse(eggs == TRUE, yes = 6, no = 1)
```

This `ifelse()` function is doing exactly the same as the more fleshed out version from earlier, but is now condensed down into a single line of code. It has the added benefit of working on vectors as opposed to single values (more on this later when we introduce loops). The logic is read in the same way; "If there are eggs, assign a value of 6 to `n.milk`, if there isn't any eggs, assign the value 1 to `n.milk`".

We can check again to make sure the logic is still returning 6 cartons of milk:

```
n.milk
```

```
[1] 6
```

Currently we'd have to copy and paste code if we wanted to change if eggs were in the store or not. We learned above how to avoid lots of copy and pasting by creating a function. Just as with the simple `x * y` expression in our previous `multiply_columns()` function, the logical statements above are straightforward to code and well suited to be turned into a function. How about we do just that and wrap this logical statement up in a function?

```
milk <- function(eggs) {
  if (eggs == TRUE) {
    6
  } else {
    1
  }
}
```

We've now created a function called `milk()` where the only argument is `eggs`. The user of the function specifies if eggs is either `TRUE` or `FALSE`, and the function will then use a conditional statement to determine how many cartons of milk are returned.

Let's quickly try:

```
milk(eggs = TRUE)
```

```
[1] 6
```

And the joke is maintained. Notice in this case we have actually specified that we are fulfilling the `eggs` argument (`eggs = TRUE`). In some functions, as with ours here, when a function only has a single argument we can be lazy and not name which argument we are fulfilling. In reality, it's generally viewed as better practice to explicitly state which arguments you are fulfilling to avoid potential mistakes.

OK, lets go back to the `multiply_columns()` function we created above and explain how we've used conditional statements to warn the user if `NA` values are produced when we multiple any two columns together.

```
multiply_columns <- function(x, y) {
  temp_var <- x * y
  if (any(is.na(temp_var))) {
    warning("The function has produced NAs")
    return(temp_var)
  } else {
    return(temp_var)
  }
}
```

In this new version of the function we still use `x * y` as before but this time we've assigned the values from this calculation to a temporary vector called `temp_var` so we can use it in our conditional statements. Note, this `temp_var` variable is *local* to our function and will not exist outside of the function due something called R's scoping rules. We then use an `if` statement to determine whether our `temp_var` variable contains any `NA` values. The way this works is that we first use the `is.na()` function to test whether each value in our `temp_var` variable is an `NA`. The `is.na()` function returns `TRUE` if the value is an `NA` and `FALSE` if the value isn't an `NA`. We then nest the `is.na(temp_var)` function inside the function `any()` to test whether **any** of the values returned by `is.na(temp_var)` are `TRUE`. If at least one value is `TRUE` the `any()` function will return a `TRUE`. So, if there are any `NA` values in our `temp_var`

variable the condition for the `if()` function will be `TRUE` whereas if there are no `NA` values present then the condition will be `FALSE`. If the condition is `TRUE` the `warning()` function generates a warning message for the user and then returns the `temp_var` variable. If the condition is `FALSE` the code below the `else` statement is executed which just returns the `temp_var` variable.

So if we run our modified `multiple_columns()` function on the columns `city$Aberdeen` and `city$nairobi` (which contains `NA`s) we will receive an warning message.

```
aberdeen_nairobi_func <- multiply_columns(city$aberdeen, city$nairobi)
```

```
Warning in multiply_columns(city$aberdeen, city$nairobi): The function has
produced NAs
```

Whereas if we multiple two columns that don't contain `NA` values we don't receive a warning message

```
porto_aberdeen_func <- multiply_columns(city$porto, city$aberdeen)
```

6.4. Combining logical operators

The functions that we've created so far have been perfectly suited for what we need, though they have been fairly simplistic. Let's try creating a function that has a little more complexity to it. We'll make a function to determine if today is going to be a good day or not based on two criteria. The first criteria will depend on the day of the week (Friday or not) and the second will be whether or not your code is working (TRUE or FALSE). To accomplish this, we'll be using `if` and `else` statements. The complexity will come from `if` statements immediately following the relevant `else` statement. We'll use such conditional statements four times to achieve all combinations of it being a Friday or not, and if your code is working or not.

```
good.day <- function(code.working, day) {
  if (code.working == TRUE && day == "Friday") {
    "BEST.
DAY.
EVER.
Stop while you are ahead and go to the pub!"
  } else if (code.working == FALSE && day == "Friday") {
```

```
    "Oh well, but at least it's Friday! Pub time!"
  } else if (code.working == TRUE && day != "Friday") {
    "So close to a good day...
shame it's not a Friday"
  } else if (code.working == FALSE && day != "Friday") {
    "Hello darkness."
  }
}

good.day(code.working = TRUE, day = "Friday")
```

```
[1] "BEST.\nDAY.\nEVER.\nStop while you are ahead and go to the pub!"
```

```
good.day(FALSE, "Tuesday")
```

```
[1] "Hello darkness."
```

Notice that we never specified what to do if the day was not a Friday? That's because, for this function, the only thing that matters is whether or not it's Friday.

We've also been using logical operators whenever we've used `if` statements. Logical operators are the final piece of the logical conditions jigsaw. Below is a table which summarises operators. The first two are logical operators and the final six are relational operators. You can use any of these when you make your own functions (or loops).

Operator	Technical Description	What it means	Example
`&&`	Logical AND	Both conditions must be met	`if(cond1 == test && cond2 == test)`
`||`	Logical OR	Either condition must be met	`if(cond1 == test || cond2 == test)`
`<`	Less than	X is less than Y	`if(X < Y)`
`>`	Greater than	X is greater than Y	`if(X > Y)`
`<=`	Less than or equal to	X is less/equal to Y	`if(X <= Y)`
`>=`	Greater than or equal to	X is greater/equal to Y	`if(X >= Y)`

Operator	Technical Description	What it means	Example
==	Equal to	X is equal to Y	`if(X == Y)`
!=	Not equal to	X is not equal to Y	`if(X != Y)`

6.5. Loops

R is very good at performing repetitive tasks. If we want a set of operations to be repeated several times we use what's known as a loop. When you create a loop, R will execute the instructions in the loop a specified number of times or until a specified condition is met. There are three main types of loop in R: the *for* loop, the *while* loop and the *repeat* loop.

Loops are one of the staples of all programming languages, not just R, and can be a powerful tool (although in our opinion, used far too frequently when writing R code).

6.5.1. For loop

The most commonly used loop structure when you want to repeat a task a defined number of times is the `for` loop. The most basic example of a `for` loop is:

```
for (i in 1:5) {
  print(i)
}
```

```
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
```

But what's the code actually doing? This is a dynamic bit of code were an index `i` is iteratively replaced by each value in the vector `1:5`. Let's break it down. Because the first value in our sequence (`1:5`) is `1`, the loop starts by replacing

`i` with `1` and runs everything between the `{ }`. Loops conventionally use `i` as the counter, short for iteration, but you are free to use whatever you like, even your pet's name, it really does not matter (except when using nested loops, in which case the counters must be called different things, like `SenorWhiskers` and `HerrFlufferkins`.

So, if we were to do the first iteration of the loop manually

```
i <- 1
print(i)
```

```
[1] 1
```

Once this first iteration is complete, the for loop *loops* back to the beginning and replaces `i` with the next value in our `1:5` sequence (`2` in this case):

```
i <- 2
print(i)
```

```
[1] 2
```

This process is then repeated until the loop reaches the final value in the sequence (`5` in this example) after which point it stops.

To reinforce how `for` loops work and introduce you to a valuable feature of loops, we'll alter our counter within the loop. This can be used, for example, if we're using a loop to iterate through a vector but want to select the next row (or any other value). To show this we'll simply add 1 to the value of our index every time we iterate our loop.

```
for (i in 1:5) {
  print(i + 1)
}
```

```
[1] 2
[1] 3
[1] 4
[1] 5
[1] 6
```

As in the previous loop, the first value in our sequence is 1. The loop begins by replacing `i` with `1`, but this time we've specified that a value of `1` must be added to `i` in the expression resulting in a value of `1 + 1`.

```
i <- 1
i + 1
```

```
[1] 2
```

As before, once the iteration is complete, the loop moves onto the next value in the sequence and replaces `i` with the next value (2 in this case) so that `i + 1` becomes `2 + 1`.

```
i <- 2
i + 1
```

```
[1] 3
```

And so on. We think you get the idea! In essence this is all a `for` loop is doing and nothing more.

Whilst above we have been using simple addition in the body of the loop, you can also combine loops with functions.

Let's go back to our data frame `city`. Previously in the Chapter we created a function to multiply two columns and used it to create our `porto_aberdeen`, `aberdeen_nairobi`, and `nairobi_genoa` objects. We could have used a loop for this. Let's remind ourselves what our data look like and the code for the `multiple_columns()` function.

```
# Recreating our dataset
city <- data.frame(
  porto = rnorm(100),
  aberdeen = rnorm(100),
  nairobi = c(rep(NA, 10), rnorm(90)),
  genoa = rnorm(100)
)


# Our function
multiply_columns <- function(x, y) {
  temp <- x * y
  if (any(is.na(temp))) {
```

```
    warning("The function has produced NAs")
    return(temp)
  } else {
    return(temp)
  }
}
```

To use a list to iterate over these columns we need to first create an empty list (remember lists?) which we call `temp` (short for temporary) which will be used to store the output of the `for` loop.

```
temp <- list()
for (i in 1:(ncol(city) - 1)) {
  temp[[i]] <- multiply_columns(x = city[, i], y = city[, i + 1])
}
```

```
Warning in multiply_columns(x = city[, i], y = city[, i + 1]): The function has
produced NAs
```

```
Warning in multiply_columns(x = city[, i], y = city[, i + 1]): The function has
produced NAs
```

When we specify our `for` loop notice how we subtracted 1 from `ncol(city)`. The `ncol()` function returns the number of columns in our `city` data frame which is `4` and so our loop runs from `i = 1` to `i = 4 - 1` which is `i = 3`. We'll come back to why we need to subtract 1 from this in a minute.

So in the first iteration of the loop `i` takes on the value `1`. The `multiply_columns()` function multiplies the `city[, 1]` (`porto`) and `city[, 1 + 1]` (`aberdeen`) columns and stores it in the `temp[[1]]` which is the first element of the `temp` list.

The second iteration of the loop `i` takes on the value `2`. The `multiply_columns()` function multiplies the `city[, 2]` (`aberdeen`) and `city[, 2 + 1]` (`nairobi`) columns and stores it in the `temp[[2]]` which is the second element of the `temp` list.

The third and final iteration of the loop `i` takes on the value `3`. The `multiply_columns()` function multiplies the `city[, 3]` (`nairobi`) and `city[, 3 + 1]` (`genoa`) columns and stores it in the `temp[[3]]` which is the third element of the `temp` list.

So can you see why we used `ncol(city) - 1` when we first set up our loop? As we have four columns in our `city` data frame if we didn't use `ncol(city) - 1` then eventually we'd try to add the 4th column with the non-existent 5th column.

Again, it's a good idea to test that we are getting something sensible from our loop (remember, check, check and check again!). To do this we can use the `identical()` function to compare the variables we created `by hand` with each iteration of the loop manually.

```
porto_aberdeen_func <- multiply_columns(city$porto, city$aberdeen)
i <- 1
identical(multiply_columns(city[, i], city[, i + 1]), porto_aberdeen_func)
```

```
[1] TRUE
```

```
aberdeen_nairobi_func <- multiply_columns(city$aberdeen, city$nairobi)
```

```
Warning in multiply_columns(city$aberdeen, city$nairobi): The function has
produced NAs
```

```
i <- 2
identical(multiply_columns(city[, i], city[, i + 1]), aberdeen_nairobi_func)
```

```
Warning in multiply_columns(city[, i], city[, i + 1]): The function has
produced NAs
```

```
[1] TRUE
```

If you can follow the examples above, you'll be in a good spot to begin writing some of your own for loops. That said there are other types of loops available to you.

6.5.2. While loop

Another type of loop that you may use (albeit less frequently) is the `while` loop. The `while` loop is used when you want to keep looping until a specific logical condition is satisfied (contrast this with the `for` loop which will always iterate through an entire sequence).

The basic structure of the while loop is:

```
while(logical_condition){ expression }
```

A simple example of a while loop is:

```
i <- 0
while (i <= 4) {
  i <- i + 1
  print(i)
}
```

```
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
```

Here the loop will only continue to pass values to the main body of the loop (the `expression` body) when `i` is less than or equal to 4 (specified using the `<=` operator in this example). Once `i` is greater than 4 the loop will stop.

There is another, very rarely used type of loop; the `repeat` loop. The `repeat` loop has no conditional check so can keep iterating indefinitely (meaning a break, or "stop here", has to be coded into it). It's worthwhile being aware of it's existence, but for now we don't think you need to worry about it; the `for` and `while` loops will see you through the vast majority of your looping needs.

6.5.3. When to use a loop?

Loops are fairly commonly used, though sometimes a little overused in our opinion. Equivalent tasks can be performed with functions, which are often more efficient than loops. Though this raises the question when should you use a loop?

In general loops are implemented inefficiently in R and should be avoided when better alternatives exist, especially when you're working with large datasets. However, loop are sometimes the only way to achieve the result we want.

Some examples of when using loops can be appropriate:

- Some simulations (e.g. the Ricker model can, in part, be built using loops)

- Recursive relationships (a relationship which depends on the value of the previous relationship ["to understand recursion, you must understand recursion"])
- More complex problems (e.g., how long since the last badger was seen at site j, given a pine marten was seen at time t, at the same location j as the badger, where the pine marten was detected in a specific 6 hour period, but exclude badgers seen 30 minutes before the pine marten arrival, repeated for all pine marten detections)
- While loops (keep jumping until you've reached the moon)

6.5.4. If not loops, then what?

In short, use the apply family of functions; `apply()`, `lapply()`, `tapply()`, `sapply()`, `vapply()`, and `mapply()`. The apply functions can often do the tasks of most "home-brewed" loops, sometimes faster (though that won't really be an issue for most people) but more importantly with a much lower risk of error. A strategy to have in the back of your mind which may be useful is; for every loop you make, try to remake it using an apply function (often `lapply` or `sapply` will work). If you can, use the apply version. There's nothing worse than realising there was a small, tiny, seemingly meaningless mistake in a loop which weeks, months or years down the line has propagated into a huge mess. We strongly recommend trying to use the apply functions whenever possible.

lapply

Your go to apply function will often be `lapply()` at least in the beginning. The way that `lapply()` works, and the reason it is often a good alternative to for loops, is that it will go through each element in a list and perform a task (i.e. run a function). It has the added benefit that it will output the results as a list - something you'd have to otherwise code yourself into a loop.

An `lapply()` has the following structure:

```
lapply(X, FUN)
```

Here `X` is the vector which we want to do *something* to. `FUN` stands for how much fun this is (just kidding!). It's also short for "function".

Let's start with a simple demonstration first. Let's use the `lapply()` function create a sequence from 1 to 5 and add 1 to each observation (just like we did when we used a for loop):

```
lapply(0:4, function(a) {a + 1})
```

```
[[1]]
[1] 1

[[2]]
[1] 2

[[3]]
[1] 3

[[4]]
[1] 4

[[5]]
[1] 5
```

Notice that we need to specify our sequence as `0:4` to get the output `1 ,2 ,3 ,4 , 5` as we are adding `1` to each element of the sequence. See what happens if you use `1:5` instead.

Equivalently, we could have defined the function first and then used the function in `lapply()`

```
add_fun <- function(a) {a + 1}
lapply(0:4, add_fun)
```

```
[[1]]
[1] 1

[[2]]
[1] 2

[[3]]
[1] 3
```

```
[[4]]
[1] 4

[[5]]
[1] 5
```

The `sapply()` function does the same thing as `lapply()` but instead of storing the results as a list, it stores them as a vector.

