Building reproducible analytical pipelines with R

Bruno Rodrigues, ...

1/6/23

Table of contents

Preface

This is a Quarto book.

To learn more about Quarto books visit https://quarto.org/docs/books.

1 Introduction

This book will teach how to structure your projects in such a way as to make them reproducible.

I think we should also explain that this book presents one way of doing things, and that it is by no means the only, canonic way, of solving the problems we will be talking about.

1.1 Prerequisites

You should be comfortable with the R programming language. This book will assume that you have been using R for some projects already, and want to improve not only your knowledge of the language itself, but also how to successfully manage complex projects.

1.2 What is reproducibility?

1.3 Are there different types of reproducibility?

Reproducibility is on a continuum.

Part I

Part 1

2 Project start

In this chapter, we are going to work together on a very simple project. This project will stay with us until the end of the book. For now, we are going to keep it simple; our goal here is to get an analysis done. We are going to download some data, and analyse it. Once this is done, we are going to think about the issues with our approach, and improve our analysis after we have learned about a new topic, as explained in the intro. At the end of each chapter, we will improve our analysis by directly applying what we've learned.

But for now, our main concern is to get our work done.

2.1 Housing in Luxembourg

We are going to download data about house prices in Luxembourg. Luxembourg is a little Western European country that looks like a shoe and is about the size of .98 Rhode Islands from the author hails from. Did you know that Luxembourg was a constitutional monarchy, and not a kingdom like Belgium, but a Grand-Duchy, and actually the last Grand-Duchy in the Word in the World? Also, what you should know to understand what we will be doing is that the country of Luxembourg is divided into Cantons, and each Cantons into Communes. Basically, if Luxembourg was the USA, Cantons would be States and Communes would be Counties (or Parishes or Boroughs). What's confusing is that "Luxembourg" is also the name of a Canton, and of a Commune, which also has the status of a city and is the capital of the country. So Luxembourg the country, is divided into Cantons, one of which is called Luxembourg as well, cantons are divided into communes, and inside the canton of Luxembourg there's the commune of Luxembourg which is also the city of Luxembourg, sometimes called Luxembourg-City, which is the capital of the country.

What you should also know is that the population is about 645.000 as of writing (January 2023), half of which are foreigners. Around 400.000 persons work in Luxembourg, of which half do not live in Luxembourg; so every morning from Monday to Friday, 200.000 people enter the country to work, and leave on the evening to go back to either Belgium, France or Germany, the neighbouring countries. As you can imagine, this puts enormous pressure on the transportation system and on the roads, but also on the housing market; everyone wants to live in Luxembourg to avoid the horrible daily commute, and everyone wants to live either in the capital city, or in the second largest urban area in the south, in a city called Esch-sur-Alzette.

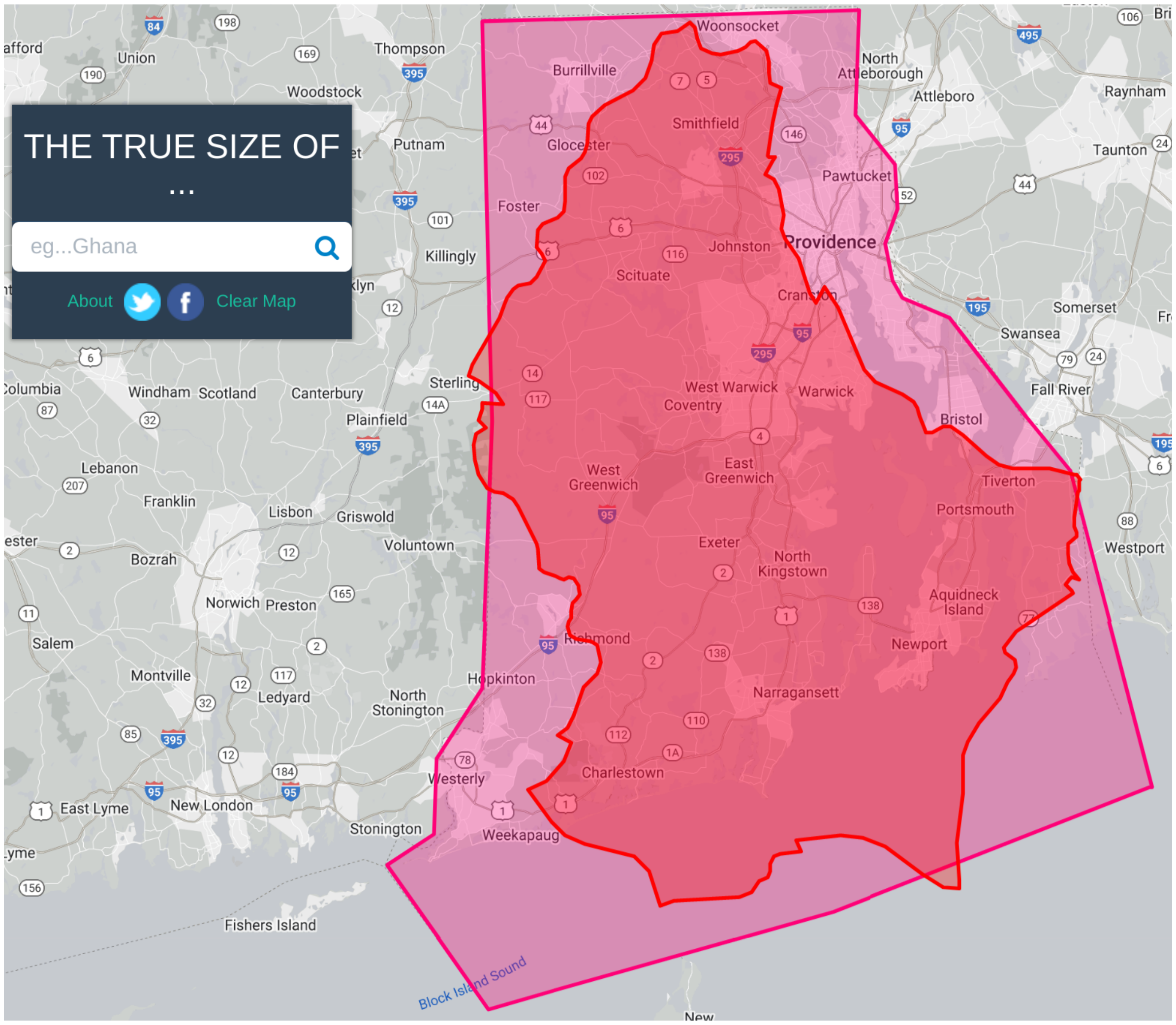
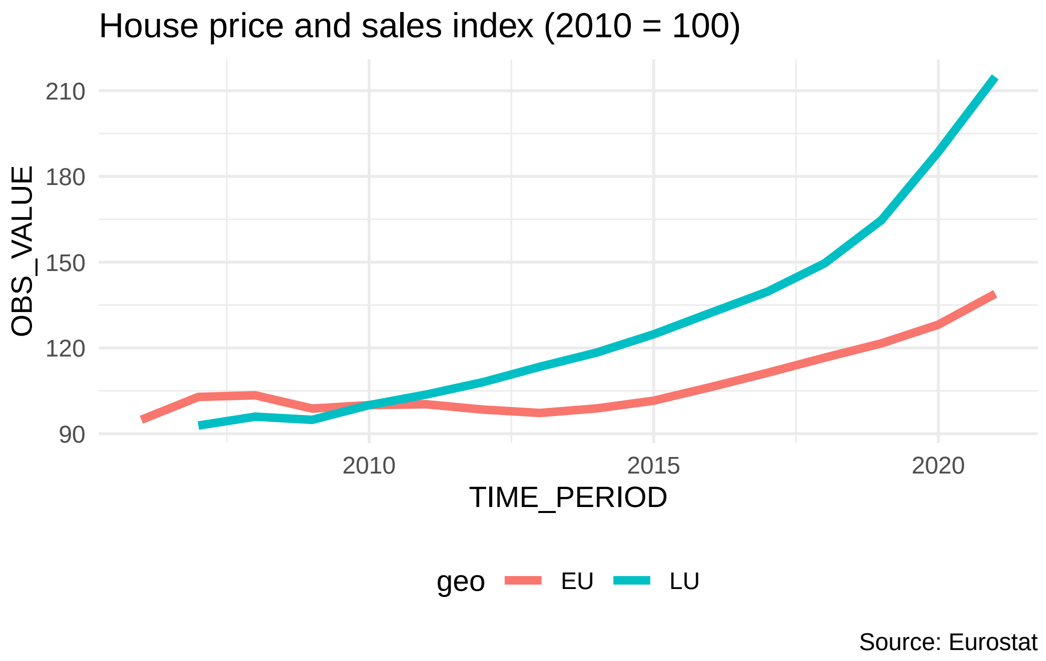


Figure 2.1: Luxembourg is about as big as the US State of Rhode Island

The plot below shows the value of the House Price Index through time for Luxembourg and the European Union:



If you want to download the data, click here.

Let us paste the definition of the HPI in here (taken from the HPI's metadata page):

The House Price Index (HPI) measures inflation in the residential property market. The HPI captures price changes of all types of dwellings purchased by households (flats, detached houses, terraced houses, etc.). Only transacted dwellings are considered, self-build dwellings are excluded. The land component of the dwelling is included.

So from the plot, we can see that the price of dwellings more than doubled between 2010 and 2021; the value of the index is 214.81 in 2021 for Luxembourg, and 138.92 for the European Union as a whole.

There is a lot of heterogeneity though; the capital and the communes immediately next to the capital are much more expensive that communes from the less urbanised north, for example. The south of the country is also more expensive than the north, but not as much as the capital and surrounding communes. Not only is price driven by hand demand, but also by scarcity; in 2021, .5% of residents owned 50% of the buildable land for housing purposes (Source: *Observatoire de l'Habitat, Note 29*, archived download link).

Our project will be quite simple; we are going to download some data, supplied as an Excel file, compiled by the Housing Observatory (*Observatoire de l'Habitat*), a service from the Ministry of Housing, which monitors the evolution of prices in the housing market, among other useful services like the identification of vacant lots for example. The advantage of their data when compared to Eurostat's data is that the data is disaggregated by commune. The disadvantage is that they only supply nominal prices, and no index. Nominal prices are the prices that you read on price tags in shops. The problem with nominal prices is that it is difficult to compare them through time. Ask yourself the following question: would you prefer to have had 500€ (or USDs) in 2003 or in 2023? You probably would have preferred them in 2003, as you could purchase a lot more with 500€ then than now. In fact, according to a random inflation calculator I googled, to match the purchasing power of $500 in 2003, you'd need to have $793 in 2023 (and I'd say that we find very similar values for €). But it doesn't really matter if that calculation is 100% correct: what matters is that the value of money changes, and comparisons through time are difficult, hence why an index is quite useful. So we are going to convert these nominal prices to real prices. Real prices take inflation into account and so allow us to compare prices through time. So we will need to also get some data to achieve this.

So to summarise; our goal is to:

- Get data trapped inside an Excel file into a neat data frame;
- Convert nominal to real prices using a simple method;
- Make some tables and plots and call it a day (for now).

We are going to start in the most basic way possible; we are simply going to write a script and deal with each step separataley.