```
sapply(0:4, function(a) {a + 1})
```

```
[1] 1 2 3 4 5
```

As you can see, in both cases, we get exactly the same results as when we used the for loop.

Chapter 7

Reproducible reports with R markdown / Quarto

> ⚠ Warning
>
> in the process of being updated to Quarto screenshot are still with Rmarkdown links need to be updated too
>
> need to describe YAML code chunk notation

This chapter will introduce you to creating reproducible reports using R markdown / Quarto to encourage best (or better) practice to facilitate open science. It will first describe what R markdown and Quarto are and why you might want to consider using it, describe how to create an R markdown document using RStudio and then how to convert this document to a html or pdf formatted report. During this Chapter you will learn about the different components of an R markdown document, how to format text, graphics and tables within the document and finally how to avoid some of the common difficulties using R markdown.

7.1. What is R markdown?

R markdown is a simple and easy to use plain text language used to combine your R code, results from your data analysis (including plots and tables) and written commentary into a single nicely formatted and reproducible document (like a report, publication, thesis chapter or a web page like this one).

Technically, R markdown is a combination of three languages, R, Mardown and YAML (yet another markup language). Both Markdown and YAML are a type of 'markup' language. A markup language simply provides a way of creating an easy to read plain text file which can incorporate formatted text, images, headers and links to other documents. If you're interested you can find more information about markup languages here. Actually, you are exposed to a markup language on a daily basis, as most of the internet content you digest every day is underpinned by a markup language called HTML (**H**yper**t**ext **M**arkup **L**anguage). Anyway, the main point is that R markdown is very easy to learn

(much, much easier than HTML) and when used with a good IDE (RStudio or VS Code) it's ridiculously easy to integrate into your workflow to produce feature rich content (so why wouldn't you?!).

7.2. What is Quarto?

Quarto is a multi-language, next generation version of R Markdown from Posit, with many new new features and capabilities and is compatible not only with R but also with other language like Python and Julia. Like R Markdown, Quarto uses knitr to execute R code, and is therefore able to render most existing Rmd files without modification. However, it also comes with a plethora of new functionalities. More importantly, it makes it much easier to create different type of output since the coding is homogenize for specific format without having to rely on different r packages each with there own specificity (*e.g* bookdown, hugodown, blogdown, thesisdown, rticles, xaringan, …).

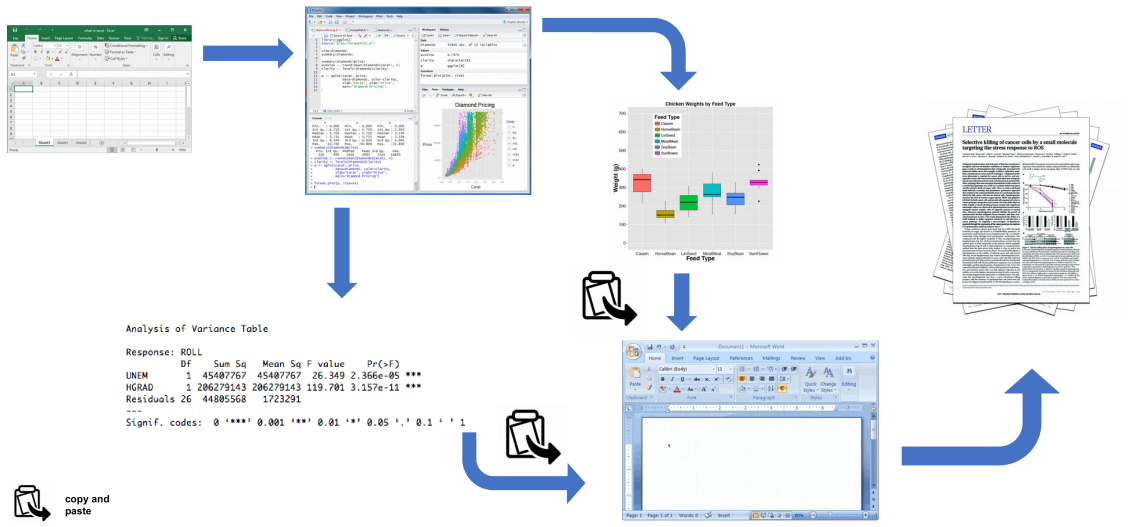
In the rest of this chapter, we will talk about Quarto but nearly everything can be done with R markdown. Quarto uses `.qmd` files while R markdown works with `.Rmd`. Notes that Quarto is also able to knit and render `.Rmd` files.

7.3. Why use Quarto?

During the previous Chapters we talked a lot about conducting your research in a robust and reproducible manner to facilitate open science. In a nutshell, open science is about doing all we can to make our data, methods, results and inferences transparent and available to everyone. Some of the main tenets of open science are described here and include:

- Transparency in experimental methodology, observation, collection of data and analytical methods.
- Public availability and re-usability of scientific data
- Public accessibility and transparency of scientific communication
- Using web-based tools to facilitate scientific collaboration

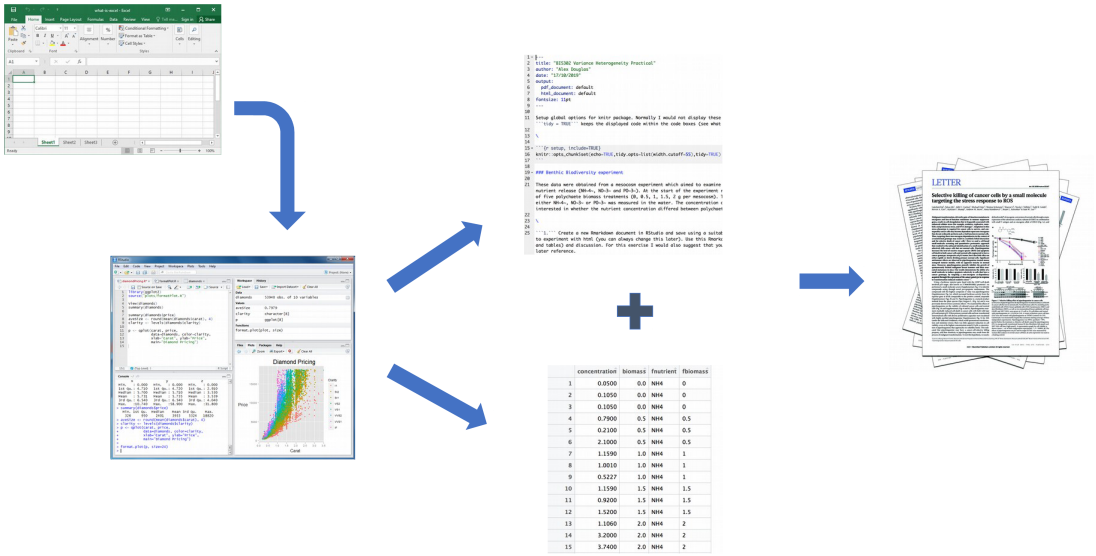
By now all of you will (hopefully) be using R to explore and analyse your interesting data. As such, you're already well along the road to making your analysis more reproducible, transparent and shareable. However, perhaps your current workflow looks something like this:



Your data is imported from your favourite spreadsheet software into R, you write your R code to explore and analyse your data, you save plots as external files, copy tables of analysis output and then manually combine all of this and your written prose into a single MS Word document (maybe a paper or thesis chapter). Whilst there is nothing particularly wrong with this approach (and it's certainly better than using point and click software to analyse your data) there are some limitations:

- It's not particularly reproducible. Because this workflow separates your R code from the final document there are multiple opportunities for undocumented decisions to be made (which plots did you use? what analysis did/didn't you include? etc).
- It's inefficient. If you need to go back and change something (create a new plot or update your analysis etc) you will need to create or amend multiple documents increasing the risk of mistakes creeping into your workflow.
- It's difficult to maintain. If your analysis changes you again need to update multiple files and documents.
- It can be difficult to decide what to share with others. Do you share all of your code (initial data exploration, model validation etc) or just the code specific to your final document? It's quite a common (and bad!) practice for researchers to maintain two R scripts, one used for the actual analysis and one to share with the final paper or thesis chapter. This can be both time consuming and confusing and should be avoided.

Perhaps a more efficient and robust workflow would look something like this:



Your data is imported into R as before but this time all of the R code you used to analyse your data, produce your plots and your written text (Introduction, Materials and Methods, Discussion etc) is contained within a single Quarto document which is then used (along with your data) to automatically create your final document. This is exactly what Quarto allows you to do.

Some of the advantages of using Quarto include:

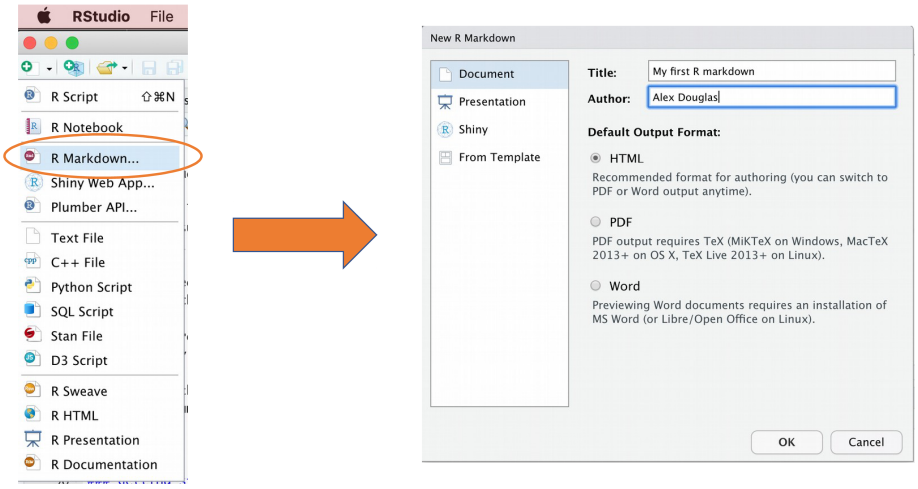
- Explicitly links your data with your R code and output creating a fully reproducible workflow. **ALL** of the R code used to explore, summarise and analyse your data can be included in a single easy to read document. You can decide what to include in your final document (as you will learn below) but all of your R code can be included in the Quarto document.
- You can create a wide variety of output formats (pdf, html web pages, MS Word and many others) from a single Quarto document which enhances both collaboration and communication.
- Enhances transparency of your research. Your data and Quarto file can be included with your publication or thesis chapter as supplementary material or hosted on a GitHub repository (see the GitHub Chapter).
- Increases the efficiency of your workflow. If you need to modify or extend your current analysis you just need to update your Quarto document and these changes will automatically be included in your final document.

7.4. Get started with Quarto

To use Quarto you will first need to install the `Quarto` software and the `quarto` R package (with its dependencies). You can find instructions on how to do this for both Windows and Mac OSX operating systems here. If you would like to create pdf documents (or MS Word documents) from your Quarto file you will also need to install a version of LaTeX on your computer. If you've not installed LaTeX before, we recommend that you install TinyTeX. Again, instructions on how to do this can be found here.

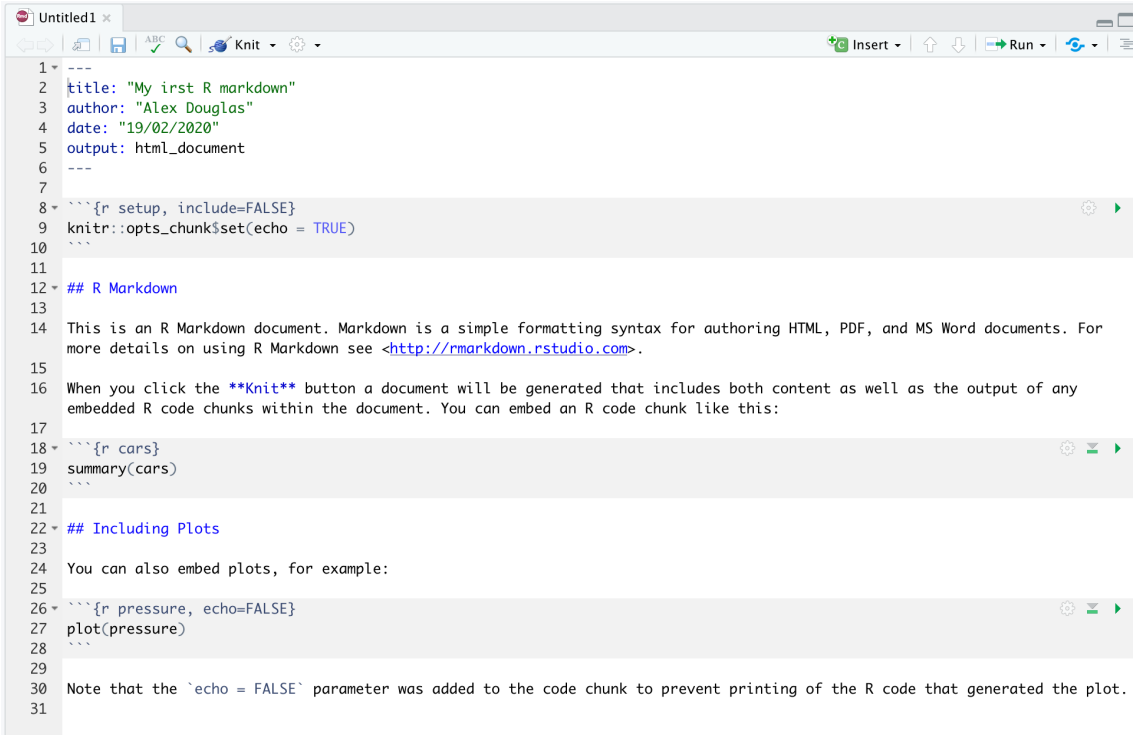
7.5. Create a Quarto document, `.qmd`

Right, time to create your first Quarto document. Within RStudio, click on the menu `File -> New File -> Quarto...`. In the pop up window, give the document a 'Title' and enter the 'Author' information (your name) and select HTML as the default output. We can change all of this later so don't worry about it for the moment.



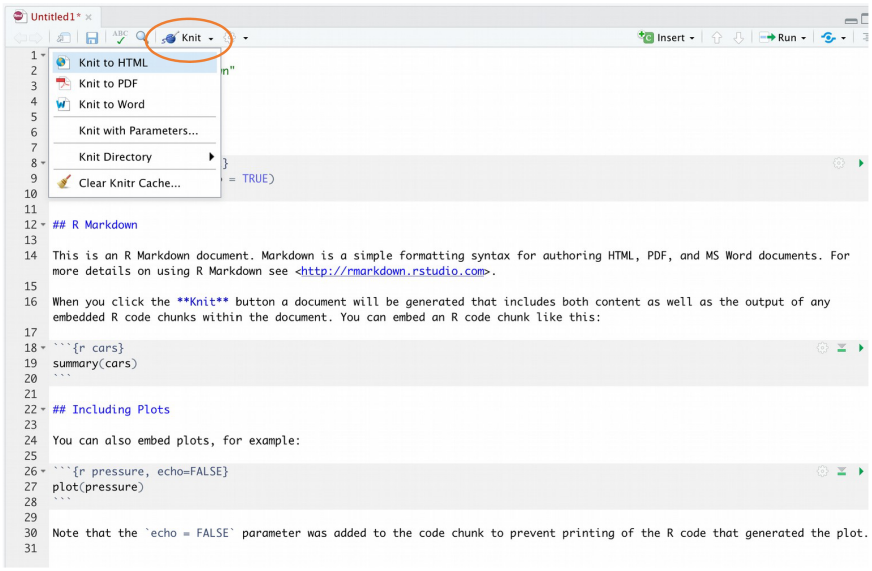
You will notice that when your new Quarto document is created it includes some example Quarto code. Normally you would just highlight and delete everything in the document except the information at the top between the `---` delimiters (this is called the YAML header which we will discuss in a bit) and then start writing your own code.

However, just for now we will use this document to practice converting Quarto to both html and pdf formats and check everything is working.

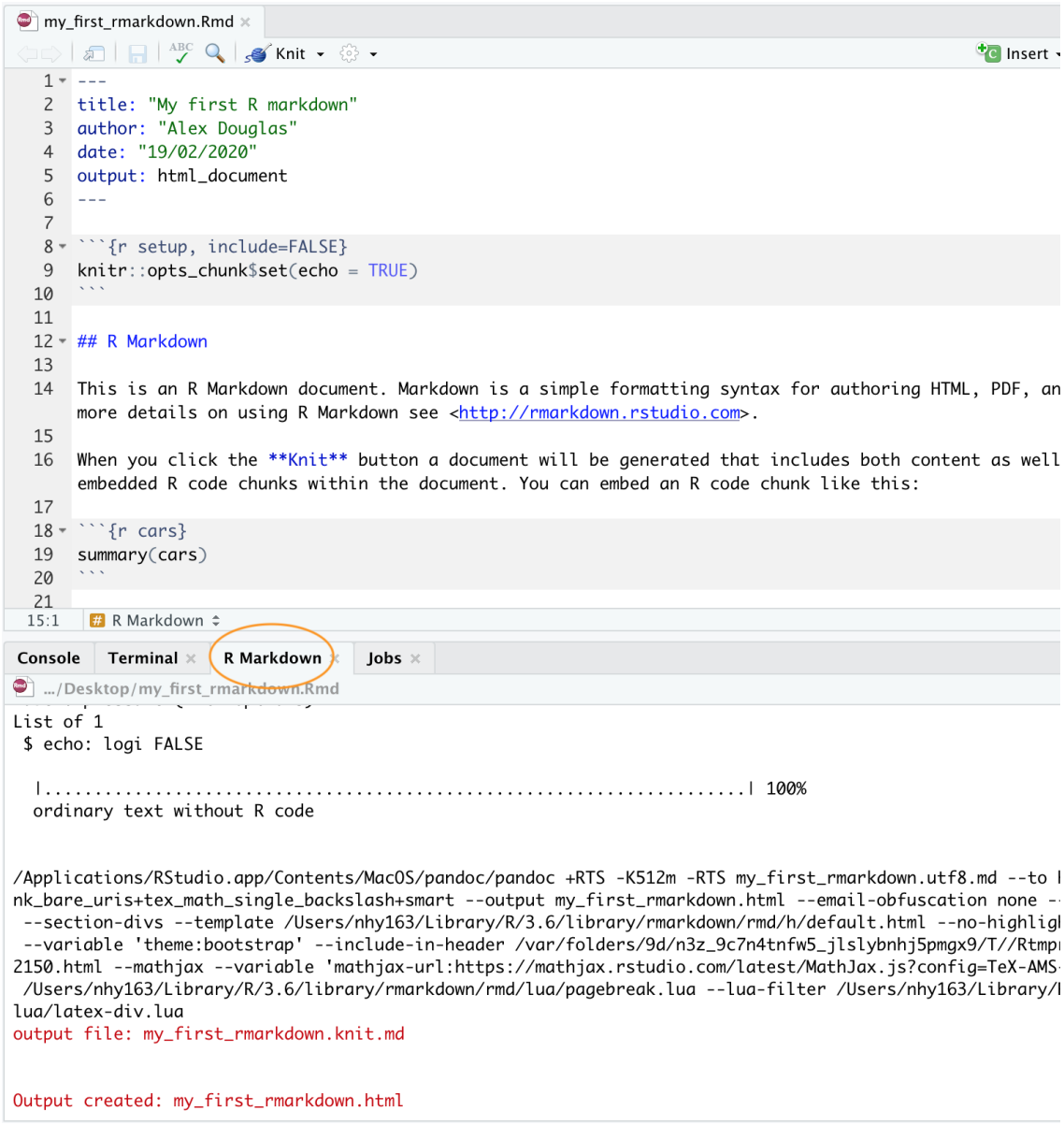


Once you've created your Quarto document it's good practice to save this file somewhere convenient. You can do this by selecting `File -> Save` from RStudio menu (or use the keyboard shortcut ctrl + s on Windows or cmd + s on a Mac) and enter an appropriate file name (maybe call it `my_first_rmarkdown`). Notice the file extension of your new Quarto file is `.qmd`.

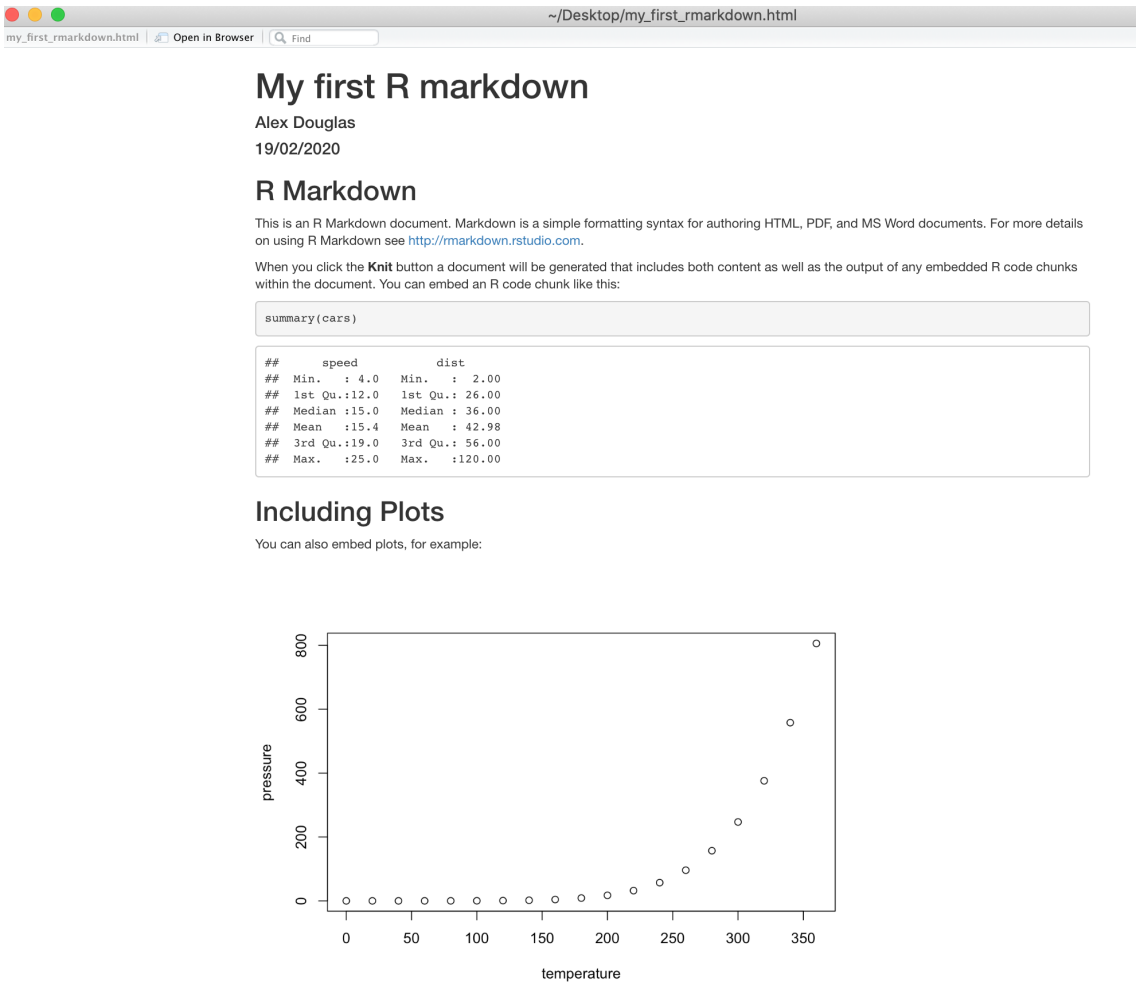
Now, to convert your `.qmd` file to a HTML document click on the little black triangle next to the `Knit` icon at the top of the source window and select `knit to HTML`



RStudio will now 'knit' (or render) your `.qmd` file into a HTML file. Notice that there is a new `Quarto` tab in your console window which provides you with information on the rendering process and will also display any errors if something goes wrong.



If everything went smoothly a new HTML file will have been created and saved in the same directory as your `.Rmd` file (ours will be called `my_first_rmarkdown.html`). To view this document simply double click on the file to open in a browser (like Chrome or Firefox) to display the rendered content. RStudio will also display a preview of the rendered file in a new window for you to check out (your window might look slightly different if you're using a Windows computer).



Great, you've just rendered your first Quarto document. If you want to knit your `.Rmd` file to a pdf document then all you need to do is choose `knit to PDF` instead of `knit to HTML` when you click on the `knit` icon. This will create a file called `my_first_rmarkdown.pdf` which you can double click to open. Give it a go!

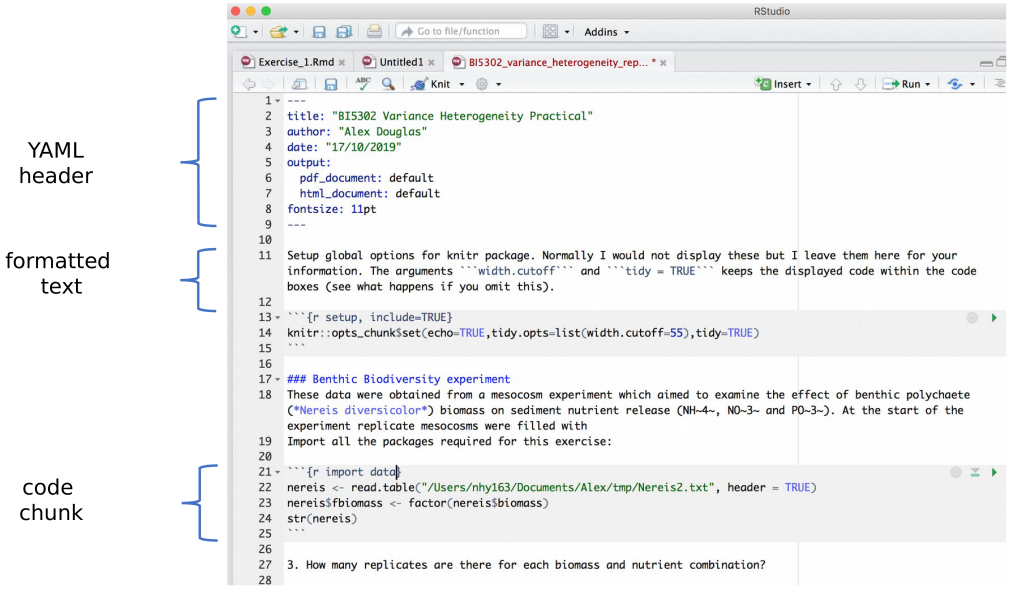
You can also knit an `.Rmd` file using the command line in the console rather than by clicking on the knit icon. To do this, just use the `render()` function from the `rmarkdown` package as shown below. Again, you can change the output format using the `output_format=` argument as well as many other options.

```
library(rmarkdown)

render('my_first_rmarkdown.Rmd', output_format = 'html_document')
```

```
# alternatively if you don't want to load the rmarkdown package

rmarkdown::render('my_first_rmarkdown.Rmd', output_format = 'html_document')

# see ?render for more options
```

7.6. Quarto anatomy

OK, now that you can render a Quarto file in RStudio into both HTML and pdf formats let's take a closer look at the different components of a typical Quarto document. Normally each Quarto document is composed of 3 main components, 1) a YAML header, 2) formatted text and 3) code chunks.



7.6.1. YAML header

YAML stands for '**Y**AML **A**in't **M**arkup **L**anguage' (it's an 'in' joke!) and this optional component contains the metadata and options for the entire document such as the author name, date, output format, etc. The YAML header is surrounded before and after by a `---` on its own line. In RStudio a minimal YAML header is automatically created

for you when you create a new Quarto document as we did above but you can change this any time. A simple YAML header may look something like this:

```
---
title: My first Quarto document
author: Jane Doe
date: March 01, 2020
output: html_document
---
```

In the YAML header above the output format is set to HTML. If you would like to change the output to pdf format then you can change it from `output: html_document` to `output: pdf_document` (you can also set more than one output format if you like). You can also change the default font and font size for the whole document and even include fancy options such as a table of contents and inline references and a bibliography. If you want to explore the plethora of other options see here. Just a note of caution, many of the options you can specify in the YAML header will work with both HTML and pdf formatted documents, but not all. If you need multiple output formats for your Quarto document check whether your YAML options are compatible between these formats. Also, indentation in the YAML header has a meaning, so be careful when aligning text. For example, if you want to include a table of contents you would modify the `output:` field in the YAML header as follows

```
---
title: My first Quarto document
author: Jane Doe
date: March 01, 2020
output:
  html_document:
    toc: yes
---
```

7.6.2. Formatted text

As mentioned above, one of the great things about Quarto is that you don't need to rely on your word processor to bring your R code, analysis and writing together. Quarto is able to render (almost) all of the text formatting that you are likely to need such as italics, bold, strike-through, super and subscript as well as bulleted and numbered lists, headers and footers, images, links to other documents or web pages and also equations. However, in contrast to your

familiar *What-You-See-Is-What-You-Get* (WYSIWYG) word processing software you don't see the final formatted text in your Quarto document (as you would in MS Word), rather you need to 'markup' the formatting in your text ready to be rendered in your output document. At first, this might seem like a right pain in the proverbial but it's actually very easy to do and also has many advantages (do you find yourself spending more time on making your text look pretty in MS Word rather than writing good content?!).

Here is an example of marking up text formatting in an Quarto document

```
#### Benthic Biodiversity experiment
These data were obtained from a mesocosm experiment which aimed to examine the effect
of benthic polychaete (*Nereis diversicolor*) biomass on sediment nutrient
(NH~4~, NO~3~ and PO~3~) release.
At the start of the experiment 15 replicate mesocosms
were filled with 20 cm^2^ of **homogenised** marine sediment and assigned to one of five
polychaete biomass treatments (0, 0.5, 1, 1.5, 2 g per mesocosm).
```

which would look like this in the final rendered document (can you spot the markups?)

Benthic Biodiversity experiment

These data were obtained from a mesocosm experiment which aimed to examine the effect of benthic polychaete (*Nereis diversicolor*) biomass on sediment nutrient (NH_4, NO_3 and PO_3) release. At the start of the experiment replicate mesocosms were filled with 20 cm^2 of **homogenised** marine sediment and assigned to one of five polychaete biomass treatments (0, 0.5, 1, 1.5, 2 g per mesocosm).

Emphasis

Some of the most common Quarto syntax for providing emphasis and formatting text is given below.

Goal	Quarto	output
bold text	`**mytext**`	**mytext**
italic text	`*mytext*`	*mytext*
strikethrough	`~~mytext~~`	~~mytext~~

Goal	Quarto	output
superscript	`mytext^2^`	mytext^2
subscript	`mytext~2~`	mytext$_2$

Interestingly there is no underline in R markdown syntax by default, for multiple more or less esoteric reasons, but Quarto fixed that problem. An underline is considered a stylistic element (there may well be other reasons). If you are using Quarto you can simply do `[text to underline]{.underline}` to underline your text.

White space and line breaks

One of the things that can be confusing for new users of Quarto is the use of spaces and carriage returns (the enter key on your keyboard). In Quarto multiple spaces within the text are generally ignored as are carriage returns. For example this Quarto text

```
These      data were      obtained from a
mesocosm experiment which    aimed to examine the
effect
of          benthic polychaete (*Nereis diversicolor*) biomass.
```

will be rendered as

> These data were obtained from a mesocosm experiment which aimed to examine the effect of benthic polychaete (*Nereis diversicolor*) biomass.

This is generally a good thing (no more random multiple spaces in your text). If you want your text to start on a new line then you can simply add two blank spaces at the end of the preceding line

> These data were obtained from a
> mesocosm experiment which aimed to examine the
> effect benthic polychaete (*Nereis diversicolor*) biomass.

If you really want multiple spaces within your text then you can use the **N**on **b**reaking **sp**ace tag ` `

```
These       data were         obtained from a
mesocosm experiment which     aimed to examine the
effect         benthic polychaete (*Nereis diversicolor*) biomass.
```

These data were obtained from a
mesocosm experiment which aimed to examine the
effect benthic polychaete (*Nereis diversicolor*) biomass.

Headings

You can add headings and subheadings to your Quarto document by using the # symbol at the beginning of the line. You can decrease the size of the headings by simply adding more # symbols. For example

```
# Benthic Biodiversity experiment
## Benthic Biodiversity experiment
### Benthic Biodiversity experiment
#### Benthic Biodiversity experiment
##### Benthic Biodiversity experiment
###### Benthic Biodiversity experiment
```

results in headings in decreasing size order

Benthic Biodiversity experiment

Benthic Biodiversity experiment

Benthic Biodiversity experiment

Benthic Biodiversity experiment

Benthic Biodiversity experiment

Comments

As you can see above the meaning of the # symbol is different when formatting text in an Quarto document compared to a standard R script (which is used to included a comment - remember?!). You can, however, use a # symbol to comment code inside a code chunk as usual (more about this in a bit). If you want to include a comment in your Quarto document outside a code chunk which won't be included in the final rendered document then enclose your comment between `<!--` and `-->`.

```
<!--
this is an example of how to format a comment using Quarto.
-->
```

Lists

If you want to create a bullet point list of text you can format an unordered list with sub items. Notice that the sub-items need to be indented.

```
- item 1
- item 2
   + sub-item 2
   + sub-item 3
- item 3
- item 4
```

- item 1
- item 2
  - sub-item 2
  - sub-item 3
- item 3
- item 4

If you need an ordered list

```
1.
item 1
2.
item 2
     + sub-item 2
```

```
     + sub-item 3
3.
item 3
4.
item 4
```

1. item 1
2. item 2

    - sub-item 2
    - sub-item 3

3. item 3
4. item 4

Images

Another useful feature is the ability to embed images and links to web pages (or other documents) into your Quarto document. You can include images into your Quarto document in a number of different ways. Perhaps the simplest method is to use

```
![Cute grey kitten](images/Cute_grey_kitten.jpg)
```

resulting in:

Figure 7.1.: Cute grey kitten

The code above will only work if the image file (`Cute_grey_kitten.jpg`) is in the right place relative to where you saved your `.Rmd` file. In the example above the image file is in a sub directory (folder) called `images` in the directory where we saved our `my_first_rmarkdown.Rmd` file. You can embed images saved in many different file types but perhaps the most common are `.jpg` and `.png`.

We think a more flexible way of including images in your document is to use the `include_graphics()` function from the `knitr` package as this gives finer control over the alignment and image size (it also works more or less the same with both HTML and pdf output formats). However, to do this you will need to include this R code in a 'code chunk' which we haven't covered yet. Despite this we'll leave the code here for later reference. This code center aligns the image and scales it to 50% of it's original size. See `?include_graphics` for more options.

````
```{r, echo=FALSE, fig.align='center', out.width='50%'}
library(knitr)
include_graphics("images/Cute_grey_kitten.jpg")
```
````

Links

In addition to images you can also include links to webpages or other links in your document. Use the following syntax to create a clickable link to an existing webpage. The link text goes between the square brackets and the URL for the webpage between the round brackets immediately after.

```
You can include a text for your clickable [link](https://www.worldwildlife.org)
```

which gives you:

You can include a text for your clickable link

7.6.1. Code chunks

Now to the heart of the matter. To include R code into your Quarto document you simply place your code into a 'code chunk'. All code chunks start and end with three backticks ```. Note, these are also known as 'grave accents' or 'back quotes' and are not the same as an apostrophe! On most keyboards you can find the backtick on the same key as tilde (~).

````
```{r}
Any valid R code goes here
```
````

You can insert a code chunk by either typing the chunk delimiters ```{r} and ``` manually or use your IDE option (RStudio toolbar (the Insert button) or by clicking on the menu `Code -> Insert Chunk`. IN VS Code you can use code snippets) Perhaps an even better way is to get familiar with the keyboard shortcuts for you IDE.

There are a many things you can do with code chunks: you can produce text output from your analysis, create tables and figures and insert images amongst other things. Within the code chunk you can place rules and arguments between the curly brackets `{}` that give you control over how your code is interpreted and output is rendered. These are known as chunk options. The only mandatory chunk option is the first argument which specifies which language you're using (`r` in our case but other languages are supported). Note, chunk options can be written in two ways:

1. either all of your chunk options must be written between the curly brackets on one line with no line breaks
2. or they can be written using a YAML notation within the code chunk using #| notation at the beginning of the line.

You can also specify an optional code chunk name (or label) which can be useful when trying to debug problems and when performing advanced document rendering. In the following block we name the code chunk `summary-stats`, create a dataframe (`dataf`) with two variables `x` and `y` and then use the `summary()` function to display some summary statistics . When we run the code chunk both the R code and the resulting output are displayed in the final document.

````
```{r, summary-stats, echo = TRUE}
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)

summary(dataf)
```
````

````
```{r}
#| label: summary-stats
#| echo: true
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)

summary(dataf)
```
````

```r
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)

summary(dataf)
```

```
       x                y         
 Min.   : 1.00   Min.   : 1.00  
 1st Qu.: 3.25   1st Qu.: 3.25  
 Median : 5.50   Median : 5.50  
 Mean   : 5.50   Mean   : 5.50  
 3rd Qu.: 7.75   3rd Qu.: 7.75  
 Max.   :10.00   Max.   :10.00  
```

When using chunk names make sure that you don't have duplicate chunk names in your Quarto document and avoid spaces and full stops as this will cause problems when you come to knit your document (We use a - to separate words in our chunk names).

If we wanted to only display the output of our R code (just the summary statistics for example) and not the code itself in our final document we can use the chunk option `echo=FALSE`

````
```{r, summary-stats, echo=FALSE}
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)
summary(dataf)
```
````

```
       x                y        
 Min.   : 1.00   Min.   : 1.00  
 1st Qu.: 3.25   1st Qu.: 3.25  
 Median : 5.50   Median : 5.50  
 Mean   : 5.50   Mean   : 5.50  
 3rd Qu.: 7.75   3rd Qu.: 7.75  
 Max.   :10.00   Max.   :10.00  
```

To display the R code but not the output use the `results='hide'` chunk option.

````
```{r}
#| label: summary-stats
#| results: 'hide'
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)
summary(dataf)
```
````

```r
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)
summary(dataf)
```

Sometimes you may want to execute a code chunk without showing any output at all. You can suppress the entire output using the chunk option `include=FALSE`.

````
```{r, summary-stats, include=FALSE}
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)
summary(dataf)
```
````

There are a large number of chunk options documented here with a more condensed version here. Perhaps the most commonly used are summarised below with the default values shown.

Chunk option	default value	Function
echo	`echo=TRUE`	If FALSE, will not display the code in the final document
results	`results='markup'`	If 'hide', will not display the code's results in the final document.

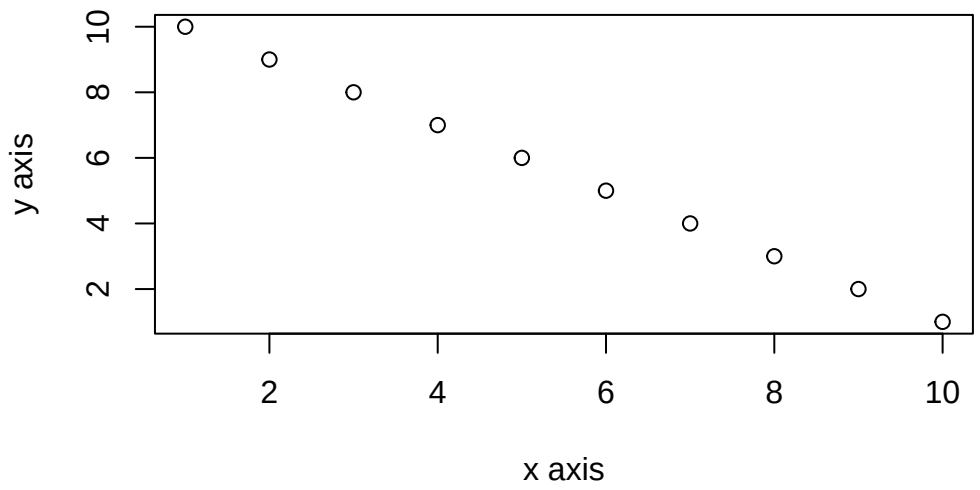
If 'hold', will delay displaying all output pieces until the end of the chunk. If 'asis', will pass through results without reformatting them. | | include | `include=TRUE` | If FALSE, will run the chunk but not include the chunk in the final document. | | eval | `eval=TRUE` | If FALSE, will not run the code in the code chunk. | | message | `message=TRUE` | If FALSE, will not display any messages generated by the code. | | warning | `warning=TRUE` | If FALSE, will not display any warning messages generated by the code. |

7.6.2. Adding figures

By default, figures produced by R code will be placed immediately after the code chunk they were generated from. For example:

````
```{r, simple-plot}
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)
plot(dataf$x, dataf$y, xlab = "x axis", ylab = "y axis")
```
````

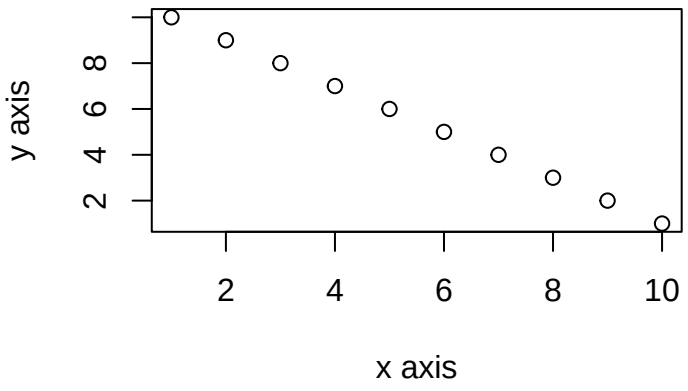
```r
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)
plot(dataf$x, dataf$y, xlab = "x axis", ylab = "y axis")
```



If you want to change the plot dimensions in the final document you can use the `fig.width=` and `fig.height=` chunk options (in inches!). You can also change the alignment of the figure using the `fig.align=` chunk option.

````
```{r, simple-plot, fig.width=4, fig.height=3, fig.align='center'}
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)
plot(dataf$x, dataf$y, xlab = "x axis", ylab = "y axis")
```
````

```
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)
plot(dataf$x, dataf$y, xlab = "x axis", ylab = "y axis")
```



You can add a figure caption using the `fig.cap=` option.

````
```{r, simple-plot-cap, fig.cap="A simple plot", fig.align='center'}
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)
plot(dataf$x, dataf$y, xlab = "x axis", ylab = "y axis")
```
````

```
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)
plot(dataf$x, dataf$y, xlab = "x axis", ylab = "y axis")
```

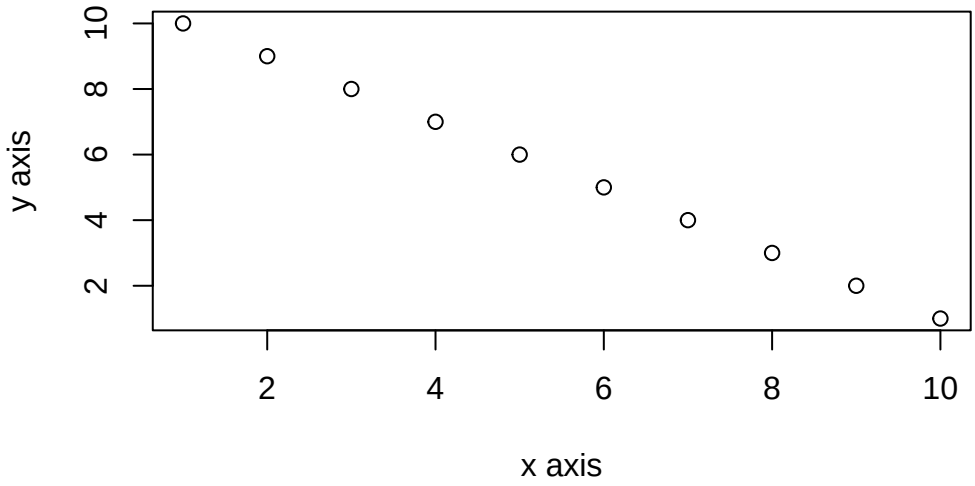


Figure 7.2.: A simple plot

If you want to suppress the figure in the final document use the `fig.show='hide'` option.

````
```{r, simple-plot, fig.show='hide'}
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)
plot(dataf$x, dataf$y, xlab = "x axis", ylab = "y axis")
```
````

```r
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)
plot(dataf$x, dataf$y, xlab = "x axis", ylab = "y axis")
```

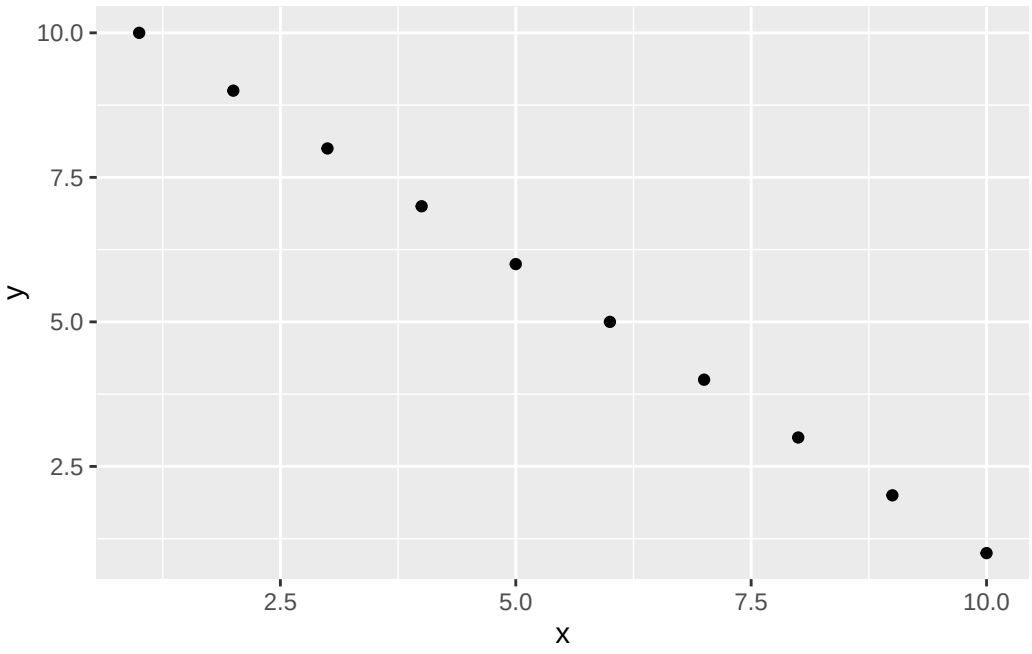
If you're using a package like ggplot2 to create your plots then don't forget you will need to make the package available with the `library()` function in the code chunk (or in a preceding code chunk).

```
```{r}
#| label: simple-ggplot
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)

library(ggplot2)
ggplot(dataf, aes(x = x, y = y)) +
  geom_point()
```
```

```r
x <- 1:10    # create an x variable
y <- 10:1    # create a y variable
dataf <- data.frame(x = x, y = y)

library(ggplot2)
ggplot(dataf, aes(x = x, y = y)) +
  geom_point()
```



Again, there are a large number of chunk options specific to producing plots and figures. See here for more details.

7.6.3. Adding tables

Quarto can print the contents of a dataframe as a table (or any other tabular object such as a summary of model output) by including the name of the dataframe in a code chunk. For example, to create a table of the first 10 rows of the inbuilt dataset `iris`

````
```{r, ugly-table}
iris[1:10,]
```
````

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa
7	4.6	3.4	1.4	0.3	setosa
8	5.0	3.4	1.5	0.2	setosa
9	4.4	2.9	1.4	0.2	setosa
10	4.9	3.1	1.5	0.1	setosa

But how ugly is that! You can create slightly nicer looking tables using native markdown syntax (this doesn't need to be in a code chunk).

```
|     x      |     y      |
|:----------:|:----------:|
|  1         |   5        |
|  2         |   4        |
|  3         |   3        |
|  4         |   2        |
|  5         |   1        |
```

x	y
1	5
2	4
3	3
4	2
5	1

The `:-------:` lets Quarto know that the line above should be treated as a header and the lines below as the body of the table. Alignment within the table is set by the position of the `:`. To center align use `:------:`, to left align `:------` and right align `------:`. Whilst it can be fun(!) to create tables with raw markup it's only practical for very small and simple tables.

The easiest way we know to include tables in an Quarto document is by using the `kable()` function from the `knitr` package (this should have already been installed when you installed the `rmarkdown` package). The `kable()` function can create tables for HTML, PDF and Word outputs.

To create a table of the first 10 rows of the `iris` dataframe using the `kable()` function simply write your code block as

```
```{r, kable-table}
library(knitr)
kable(iris[1:10,])
```
```

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa
4.6	3.4	1.4	0.3	setosa
5.0	3.4	1.5	0.2	setosa
4.4	2.9	1.4	0.2	setosa
4.9	3.1	1.5	0.1	setosa

The `kable()` function offers plenty of options to change the formatting of the table. For example, if we want to round numeric values to one decimal place use the `digits =` argument. To center justify the table contents use `align = 'c'` and to provide custom column headings use the `col.names =` argument. See `?knitr::kable` for more information.

```
```{r, kable-table2}
kable(iris[1:10,], digits = 0, align = 'c',
      col.names = c('sepal length', 'sepal width',
      'petal length', 'petal width', 'species'))
```
```

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa
4.6	3.4	1.4	0.3	setosa
5.0	3.4	1.5	0.2	setosa
4.4	2.9	1.4	0.2	setosa
4.9	3.1	1.5	0.1	setosa

sepal length	sepal width	petal length	petal width	species
5	4	1	0	setosa
5	3	1	0	setosa
5	3	1	0	setosa
5	3	2	0	setosa
5	4	1	0	setosa
5	4	2	0	setosa
5	3	1	0	setosa
5	3	2	0	setosa
4	3	1	0	setosa
5	3	2	0	setosa

You can further enhance the look of your `kable` tables using the `kableExtra` package (don't forget to install the package first!). See here 📦 for more details and a helpful tutorial.

````
```{r, kableExtra-table}
library(kableExtra)
kable(iris[1:10,]) %>%
    kable_styling(bootstrap_options = "striped", font_size = 10)
```
````

If you want even more control and customisation options for your tables take a look at the [gt][gt] package. `gt`stands for grammar of tables and is based on similar principle for tables that are used for plots in ggplot.

7.6.4. Inline R code

Up till now we've been writing and executing our R code in code chunks. Another great reason to use Quarto is that we can also include our R code directly within our text. This is known as 'inline code'. To include your code in your Quarto text you simply write `` `r write your code here` ``. This can come in really useful when you want to include summary statistics within your text. For example, we could describe the `iris` dataset as follows:

```
Morphological characteristics (variable names:
`r names(iris)[1:4]`) were measured from
`r nrow(iris)` *Iris sp.* plants from
`r length(levels(iris$Species))` different species.
The mean Sepal length was
`r round(mean(iris$Sepal.Length), digits = 2)` mm.
```

which will be rendered as

> Morphological characteristics (variable names: Sepal.Length, Sepal.Width, Petal.Length, Petal.Width) were measured from 150 *iris* plants from 3 different species. The mean Sepal length was 5.84 mm.

The great thing about including inline R code in your text is that these values will automatically be updated if your data changes.

7.7. Some tips and tricks

Problem :

When rendering my Quarto document to pdf my code runs off the edge of the page.

Solution:

Add a global_options argument at the start of your .Rmd file in a code chunk:

````
```{r, global_options, include=FALSE}
knitr::opts_chunk$set(message=FALSE, tidy.opts=list(width.cutoff=60), tidy=TRUE)
```
````

This code chunk won't be displayed in the final document due to the `include = FALSE` argument and you should place the code chunk immediately after the YAML header to affect everything below that.

`tidy.opts = list(width.cutoff = 60), tidy=TRUE` defines the margin cutoff point and wraps text to the next line. Play around with this value to get it right (60-80 should be OK for most documents).

Problem:

When I load a package in my Quarto document my rendered output contains all of the startup messages and/or warnings.

Solution:

You can load all of your packages at the start of your Quarto document in a code chunk along with setting your global options.

````
```{r, global_options, include=FALSE}
knitr::opts_chunk$set(message=FALSE, warning=FALSE, tidy.opts=list(width.cutoff=60))
suppressPackageStartupMessages(library(ggplot2))
```
````

The `message=FALSE` and `warning=FALSE` arguments suppress messages and warnings. The `suppressPackageStartupMessag` will load the `ggplot2` package but suppress startup messages.

Problem:

When rendering my Quarto document to pdf my tables and/or figures are split over two pages.

Solution:

Add a page break using the LaTeX `\pagebreak` notation before your offending table or figure

Problem:

The code in my rendered document looks ugly!

Solution:

Add the argument `tidy=TRUE` to your global arguments. Sometimes, however, this can cause problems especially with correct code indentation.