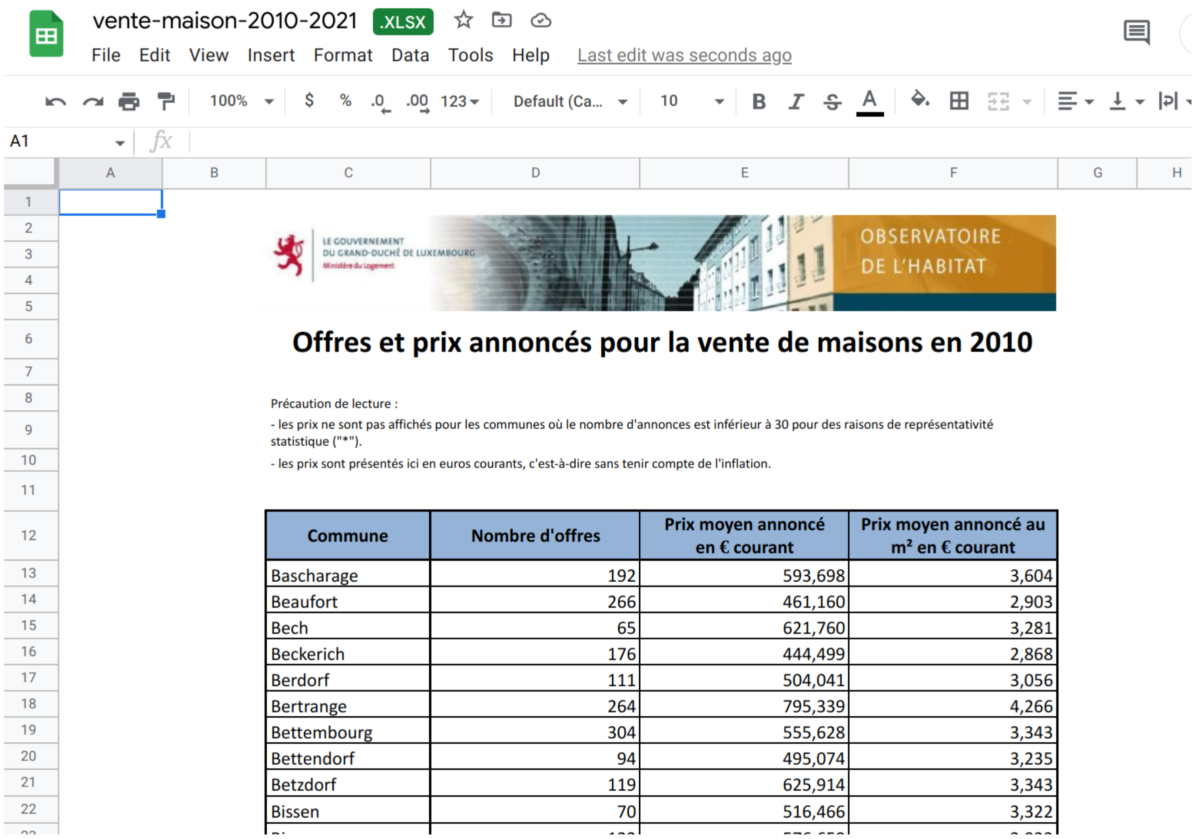
2.2 Saving trapped data from Excel

Getting data from Excel into a tidy data frame can be very tricky. This is because very often, Excel is used as some kind of dashboard, or presentation tool. So data is made human-readable, in contrast to machine readable. Let us quickly discuss this topic as it is essential to grasp the difference between the two (and in our experience, a lot of collective pain inflicted to statisticians and researchers could have been avoided if this concept was more well-known). The picture below shows an Excel made for human consumption:

So why is this file not machine-readable? Here are some issues:

- The table does not start in the top-left corner of the spreadsheet, which is where most importing tools expect it to be;
- The spreadsheet start with a head that contains an image and some text;
- Numbers are text and use "," as the thousands separator;
- You don't see it in the screenshot, but each year is in a separate sheet.

That being said, this one is still very nice, and going from this Excel to a tidy dataframe will not be too difficult. In fact, we suspect that whoever made this Excel file is well aware of the


vente-maison-2010-2021 .XLSX
File Edit View Insert Format Data Tools Help Last edit was seconds ago
100% $ % .0 .00 123 Default (Ca... 10
A1
LE GOUVERNEMENT DU GRAND-DUCHÉ DE LUXEMBOURG Ministère du Logement
OBSERVATOIRE DE L'HABITAT

Offres et prix annoncés pour la vente de maisons en 2010

Précaution de lecture :
- les prix ne sont pas affichés pour les communes où le nombre d'annonces est inférieur à 30 pour des raisons de représentativité statistique ("*").
- les prix sont présentés ici en euros courants, c'est-à-dire sans tenir compte de l'inflation.

Commune	Nombre d'offres	Prix moyen annoncé en € courant	Prix moyen annoncé au m² en € courant
Bascharage	192	593,698	3,604
Beaufort	266	461,160	2,903
Bech	65	621,760	3,281
Beckerich	176	444,499	2,868
Berdorf	111	504,041	3,056
Bertrange	264	795,339	4,266
Bettembourg	304	555,628	3,343
Bettendorf	94	495,074	3,235
Betzdorf	119	625,914	3,343
Bissen	70	516,466	3,322

Figure 2.2: An Excel file meant for human eyes

contradicting requirements of human and machine readable formatting of data, and strove to find a compromise. Because more often than not, getting human readable data into a machine readable formatting is a nightmare.

This is actually the file that we are going to use for our project, so if you want to follow along, you can download it here (downloaded on January 2023 from the luxembourguish open data portal).

Each sheet contains a dataset with the following columns:

- Commune: the commune
- Nombre d'offres: the total number of selling offers
- Prix moyen annoncé en Euros courants: Average selling price in nominal Euros
- Prix moyen annoncé au m2 en Euros courants: Average selling price in square meters in nominal Euros

For ease of presentation, we are going to show you each function here separately, but we'll be putting everything together in a single script once we're done explaining each step. So first, let's read in the data. The following lines do just that:

```r
library(dplyr)
```

```
Attaching package: 'dplyr'


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

    filter, lag


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

    intersect, setdiff, setequal, union
```

```r
library(purrr)
library(readxl)
library(stringr)
library(janitor)
```

```
Attaching package: 'janitor'
```

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

    chisq.test, fisher.test
```

```r
url <- "https://github.com/b-rodrigues/rap4all/raw/master/datasets/vente-maison-2010-2021.

raw_data <- tempfile(fileext = ".xlsx")

download.file(url, raw_data)

sheets <- excel_sheets(raw_data)

read_clean <- function(..., sheet){
  read_excel(..., sheet = sheet) |>
    mutate(year = sheet)
}

raw_data <- map(
  sheets,
  ~read_clean(raw_data,
              skip = 10,
              sheet = .)
                   ) |>
  bind_rows() |>
  clean_names()
```

```
New names:
* `*` -> `*...3`
* `*` -> `*...4`
```

```r
raw_data <- raw_data |>
  rename(
    locality = commune,
    n_offers = nombre_doffres,
    average_price_nominal_euros = prix_moyen_annonce_en_courant,
    average_price_m2_nominal_euros = prix_moyen_annonce_au_m2_en_courant,
    average_price_m2_nominal_euros = prix_moyen_annonce_au_m2_en_courant
  ) |>
  mutate(locality = str_trim(locality)) |>
  select(year, locality, n_offers, starts_with("average"))
```

If you are familiar with the {tidyverse} the above code should be quite easy to follow. We start by downloading the raw Excel file and save the sheet names into a variable. We then use a function called read_clean(), which takes the path to the Excel file and the sheet names as an argument to read the required sheet into a data frame. We use skip = 10 to skip the first 10 lines in each Excel sheet because the first 10 lines contain a header. The last thing this function is add a new column called year which contains the year of the data. We're lucky, because the sheet names are simply years: "2010", "2011" and so on. We then map this function to the list of sheet names, thus reading in all the data from all the sheets into one list of data frames, which then bind by row into a new data frame. Finally, we remane the columns (by translating their names from French to English) and only select the required columns.

Running this code results in a neat data set:

```
str(raw_data)
```

```
tibble [1,343 x 5] (S3: tbl_df/tbl/data.frame)
 $ year                          : chr [1:1343] "2010" "2010" "2010" "2010" ...
 $ locality                      : chr [1:1343] "Bascharage" "Beaufort" "Bech" "Beckerich" .
 $ n_offers                      : num [1:1343] 192 266 65 176 111 264 304 94 119 70 ...
 $ average_price_nominal_euros   : chr [1:1343] "593698.31000000006" "461160.29" "621760.22"
 $ average_price_m2_nominal_euros: chr [1:1343] "3603.57" "2902.76" "3280.51" "2867.88" ...
```

But there's a problem: columns that should be of type numeric are of type character instead (average_price_nominal_euros and average_price_m2_nominal_euros). There's also another issue, which you would eventually catch as you would be exploring the data: naming of the communes is not consistent. Let's take a look:

```
raw_data |>
  dplyr::filter(grepl("Luxembourg", locality)) |>
  dplyr::count(locality)
```

```
# A tibble: 2 x 2
  locality             n
  <chr>            <int>
1 Luxembourg           9
2 Luxembourg-Ville     2
```

We can see that the city of Luxembourg is spelled in two different ways. It's the same with another commune, Pétange:

```
raw_data |>
  dplyr::filter(grepl("P.tange", locality)) |>
  dplyr::count(locality)
```

```
# A tibble: 2 x 2
  locality     n
  <chr>    <int>
1 Petange      9
2 Pétange      2
```

So sometimes it is spelled correctly, with an “é”, sometimes not. Let’s write some code to correct this:

```
raw_data <- raw_data |>
  mutate(locality = ifelse(grepl("Luxembourg-Ville", locality),
                           "Luxembourg",
                           locality),
         locality = ifelse(grepl("P.tange", locality),
                           "Pétange",
                           locality)
         ) |>
  mutate(across(starts_with("average"), as.numeric))
```

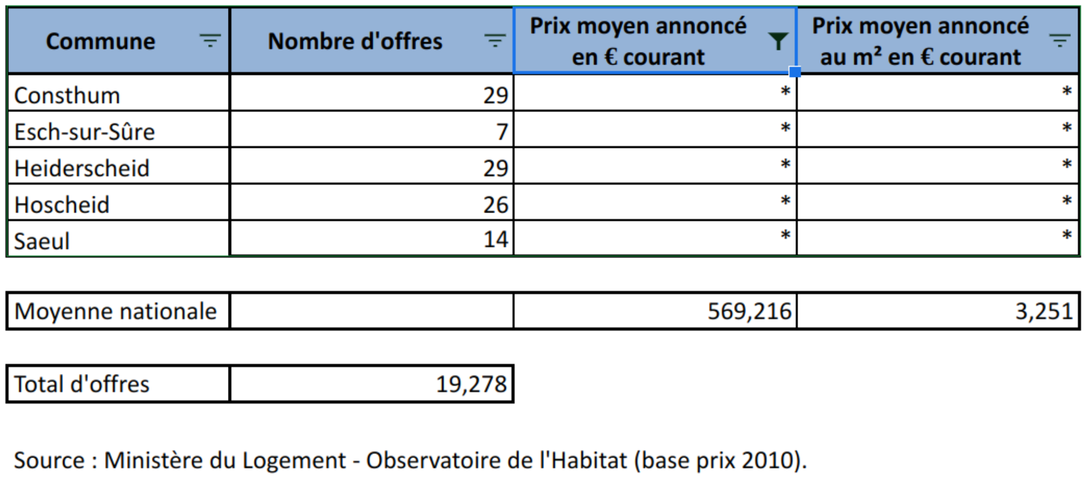
```
Warning in mask$eval_all_mutate(quo): NAs introduced by coercion