````
```{r, global_options, include=FALSE}
knitr::opts_chunk$set(message=FALSE, tidy.opts=list(width.cutoff=60), tidy=TRUE)
```
````

7.8. Further Information

Although we've covered more than enough to get you quite far using Quarto, as with most things R related, we've really only had time to scratch the surface. Happily, there's a wealth of information available to you should you need to expand your knowledge and experience. A good place to start is the excellent quarto website here.

Another useful and concise Quarto reference guide can be found here

A quick and easy R Markdown cheatsheet

Chapter 8

Version control with Git and GitHub

This Chapter will introduce you to the basics of using a version control system to keep track of all your important R code and facilitate collaboration with colleagues and the wider world. This Chapter will focus on using the software 'Git' in combination with the web-based hosting service 'GitHub'. By the end of the Chapter, you will be able to install and configure Git and GitHub on your computer and setup and work with a version controlled project in RStudio. We won't be covering more advanced topics such as branching, forking and pull requests in much detail but we do give an overview later on in the Chapter.

Just a few notes of caution. In this Chapter we'll be using RStudio to interface with Git as it gives you a nice friendly graphical user interface which generally makes life a little bit easier (and who doesn't want that?). However, one downside to using RStudio with Git is that RStudio only provides pretty basic Git functionality through its menu system. That's fine for most of what we'll be doing during this Chapter (although we will introduce a few Git commands as we go along) but if you really want to benefit from using Git's power you will need to learn some Git commands and syntax and change for another IDE such as VSCode which is much much better when it comes to integration with github. Git can become a little bewildering and frustrating when you first start using it. This is mostly due to the terminology and liberal use of jargon associated with Git, but there's no hiding the fact that it's quite easy to get yourself and your Git repository into a pickle. Therefore, we've tried hard to keep things as straight forward as we can during this Chapter and as a result we do occasionally show you a couple of very 'un-Git' ways of doing things (mostly about reverting to previous versions of documents). Don't get hung up about this, there's no shame to using these low tech solutions and if it works then it works. Lastly, GitHub was not designed to host very large files and will warn you if you try to add files greater than 50 MB and block you adding files greater than 100 MB. If your project involves using large file sizes there are a few solutions but we find the easiest solution is to host these files elsewhere (Googledrive, Dropbox etc) and create a link to them in a README file or R markdown document on Github.

8.1. What is version control?

A Version Control System (VCS) keeps a record of all the changes you make to your files that make up a particular project and allows you to revert to previous versions of files if you need to. To put it another way, if you muck things up or accidentally lose important files you can easily roll back to a previous stage in your project to sort things out. Version control was originally designed for collaborative software development, but it's equally useful for scientific research and collaborations (although admittedly a lot of the terms, jargon and functionality are focused on the software development side). There are many different version control systems currently available, but we' we'll focus on using *Git*, because it's free and open source and it integrates nicely with RStudio. This means that its can easily become part of your usual workflow with minimal additional overhead.

8.2. Why use version control?

So why should you worry about version control? Well, first of all it helps avoid this (familiar?) situation when you're working on a project

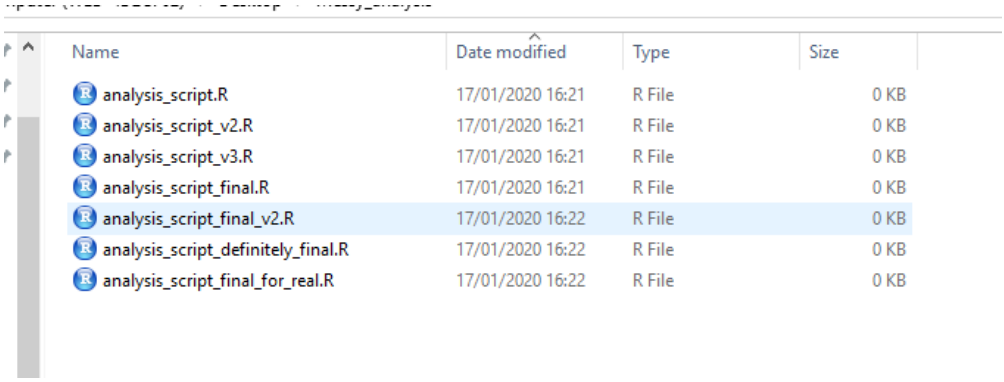
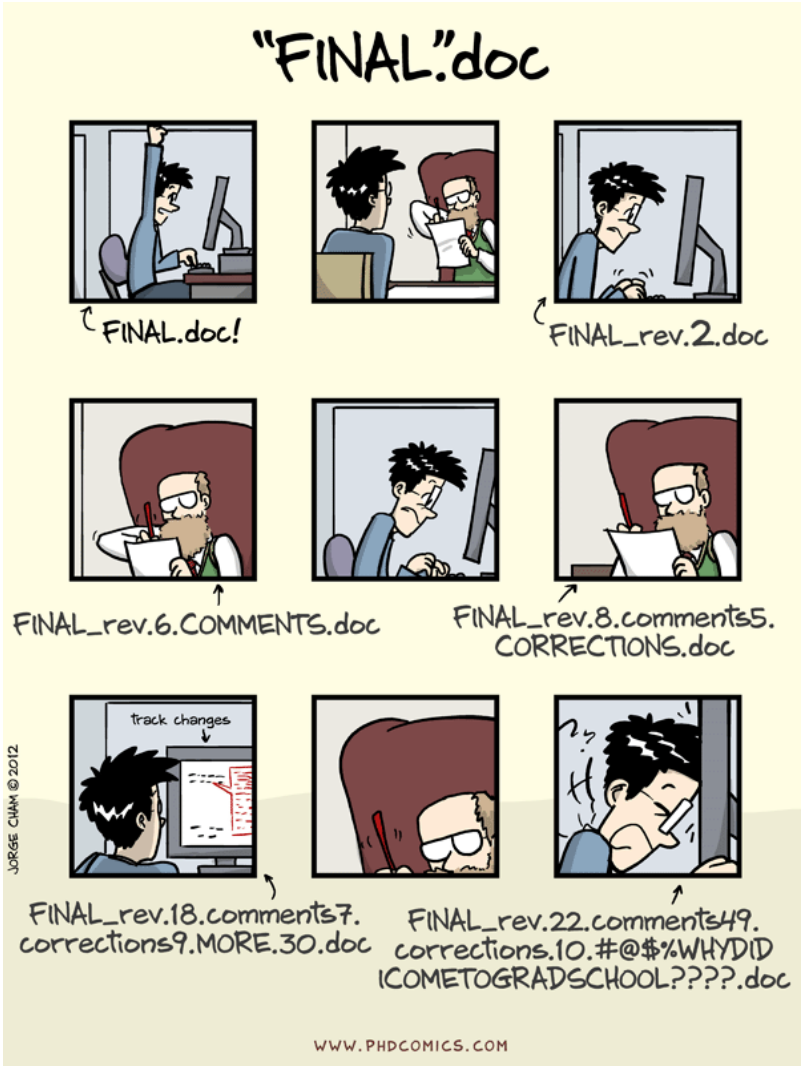


Figure 8.1.: You need version control

usually arising from this (familiar?) scenario



Version control automatically takes care of keeping a record of all the versions of a particular file and allows you to revert back to previous versions if you need to. Version control also helps you (especially the future you) keep track of all your files in a single place and it helps others (especially collaborators) review, contribute to and reuse your work through the GitHub website. Lastly, your files are always available from anywhere and on any computer, all you need is an internet connection.

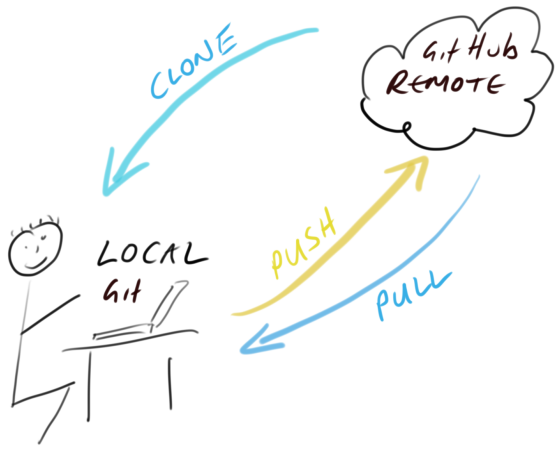
8.3. What is Git and GitHub?

Git is a version control system originally developed by Linus Torvalds that lets you track changes to a set of files. These files can be any type of file including the menagerie of files that typically make up a data orientated project

(.pdf, .Rmd, .docx, .txt, .jpg etc) although plain text files work the best. All the files that make up a project is called a **repository** (or just **repo**).

GitHub is a web-based hosting service for Git repositories which allows you to create a remote copy of your local version-controlled project. This can be used as a backup or archive of your project or make it accessible to you and to your colleagues so you can work collaboratively.

At the start of a project we typically (but not always) create a **remote** repository on GitHub, then **clone** (think of this as copying) this repository to our **local** computer (the one in front of you). This cloning is usually a one time event and you shouldn't need to clone this repository again unless you really muck things up. Once you have cloned your repository you can then work locally on your project as usual, creating and saving files for your data analysis (scripts, R markdown documents, figures etc). Along the way you can take snapshots (called **commits**) of these files after you've made important changes. We can then **push** these changes to the remote GitHub repository to make a backup or make available to our collaborators. If other people are working on the same project (**repository**), or maybe you're working on a different computer, you can **pull** any changes back to your local repository so everything is synchronised.

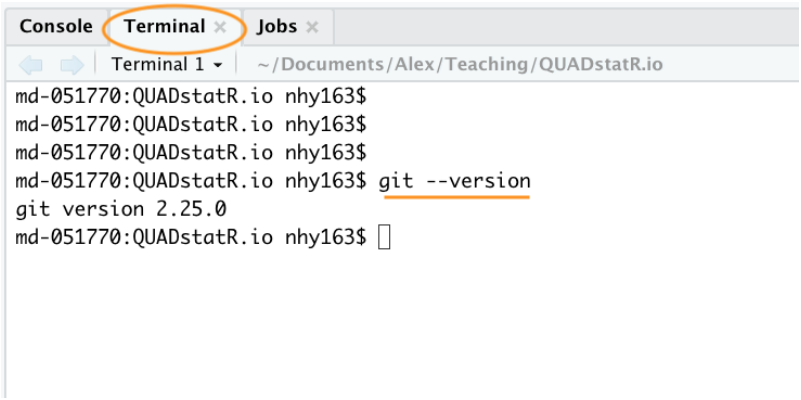


8.4. Getting started

This Chapter assumes that you have already installed the latest versions of R and an IDE (RStudio or VSCode). If you haven't done this yet you can find instructions here.

8.4.1. Install Git

To get started, you first need to install Git. If you're lucky you may already have Git installed (especially if you have a Mac or Linux computer). You can check if you already have Git installed by clicking on the Terminal tab in the Console window in RStudio and typing `git --version` (the space after the `git` command is important). If you see something that looks like `git version 2.25.0` (the version number may be different on your computer) then you already have Git installed (happy days). If you get an error (something like `git: command not found`) this means you don't have Git installed (yet!).



You can also do this check outside RStudio by opening up a separate Terminal if you want. On Windows go to the 'Start menu' and in the search bar (or run box) type `cmd` and press enter. On a Mac go to 'Applications' in Finder, click on the 'Utilities' folder and then on the 'Terminal' program. On a Linux machine simply open the Terminal (Ctrl+Alt+T often does it).

To install Git on a **Windows** computer we recommend you download and install Git for Windows (also known as 'Git Bash'). You can find the download file and installation instructions here.

For those of you using a **Mac** computer we recommend you download Git from here and install in the usual way (double click on the installer package once downloaded). If you've previously installed Xcode on your Mac and want

to use a more up to date version of Git then you will need to follow a few more steps documented here. If you've never heard of Xcode then don't worry about it!

For those of you lucky enough to be working on a **Linux** machine you can simply use your OS package manager to install Git from the official repository. For Ubuntu Linux (or variants of) open your Terminal and type

```
sudo apt update
sudo apt install git
```

You will need administrative privileges to do this. For other versions of Linux see here for further installation instructions.

Whatever version of Git you're installing, once the installation has finished verify that the installation process has been successful by running the command `git --version` in the Terminal tab in RStudio (as described above). On some installations of Git (yes we're looking at you MS Windows) this may still produce an error as you will also need to setup RStudio so it can find the Git executable (described below).

8.4.2. Configure Git

After installing Git, you need to configure it so you can use it. Click on the Terminal tab in the Console window again and type the following:

```
git config --global user.email 'you@youremail.com'
```

```
git config --global user.name 'Your Name'
```

substituting `'Your Name'` for your actual name and `'you@youremail.com'` with your email address. We recommend you use your University email address (if you have one) as you will also use this address when you register for your GitHub account (coming up in a bit).

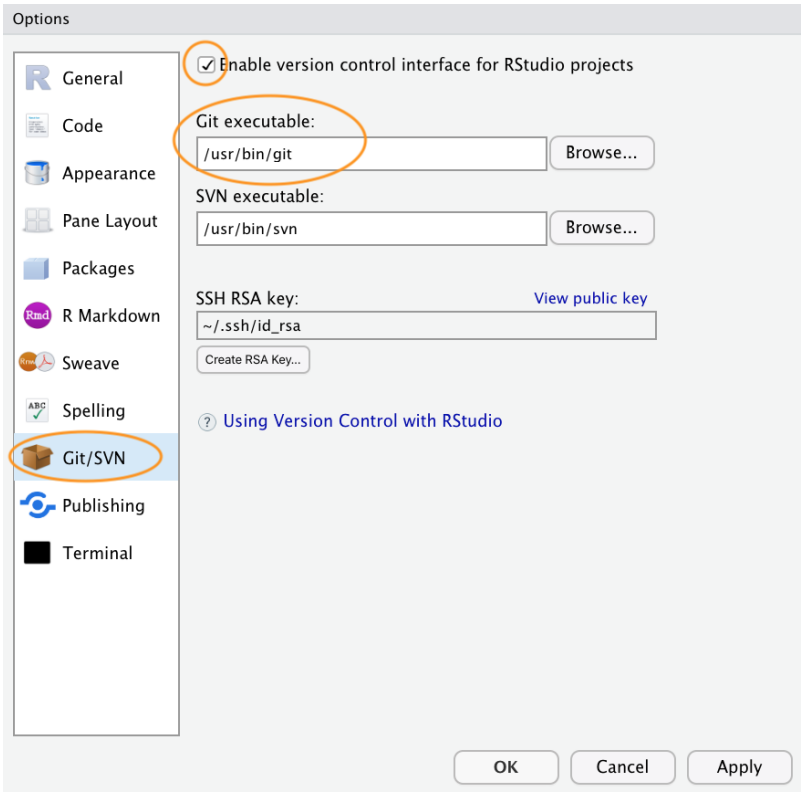
If this was successful, you should see no error messages from these commands. To verify that you have successfully configured Git type the following into the Terminal

```
git config --global --list
```

You should see both your `user.name` and `user.email` configured.

8.4.3. Configure RStudio

As you can see above, Git can be used from the command line, but it also integrates well with RStudio, providing a friendly graphical user interface. If you want to use RStudio's Git integration (we recommend you do - at least at the start), you need to check that the path to the Git executable is specified correctly. In RStudio, go to the menu `Tools -> Global Options -> Git/SVN` and make sure that 'Enable version control interface for RStudio projects' is ticked and that the 'Git executable:' path is correct for your installation. If it's not correct hit the `Browse...` button and navigate to where you installed git and click on the executable file. You will need to restart RStudio after doing this.



8.4.4. Configure VSCode

to develop

8.4.5. Register a GitHub account

If all you want to do is to keep track of files and file versions on your local computer then Git is sufficient. If however, you would like to make an off-site copy of your project or make it available to your collaborators then you will need

a web-based hosting service for your Git repositories. This is where GitHub comes into play (there are also other services like GitLab, Bitbucket and Savannah). You can sign up for a free account on GitHub here. You will need to specify a username, an email address and a strong password. We suggest that you use your University email address (if you have one) as this will also allow you to apply for a free educator or researcher account later on which gives you some useful benefits (don't worry about this now though). When it comes to choosing a username we suggest you give this some thought. Choose a short(ish) rather than a long username, use all lowercase and hyphenate if you want to include multiple words, find a way of incorporating your actual name and lastly, choose a username that you will feel comfortable revealing to your future employer!

Next click on the 'Select a plan' (you may have to solve a simple puzzle first to verify you're human) and choose the 'Free Plan' option. Github will send an email to the email address you supplied for you to verify.

Once you've completed all those steps you should have both Git and GitHub setup up ready for you to use (Finally!).

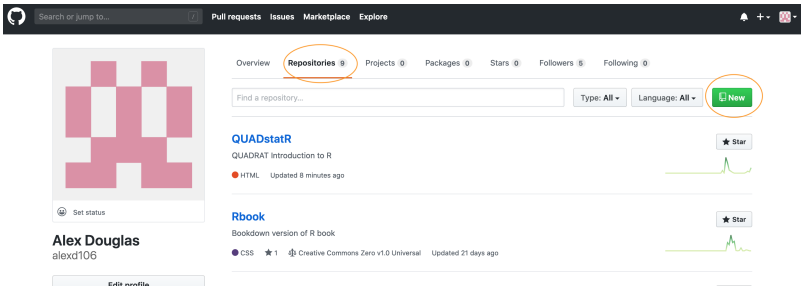
8.5. Setting up a project

8.5.1. in RStudio

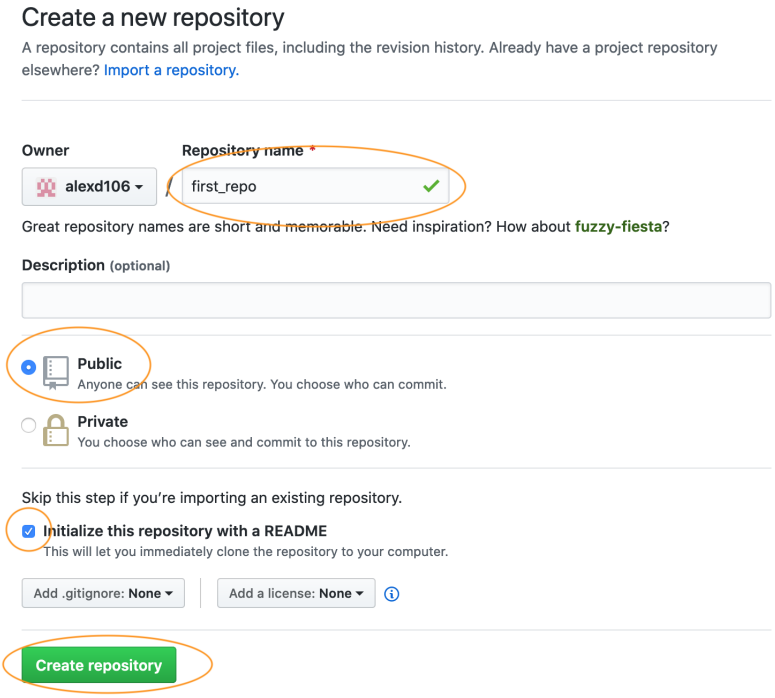
Now that you're all set up, let's create your first version controlled RStudio project. There are a couple of different approaches you can use to do this. You can either setup a remote GitHub repository first then connect an RStudio project to this repository (we'll call this Option 1). Another option is to setup a local repository first and then link a remote GitHub repository to this repository (Option 2). You can also connect an existing project to a GitHub repository but we won't cover this here. We suggest that if you're completely new to Git and GitHub then use Option 1 as this approach sets up your local Git repository nicely and you can **push** and **pull** immediately. Option 2 requires a little more work and therefore there are more opportunities to go wrong. We will cover both of these options below.

8.5.2. Option 1 - GitHub first

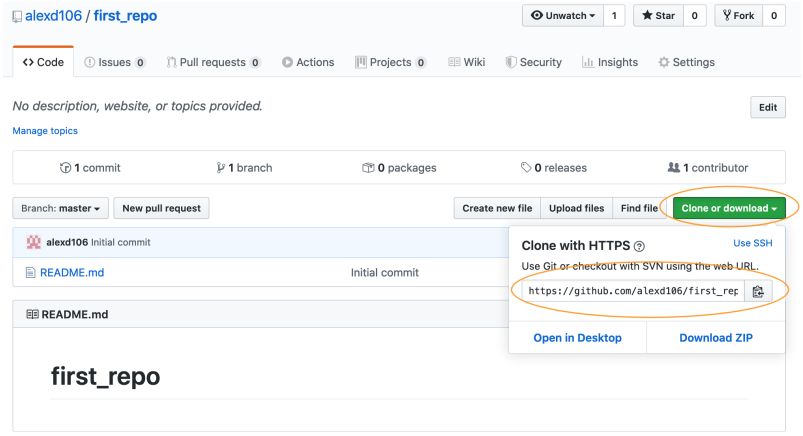
To use the GitHub first approach you will first need to create a **repository (repo)** on GitHub. Go to your GitHub page and sign in if necessary. Click on the 'Repositories' tab at the top and then on the green 'New' button on the right



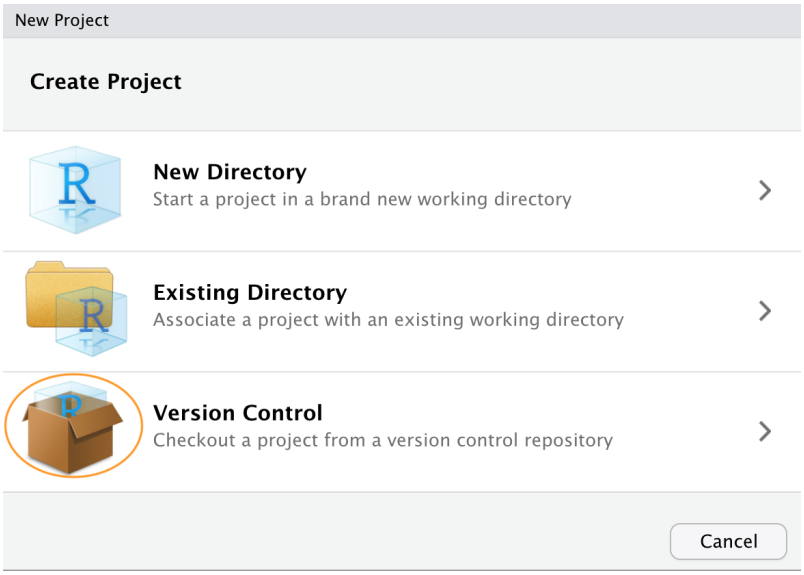
Give your new repo a name (let's call it `first_repo` for this Chapter), select 'Public', tick on the 'Initialize this repository with a README' (this is important) and then click on 'Create repository' (ignore the other options for now).



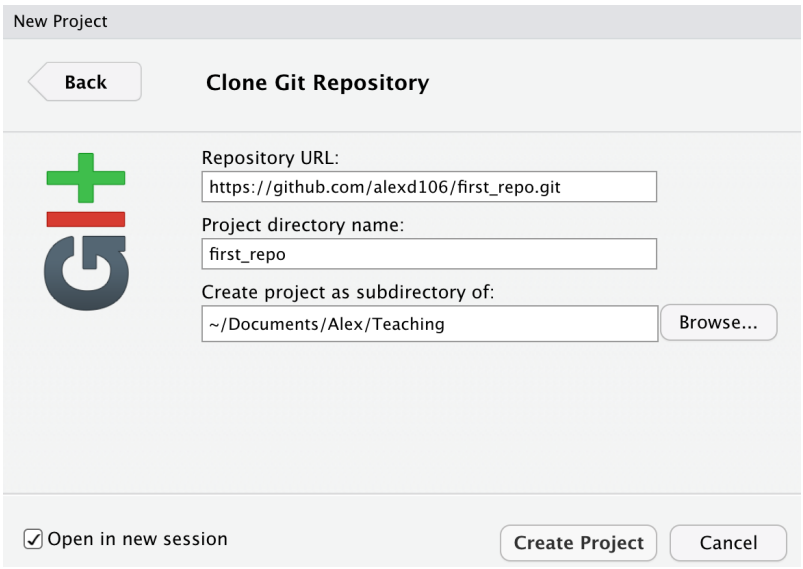
Your new GitHub repository will now be created. Notice the README has been rendered in GitHub and is in markdown (.md) format (see Chapter 8 on R markdown if this doesn't mean anything to you). Next click on the green 'Clone or Download' button and copy the `https//...` URL that pops up for later (either highlight it all and copy or click on the copy to clipboard icon to the right).



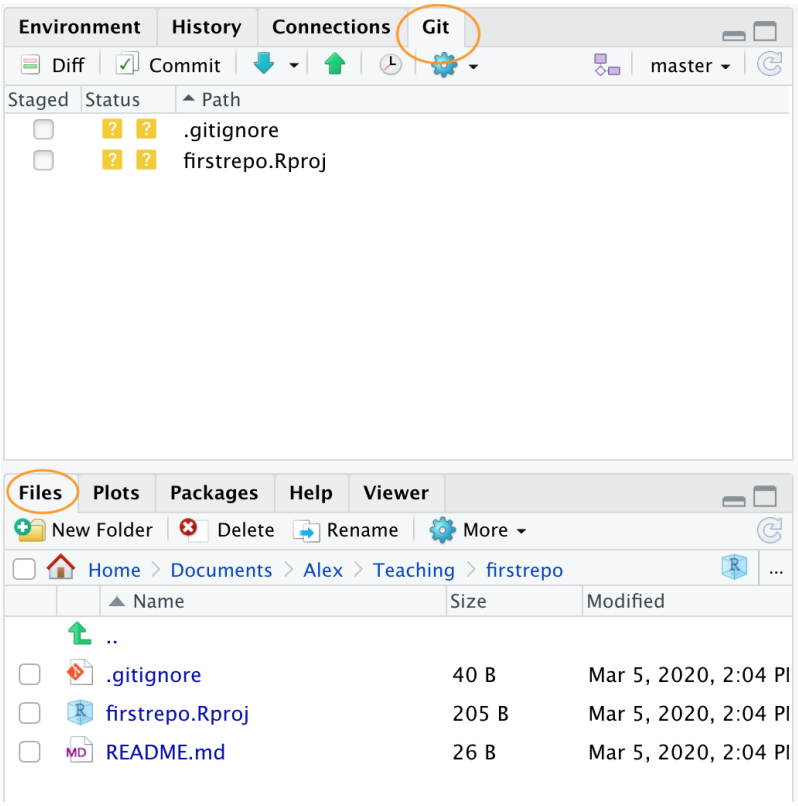
Ok, we now switch our attention to RStudio. In RStudio click on the `File -> New Project` menu. In the pop up window select `Version Control`.



Now paste the the URL you previously copied from GitHub into the `Repository URL:` box. This should then automatically fill out the `Project Directory Name:` section with the correct repository name (it's important that the name of this directory has the same name as the repository you created in GitHub). You can then select where you want to create this directory by clicking on the `Browse` button opposite the `Create project as a subdirectory of:` option. Navigate to where you want the directory created and click OK. We also tick the `Open in new session` option.



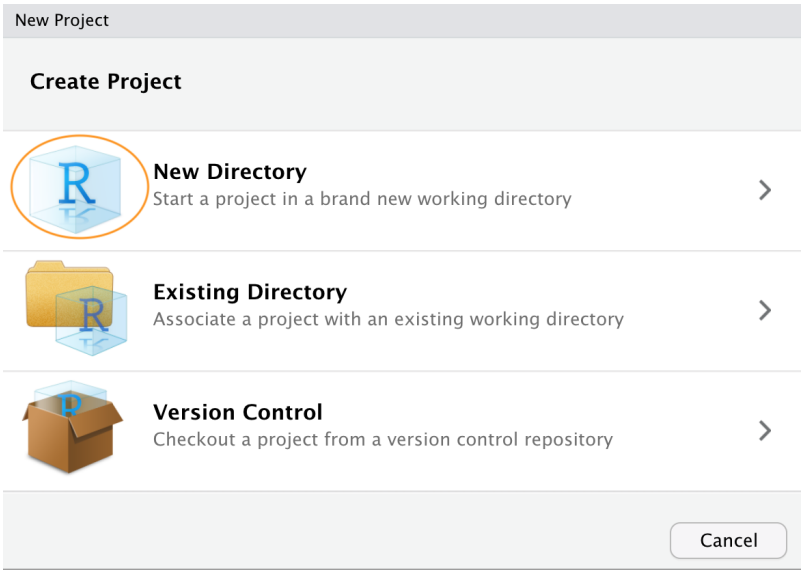
RStudio will now create a new directory with the same name as your repository on your local computer and will then **clone** your remote repository to this directory. The directory will contain three new files; `first_repo.Rproj` (or whatever you called your repository), `README.md` and `.gitignore`. You can check this out in the `Files` tab usually in the bottom right pane in RStudio. You will also have a `Git` tab in the top right pane with two files listed (we will come to this later on in the Chapter). That's it for Option 1, you now have a remote GitHub repository set up and this is linked to your local repository managed by RStudio. Any changes you make to files in this directory will be version controlled by Git.



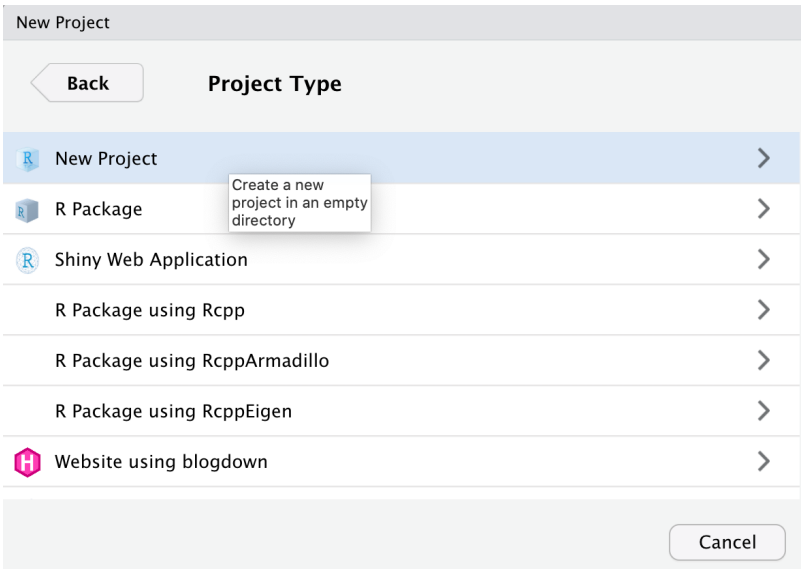
8.5.3. Option 2 - RStudio first

An alternative approach is to create a local RStudio project first and then link to a remote Github repository. As we mentioned before, this option is more involved than Option 1 so feel free to skip this now and come back later to it if you're interested. This option is also useful if you just want to create a local RStudio project linked to a local Git repository (i.e. no GitHub involved). If you want to do this then just follow the instructions below omitting the GitHub bit.

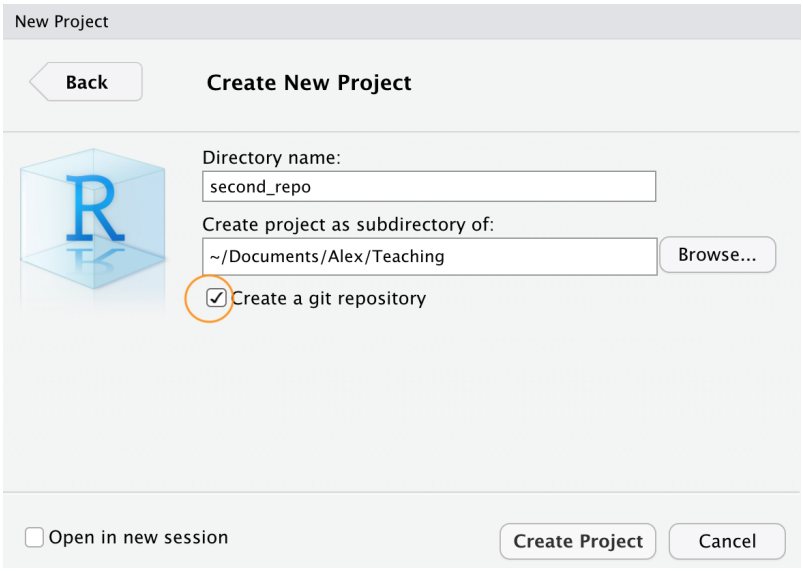
In RStudio click on the `File -> New Project` menu and select the `New Directory` option.



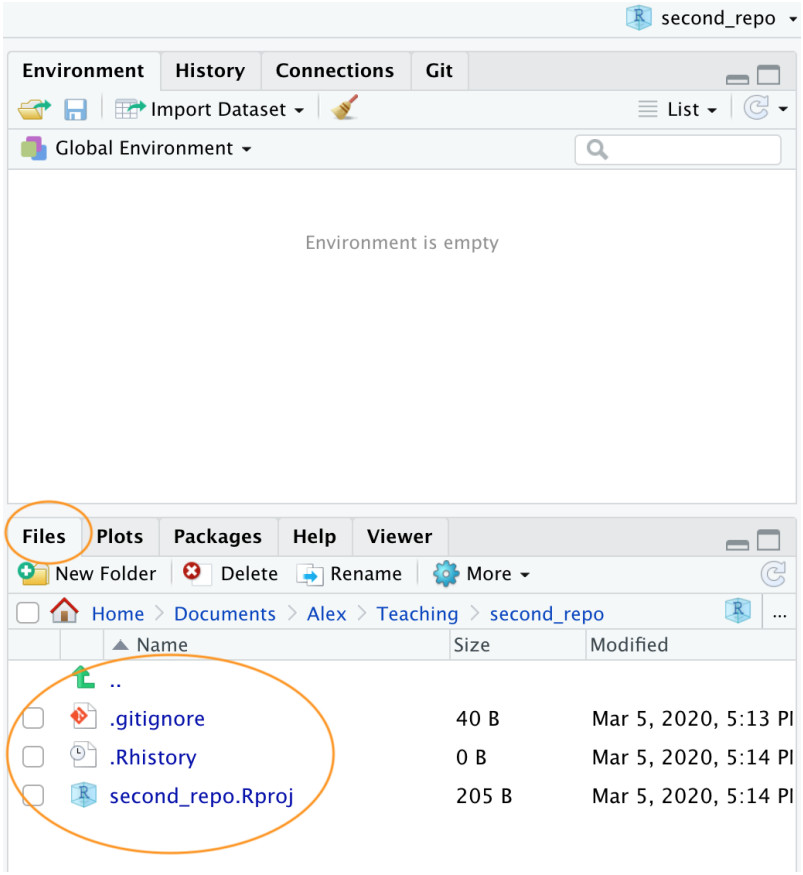
In the pop up window select the `New Project` option



In the New Project window specify a `Directory name` (choose `second_repo` for this Chapter) and select where you would like to create this directory on you computer (click the `Browse` button). Make sure the `Create a git repository` option is ticked

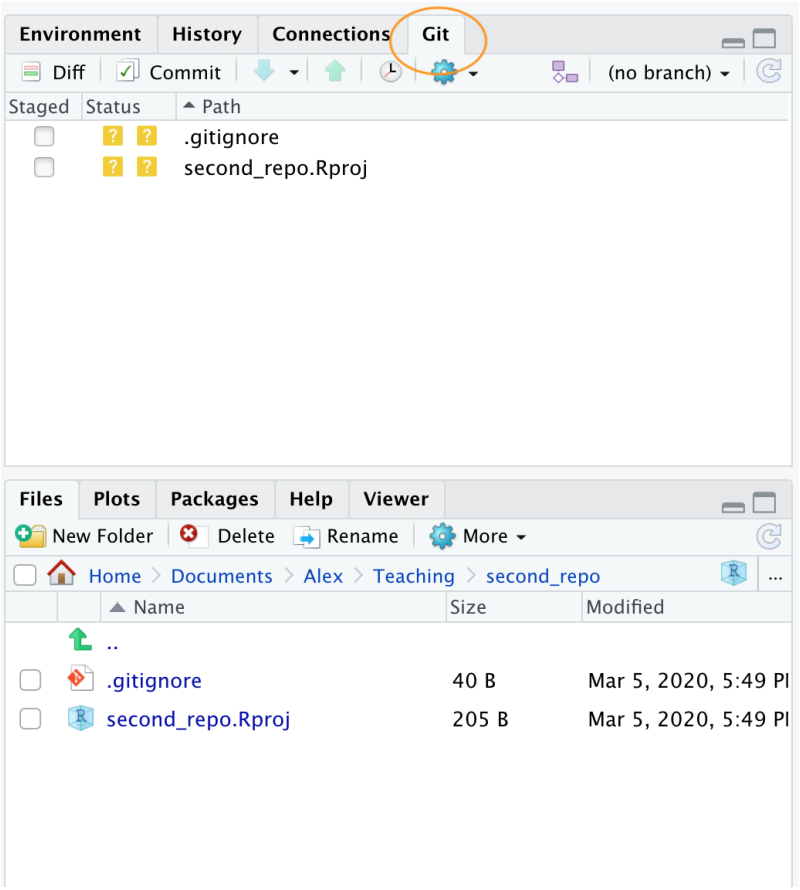


This will create a version controlled directory called `second_repo` on your computer that contains two files, `second_repo.Rproj` and `.gitignore` (there might also be a `.Rhistory` file but ignore this). You can check this by looking in the `Files` tab in RStudio (usually in the bottom right pane).

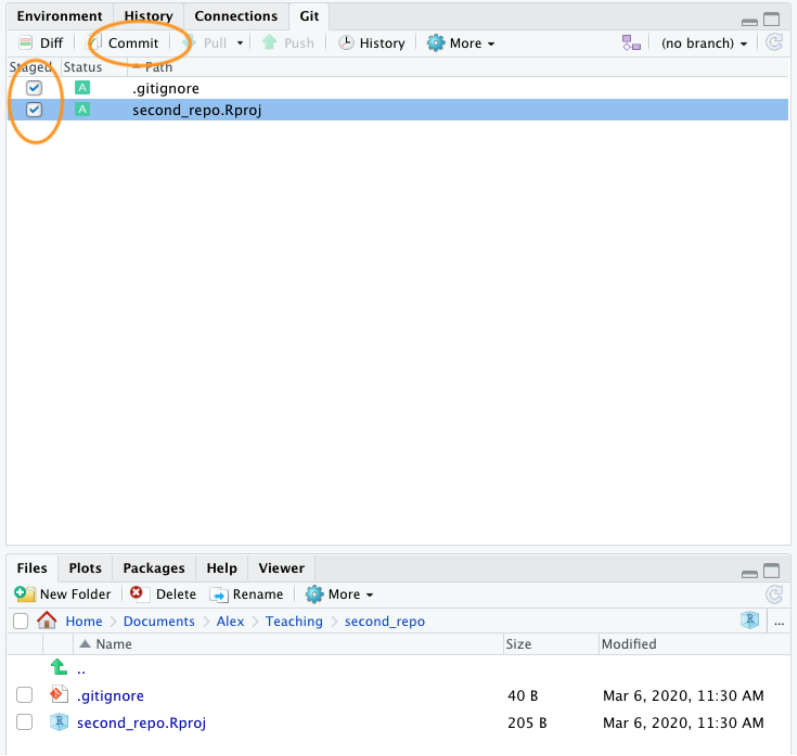


OK, before we go on to create a repository on GitHub we need to do one more thing - we need to place our `second_repo.Rproj` and `.gitignore`files under version control. Unfortunately we haven't covered this in detail yet so just follow the next few instructions (blindly!) and we'll revisit them in the Using Git section of this Chapter.

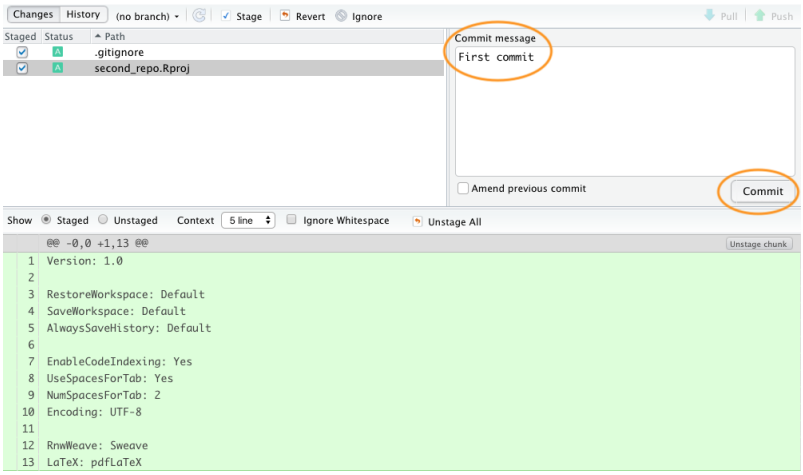
To get our two files under version control click on the 'Git' tab which is usually in the top tight pane in RStudio



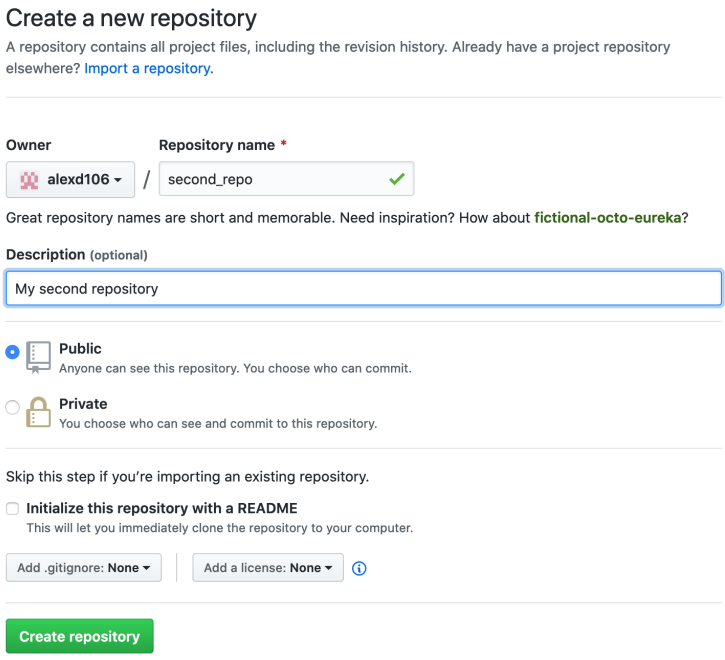
You can see that both files are listed. Next, tick the boxes under the 'Staged' column for both files and then click on the 'Commit' button.



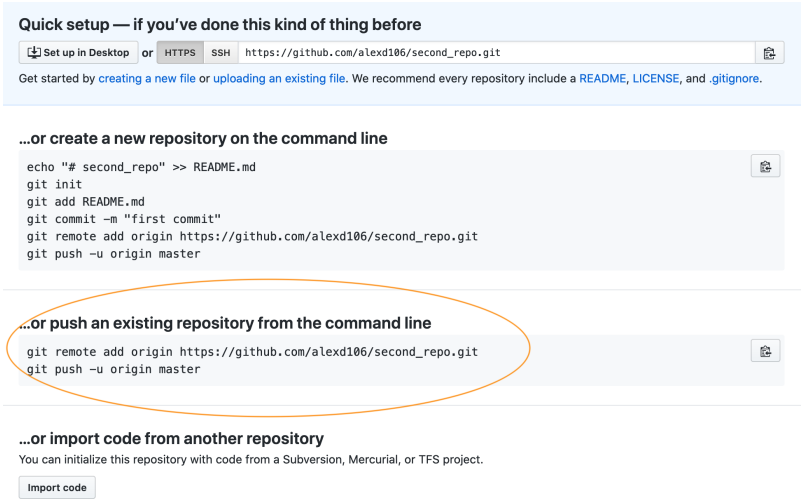
This will take you to the 'Review Changes' window. Type in the commit message 'First commit' in the 'Commit message' window and click on the 'Commit' button. A new window will appear with some messages which you can ignore for now. Click 'Close' to close this window and also close the 'Review Changes' window. The two files should now have disappeared from the Git pane in RStudio indicating a successful commit.



OK, that's those two files now under version control. Now we need to create a new repository on GitHub. In your browser go to your GitHub page and sign in if necessary. Click on the 'Repositories' tab and then click on the green 'New' button on the right. Give your new repo the name `second_repo` (the same as your version controlled directory name) and select 'Public'. This time **do not** tick the 'Initialize this repository with a README' (this is important) and then click on 'Create repository'.



This will take you to a Quick setup page which provides you with some code for various situations. The code we are interested in is the code under `...or push an existing repository from the command line` heading.



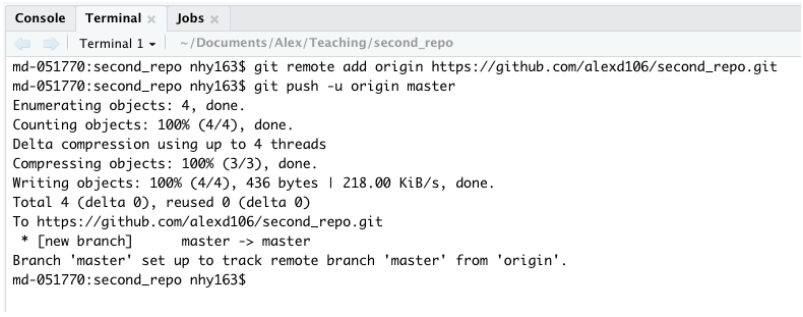
Highlight and copy the first line of code (note: yours will be slightly different as it will include your GitHub username not mine)

```
git remote add origin https://github.com/alexd106/second_repo.git
```

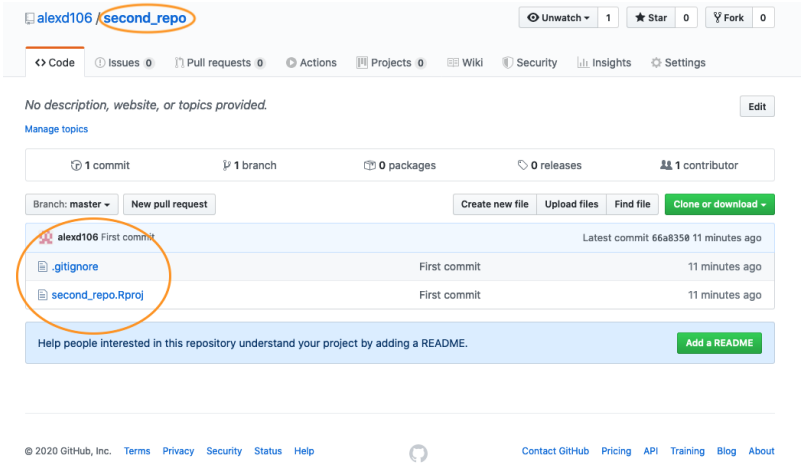
Switch to RStudio, click on the 'Terminal' tab and paste the command into the Terminal. Now go back to GitHub and copy the second line of code

```
git push -u origin master
```

and paste this into the Terminal in RStudio. You should see something like this

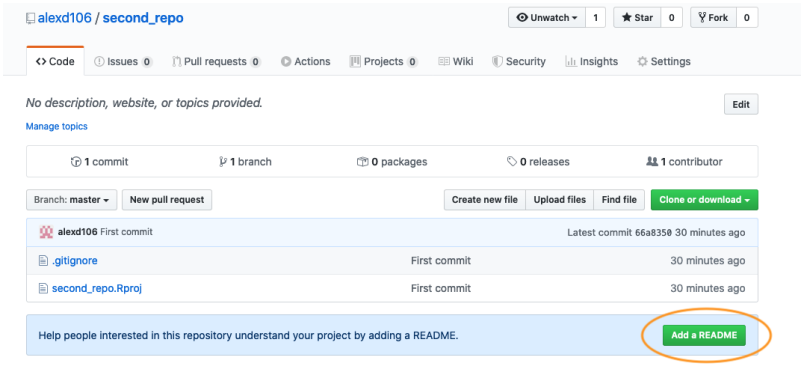


If you take a look at your repo back on GitHub (click on the `/second_repo` link at the top) you will see the `second_repo.Rproj` and `.gitignore` files have now been **pushed** to GitHub from your local repository.

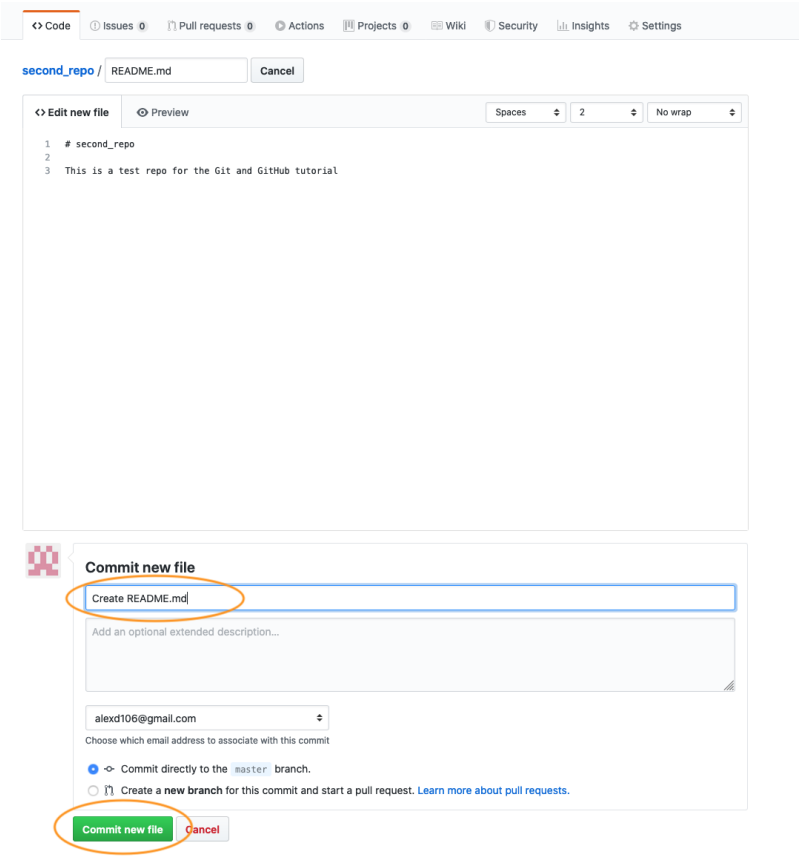


The last thing we need to do is create and add a **README** file to your repository. A README file describes your project and is written using the same Markdown language you learned in the R markdown Chapter. A good README file makes it easy for others (or the future you!) to use your code and reproduce your project. You can create a README file in RStudio or in GitHub. Let's use the second option.

In your repository on GitHub click on the green `Add a README` button.



Now write a short description of your project in the `<> Edit new file` section and then click on the green `Commit new file` button.



You should now see the `README.md` file listed in your repository. It won't actually exist on your computer yet as you will need to **pull** these changes back to your local repository, but more about that in the next section.

Whether you followed Option 1 or Option 2 (or both) you have now successfully setup a version controlled RStudio project (and associated directory) and linked this to a GitHub repository. Git will now monitor this directory for any changes you make to files and also if you add or delete files. If the steps above seem like a bit of an ordeal, just remember, you only need to do this once for each project and it gets much easier over time.

8.5.4. in VSCode

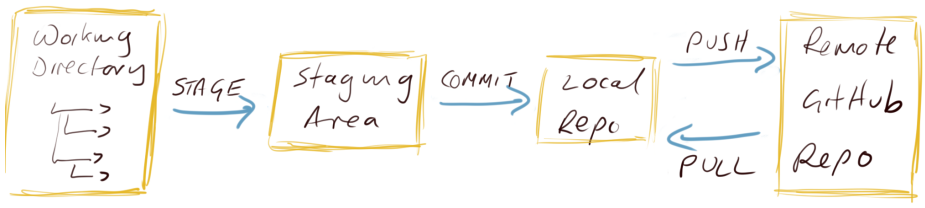
to develop

8.6. Using Git with RStudio

Now that we have our project and repositories (both local and remote) set up, it's finally time to learn how to use Git in your IDE!

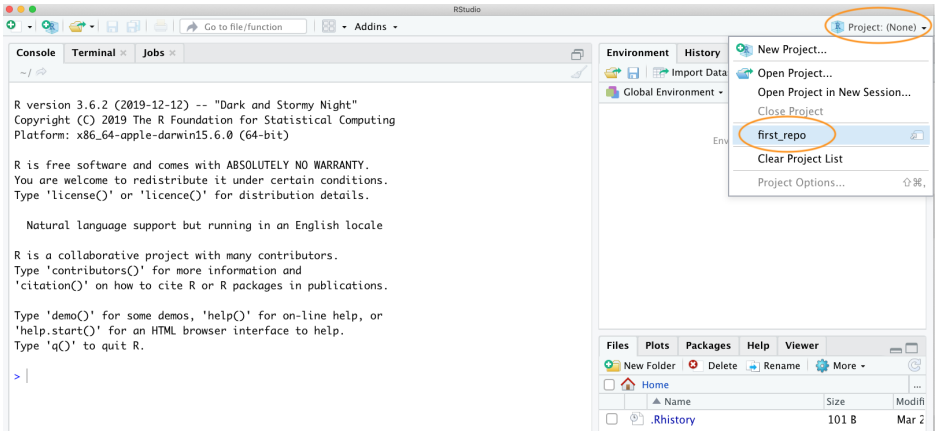
Typically, when using Git your workflow will go something like this:

1. You create/delete and edit files in your project directory on your computer as usual (saving these changes as you go)
2. Once you've reached a natural 'break point' in your progress (i.e. you'd be sad if you lost this progress) you **stage** these files
3. You then **commit** the changes you made to these staged files (along with a useful commit message) which creates a permanent snapshot of these changes
4. You keep on with this cycle until you get to a point when you would like to **push** these changes to GitHub
5. If you're working with other people on the same project you may also need to **pull** their changes to your local computer



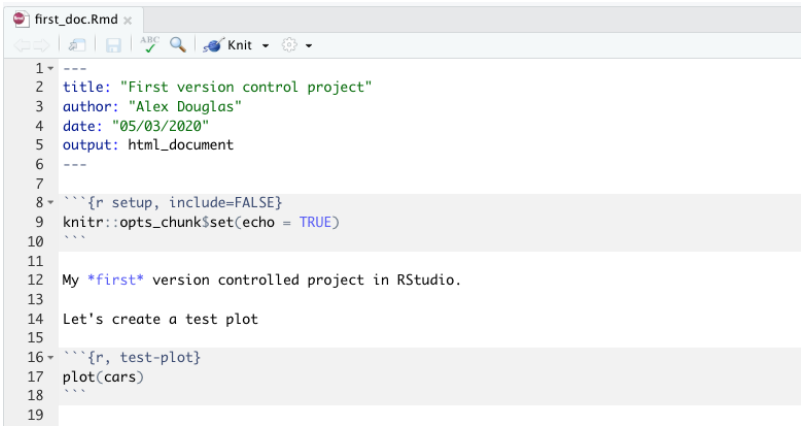
OK, let's go through an example to help clarify this workflow.

Open up the `first_repo.Rproj` you created previously during Option 1. Either use the `File -> Open Project` menu or click on the top right project icon and select the appropriate project.

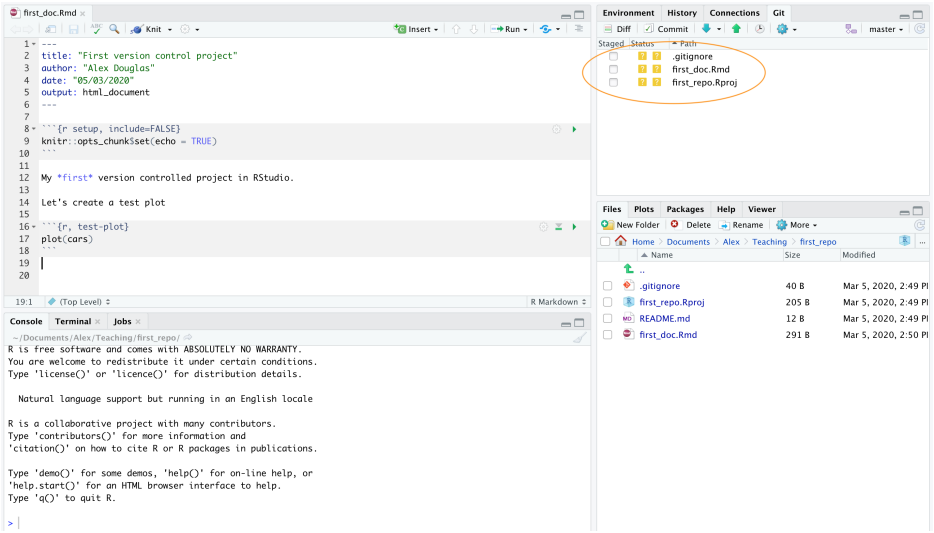


Create an R markdown document inside this project by clicking on the `File` -> `New File` -> `R markdown` menu (remember from the R markdown Chapter?).

Once created, we can delete all the example R markdown code (except the YAML header) as usual and write some interesting R markdown text and include a plot. We'll use the inbuilt `cars` dataset to do this. Save this file (cmd + s for Mac or ctrl + s in Windows). Your R markdown document should look something like the following (it doesn't matter if it's not exactly the same).

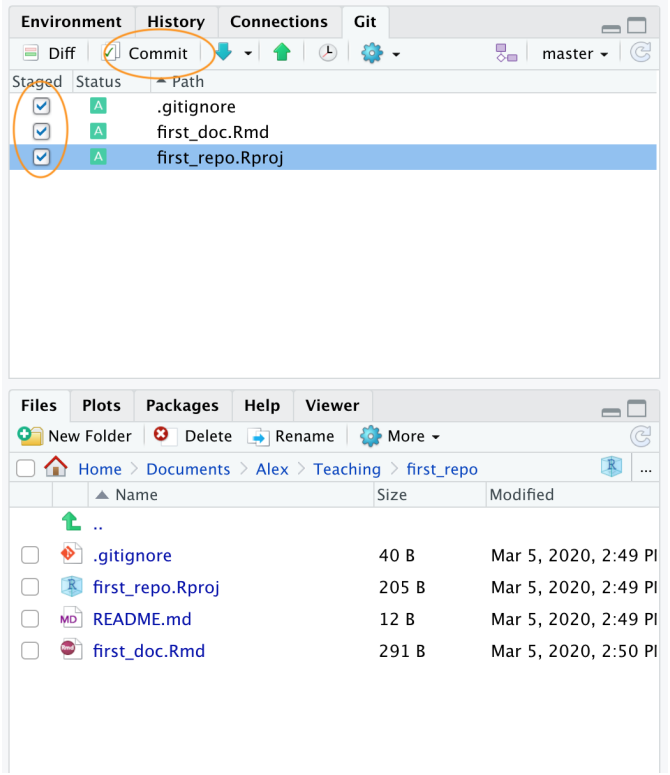


Take a look at the 'Git' tab which should list your new R markdown document (`first_doc.Rmd` in this example) along with `first_repo.Rproj`, and `.gitignore` (you created these files previously when following Option 1).

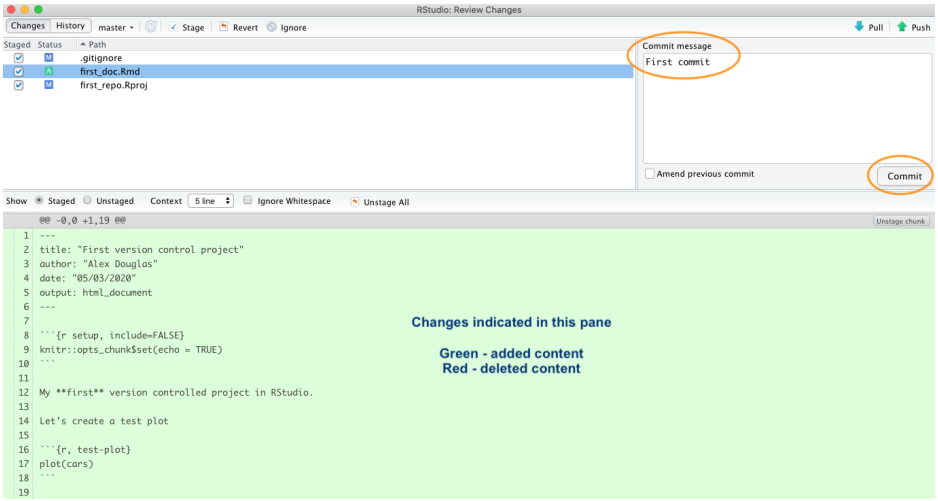


Following our workflow, we now need to **stage** these files. To do this tick the boxes under the 'Staged' column for all files. Notice that there is a status icon next to the box which gives you an indication of how the files were changed. In our case all of the files are to be added (capital A) as we have just created them.

After you have staged the files the next step is to **commit** the files. This is done by clicking on the 'Commit' button.

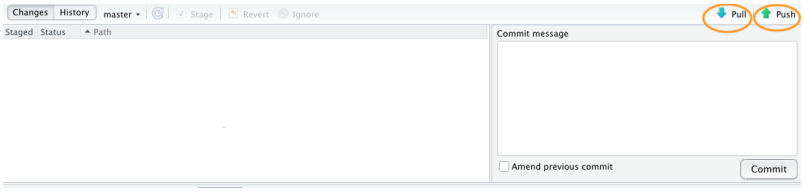


After clicking on the 'Commit' button you will be taken to the 'Review Changes' window. You should see the three files you staged from the previous step in the left pane. If you click on the file name `first_doc.Rmd` you will see the changes you have made to this file highlighted in the bottom pane. Any content that you have added is highlighted in green and deleted content is highlighted in red. As you have only just created this file, all the content is highlighted in green. To commit these files (take a snapshot) first enter a mandatory commit message in the 'Commit message' box. This message should be relatively short and informative (to you and your collaborators) and indicate why you made the changes, not what you changed. This makes sense as Git keeps track of *what* has changed and so it is best not to use commit messages for this purpose. It's traditional to enter the message 'First commit' (or 'Initial commit') when you commit files for the first time. Now click on the 'Commit' button to commit these changes.

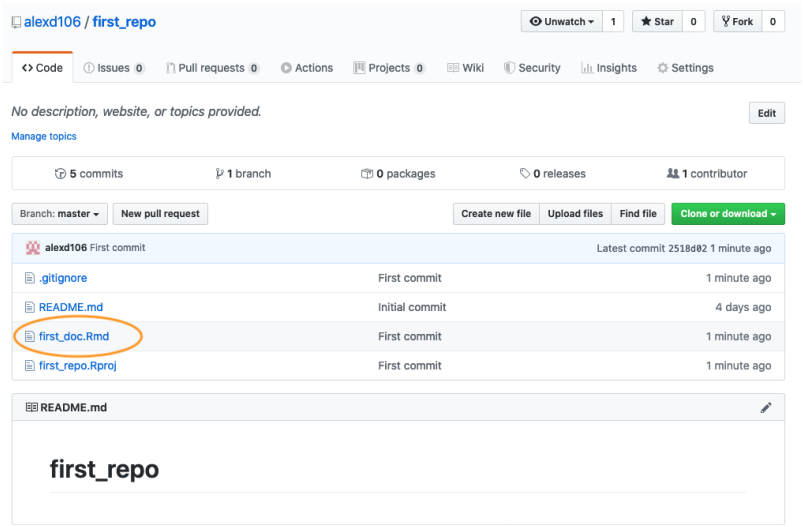


A summary of the commit you just performed will be shown. Now click on the 'Close' button to return to the 'Review Changes' window. Note that the staged files have now been removed.

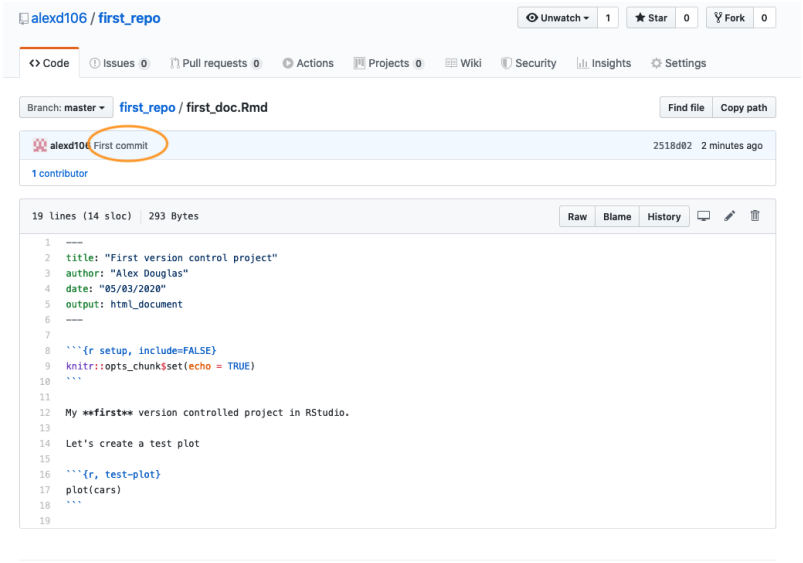
Now that you have committed your changes the next step is to **push** these changes to GitHub. Before you push your changes it's good practice to first **pull** any changes from GitHub. This is especially important if both you and your collaborators are working on the same files as it keeps you local copy up to date and avoids any potential conflicts. In this case your repository will already be up to date but it's a good habit to get into. To do this, click on the 'Pull' button on the top right of the 'Review Changes' window. Once you have pulled any changes click on the green 'Push' button to push your changes. You will see a summary of the push you just performed. Hit the 'Close' button and then close the 'Review Changes' window.



To confirm the changes you made to the project have been pushed to GitHub, open your GitHub page, click on the Repositories link and then click on the `first_repo` repository. You should see four files listed including the `first_doc.Rmd` you just pushed. Along side the file name you will see your last commit message ('First commit' in this case) and when you made the last commit.



To see the contents of the file click on the `first_doc.Rmd` file name.

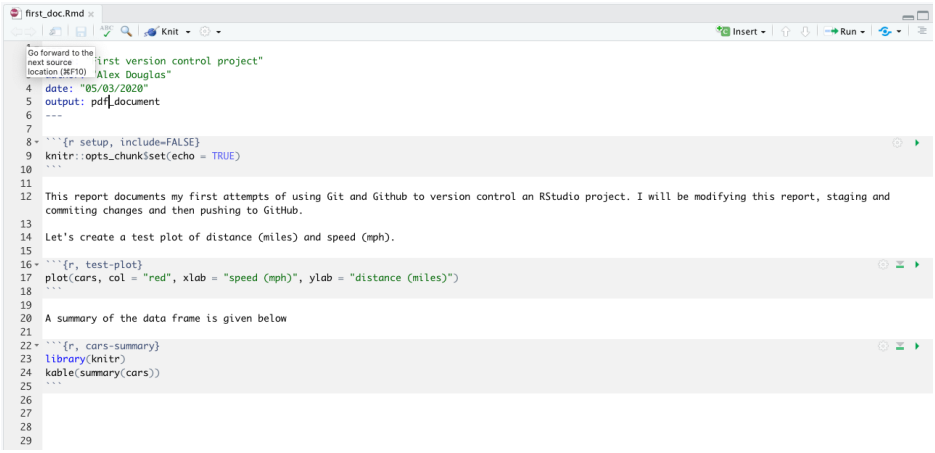


8.6.1. Tracking changes

After following the steps outlined above, you will have successfully modified an RStudio project by creating a new R markdown document, staged and then committed these changes and finally pushed the changes to your GitHub repository. Now let's make some further changes to your R markdown file and follow the workflow once again but this time we 'll take a look at how to identify changes made to files, examine the commit history and how to restore to a previous version of the document.

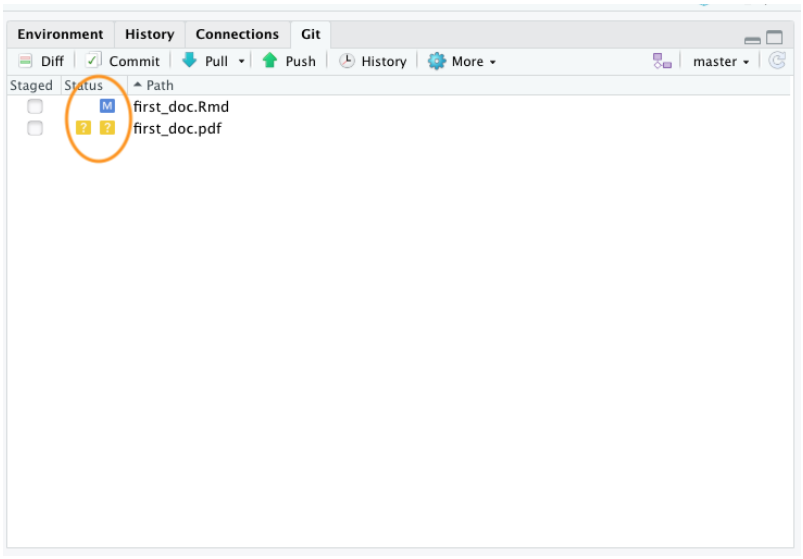
In RStudio open up the `first_repo.Rproj` file you created previously (if not already open) then open the `first_doc.Rmd` file (click on the file name in the `Files` tab in RStudio).

Let's make some changes to this document. Delete the line beginning with 'My first version controlled …' and replace it with something more informative (see figure below). We will also change the plotted symbols to red and give the plot axes labels. Lastly, let's add a summary table of the dataframe using the `kable()` and `summary()` functions (you may need to install the `knitr` package if you haven't done so previously to use the `kable()` function) and finally render this document to pdf by changing the YAML option to `output: pdf_document`.

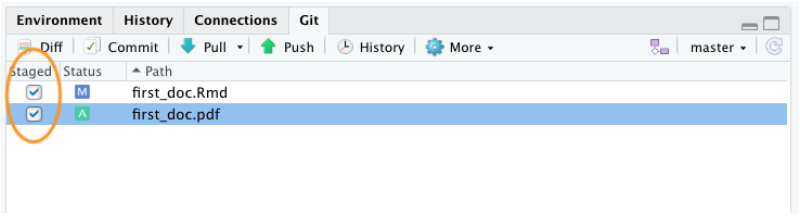


Now save these changes and then click the `knit` button to render to pdf. A new pdf file named `first_doc.pdf` will be created which you can view by clicking on the file name in the `Files` tab in RStudio.

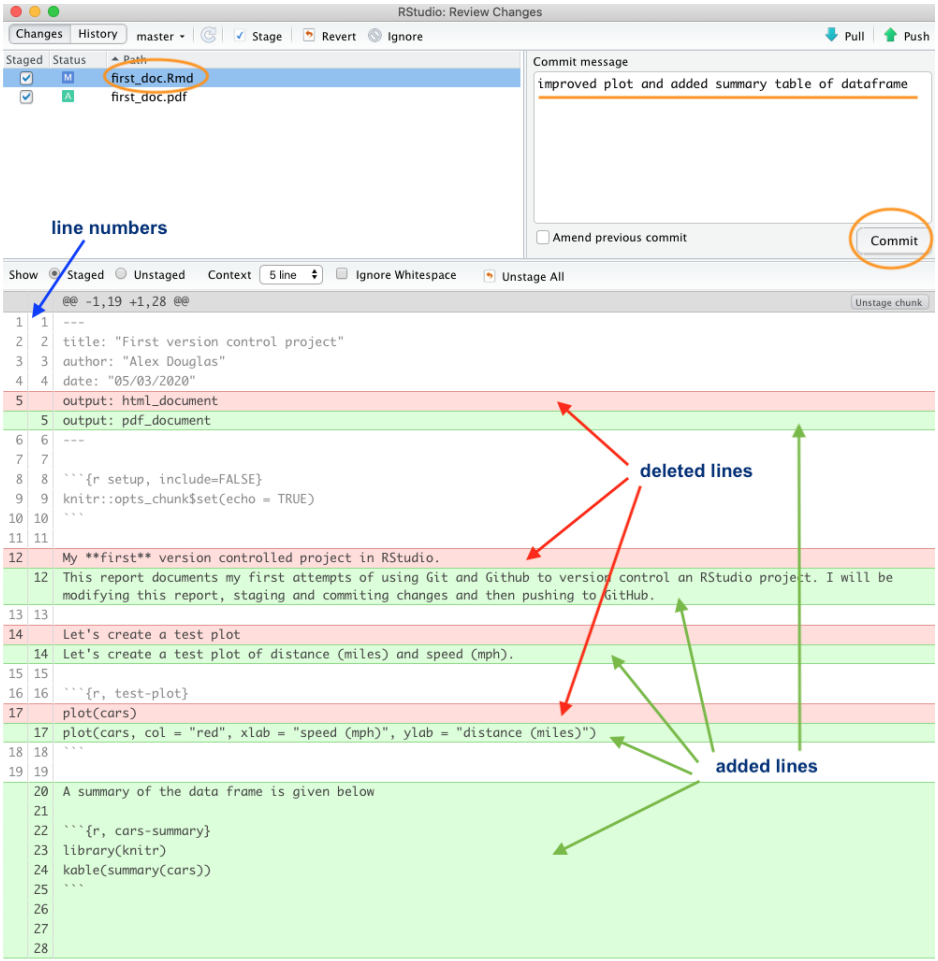
Notice that these two files have been added to the `Git` tab in RStudio. The status icons indicate that the `first_doc.Rmd` file has been modified (capital M) and the `first_doc.pdf` file is currently untracked (question mark).



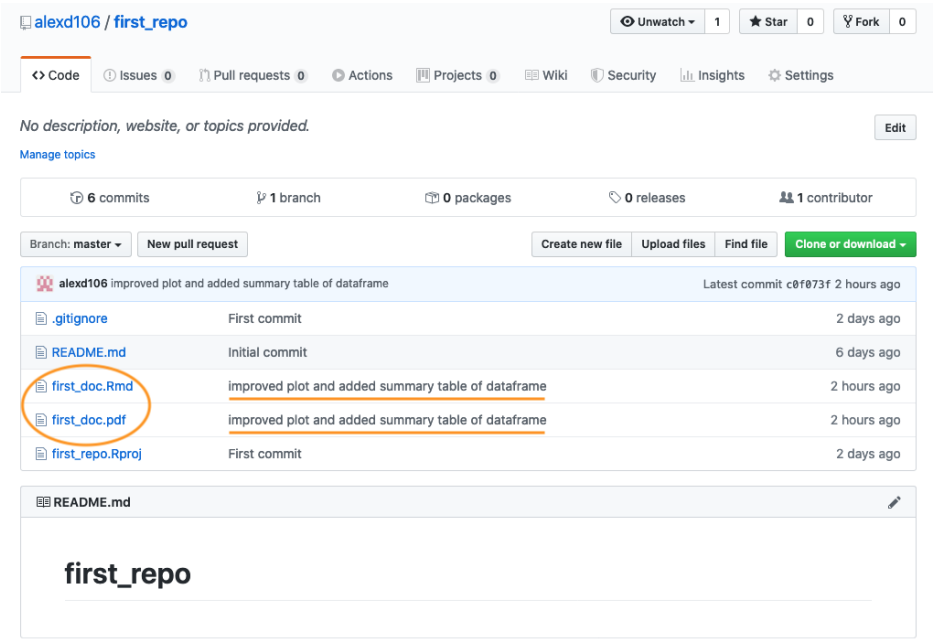
To stage these files tick the 'Staged' box for each file and click on the 'Commit' button to take you to the 'Review Changes' window



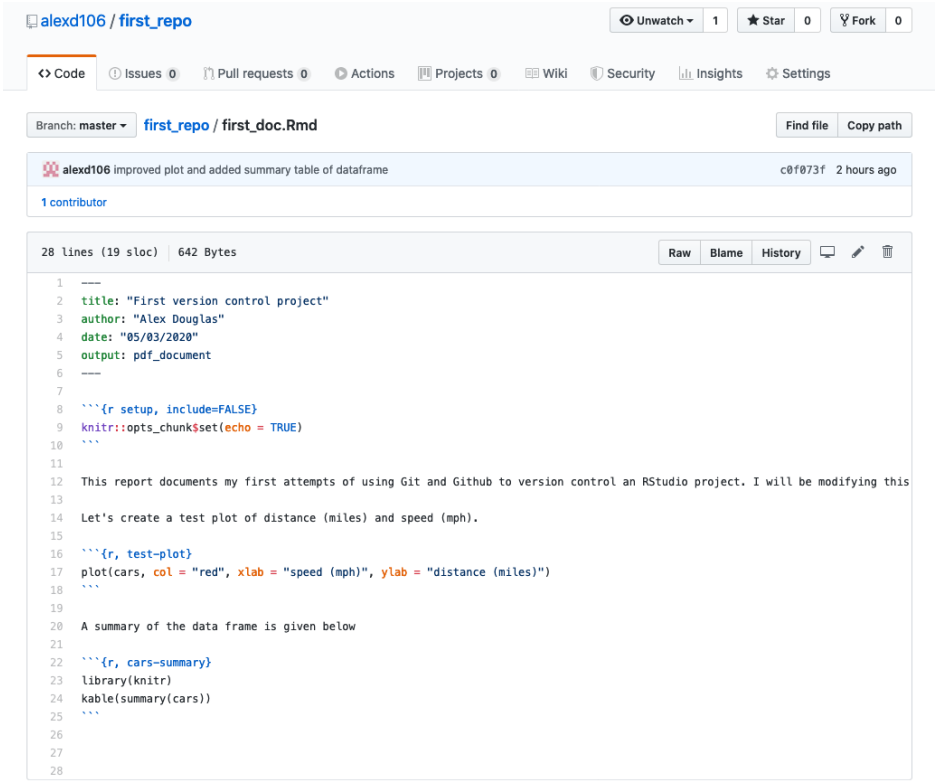
Before you commit your changes notice the status of `first_doc.pdf` has changed from untracked to added (A). You can view the changes you have made to the `first_doc.Rmd` by clicking on the file name in the top left pane which will provide you with a useful summary of the changes in the bottom pane (technically called diffs). Lines that have been deleted are highlighted in red and lines that have been added are highlighted in green (note that from Git's point of view, a modification to a line is actually two operations: the removal of the original line followed by the creation of a new line). Once you're happy, commit these changes by writing a suitable commit message and click on the 'Commit' button.



To push the changes to GitHub, click on the 'Pull' button first (remember this is good practice even though you are only collaborating with yourself at the moment) and then click on the 'Push' button. Go to your online GitHub repository and you will see your new commits, including the `first_doc.pdf` file you created when you rendered your R markdown document.



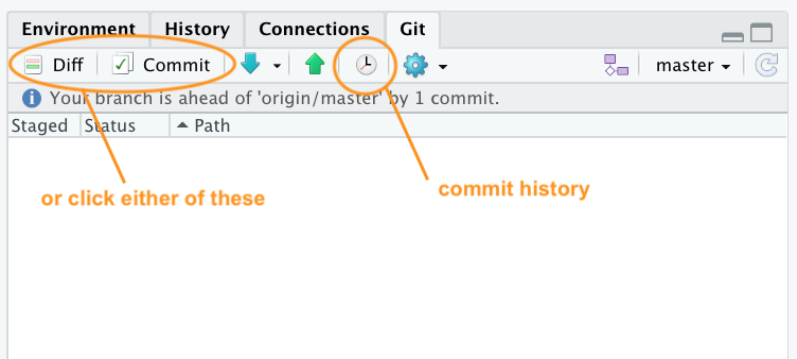
To view the changes in `first_doc.Rmd` click on the file name for this file.



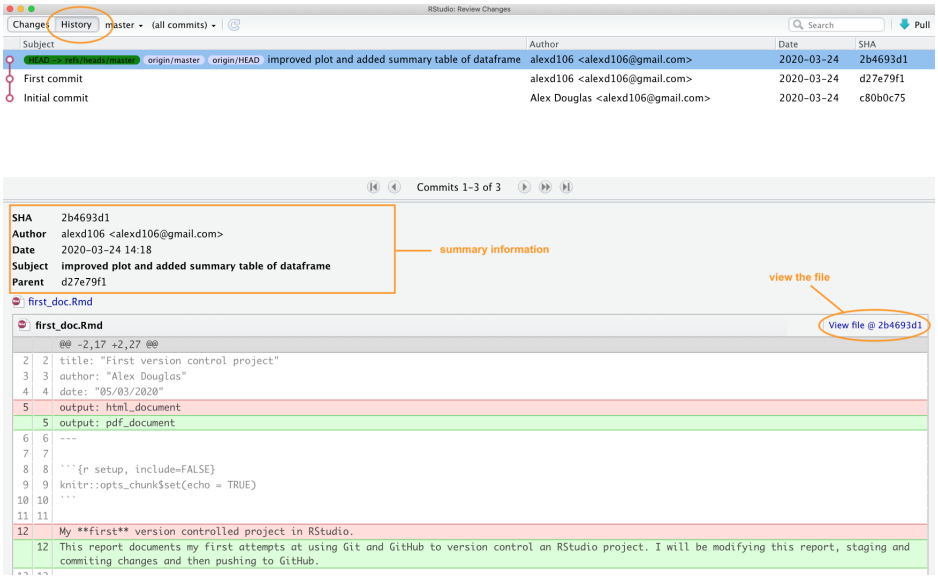
8.6.2. Commit history

One of the great things about Git and GitHub is that you can view the history of all the commits you have made along with the associated commit messages. You can do this locally using RStudio (or the Git command line) or if you have pushed your commits to GitHub you can check them out on the GitHub website.

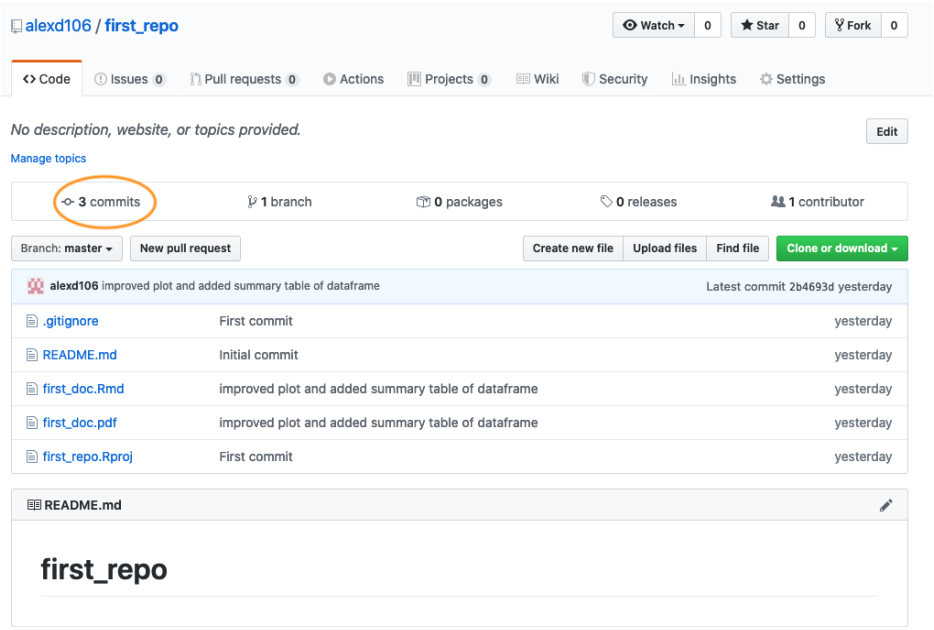
To view your commit history in RStudio click on the 'History' button (the one that looks like a clock) in the Git pane to bring up the history view in the 'Review Changes' window. You can also click on the 'Commit' or 'Diff' buttons which takes you to the same window (you just need to additionally click on the 'History' button in the 'Review Changes' window).



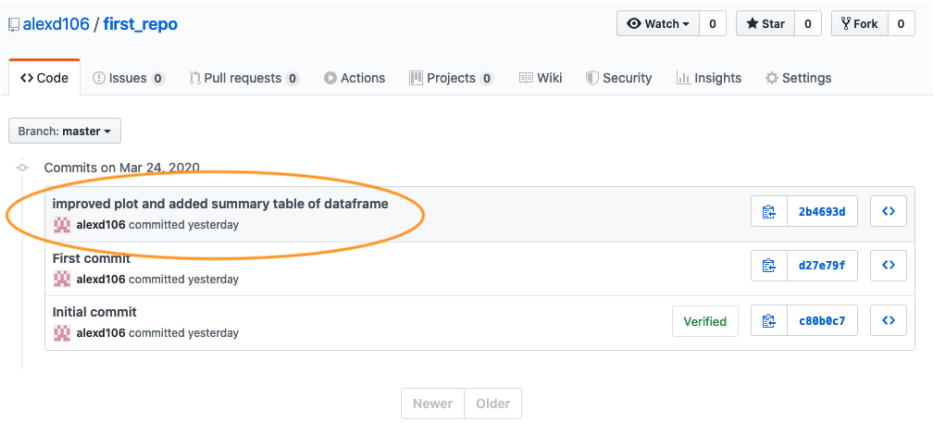
The history window is split into two parts. The top pane lists every commit you have made in this repository (with associated commit messages) starting with the most recent one at the top and oldest at the bottom. You can click on each of these commits and the bottom pane shows you the changes you have made along with a summary of the **Date** the commit was made, **Author** of the commit and the commit message (**Subject**). There is also a unique identifier for the commit (**SHA** - Secure Hash Algorithm) and a **Parent** SHA which identifies the previous commit. These SHA identifiers are really important as you can use them to view and revert to previous versions of files (details below). You can also view the contents of each file by clicking on the 'View file @ SHA key' link (in our case 'View file @ 2b4693d1').



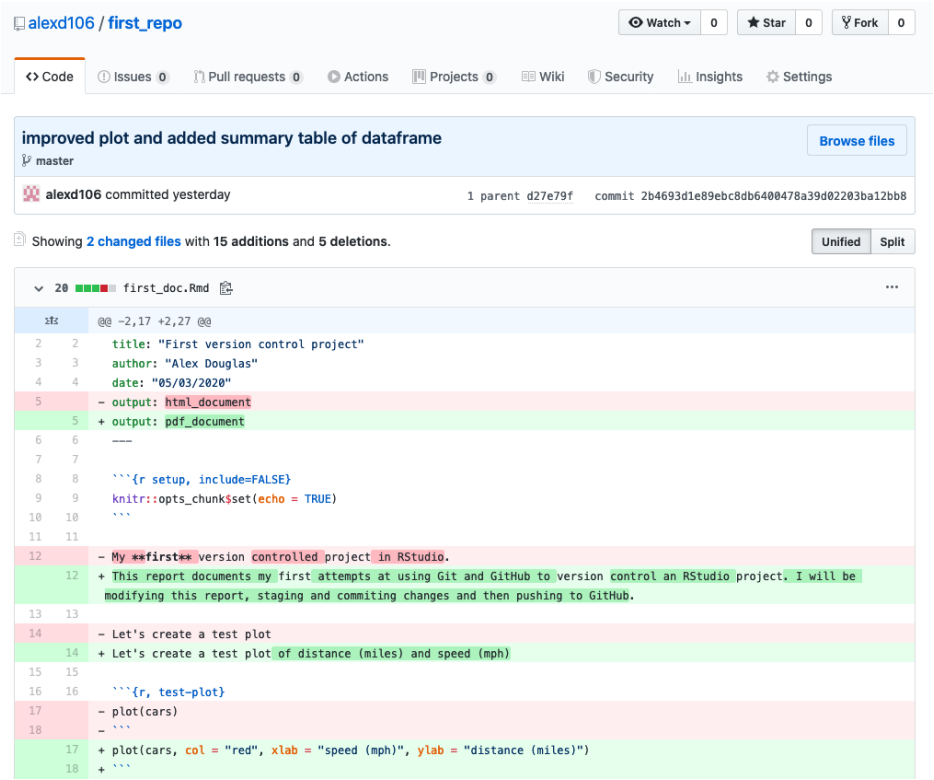
You can also view your commit history on GitHub website but this will be limited to only those commits you have already pushed to GitHub. To view the commit history navigate to the repository and click on the 'commits' link (in our case the link will be labelled '3 commits' as we have made 3 commits).



You will see a list of all the commits you have made, along with commit messages, date of commit and the SHA identifier (these are the same SHA identifiers you saw in the RStudio history). You can even browse the repository at a particular point in time by clicking on the <> link. To view the changes in files associated with the commit simply click on the relevant commit link in the list.



Which will display changes using the usual format of green for additions and red for deletions.

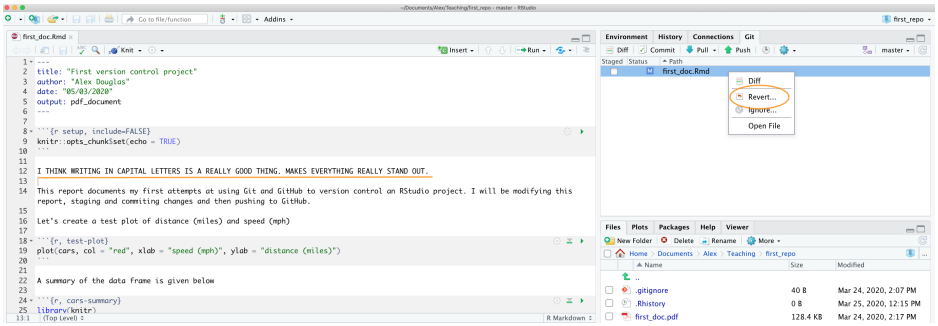


8.6.3. Reverting changes

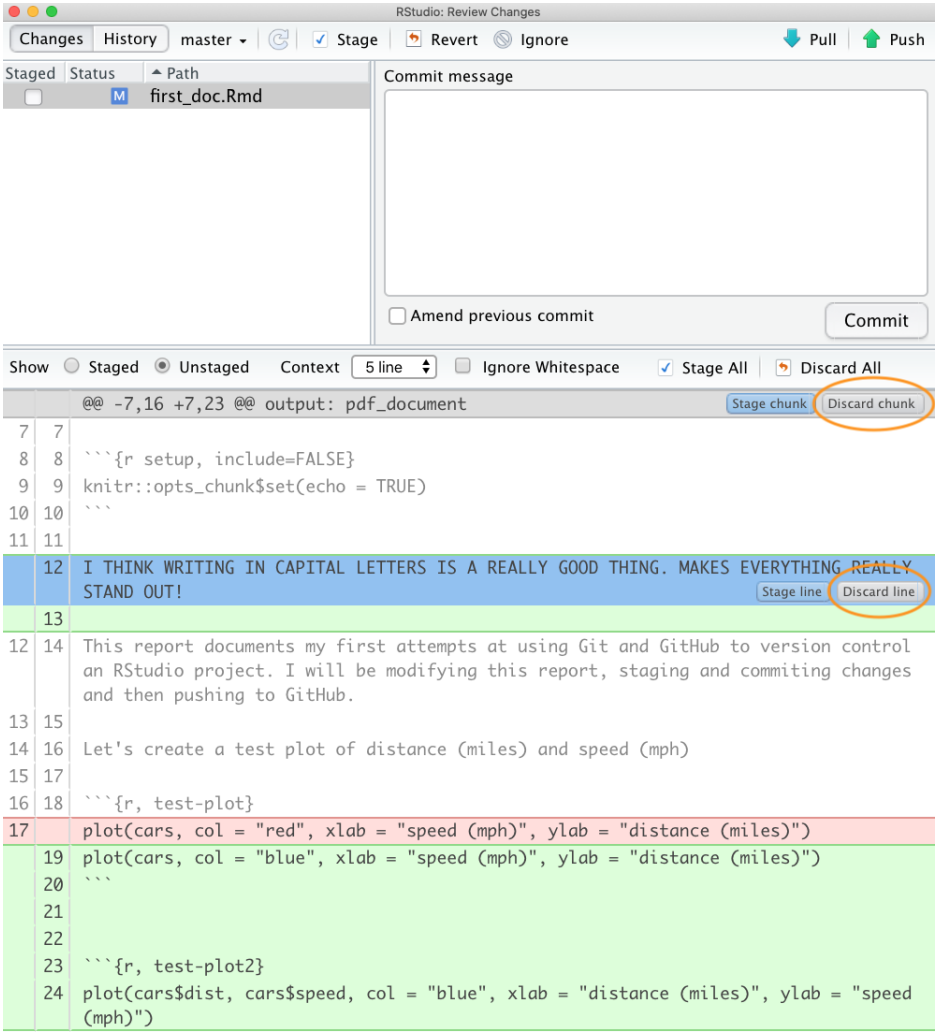
One the great things about using Git is that you are able to revert to previous versions of files if you've made a mistake, broke something or just prefer and earlier approach. How you do this will depend on whether the changes you want to discard have been staged, committed or pushed to GitHub. We'll go through some common scenarios below mostly using RStudio but occasionally we will need to resort to using the Terminal (still in RStudio though).

Changes saved but not staged, committed or pushed

If you have saved changes to your file(s) but not staged, committed or pushed these files to GitHub you can right click on the offending file in the Git pane and select 'Revert …'. This will roll back all of the changes you have made to the same state as your last commit. Just be aware that you cannot undo this operation so use with caution.



You can also undo changes to just part of a file by opening up the 'Diff' window (click on the 'Diff' button in the Git pane). Select the line you wish to discard by double clicking on the line and then click on the 'Discard line' button. In a similar fashion you can discard chunks of code by clicking on the 'Discard chunk' button.

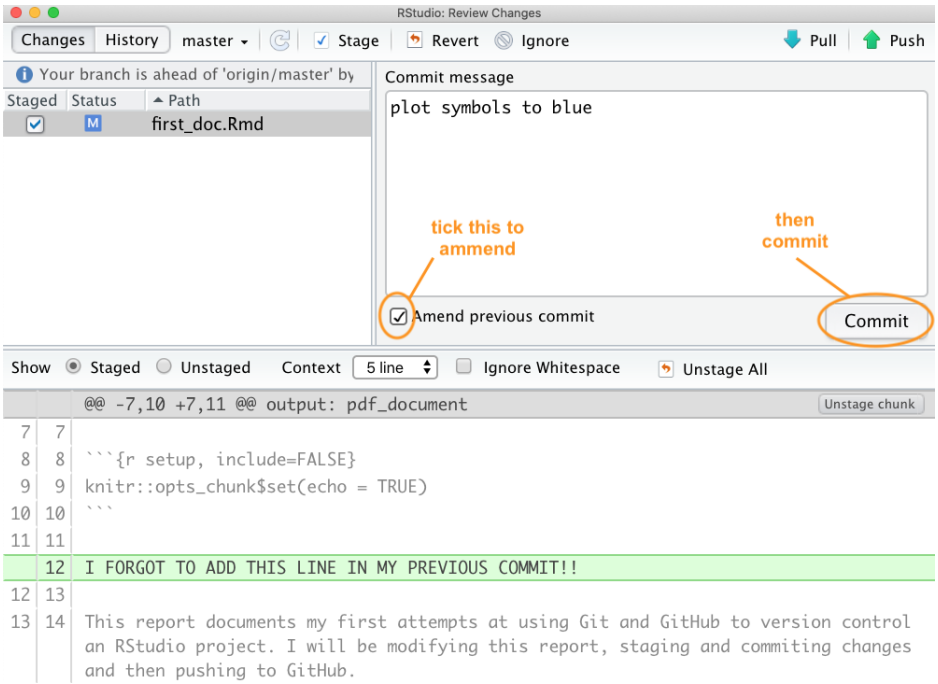


Staged but not committed and not pushed

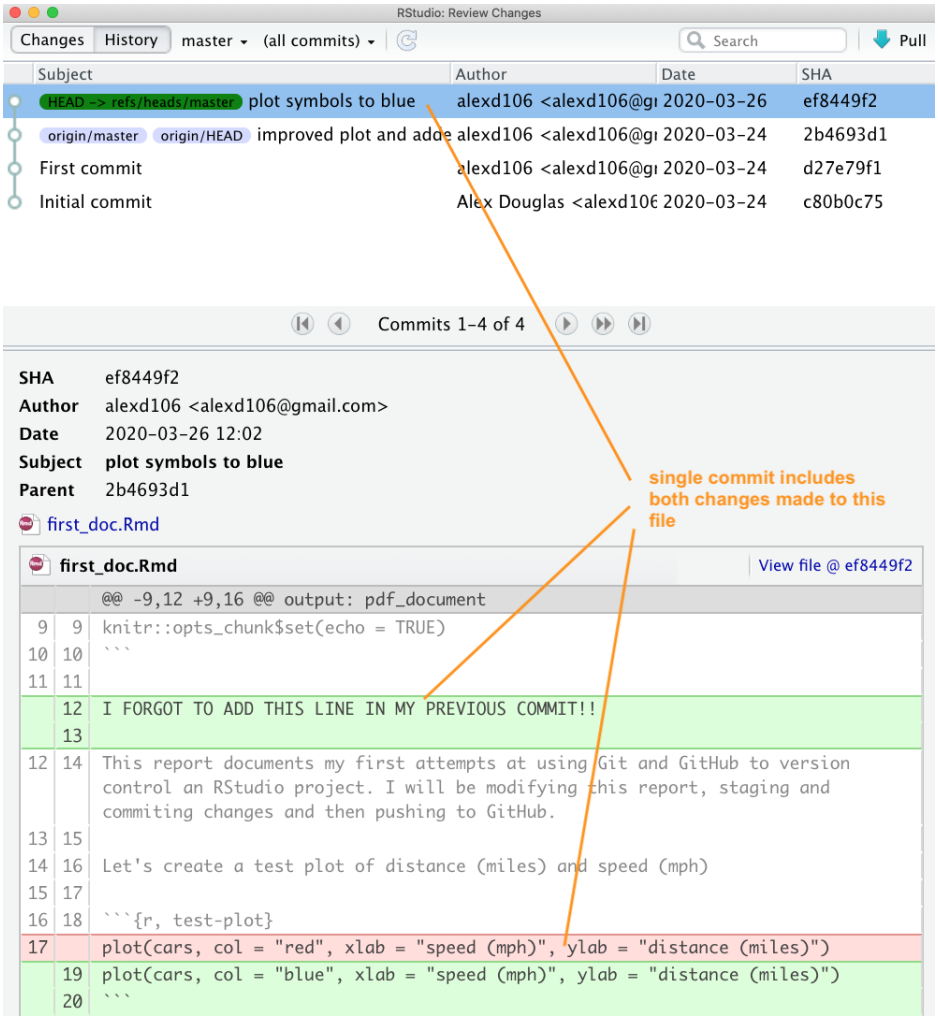
If you have staged your files, but not committed them then simply unstage them by clicking on the 'Staged' check box in the Git pane (or in the 'Review Changes' window) to remove the tick. You can then revert all or parts of the file as described in the section above.

Staged and committed but not pushed

If you have made a mistake or have forgotten to include a file in your last commit which you have not yet pushed to GitHub, you can just fix your mistake, save your changes, and then amend your previous commit. You can do this by staging your file and then tick the 'Amend previous commit' box in the 'Review Changes' window before committing.

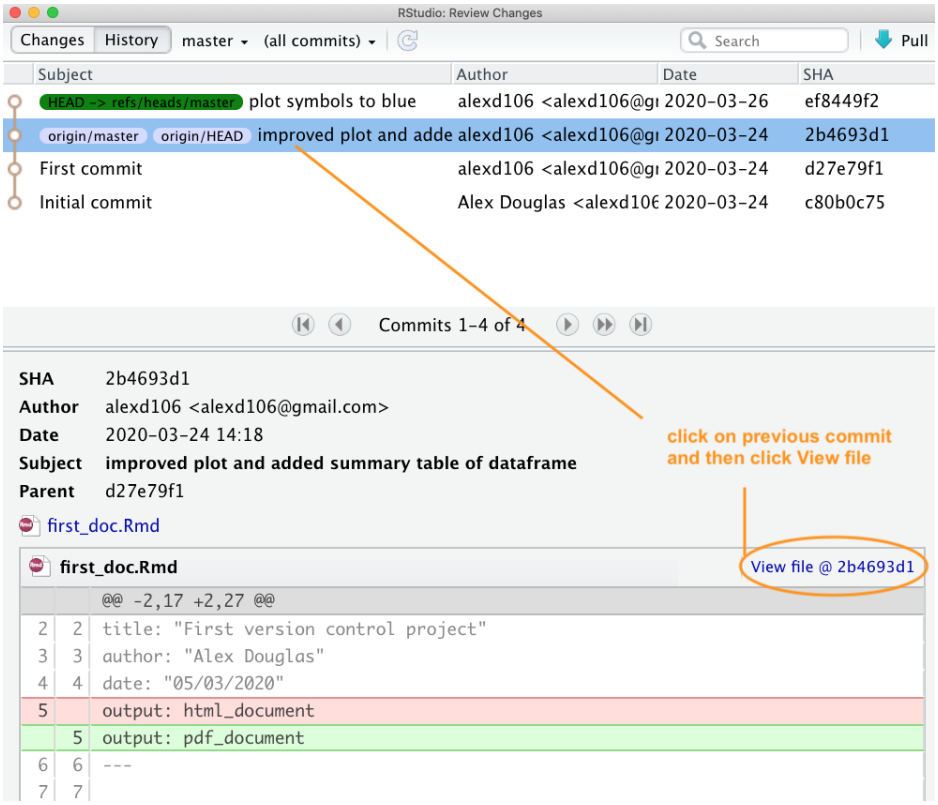


If we check out our commit history you can see that our latest commit contains both changes to the file rather than having two separate commits. We use the amend commit approach alot but it's important to understand that you should **not** do this if you have already pushed your last commit to GitHub as you are effectively rewriting history and all sorts bad things may happen!

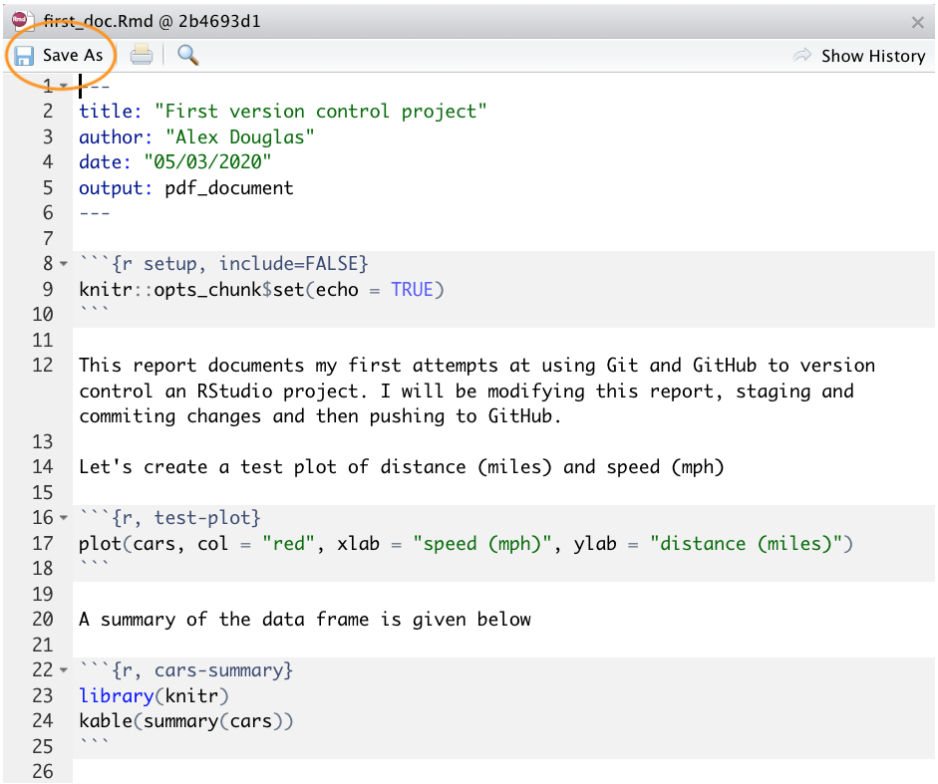


If you spot a mistake that has happened multiple commits back or you just want to revert to a previous version of a document you have a number of options.

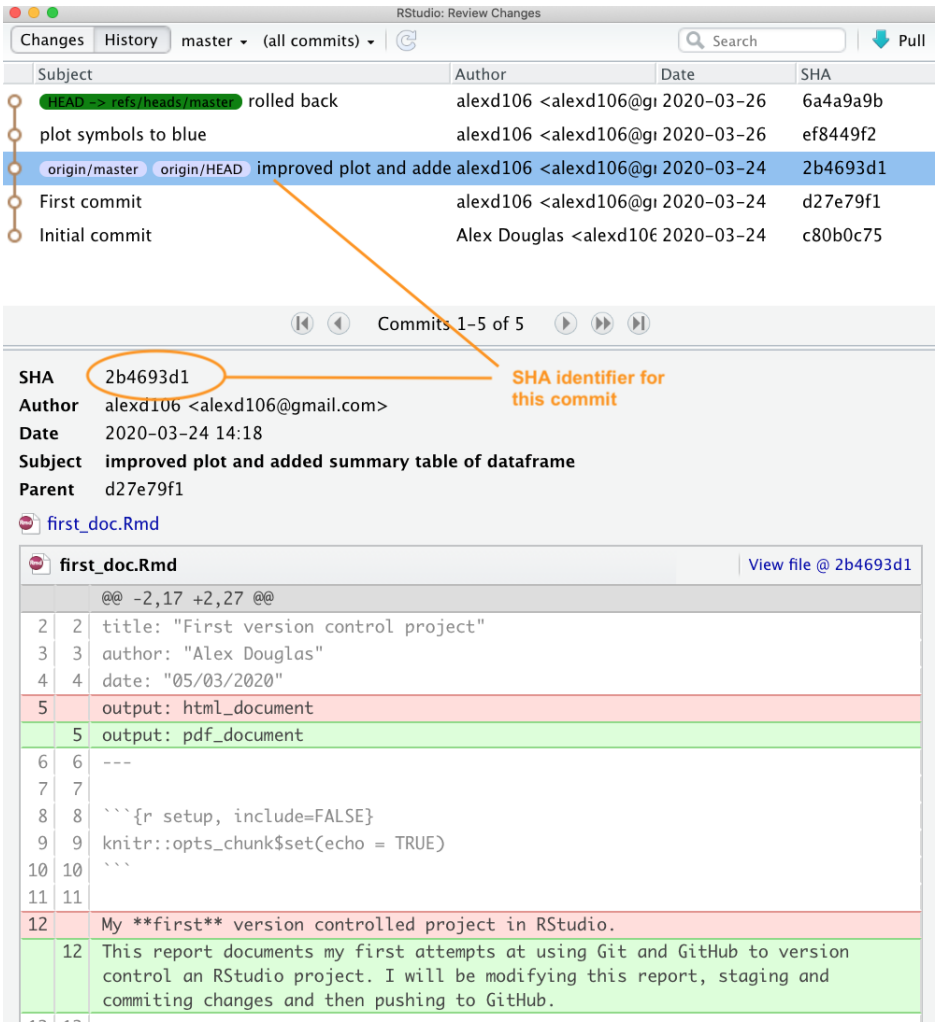
Option 1 - (probably the easiest but very unGit - but like, whatever!) is to look in your commit history in RStudio, find the commit that you would like to go back to and click on the 'View file @' button to show the file contents.



You can then copy the contents of the file to the clipboard and paste it into your current file to replace your duff code or text. Alternatively, you can click on the 'Save As' button and save the file with a different file name. Once you have saved your new file you can delete your current unwanted file and then carry on working on your new file. Don't forget to stage and commit this new file.



Option 2 - (Git like) Go to your Git history, find the commit you would like to roll back to and write down (or copy) its SHA identifier.



Now go to the Terminal in RStudio and type `git checkout <SHA> <filename>`. In our case the SHA key is `2b4693d1` and the filename is `first_doc.Rmd` so our command would look like this:

```
git checkout 2b4693d1 first_doc.Rmd
```

The command above will copy the selected file version from the past and place it into the present. RStudio may ask you whether you want to reload the file as it now changed - select yes. You will also need to stage and commit the file as usual.

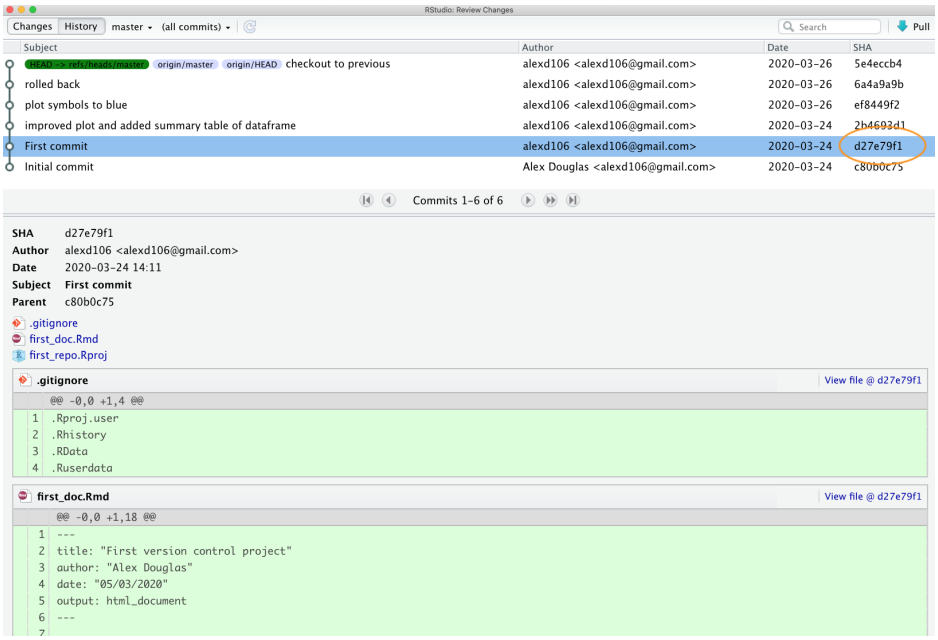
If you want to revert all your files to the same state as a previous commit rather than just one file you can use (the single 'dot' `.` is important otherwise your HEAD will detach!):

```
git rm -r .
git checkout 2b4693d1 .
```

Note that this will delete all files that you have created since you made this commit so be careful!

Staged, committed and pushed

If you have already pushed your commits to GitHub you can use the `git checkout` strategy described above and then commit and push to update GitHub (although this is not really considered 'best' practice). Another approach would be to use `git revert` (Note: as far as we can tell `git revert` is not the same as the 'Revert' option in RStudio). The `revert` command in Git essentially creates a new commit based on a previous commit and therefore preserves all of your commit history. To rollback to a previous state (commit) you first need to identify the SHA for the commit you wish to go back to (as we did above) and then use the `revert` command in the Terminal. Let's say we want to revert back to our 'First commit' which has a SHA identifier `d27e79f1`.

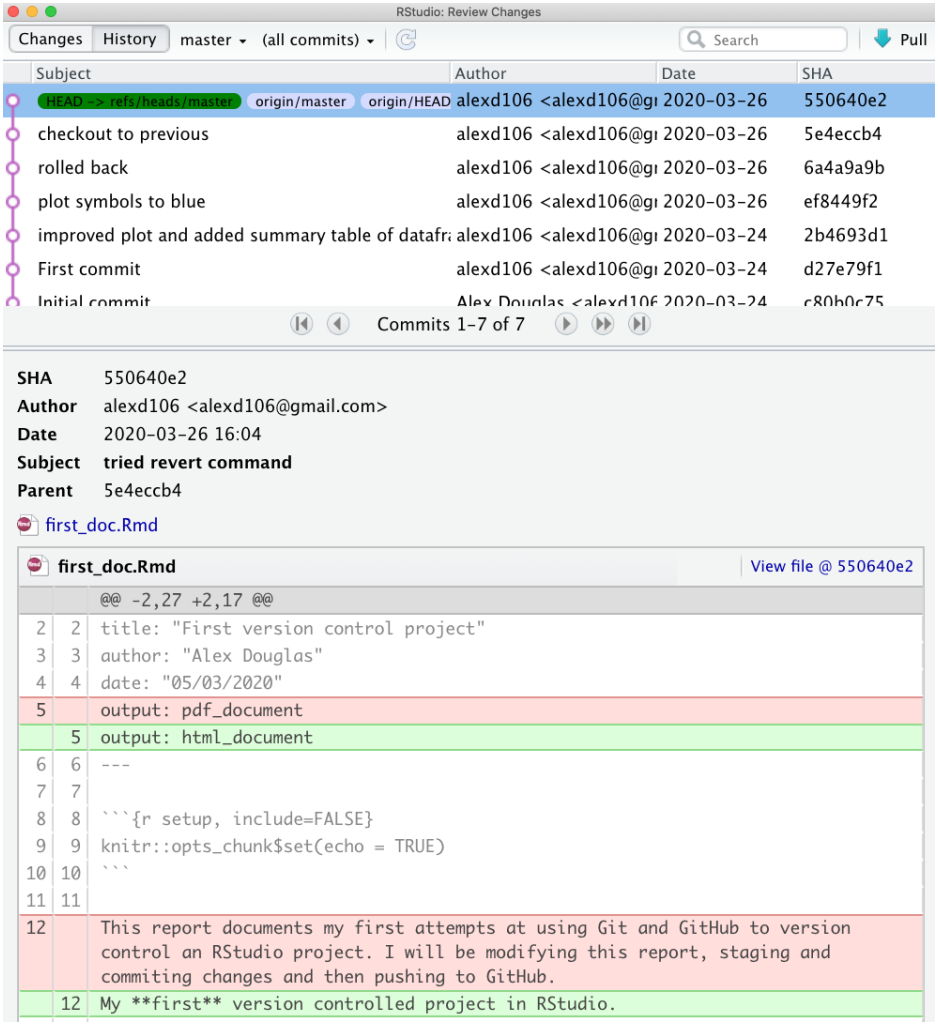


We can use the `revert` command as shown below in the Terminal. The `--no-commit` option is used to prevent us from having to deal with each intermediate commit.

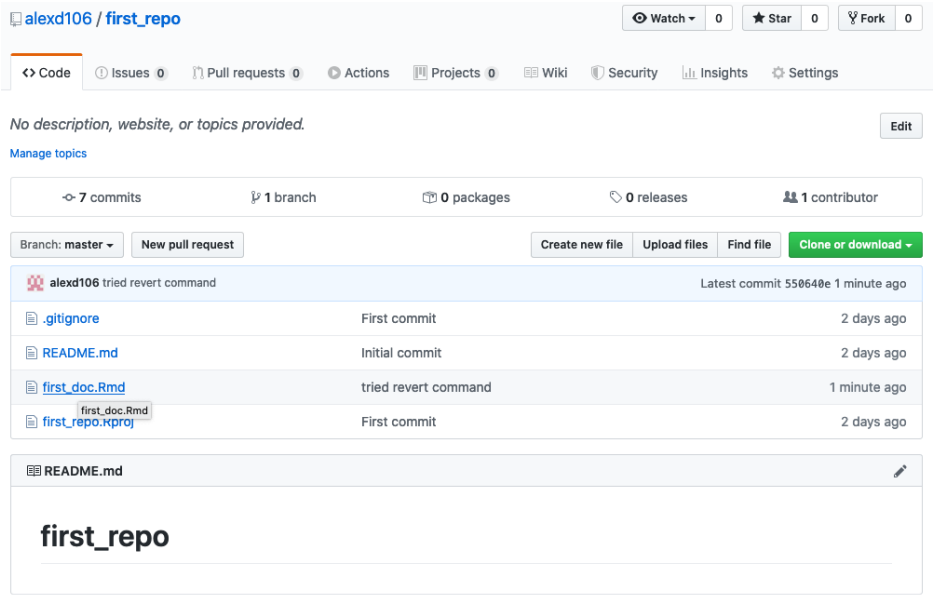
```
git revert --no-commit d27e79f1..HEAD
```

Your `first_doc.Rmd` file will now revert back to the same state as it was when you did your 'First commit'. Notice also that the `first_doc.pdf` file has been deleted as this wasn't present when we made our first commit. You can

now stage and commit these files with a new commit message and finally push them to GitHub. Notice that if we look at our commit history all of the commits we have made are still present.



and our repo on GitHub also reflects these changes



8.7. Using Git with VSCode

Now that we have our project and repositories (both local and remote) set up, it's finally time to learn how to use Git in VSCode!

Typically, when using Git your workflow will go something like this:

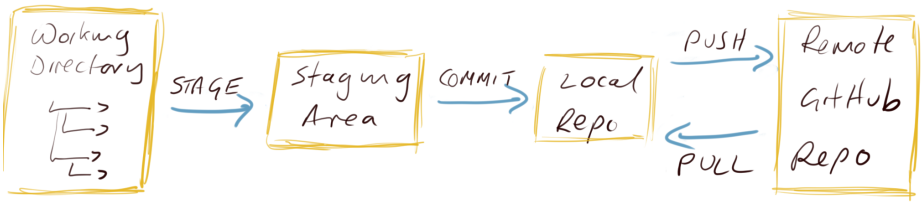
1. You create/delete and edit files in your project directory on your computer as usual (saving these changes as you go)

2. Once you've reached a natural 'break point' in your progress (i.e. you'd be sad if you lost this progress) you **stage** these files

3. You then **commit** the changes you made to these staged files (along with a useful commit message) which creates a permanent snapshot of these changes

4. You keep on with this cycle until you get to a point when you would like to **push** these changes to GitHub

5. If you're working with other people on the same project you may also need to **pull** their changes to your local computer



OK, let's go through an example to help clarify this workflow.

Tracking changes

Commit History

Reverting changes

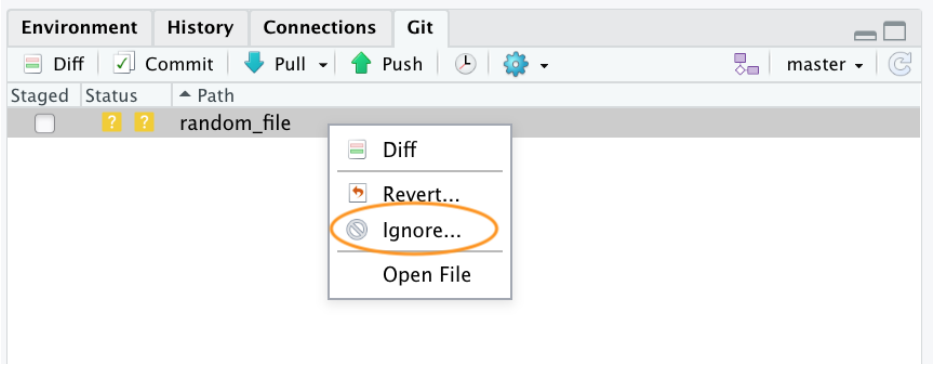
8.8. Collaborate with Git

GitHub is a great tool for collaboration, it can seem scary and complicated at first, but it is worth investing some time to learn how it works. What makes GitHub so good for collaboration is that it is a *distributed system*, which means that every collaborator works on their own copy of the project and changes are then merged together in the remote repository. There are two main ways you can set up a collaborative project on GitHub. One is the workflow we went through above, where everybody connects their local repository to the same remote one; this system works well with small projects where different people mainly work on different aspects of the project but can quickly become unwieldy if many people are collaborating and are working on the same files (merge misery!). The second approach consists of every collaborator creating a copy (or **fork**) of the main repository, which becomes their remote repository. Every collaborator then needs to send a request (a **pull request**) to the owner of the main repository to incorporate any changes into the main repository and this includes a review process before the changes are integrated. More detail of these topics can be found in the Further resources section.

8.9. Git tips

Generally speaking you should commit often (including amended commits) but push much less often. This makes collaboration easier and also makes the process of reverting to previous versions of documents much more straight forward. We generally only push changes to GitHub when we're happy for our collaborators (or the rest of the world) to see our work. However, this is entirely up to you and depends on the project (and who you are working with) and what your priorities are when using Git.

If you don't want to track a file in your repository (maybe they are too large or transient files) you can get Git to ignore the file by adding it to the `.gitignore` file. On RStudio, in the git pane, you can right clicking on the filename to exclude and selecting 'Ignore…'



This will add the filename to the `.gitignore` file. If you want to ignore multiple files or a particular type of file you can also include wildcards in the `.gitignore` file. For example to ignore all `png` files you can include the expression `*.png` in your `.gitignore` file and save.

If it all goes pear shaped and you end up completely trashing your Git repository don't despair (we've all been there!). As long as your GitHub repository is good, all you need to do is delete the offending project directory on your computer, create a new RStudio project and link this with your remote GitHub repository using Option 2. Once you have cloned the remote repository you should be good to go.

8.10. Further resources

There are many good online guides to learn more about git and GitHub and as with any open source software there is a huge community that can be a great resource:

- The British Ecological Society guide to Reproducible Code
- The GitHub guides
- The Mozilla Science Lab GitHub for Collaboration on Open Projects guide
- Jenny Bryan's Happy Git and GitHub. We borrowed the idea (but with different content) of RStudio first, RStudio second in the 'Setting up a version controlled Project in RStudio' section.
- Melanie Frazier's GitHub: A beginner's guide to going back in time (aka fixing mistakes). We followed this structure (with modifications and different content) in the 'Reverting changes' section.
- If you have done something terribly wrong and don't know how to fix it try Oh Shit, Git or if you're easily offended Dangit, Git

These are only a couple of examples, all you need to do is Google "version control with git and GitHub" to see how huge the community around these open source projects is and how many free resources are available for you to become a version control expert.

References

R packages

This book was produced all packages (excluding dependencies) listed in table Table 8.1. As recommended by the 'tidyverse' team, all citations to tidyverse packages are collapsed into a single citation.

Table 8.1.: R packages used in this book

Package	Version	Citation
babeldown	0.0.0.9000	Salmon (2024)
base	4.3.3	R Core Team (2024)
GGally	2.2.1	Schloerke et al. (2024)
ggcleveland	0.1.0	Prunello and Mari (2021)
ggfortify	0.4.16	Tang et al. (2016); Horikoshi and Tang (2018)
ggpubr	0.6.0	Kassambara (2023)
grateful	0.2.4	Francisco Rodriguez-Sanchez and Connor P. Jackson (2023)
hexbin	1.28.3	Carr et al. (2023)
kableExtra	1.4.0	Zhu (2024)
keyring	1.3.2	Csárdi (2023)
knitr	1.45	Xie (2014); Xie (2015); Xie (2023)
patchwork	1.2.0	Pedersen (2024)
quantreg	5.97	Koenker (2023)
quarto	1.4.1	Allaire and Dervieux (2024)
reshape2	1.4.4	Wickham (2007)
rmarkdown	2.26	Xie et al. (2018); Xie et al. (2020); Allaire et al. (2024)
tidyverse	2.0.0	Wickham et al. (2019)
vioplot	0.4.0	Adler et al. (2022)

Bibliography

Adler, D., S. T. Kelly, T. Elliott, and J. Adamson. 2022. vioplot: Violin plot.

Allaire, J., and C. Dervieux. 2024. quarto: R interface to "Quarto" markdown publishing system.

Allaire, J., Y. Xie, C. Dervieux, J. McPherson, J. Luraschi, K. Ushey, A. Atkins, H. Wickham, J. Cheng, W. Chang, and R. Iannone. 2024. rmarkdown: Dynamic documents for r.

Carr, D., ported by Nicholas Lewin-Koh, M. Maechler, and contains copies of lattice functions written by Deepayan Sarkar. 2023. hexbin: Hexagonal binning routines.

Csárdi, G. 2023. keyring: Access the system credential store from r.

Douglas, A. 2023. The Grammar of Graphics.

Francisco Rodriguez-Sanchez, and Connor P. Jackson. 2023. grateful: Facilitate citation of r packages.

Horikoshi, M., and Y. Tang. 2018. ggfortify: Data visualization tools for statistical analysis results.

Kassambara, A. 2023. ggpubr: "ggplot2" based publication ready plots.

Koenker, R. 2023. quantreg: Quantile regression.

Pedersen, T. L. 2024. patchwork: The composer of plots.

Prunello, M., and G. Mari. 2021. ggcleveland: Implementation of plots from cleveland's visualizing data book.

R Core Team. 2024. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.

Salmon, M. 2024. babeldown: Helpers for automatic translation of markdown-based content.

Schloerke, B., D. Cook, J. Larmarange, F. Briatte, M. Marbach, E. Thoen, A. Elberg, and J. Crowley. 2024. GGally: Extension to "ggplot2".

Tang, Y., M. Horikoshi, and W. Li. 2016. ggfortify: Unified interface to visualize statistical result of popular r packages. The R Journal 8:474–485.

Wickham, H. 2007. Reshaping data with the reshape package. Journal of Statistical Software 21:1–20.

Wickham, H., M. Averick, J. Bryan, W. Chang, L. D. McGowan, R. François, G. Grolemund, A. Hayes, L. Henry, J. Hester, M. Kuhn, T. L. Pedersen, E. Miller, S. M. Bache, K. Müller, J. Ooms, D. Robinson, D. P. Seidel, V. Spinu, K. Takahashi, D. Vaughan, C. Wilke, K. Woo, and H. Yutani. 2019. Welcome to the tidyverse. Journal of Open Source Software 4:1686.

Wilkinson, L. 2005. The Grammar of Graphics. Springer Science & Business Media.

Xie, Y. 2014. knitr: A comprehensive tool for reproducible research in R. *in* V. Stodden, F. Leisch, and R. D. Peng, editors. Implementing reproducible computational research. Chapman; Hall/CRC.

Xie, Y. 2015. Dynamic documents with R and knitr. 2nd edition. Chapman; Hall/CRC, Boca Raton, Florida.

Xie, Y. 2023. knitr: A general-purpose package for dynamic report generation in r.

Xie, Y., J. J. Allaire, and G. Grolemund. 2018. R markdown: The definitive guide. Chapman; Hall/CRC, Boca Raton, Florida.

Xie, Y., C. Dervieux, and E. Riederer. 2020. R markdown cookbook. Chapman; Hall/CRC, Boca Raton, Florida.

Zhu, H. 2024. kableExtra: Construct complex table with "kable" and pipe syntax.

Appendix A

Data used in this book

check what is done for BIO8940

use downlaod this to create nice downlaod options potentially

```
path_files <- list.files(path = system.file("assets/css", package = "downloadthis"), full.names =


download_file(
  path = path_files,
  output_name = "Files from downloadthis",
  button_label = "Download files",
  button_type = "danger",
  has_icon = TRUE,
  icon = "fa fa-save",
  self_contained = FALSE
)
```

Appendix B

Installing R Markdown and LateX

Installing R markdown on your computer is pretty straight forward and should be painless. If you're getting started with R markdown we suggest that you use RStudio but of course RStudio is not required and there are other options available. You will also need to install some additional software if you want to render your R markdown documents to PDF format.

This guide assumes you have already installed R and an IDE (RStudio IDE or VSCode. An IDE is not required but recommended, because it makes it easier to work with R Markdown. If you don't have RStudio IDE installed, you will also have to install Pandoc. If you have RStudio installed there is no need to install Pandoc separately because it's bundled with RStudio. Next you can install the `rmarkdown` 📦 package in RStudio using the following code:

```
install.packages("rmarkdown", dep = TRUE)
```

The `dep = TRUE` argument will also install a bunch of additional R packages on which rmarkdown depends.

If you want to generate PDF output, you will need to install LaTeX. For R Markdown users who have not installed LaTeX before, we recommend that you install TinyTeX. You can install TinyTex from within R using the `tinytex` 📦 package with the following code:

```
install.packages('tinytex')
tinytex::install_tinytex()  # install TinyTeX
```

TinyTeX is a lightweight, portable, cross-platform, and easy-to-maintain LaTeX distribution. The R companion package `tinytex` 📦 can help you automatically install missing LaTeX packages when compiling LaTeX or R Markdown documents to PDF.

B.1. MS Windows

An alternative option would be to install MiKTeX instead. You can download the latest distribution of MiKTeX. Installing MiKTeX is pretty straight forward, but it can sometimes be a pain to get it to play nicely with RStudio. If at all possible we recommend that you use TinyTex.

B.2. Mac OSX

If for some reason TinyTeX does not work on your Mac computer then you can try to install MacTeX instead. You can download the latest version of MacTeX here.

B.3. Linux

An alternative to TinyTex on linux would be to use a full fledge distribution of LaTeX such as TexLive