Warning in mask$eval_all_mutate(quo): NAs introduced by coercion
```

Now this is interesting – converting the `average` columns to numeric resulted in some `NA` values. Let’s see what happened:

```
raw_data |>
  filter(is.na(average_price_nominal_euros))
```

```
# A tibble: 290 x 5
   year  locality                                    n_off~1 avera~2 avera~3
   <chr> <chr>                                         <dbl>   <dbl>   <dbl>
 1 2010  Consthum                                         29      NA      NA
 2 2010  Esch-sur-Sûre                                     7      NA      NA
 3 2010  Heiderscheid                                     29      NA      NA
 4 2010  Hoscheid                                       26      NA      NA
 5 2010  Saeul                                          14      NA      NA
 6 2010  <NA>                                           NA      NA      NA
 7 2010  <NA>                                           NA      NA      NA
 8 2010  Total d'offres                              19278      NA      NA
 9 2010  <NA>                                           NA      NA      NA
10 2010  Source : Ministère du Logement - Observatoire ~      NA      NA      NA
# ... with 280 more rows, and abbreviated variable names 1: n_offers,
#   2: average_price_nominal_euros, 3: average_price_m2_nominal_euros
```

It turns out that there are no prices for certain communes, but that we also have some rows with garbage in there. Let's go back to the raw data to see what this is about:



Commune	Nombre d'offres	Prix moyen annoncé en € courant	Prix moyen annoncé au m² en € courant
Consthum	29	*	*
Esch-sur-Sûre	7	*	*
Heiderscheid	29	*	*
Hoscheid	26	*	*
Saeul	14	*	*

Moyenne nationale		569,216	3,251

Total d'offres	19,278

Source : Ministère du Logement - Observatoire de l'Habitat (base prix 2010).

Figure 2.3: Always look at your data

So it turns out that indeed, there are some rows that we need to remove. We can start by removing rows where `locality` is missing. Then we have a row where `locality` is equal to "Total d'offres". This is simply the total of every offer from every commune. We could keep that in a separate data frame, or even remove it. Finally there's a row, the last one, that states the source of the data, which we can remove.

In the screenshot above, we see another row that we don't see in our filtered data frame: one where `n_offers` is missing. This row gives the national average for columns `average_prince_nominal_euros` and `average_price_m2_nominal_euros`. What we are going to do is create two datasets: one with data on communes, and the other on national prices. Let's first remove the rows stating the sources:

```r
raw_data <- raw_data |>
  filter(!grepl("Source", locality))
```

Let's now only keep the communes in our data:

```r
commune_level_data <- raw_data |>
    filter(!grepl("nationale|offres", locality),
           !is.na(locality))
```

And let's create a dataset with the national data as well:

```r
country_level <- raw_data |>
  filter(grepl("nationale", locality)) |>
  select(-n_offers)

offers_country <- raw_data |>
  filter(grepl("Total d.offres", locality)) |>
  select(year, n_offers)

country_level_data <- full_join(country_level, offers_country) |>
  select(year, locality, n_offers, everything()) |>
  mutate(locality = "Grand-Duchy of Luxembourg")
```

```
Joining, by = "year"
```

Now the data looks clean, and we can start the actual analysis… or can we? Before proceeding, it would be nice to make sure that we got every commune in there. For this, we need a list of communes from Luxembourg. Thankfully, Wikipedia has such a list.

Let's scrape and save this list:

```r
current_communes <- "https://en.wikipedia.org/wiki/List_of_communes_of_Luxembourg" |>
  rvest::read_html() |>
  rvest::html_table() |>
  purrr::pluck(1) |>
  janitor::clean_names()
```

We scrape the table from the Wikipedia page using `{rvest}`. `rvest::html_table()` returns a list of tables from the Wikipedia table, and then we use `purrr::pluck()` to keep the first table from the website, which is what we need.

Let's see if we have all the communes in our data:

```
setdiff(unique(commune_level_data$locality), current_communes$commune)
```

```
 [1] "Bascharage"          "Boevange-sur-Attert" "Burmerange"         
 [4] "Clémency"            "Consthum"            "Ermsdorf"           
 [7] "Erpeldange"          "Eschweiler"          "Heiderscheid"       
[10] "Heinerscheid"        "Hobscheid"           "Hoscheid"           
[13] "Hosingen"            "Luxembourg"          "Medernach"          
[16] "Mompach"             "Munshausen"          "Neunhausen"         
[19] "Redange-sur-Attert"  "Rosport"             "Septfontaines"      
[22] "Tuntange"            "Wellenstein"         "Kaerjeng"           
```

We see many communes that are in our `commune_level_data`, but not in `current_communes`. There's one obvious reason: differences in spelling, for example, "Kaerjeng" in our data, but "Käerjeng" in the table from Wikipedia. But there's also a less obvious reason; since 2010, several communes have merged into new ones. So there are communes that are in our data, say, in 2010 and 2011, but disappear from 2012 onwards. So we need to do several things: first, get a list of all existing communes from 2010 onwards, and then, harmonise spelling. Here again, we can use a list of Wikipedia:

```
former_communes <- "https://en.wikipedia.org/wiki/Communes_of_Luxembourg#Former_communes"
  rvest::read_html() |>
  rvest::html_table() |>
  purrr::pluck(3) |>
  janitor::clean_names() |>
  dplyr::filter(year_dissolved > 2009)

former_communes
```

```
# A tibble: 20 x 3
   name                 year_dissolved reason                         
   <chr>                         <int> <chr>                          
 1 Bascharage                     2011 merged to form Käerjeng        
 2 Boevange-sur-Attert            2018 merged to form Helperknapp     
 3 Burmerange                     2011 merged into Schengen           
 4 Clemency                       2011 merged to form Käerjeng        
 5 Consthum                       2011 merged to form Parc Hosingen   
 6 Ermsdorf                       2011 merged to form Vallée de l'Ernz
 7 Eschweiler                     2015 merged into Wiltz              
 8 Heiderscheid                   2011 merged into Esch-sur-Sûre      
 9 Heinerscheid                   2011 merged into Clervaux           
```

```
10 Hobscheid                      2018 merged to form Habscht
11 Hoscheid                       2011 merged to form Parc Hosingen
12 Hosingen                       2011 merged to form Parc Hosingen
13 Mompach                        2018 merged to form Rosport-Mompach
14 Medernach                      2011 merged to form Vallée de l'Ernz
15 Munshausen                     2011 merged into Clervaux
16 Neunhausen                     2011 merged into Esch-sur-Sûre
17 Rosport                        2018 merged to form Rosport-Mompach
18 Septfontaines                  2018 merged to form Habscht
19 Tuntange                       2018 merged to form Helperknapp
20 Wellenstein                    2011 merged into Schengen
```

As you can see, since 2010 many communes have merged to form new ones. We can now combine the list of current and former communes, as well as harmonise their names:

```r
communes <- unique(c(former_communes$name, current_communes$commune))
# we need to rename some communes

# Different spelling of these communes between wikipedia and the data

communes[which(communes == "Clemency")] <- "Clémency"
communes[which(communes == "Redange")] <- "Redange-sur-Attert"
communes[which(communes == "Erpeldange-sur-Sûre")] <- "Erpeldange"
communes[which(communes == "Luxembourg-City")] <- "Luxembourg"
communes[which(communes == "Käerjeng")] <- "Kaerjeng"
communes[which(communes == "Petange")] <- "Pétange"
```

Let's run our test again:

```r
setdiff(unique(commune_level_data$locality), communes)
```

```
character(0)
```

Great! When we compare the communes that are in our data with every commune that has existed since 2010, we don't have any commune that is unaccounted for. So are we done with cleaning the data? Yes, we can now actually start with analysing the data. Take a look here to see the finalized script. Also read some of the comments the we've added. This is a typical R script, and at first glance, one might wonder what is wrong with it. Actually, not much, but the problem if you leave this script as it is, is that it is very likely that we will have problems rerunning it in the future. As it turns out, this script is not reproducible. But we will discuss this in much more detail later on. For now, let's analyze our cleaned data.

2.3 Analysing the data

We are now going to analyse the data. The first thing we are going to do is compute a Laspeyeres price index. This price index allows us to make comparisons through time; for example, the index at year 2012 measures how much more expensive (or cheaper) housing became relative to the base year (2010). However, since we only have one good, this index becomes quite simple to compute: it is nothing but the prices at year t divided by the prices in 2010 (if we had a basket of goods, we would need to use the Laspeyeres index formula to compute the index at all periods).

For this section, we will perform a rather simple analysis. We will immediately show you the R script: take a look at it here. For our analysis we selected 5 communes and plotted the evolution of prices compared to the national average.

This analysis might seem trivially simple, but it contains all the needed ingredients to illustrate everything else that we're going to teach you in this book.

Most analyses would stop here: after all, we have what we need; our goal was to get the plots for the 5 communes of Luxemourg, Esch-sur-Alzette, Mamer, Schengen (which gave its name to the Schengen Area and Wincrange. However, let's ask ourselves the following important questions:

- How easy would it be for someone else to rerun the analysis?
- How easy would it be to update the analysis once new data gets published?
- How easy would it be to reuse this code for other projects?
- What guarantee do we have that if the scripts get run in 5 years, with the same input data, we get the same output?

Let's answer these questions one by one.

2.4 Your project is not done

2.4.1 How easy would it be for someone else to rerun the analysis?

The analysis is composed of two R scripts, one to prepare the data, another to actually run the analysis proper. This might seem quite easy, because each script contains comments as to what is going on, and the code is not that complicated. However, we are missing any project-level documentation, that would provide clear instructions as to how to run it. This might seem simple for us who wrote these scripts, but we are familiar with R, and this is still fresh in our brains. Should someone less familiar with R have to run the script, there is no clue for them as to how they should do it. And of course, should the analysis be more complex (suppose it's composed of a dozens scripts), this gets even worse. It might not even be easy for you to remember how to run this in 5 months!

And what about the required dependencies? Many packages were used in the analysis. How should these get installed? Ideally, the same versions of the packages you used and the same version of R should get used by that person to rerun the analysis.

All of this still needs to get documented.

2.4.2 How easy would it be to update the project?

If new data gets published, all the points discussed previously are still valid, plus you need to make sure that the updated data is still close enough to the previous data that it can pass through the data cleaning steps you wrote. You should also make sure that the update did not introduce a mistake in past data, or at least alert you if that is the case. Sometimes, when new years get added, data for previous years also get corrected, so it would be nice to make sure that you know this. Also, in the specific case of our data, communes might get fused into a new one, or maybe even divided into smaller communes (even though this is has not happened in a long time, it is not entirely out of the question).

In summary, what is missing from the current project are enough tests to make sure that an update to the data can happen smoothly.

2.4.3 How easy would it be to reuse this code for another project?

Said plainly, not very easy. With code in this state you have no choice but to copy and paste it into a new script and change it adequately. For reusability, nothing beat structuring your code into functions and ideally you would even package them. We are going to learn just that in future chapters of this book.

But sometimes you might not be interested in reusing code for another project: however, even if that's the case, structuring your code into functions and package them makes it easy to reuse even inside the same project. Look at the last part of the `analysis.R` script: we copy and pasted the same code 5 times and only slightly changed it. We are going to learn how not to repeat ourselves by using functions and you will immediately see the benefits of writing functions, even when simply to reuse inside the same project.

2.4.4 What guarantee do we have that the output is stable?

Now this might seem weird: after all, if we start from the same dataset, does it matter *when* we run the scripts? We should be getting the same result if we build the project today, in 5 months or in 5 years. Well, not necessarily. While it is true that R is quite stable, this cannot necessarily be said of the packages that get used. There is no guarantee that the authors of the packages will not change the package's functions to work differently, or take arguments in a different order, or even that the packages will all be available at all in 5 years. And even if the packages are still available and work the same, bugs in the packages might get corrected that could now alter the result. This might seem like a non-problem; after all, if bugs get corrected, should you be happy to update your results as well? But this depends on what it is we're talking about. Sometimes it is necessary to reproduce results exactly as they were, if it they were wrong.

So we also need a way to somehow snapshot and freeze the computational environment that was used to create the project originally.

2.5 Chapter conclusion

We now have a basic analysis that has all we need to get started. In the coming chapters, we are going to learn about topics that will make it easy to write code that is more robust, better documented and tested, and most importantly easy to rerun (and thus to reproduce the results). The first step will actually not involve having to start rewriting our scripts though; next we are going to learn about Git, a tool that will make our life easier by versioning our code.

3 Version control

What Miles said on the matter:

There are still a lot of people that find git intimidating and still potential for some things to go badly for a project if git is used in the wrong way. I once had a colleague who assured me they knew how to use git proceed to use a repo like their personal dropbox folder. Perhaps the details of git usage can be basically waved away, but some detail about good git workflow could be incorporated. For example: The branching model to use. IMHO trunk-based development works much better than gitflow for analysis teams. Version number discipline. Why you always bump the version number when making changes to your packages. Why keeping commits small and confined to just one target at a time if possible is useful when tracing problems with a pipeline.

Modern software development would be impossible without version control systems, and the same goes for building analytical pipelines that are reproducible and robust. It doesn't really matter what the output of the pipeline is: a simple graph, a report with a statistical analysis, a trained machine learning model that you want to hook to an API… if the code to the project is not versioned, you incur major risks.

But what is version control anyway?

Version control tools make it easy to keep track of the changes that were made to text files (like R scripts). Any change made to any file of a project is cataloged, making it possible to trace back how the file changed, who made the changes, and when these changes were made. Using version control it is also quite easy to collaborate on a project by forcing team members to deal explicitly with the potential conflicts that might arise when the same file got changed by different people at the same time. Should your computer get lost, stolen, or explode, your projects are safely backed up on a server: this is because version control tools make use of a server which keeps track of all the changes (and in some cases, this *server* is actually your team mates' computers!)

Version control tools also make it easy to experiment with new ideas. You can start new *branches* which essentially make a copy of your current project. In this new branch, you can safely experiment with new features, and if the experiments are not conclusive, you can simply discard this branch: the *original* copy of your project will remain untouched.

There are several version control tools out there, but Git is undoubtedly the most popular one. You might have heard of Github; this is service that hosts repositories for your projects, and provides other project management tools such as an issue tracker, project wiki, feature requests… and also very importantly continuous integration. Don't worry if this all sounds very abstract: by the end of this chapter you will have all the basic knowledge to use Git and Github.com for your projects.

Git is a tool that you must install on your computer to get started. Once Git is installed, you can immediately start using it; you don't need to open an account on Github (or a similar service), but it is recommended to make collaboration easier (it is possible to collaborate with several people using Git without a service like Github, by setting up a bare repository on a server on network drive you control, but this is outside the scope of this book).

You should know that private repositories are available for free, so if you don't want your work to be accessible to the public, you can. Only people that you invite to your private repositories will be able to see the code and collaborate with you. It is also possible that your work place has set up a self-hosted Git platform, ask your IT department! Usually these self-hosted platforms are Gitea or Gitlab instances. Gitea, Gitlab, Bitbucket, Codeberg, these are all similar services to Github. All have their own advantages and disadvantages. The advantage of Github is twofold:

- It has a very large community of users;
- Its continuous integration service is incredibly useful, and free for up to 2000 minutes a month.

Disadvantages are:

- It has been bought by Microsoft in 2018;
- It is not possible to self-host an instance of Github (not for free at least).

The fact it is owned by Microsoft may not seem like an issue, but Microsoft's track record of previous acquisitions is not great (Nokia, Skype), and the recent discussions about using source code hosted on Github to train machine learning models (Copilot) can make one uneasy about relying too much on Github.

So while we are going to use Github to host our projects in the remainder of this book, almost everything you are going to learn will be easily transeferable to another service such as Gitlab or Bitbucket, should you want to switch (or if your workplace has a self-hosted instance from one of Github's competitors). Installing and configuring Git will be exactly the same regardless of the hosting service we use, and all the commands we will use to actually interact with our repositories will be the same as well. So why did we write *almost everything* is the the same? Well, the two advantages we cited above really give Github an edge; many, many developers, researchers and data scientists have a Github account and so if one day you need to collaborate with people, chances are they have an account on Github. Also, the 2000 minutes of free computing time are really more than enough for the continuous integration of your project (which will be one of the last topics we will study in this book).

3.1 Installing Git

Git is a program that you install on your computer. If you're running a Linux distribution, chances are Git is already installed. Try to run the following command in a terminal to see if this is the case:

```
which git
```

If a path like `/usr/bin/git` gets shown, congratulations, you can skip the rest of this paragraph. If something like

```
/usr/bin/which: no git in (/home/username/.local/bin:/home/username/bin:/usr/local/bin:/usr/l
```

gets shown instead, then this means that Git is not installed on your system. To install Git, use your distribution's package manager, as it is very likely that Git is packaged for your system. On Ubuntu, arguably the most popular Linux distribution, this means running:

```
sudo apt-get update
sudo apt-get install git
```

On macOS and Windows, follow the instructions from the Git Book. It should be as easy as running an installer.

Depending on your operating system, a graphical user interface might have been installed with Git. It is also possible to use Git from within RStudio, if you use it and many other editors have interfaces to Git as well.

We are not going to use any graphical user interface. This is because there is no common, universal graphical user interface; they all work slightly differently. The only universal is the command line. Also, learning how to use Git via the command line will make it easier the day you will need to use it from a server, which will very likely happen. It also makes our job easier: it is simpler to tell you which commands to run and explain them to you than littering the book with dozens upon dozens of screenshots that might get outdated as soon as a new version of the interface gets released.

Don't worry, using the command line is not as hard as it sounds.

4 Functional programming

This chapter will teach you the fundamentals of functional programming. *Functional programming* might sound scary, but we will focus on only a handful of concepts that are quite accessible while providing many benefits. Using these functional programming concepts will make your code more reliable, easier to test, document, share, and ultimately rerun.

4.1 Introduction

You are very likely already familiar with some aspects of functional program. Let's start by discussing the two central elements of functional programming: functions and lists.

There are several ways that you can structure a program, called programming paradigms. Functional programming is a paradigm that relies exclusively on the evaluation of functions to achieve the desired end result. If you have already written your own functions in the past, what follows will not be very new. But in order to write a good functional program, the functions that you write and evaluate have to have certain properties. Before discussing these properties, let's start by with *state*.

4.1.1 The state of your program

Let's suppose that you start a fresh R session, and immediately run this next line:

```
ls()
```

If you did not modify any of R's configuration files that get automatically loaded on startup, you should see the following:

```
character(0)
```

Let's suppose that now you load some data:

```
data(mtcars)
```

and define a variable `a`:

```
a <- 1
```

Running `ls()` now shows the following:

```
[1] "a"      "mtcars"
```

You have just altered the state of your program. You can think of the *state* as a box that holds everything that gets defined by the user and is accessible at any time. Let's now define a simple function that prints a sentence:

```
f <- function(name){
  print(paste0(name, " likes lasagna"))
}

f("Bruno")
```

and here's the output:

```
[1] "Bruno likes lasagna"
```

Let's run `ls()` again:

```
[1] "a"      "f"      "mtcars"
```

Function `f()` is now listed there as well. This function has two nice properties:

- For a given input, it always returns exactly the same output. So `f("Bruno")` will always return "Bruno likes lasagna".
- This function does not change the state of your program, by adding new objects every time it's run.

4.1.2 Predictable functions

Let's now define another function called `g()`, that does not have the same properties as `f()`. First, let's define a function that does not always return the same output given a particular input:

```
g <- function(name){
  food <- sample(c("lasagna", "cassoulet", "feijoada"), 1)
  print(paste0(name, " likes ", food))
}
```

For the same input, “Bruno”, this function now produces (potentially) a different output:

```
g("Bruno")
[1] "Bruno likes lasagna"
```

```
g("Bruno")
[1] "Bruno likes feijoada"
```

And now let’s consider function `h()` that modifies the state of the program:

```
h <- function(name){
  food <- sample(c("lasagna", "cassoulet", "feijoada"), 1)

  if(exists("food_list")){
    food_list <<- append(food_list, food)
  } else {
    food_list <<- append(list(), food)
  }

  print(paste0(name, " likes ", food))
}
```

This function uses the `<<-` operator. This operator saves definitions that are made inside the body of functions in the global environment. Before calling this function, run `ls()` again. You should see the same objects as before, plus the new functions we’ve defined:

```
[1] "a"         "f"          "g"         "h"         "mtcars"
```

Let’s now run `h()` once:

```
h("Bruno")
[1] "Bruno likes feijoada"
```

And now `ls()` again:

```
[1] "a"         "f"         "food_list" "g"         "h"         "mtcars"
```

Running `h()` did two things: it printed the message, but also created a variable called “food_list” in the global environment with the following contents:

```
food_list
```

```
[[1]]
[1] "feijoada"
```

Let's run `h()` again:

```
h("Bruno")
[1] "Bruno likes cassoulet"
```

and let's check the contents of "food_list":

```
food_list
```

```
[[1]]
[1] "feijoada"

[[2]]
[1] "cassoulet"
```

If you keep running `h()`, this list will continue growing. Let me just say that I hesitated showing you this; this is because if you didn't know `<<-`, you might find the example above useful. But while useful, it is quite dangerous as well. Generally, we want to avoid using functions that change the state as much as possible because these function are unpredictable, especially if randomness is involved. It is much safer to define `h()` like this instead:

```
h <- function(name, food_list = list()){

  food <- sample(c("lasagna", "cassoulet", "feijoada"), 1)

  food_list <- append(food_list, food)

  print(paste0(name, " likes ", food))

  food_list
}
```

The difference now is that we made `food_list` the second argument of the function. Also, we defined it as being optional by writing:

```
food_list = list()
```

This means that if we omit this argument, the empty list will get used by default. This avoids the users having to manually specify it.

We can call it like this:

```
food_list <- h("Bruno", food_list) # since food_list is already defined, we don't need to
```

```
[1] "Bruno likes feijoada"
```

We save the output back to `food_list`. Let's now check its contents:

```
food_list
```

```
[[1]]
[1] "feijoada"

[[2]]
[1] "cassoulet"

[[3]]
[1] "feijoada"
```

The only thing that we need now to deal with is the fact that the food gets chosen randomly. I'm going to show you the simple way of dealing with this, but later in this chapter we are going to use the `{withr}` package for situations like this. Let's redefine `h()` one last time:

```
h <- function(name, food_list = list(), seed = 123){

  # We set the seed, making sure that we get the same selection of food for a given seed
  set.seed(seed)
  food <- sample(c("lasagna", "cassoulet", "feijoada"), 1)

  # We now need to unset the seed, because if we don't, guess what, the seed will stay set
  set.seed(NULL)

  food_list <- append(food_list, food)

  print(paste0(name, " likes ", food))

  food_list
}
```

Let's now call `h()` several times with its default arguments:

```
h("Bruno")
```

```
[1] "Bruno likes feijoada"
[[1]]
[1] "feijoada"
```

```
h("Bruno")
```

```
[1] "Bruno likes feijoada"
[[1]]
[1] "feijoada"
```

```
h("Bruno")
```

```
[1] "Bruno likes feijoada"
[[1]]
[1] "feijoada"
```

As you can see, every time this function runs, it now produces the same result. Users can change the seed to have this function produce, consistently, another result.

4.1.3 Referentially transparent and pure functions

A referentially transparent function is a function that does not use any variable that is not also one of its inputs. For example, the following function:

```
bad <- function(x){
  x + y
}
```

is not referentially transparent, because `y` is not one of the functions inputs. What happens if you run `bad()` is that `bad()` needs to look for `y`. Because `y` is not one of its inputs, `bad()` then looks for it in the global environment. If `y` is defined there, it then gets used. Defining and using such functions must be avoided at all costs, because these functions are unpredictable. For example:

```
y <- 10
bad <- function(x){
  x + y
}

bad(5)
```

This will return `15`. But if `y <- 45` then `bad(5)` would this time around return `50`. It is much safer, and easier to make `y` an explicit input of the function instead of having to keep track of `y`'s value:

```
good <- function(x, y){
  x + y
}
```

`good()` is a referentially transparent function; it is much safer than `bad()`. `good()` is also a pure function, because it's a function that does not interact in any way with the global environment. It does not write anything to the global environment, nor requires anything from the global environment. Function `h()` from the previous section was not pure, because it created an object and wrote it to the global environment (the `food_list` object). Turns out that pure functions are thus necesarrily referentially transparent.

So the first lesson in your functional programming journey that you have to remember is to only use pure functions.

4.2 Writing good functions

4.2.1 Functions are first class objects

In a functional programming language, functions are first class objects. Contrary to what the name implies, this means that functions, especially the ones you define yourself, are nothing special. A function is an object like any other, and can thus be manipulated as such. Think of anything that you can do with any object in R, and you can do the same thing with a function. For example, let's consider the `+()` function. It takes two numeric objects and retuns their sum:

```
1 + 5.3
```

```
[1] 6.3
```

```
# or alternatively: `+`(1, 5.3)
```

You can replace the numbers by functions that return numbers:

```r
sqrt(1) + log(5.3)
```

```
[1] 2.667707
```

It's also possible to define a function that explicitely takes another function as an input:

```r
h <- function(number, f){
  f(number)
}
```

You can call then use `h()` as a wrapper for `f()`:

```r
h(4, sqrt)
```

```
[1] 2
```

```r
h(10, log10)
```

```
[1] 1
```

Because `h()` takes another function as an argument, `h()` is called a higher-order function.

If you don't know how many arguments `f()`, the function you're wrapping, has, you can use the `...`:

```r
h <- function(number, f, ...){
  f(number, ...)
}
```

`...` are simply a placeholder for any potential additional argument that `f()` might have:

```r
h(c(1, 2, NA, 3), mean, na.rm = TRUE)
```

```
[1] 2
```

```r
h(c(1, 2, NA, 3), mean, na.rm = FALSE)
```

```
[1] NA
```

`na.rm` is an argument of `mean()`. As the developer of `h()`, I don't necessarily know what `f()` might be, or maybe I know `f()` and know all its arguments, but don't want to have to rewrite them all to make them arguments of `h()`, so I can use `...` instead. The following is also possible:

```
w <- function(...){
paste0("First argument: ", ..1, ", second argument: ", ..2, ", last argument: ", ..3)
}

w(1, 2, 3)
```

```
[1] "First argument: 1, second argument: 2, last argument: 3"
```

If you want to learn more about `...`, type `?dots` in an R console.

Because functions are nothing special, you can also write functions that return functions. As an illustration, we'll be writing a function that converts warnings to errors. This can be quite useful if you want your functions to fail early, which often makes debuging easier. For example, try running this:

```
sqrt(-5)
```

```
Warning in sqrt(-5): NaNs produced
```

```
[1] NaN
```

This only raises a warning and returns `NaN` (Not a Number). This can be quite dangerous, especially when working non-interactively, which is what we will be doing a lot later on. It is much better if a pipeline fails early due to an error, than dragging an `NaN` value. This also happens with `log()`:

```
sqrt(-10)
```

```
Warning in sqrt(-10): NaNs produced
```

```
[1] NaN
```

So it could be useful to redefine this functions to raise an error instead, for example like this:

```r
strict_sqrt <- function(x){

  if(x <= 0) stop("x is negative")

  sqrt(x)

}
```

This function now throws an error for negative `x`:

```r
strict_sqrt(-10)
```

```
Error in strict_sqrt(-10) : x is negative
```

However, it can be quite tedious to redefine every function that we need in our pipeline. This is where a function factory is useful. We can define a function that takes a function as an argument, converts any warning thrown by that function into an error, and returns the new function. For example it could look like this:

```r
strictly <- function(f){
  function(...){
    tryCatch({
      f(...)
    },
    warning = function(warning)stop("Can't do that chief"))
  }
}
```

This function makes use of `tryCatch()` which catches warnings raised by an expression (in this example the expression is `f(...)`) and then raises an error insead with the `stop()` function. It is now possible to define new functions like this:

```r
s_sqrt <- strictly(sqrt)
```

```r
s_sqrt(-4)
```

```
Error in value[[3L]](cond) : Can't do that chief
```

```r
s_log <- strictly(log)
```

```
s_log(-4)
```

```
Error in value[[3L]](cond) : Can't do that chief
```

Functions that return functions are called *functions factories* and they're incredibly useful. I use this so much that I've written a package, available on CRAN, called `{chronicler}`, that does this:

```
s_sqrt <- chronicler::record(sqrt)
```

```
result <- s_sqrt(-4)

result
```

```
NOK! Value computed unsuccessfully:
---------------
Nothing

---------------
This is an object of type `chronicle`.
Retrieve the value of this object with pick(.c, "value").
To read the log of this object, call read_log(.c).
```

Because the expression above resulted in an error, `Nothing` is returned. `Nothing` is a special value defined in the `{maybe}` package (check it out, very interesting package!). We can then even read the log to see what went wrong:

```
chronicler::read_log(result)
```

```
[1] "Complete log:"
[2] "NOK! sqrt() ran unsuccessfully with following exception: NaNs produced at 2023-02-04 20
[3] "Total running time: 0.00115704536437988 secs"
```

The `{purrr}` package also comes with function factories that you might find useful (`{possibly}`, `{safely}` and `{quietly}`).

4.2.2 Optional arguments

It is possible to make function arguments optional, by using `NULL`. For example:

```
g <- function(x, y = NULL){
  if(is.null(y)){
    print("optional argument y is NULL")
    x
  } else {
    if(y == 5) print("y is present"); x+y
  }
}
```

Calling `g(10)` prints the message "Optional argument y is NULL", and returns 10. Calling `g(10, 5)` however, prints "y is present" and returns 15. It is also possible to use `missing()`:

```
g <- function(x, y){
  if(missing(y)){
    print("optional argument y is missing")
    x
  } else {
    if(y == 5) print("y is present"); x+y
  }
}
```

I however prefer the first approach, because it is clearer which arguments are optional, which is not the case with the second approach, where you need to read the body of the function.

4.2.3 Safe functions

It is important that your functions are safe and predictable. You should avoid writing functions that behave like `nchar()`, a base R function. Let's see why this function is not safe:

```
nchar("10000000")
```

```
[1] 8
```

It returns the expected result of 8. But what if I remove the quotes?

```
nchar(10000000)
```

```
[1] 5
```

What is going on here? I'll give you a hint: simply type `10000000` in the console:

```
10000000
```

```
[1] 1e+07
```

`10000000` gets represented as `1e+07` by R. This number in scientific notation gets then converted into the character "1e+07" by `nchar()`, and this conversion happens silently. `nchar()` then counts the number of characters, and *correctly* returns 5. The problem is that it doesn't make sense to provide a number to a function that expects a character. This function should have returned an error message, or at the very least raised a warning that the number got converted into a character. Here is how you could rewrite `nchar()` to make it safer:

```
nchar2 <- function(x, result = 0){

  if(!isTRUE(is.character(x))){
    stop(paste0("x should be of type 'character', but is of type '",
                typeof(x), "' instead."))
  } else if(x == ""){
    result
  } else {
    result <- result + 1
    split_x <- strsplit(x, split = "")[[1]]
    nchar2(paste0(split_x[-1],
                  collapse = ""), result)
  }
}
```

This function now returns an error message if the input is not a character:

```
nchar2(10000000)
```

```
Error in nchar2(10000000) : x should be of type 'character', but is of type 'integer' instea
```

4.2.4 Recursive functions

You may have noticed that in the last lines of `nchar2()`, that `nchar2()` calls itself. A function that calls itself in its own body is called a recursive function. It is sometimes easier to write down a function in its recursive form than in an iterative form. The most common example is the factorial function. However, there is an issue with recursive functions (in the R programming language, other programming languages may not have the same problem, like Haskell):

while it is sometimes easier to write down a function using a recursive algorithm than an iterative algorithm, like for the factorial function, recursive functions in R are quite slow. Let's take a look at two definitions of the factorial function, one recursive, the other iterative:

```
fact_iter <- function(n){
  result = 1
  for(i in 1:n){
    result = result * i
    i = i + 1
  }
  result
}

fact_recur <- function(n){
  if(n == 0 || n == 1){
  result = 1
  } else {
    n * fact_recur(n-1)
  }
}
```

Using the `{microbenchmark}` package we can benchmark the code:

```
microbenchmark::microbenchmark(
  fact_recur(50),
  fact_iter(50)
)
```

```
Unit: microseconds
           expr    min     lq     mean median      uq    max neval
 fact_recur(50) 21.501 21.701 23.82701 21.901 22.0515 68.902   100
  fact_iter(50)  2.000  2.101  2.74599  2.201  2.3510 21.000   100
```

We see that the recursive factorial function is 10 times slower then the iterative version. In this particular example it doesn't make much of a difference, because the functions only take microseconds to run. But if you're working with more complex functions, this is a problem. If you want to keep using the recursive function and not switch to an iterative algorithm, there are workarounds. The first is called *trampolining*. I won't go into details, but if you're interested, there is an R package that allows you to use trampolining with R, aptly called `{trampoline}`. Another solution is using the `{memoise}` package.

4.2.5 Anonymous functions

It is possible to define a function and not give it a name. For example:

```
function(x)(x+1)(10)
```

Since R version 4.1, there iseven a shorthand notationfor anonymous functions:

```
(\(x)(x+1))(10)
```

Because we don't name them, we cannot reuse them. So why is this useful? Anonymous functions are useful when you need to apply a function somewhere inside a pipe once, and don't want to define a function just for this. This will become clearer once we learn about lists, but before that, let's philosophize a bit.

4.2.6 The Unix philosophy applied to R

> This is the Unix philosophy: Write programs that do one thing and do it well. Write programs to work together. Write programs to handle text streams, because that is a universal interface.

Doug McIlroy, in A Quarter Century of Unix[1]

We can take inspiration from the Unix philosophy and rewrite it like this for our purposes:

Write functions that do one thing and do it well. Write functions that work together. Write functions that handle lists, because that is a universal interface.

Strive for writing simple functions that only perform one task. Don't hesitate to split a big function into smaller ones. Small functions that only perform one task are easier to maintain, test, document and debug. These smaller functions can then be chained using the `|>` operator. In other words, it is preferable to have something like:

```
a |> f() |> g() |> h()
```

where `a` is for example a path to a data set, and where `f()`, `g()` and `h()` successively read, clean, and plot the data, than having something like:

```
big_function(a)
```

[1]https://stackoverflow.com/a/68690065/1298051

that does all the steps above in one go.

This idea of splitting the problem into smaller chunks, each chunk in turn split into even smaller units that can be handled by functions and then the results of these function combined into a final output is called composability.

The advantage of splitting `big_function()` into `f()`, `g()` and `h()` is that you can tackle big problems *one bite at a time*, and also reusing these smaller functions in other projects is much easier. So what's important is that you can make small functions work together by sharing a common interface. The list is usually a good candidate for this.

4.3 Lists: a powerful data-structure

Lists are the second important ingredient of functional programming. In the R philosophy inspired from UNIX, I stated that *lists are an universal interface* in R, so our functions should handle lists. This of course depends on what it is your doing. If you need functions to handle numbers, then there's little value in placing these numbers inside lists. But in practice, you will very likely manipulate objects that are more complex than numbers, and this is where lists come into play.

4.3.1 Lists all the way down

Lists are extremely flexible, and most very complex objects classes that you manipulate are actually lists, but just fancier. For example, a data frame is a list:

```r
data(mtcars)

typeof(mtcars)
```

```
[1] "list"
```

A fitted model is a list:

```r
my_model <- lm(hp ~ mpg, data = mtcars)

typeof(my_model)
```

```
[1] "list"
```

A `ggplot` is a list:

```
library(ggplot2)

my_plot <- ggplot(data = mtcars) +
  geom_line(aes(y = hp, x = mpg))

typeof(my_plot)
```

```
[1] "list"
```

It's lists all the way down, and it's not a coincidence. It's because, as stated, lists are very powerful. So it's important to know what you can do with lists.

4.3.2 Lists can hold many things

If you write a function that needs to return many objects, the only solution is to place them inside a list. For example, consider this function:

```
sqrt_newton <- function(a, init = 1, eps = 0.01, steps = 1){
    stopifnot(a >= 0)
    while(abs(init**2 - a) > eps){
        init <- 1/2 *(init + a/init)
        steps <- steps + 1
    }
    list(
      "result" = init,
      "steps" = steps
    )
}
```

This function returns the square root of a number using Newton's algorithm, as well as the number of steps, or iterations, it took to reach the solution:

```
result_list <- sqrt_newton(1600)

result_list
```

```
$result
[1] 40

$steps
[1] 10
```

It is quite common to instead print the number of steps to the console instead of returning them. But the issue with a function that prints something to the console instead of returning it, is that such a function is not pure, as it changes something outside of its scope. It is preferable to instead make the function pure by returning everything inside a neat list. It is then possible to separately save these objects if needed:

```
result <- result_list$result

result_steps <- result_list$steps
```

Or you could define functions that know how to deal with the list:

```
f <- function(result_list){
  list(
    "result" = result_list$result * 10,
    "steps" = result_list$steps + 1
    )
}

f(result_list)
```

```
$result
[1] 400

$steps
[1] 11
```

It all depends on what you want to do. But it is usually better to keep everything neatly inside a list.

Lists can also hold objects of differen types:

```
list(
  "a" = head(mtcars),
  "b" = ~lm(y ~ x)
  )
```

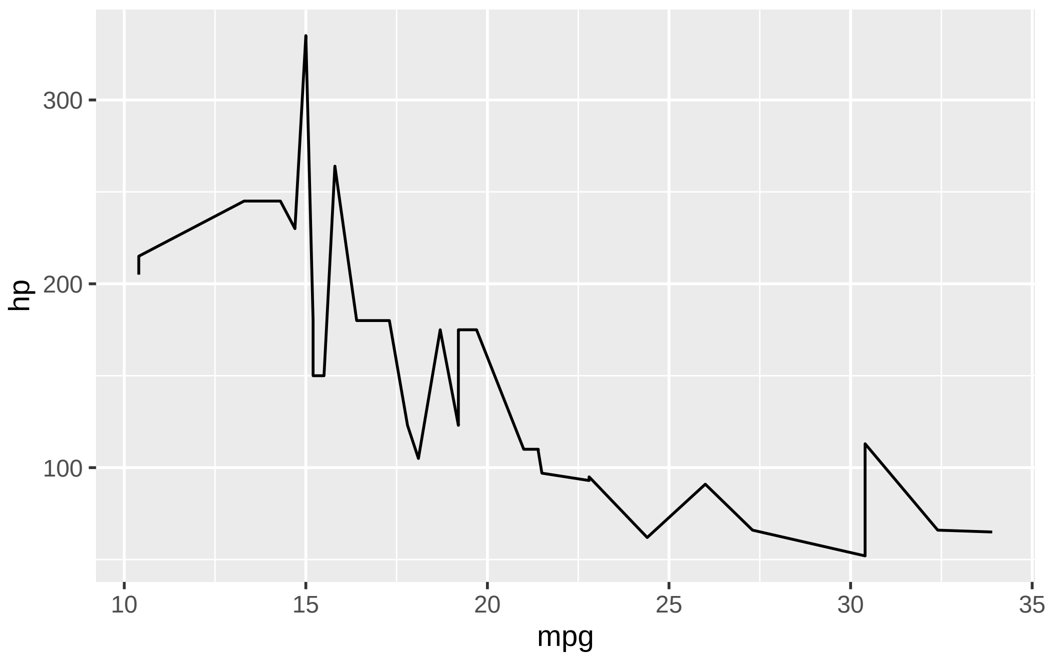
```
$a
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
```

```
Datsun 710         22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive     21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1

$b
~lm(y ~ x)
```

The list above has two elements, the first is the head of the `mtcars` data frame, the second is a formula object. Lists can even hold other lists:

```
list(
  "a" = head(mtcars),
  "b" = list(
    "c" = sqrt,
    "d" = my_plot # Remember this ggplot object from before?
    )
  )
```

```
$a
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1

$b
$b$c
function (x)  .Primitive("sqrt")

$b$d
```



Use this to your advantage.

4.3.3 Lists as the cure to loops

Loops are incredibly useful, and you are likely familiar with them. The problem with loops is that they are a concept from iterative programming, not functional programming, and this is a problem because loops rely on changing the state of your program to function. For example, let's suppose that you wish to use a for-loop to compute the sum of the first 100 integers:

```
result <- 0
for (i in 1:100){
  result <- result + i
}

print(result)
```

```
[1] 5050
```

If you run `ls()` now, you should see that there's a variable `i` in your global environment. This could cause issues further down in your pipeline if you need to re-use `i`. Also, writing loops is, in my opinion, quite error prone. But how can we avoid using loops? For looping in a functional programming language, we need to use higher-order functions and lists. A reminder: a higher-order function is a function that takes another function as an argument. Looping is a task like any other, so we can write a function that does the looping for us. We will call it `looping()`, which will take a function as an argument, as well as list. The list will serve as the container to hold our numbers:

```
looping <- function(a_list, a_func, init = NULL, ...){

  # If the user does not provide an `init` value, set the head of the list as the initial
  if(is.null(init)){
    init <- a_list[[1]]
    a_list <- tail(a_list, -1)
  }

  # Separate the head from the tail of the list and apply the function to the initial valu
  head_list = a_list[[1]]
  tail_list = tail(a_list, -1)
  init = a_func(init, head_list, ...)

  # Check if we're done: if there is still some tail, rerun the whole thing until there's
  if(length(tail_list) != 0){
    looping(tail_list, a_func, init, ...)
  }
  else {
    init
  }
}
```

Now, this might seem much more complicated than a for loop. However, now that we have abstracted the loop away inside a function, we can keep reusing this function:

```
looping(as.list(seq(1:100)), `+`)
```

```
[1] 5050
```

Of course, because this is so useful, `looping()` actually ships with R, and is called `Reduce()`:

```
Reduce(`+`, seq(1:100)) # the order of the arguments is `function` then `list` for `Reduce
```

```
[1] 5050
```

But this is not the only way that we can loop. We can also write a loop that applies a function to each element of a list, instead of operating on the whole list:

```r
result <- as.list(seq(1:5))
for (i in seq_along(result)){
  result[[i]] <- sqrt(result[[i]])
}

print(result)
```

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

[[2]]
[1] 1.414214

[[3]]
[1] 1.732051

[[4]]
[1] 2

[[5]]
[1] 2.236068
```

Here again, we have to pollute the global environment by first creating a vessel for our results, and then apply the function at each index. We can abstract this process away in a function:

```r
applying <- function(a_list, a_func, ...){

  head_list = a_list[[1]]
  tail_list = tail(a_list, -1)
  result = a_func(head_list, ...)

  # Check if we're done: if there is still some tail, rerun the whole thing until there's
  if(length(tail_list) != 0){
    append(result, applying(tail_list, a_func, ...))
  }
  else {
    result
  }
}
```

Once again this might seem complicated, and I would agree. Abstraction is complex. But once we have it, we can focus on the task at hand, instead of having to always tell the computer what we want:

```
applying(as.list(seq(1:5)), sqrt)
```

```
[1] 1.000000 1.414214 1.732051 2.000000 2.236068
```

Of course, R ships with its own, much more efficient, implementation of this function:

```
lapply(list(seq(1:5)), sqrt)
```

```
[[1]]
[1] 1.000000 1.414214 1.732051 2.000000 2.236068
```

In other programming languages, `lapply()` is often called `map()`. The `{purrr}` packages ships with other such useful higher-order functions that abstract loops away. For example, there's the function called `map2()`, that maps a function of two arguments to each element of two atomic vectors or lists, two at a time:

```
library(purrr)

map2(
  .x = seq(1:5),
  .y = seq(1:5),
  .f = `+`
  )
```

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

[[2]]
[1] 4

[[3]]
[1] 6
```

```
[[4]]
[1] 8

[[5]]
[1] 10
```

If you have more than two lists, you can use `pmap()` instead.

4.3.4 Data frames

As mentioned in the introduction of this section, data frames are a special type of list of atomic vectors. This means that just as I can use `lapply()` to compute the square root of the elements of an atomic vector, as in the previous example, I can also operate on all the columns of a data frame. For example, it is possible to determine the class of
every variable like this:

```r
lapply(iris, class)
```

```
$Sepal.Length
[1] "numeric"

$Sepal.Width
[1] "numeric"

$Petal.Length
[1] "numeric"

$Petal.Width
[1] "numeric"

$Species
[1] "factor"
```

Unlike a list however, the elements of a data frame must be of the same length. Data frames remain very flexible however, and using what we have learned until now, it is possible to use the data frame as a structure for all our computations. For example, suppose that we have a data frame that contains data on unemployment for the different subnational divisions of the Grand-Duchy of Luxembourg, the country the author of this book hails from. Let's suppose that I want to generate several plots, per subnational division and per year. Typically, we would use a loop for this, but we can use what we've learned here, as well as some functions from the `{dplyr}`, `{purrr}`, `{ggplot2}` and `{tidyr}` packages. I will be downloading data that I made available inside a package, but instead of installng the package, we will dowload the `.rda` file (which is the file format of packaged data) and then load that data into our R session:

```
# Create a temporary file
unemp_path <- tempfile(fileext = ".rda")

# Download the data and save it to the path of the temporary file
download.file("https://github.com/b-rodrigues/myPackage/raw/main/data/unemp.rda", destfile

# Load the data. The data is now available as 'unemp'
load(unemp_path)
```

Let's load the required packages and take a look at the data:

```
library(dplyr)
```

```

Attaching package: 'dplyr'


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

    filter, lag


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

    intersect, setdiff, setequal, union
```

```
library(purrr)
library(ggplot2)
library(tidyr)

glimpse(unemp)
```

```
Rows: 472
Columns: 9
$ year                         <dbl> 2013, 2013, 2013, 2013, 2013, 2013, 2013,~
$ place_name                   <chr> "Luxembourg", "Capellen", "Dippach", "Gar~
$ level                        <chr> "Country", "Canton", "Commune", "Commune"~
$ total_employed_population    <dbl> 223407, 17802, 1703, 844, 1431, 4094, 214~
$ of_which_wage_earners        <dbl> 203535, 15993, 1535, 750, 1315, 3800, 187~
$ of_which_non_wage_earners    <dbl> 19872, 1809, 168, 94, 116, 294, 272, 113,~
$ unemployed                   <dbl> 19287, 1071, 114, 25, 74, 261, 98, 45, 66~
$ active_population            <dbl> 242694, 18873, 1817, 869, 1505, 4355, 224~
$ unemployment_rate_in_percent <dbl> 7.947044, 5.674773, 6.274078, 2.876870, 4~
```

Column names are self-descriptive, but the `level` column needs some explanations. The country of Luxembourg is divided into *Cantons*, and these *Cantons* themselves into *Communes*.

You should know that the word *Luxembourg* can refer to the country, the canton or the commune of Luxembourg. Now let's suppose that I want a separate plot for the three communes of Luxembourg, Esch-sur-Alzette and Wiltz. Instead of creating three separate data frames and feeding them to the same ggplot code, I can instead take advantage of the fact that data frames are lists, and are thus quite flexible. Let's start with filtering:

```
filtered_unemp <- unemp %>%
  filter(
    level == "Commune",
    place_name %in% c("Luxembourg", "Esch-sur-Alzette", "Wiltz")
   )

glimpse(filtered_unemp)
```

```
Rows: 12
Columns: 9
$ year                         <dbl> 2013, 2013, 2013, 2014, 2014, 2014, 2015,~
$ place_name                   <chr> "Esch-sur-Alzette", "Luxembourg", "Wiltz"~
$ level                        <chr> "Commune", "Commune", "Commune", "Commune~
$ total_employed_population    <dbl> 12725, 39513, 2344, 13155, 40768, 2377, 1~
$ of_which_wage_earners        <dbl> 12031, 35531, 2149, 12452, 36661, 2192, 1~
$ of_which_non_wage_earners    <dbl> 694, 3982, 195, 703, 4107, 185, 710, 4140~
$ unemployed                   <dbl> 2054, 3855, 318, 1997, 3836, 315, 2031, 3~
$ active_population            <dbl> 14779, 43368, 2662, 15152, 44604, 2692, 1~
$ unemployment_rate_in_percent <dbl> 13.898099, 8.889043, 11.945905, 13.179778~
```

We are now going to use the fact that data frames are lists, and that lists can hold any type of object. For example, remember this list from before where one of the elements is a data frame, and the second one a formula:

```
list(
  "a" = head(mtcars),
  "b" = ~lm(y ~ x)
  )
```

```
$a
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1

$b
~lm(y ~ x)
```

`{dplyr}` comes with a function called `group_nest()` which groups the data frame by a variable (such that the next computations will be performed group-wise) and then nests the other columns into a smaller data frame. Let's try it and see what happens:

```
nested_unemp <- filtered_unemp %>%
  group_nest(place_name)
```

Let's see how this looks like:

```
nested_unemp
```

```
# A tibble: 3 x 2
  place_name                    data
  <chr>            <list<tibble[,8]>>
1 Esch-sur-Alzette            [4 x 8]
2 Luxembourg                  [4 x 8]
3 Wiltz                       [4 x 8]
```

`nested_unemp` is a new data frame of 3 rows, one per commune ("Esch-sur-Alzette", "Luxembourg", "Wiltz"), and of two columns, one for the names of the communes, and the other contains every other variable inside a smaller data frame. So this is a data frame that has one column where each element of that column is itself a data frame. Such a column is called a list-column. This is essentially a list of lists.

Let's now think about this for a moment. If the column titled `data` is a list of data frames, it should be possible to use a function like `map()` or `lapply()` to apply a function on each of these data frames. Remember that `map()` or `lapply()` require a list of elements of whatever type and a function that accepts objects of this type as input. So this means that we could apply a function that plots the data to each element of the column titled `data`. Since each element of this column is a data frame, this functions needs a data frame as an input. As a first, simple, example to illustrate this, let's suppose that we want to determine the number of rows of each data frame. This is how we would do it:

```
nested_unemp %>%
  mutate(nrows = map(data, nrow))
```

```
# A tibble: 3 x 3
  place_name                       data nrows
  <chr>              <list<tibble[,8]>> <list>
1 Esch-sur-Alzette              [4 x 8] <int [1]>
2 Luxembourg                    [4 x 8] <int [1]>
3 Wiltz                         [4 x 8] <int [1]>
```

The new column, titled `nrows` is a list of integers. We can simplify it by converting it directly to an atomic vector of integers by using `map_int()` instead of `map()`:

```
nested_unemp %>%
  mutate(nrows = map_int(data, nrow))
```

```
# A tibble: 3 x 3
  place_name                       data nrows
  <chr>              <list<tibble[,8]>> <int>
1 Esch-sur-Alzette              [4 x 8]     4
2 Luxembourg                    [4 x 8]     4
3 Wiltz                         [4 x 8]     4
```

Let's try for a more complex example now. What if we want to filter rows? (The simplest way would of course to filter the rows we need before nesting the data frame). We need to apply the function `filter()` where its first argument is a data frame and the second argument is a predicate:

```
nested_unemp %>%
  mutate(nrows = map(data, \(x)filter(x, year == 2015)))
```

```
# A tibble: 3 x 3
  place_name                       data nrows
  <chr>              <list<tibble[,8]>> <list>
```

```
1 Esch-sur-Alzette            [4 x 8] <tibble [1 x 8]>
2 Luxembourg                  [4 x 8] <tibble [1 x 8]>
3 Wiltz                       [4 x 8] <tibble [1 x 8]>
```

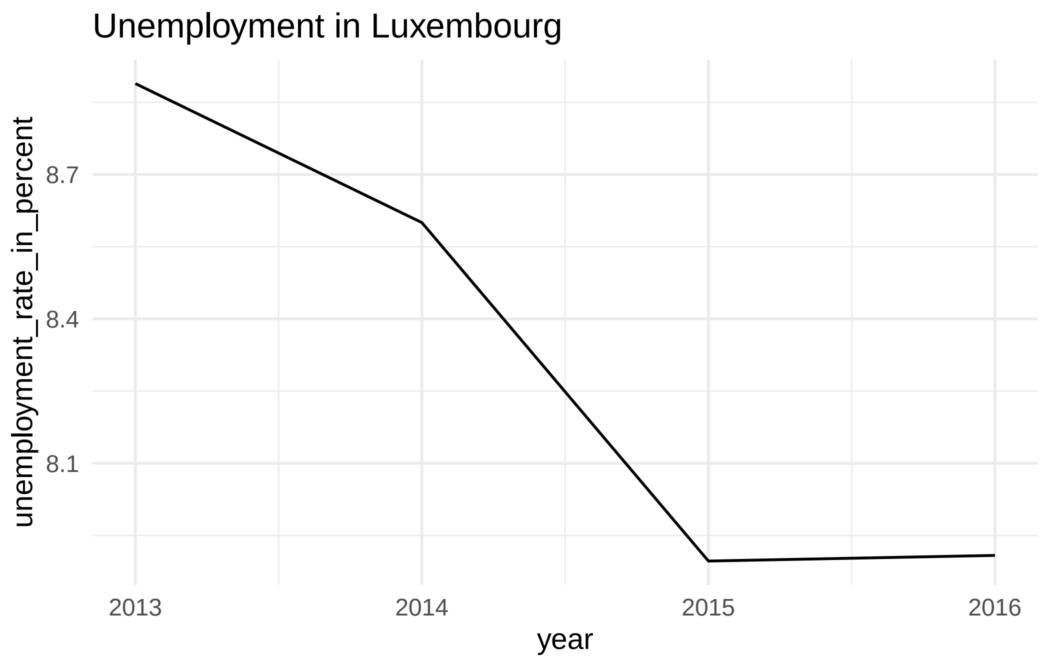
In this case here, we need to use an anonymous function. This is because `filter()` has two arguments, and we need to make clear what it is we are mapping over and what argument stays fixed; we are mapping over, or iterating if you will, data frames, but the predicate stays fixed.

We are now ready to plot our data. The best way to continue is to first get the function right by creating one plot for one single commune. Let's select the dataset for the commune of `Luxembourg`:

```
lux_data <- nested_unemp %>%
  filter(place_name == "Luxembourg") %>%
  unnest(data)
```

To plot this data, we can now write the required `ggplot2()` code:

```
ggplot(data = lux_data) +
  theme_minimal() +
  geom_line(
    aes(year, unemployment_rate_in_percent, group = 1)
   ) +
  labs(title = "Unemployment in Luxembourg")
```



To turn the lines of code above into a function, you need to think about how many arguments that function would have. There is an obvious one, the data itself (in the snippet above, the data is the `lux_data` object). Another one that is less obvious is in the title:

```
    labs(title = "Unemployment in Luxembourg")
```

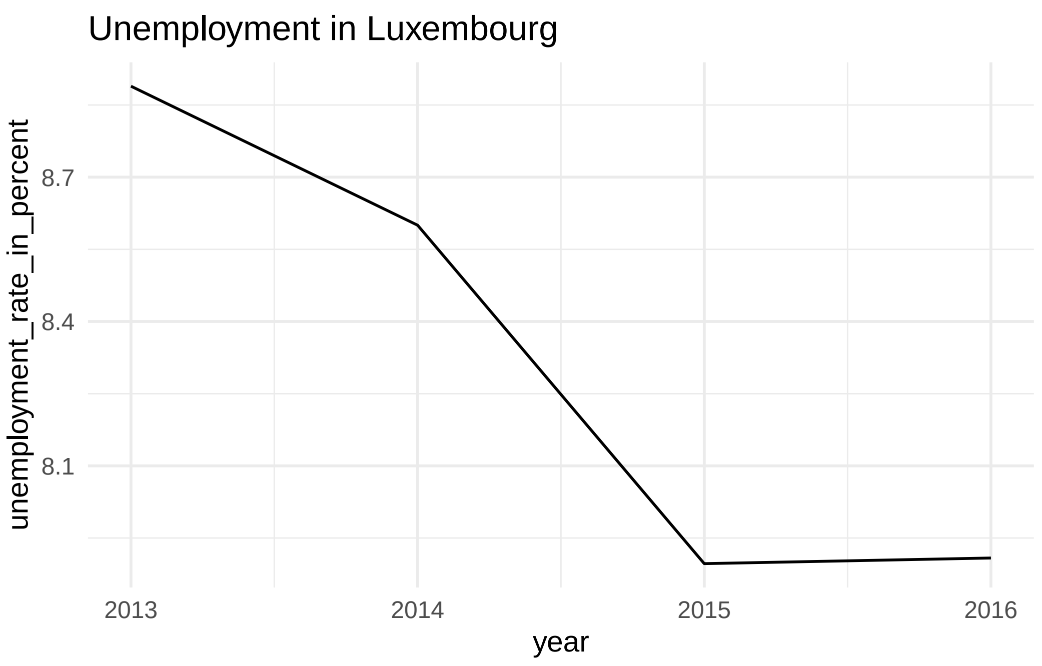
```
$title
[1] "Unemployment in Luxembourg"

attr(,"class")
[1] "labels"
```

Ideally, we would want that title to change, depending on the data set. So we could write the function like so:

```
make_plot <- function(x, y){
  ggplot(data = x) +
    theme_minimal() +
    geom_line(
      aes(year, unemployment_rate_in_percent, group = 1)
      ) +
    labs(title = paste("Unemployment in", y))
}
```

Let's try it on our data:

```
make_plot(lux_data, "Luxembourg")
```



Ok, so now, we simply need to apply this function to our nested data frame:

```
nested_unemp <- nested_unemp %>%
  mutate(plots = map2(
    .x = data,
    .y = place_name,
    .f = make_plot
  ))

nested_unemp
```

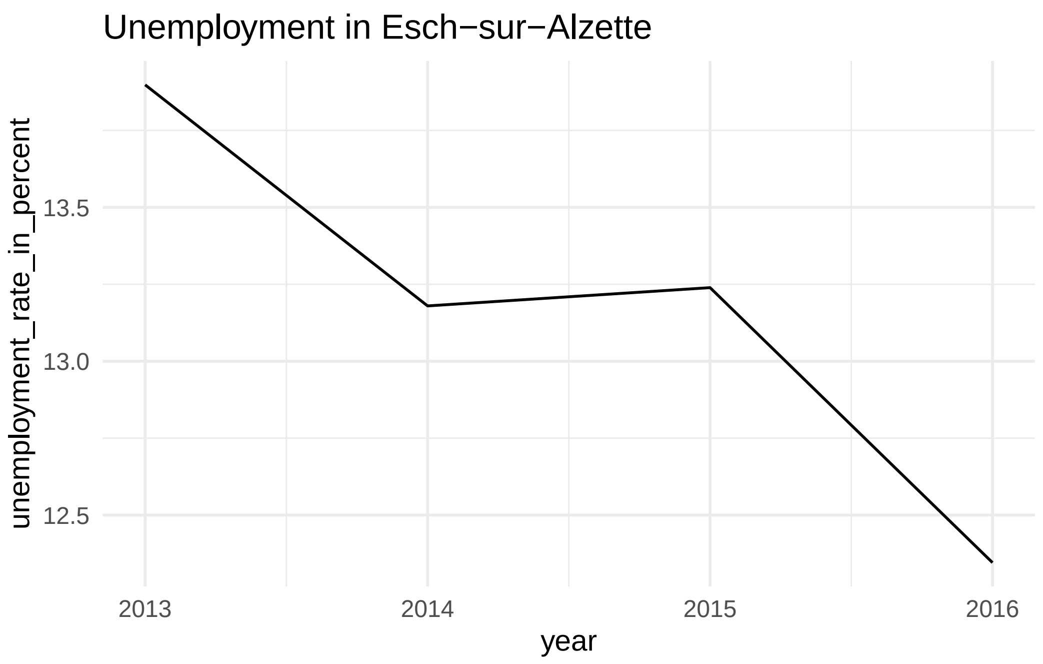
```
# A tibble: 3 x 3
  place_name                         data plots
  <chr>                <list<tibble[,8]>> <list>
```

```
1 Esch-sur-Alzette            [4 x 8] <gg>
2 Luxembourg                  [4 x 8] <gg>
3 Wiltz                       [4 x 8] <gg>
```

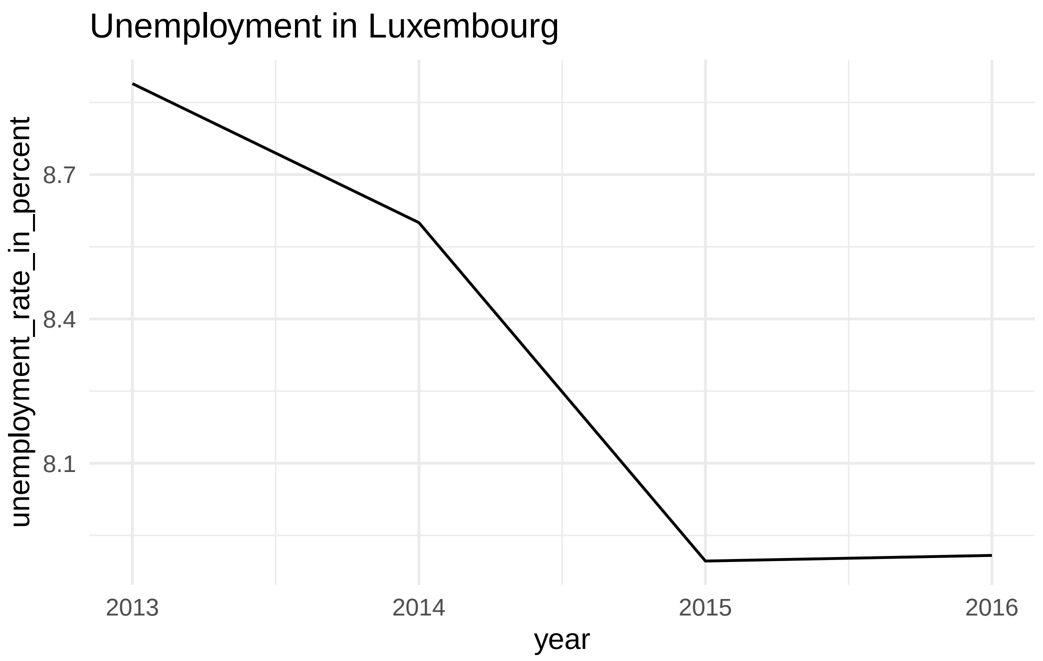
If you look at the `plots` column, you see that it is a list of `gg` objects: these are our plots. Let's take a look at them:

```
nested_unemp$plots
```

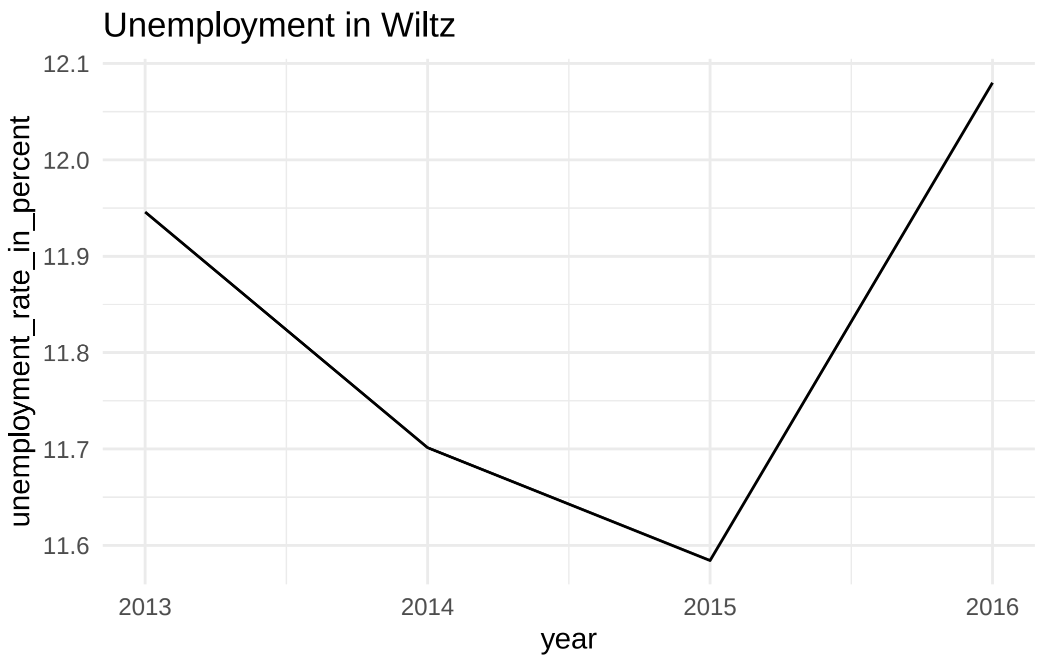
```
[[1]]
```



```
[[2]]
```


Unemployment in Luxembourg
unemployment_rate_in_percent
8.7
8.4
8.1
2013
2014
2015
2016
year

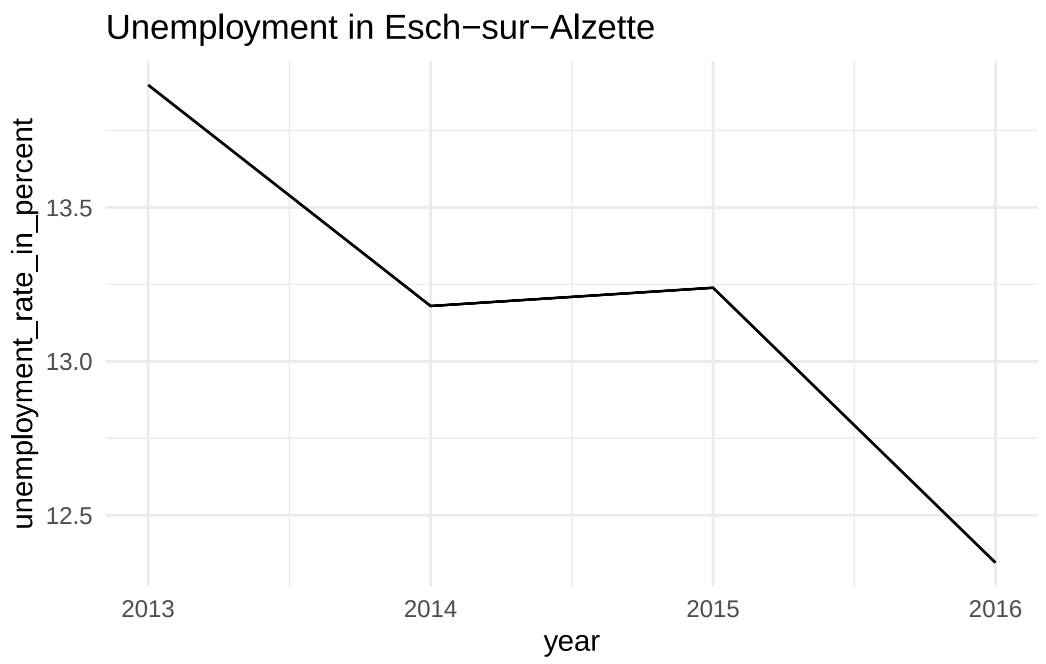
```
[[3]]
```


Unemployment in Wiltz
unemployment_rate_in_percent
12.1
12.0
11.9
11.8
11.7
11.6
2013
2014
2015
2016
year

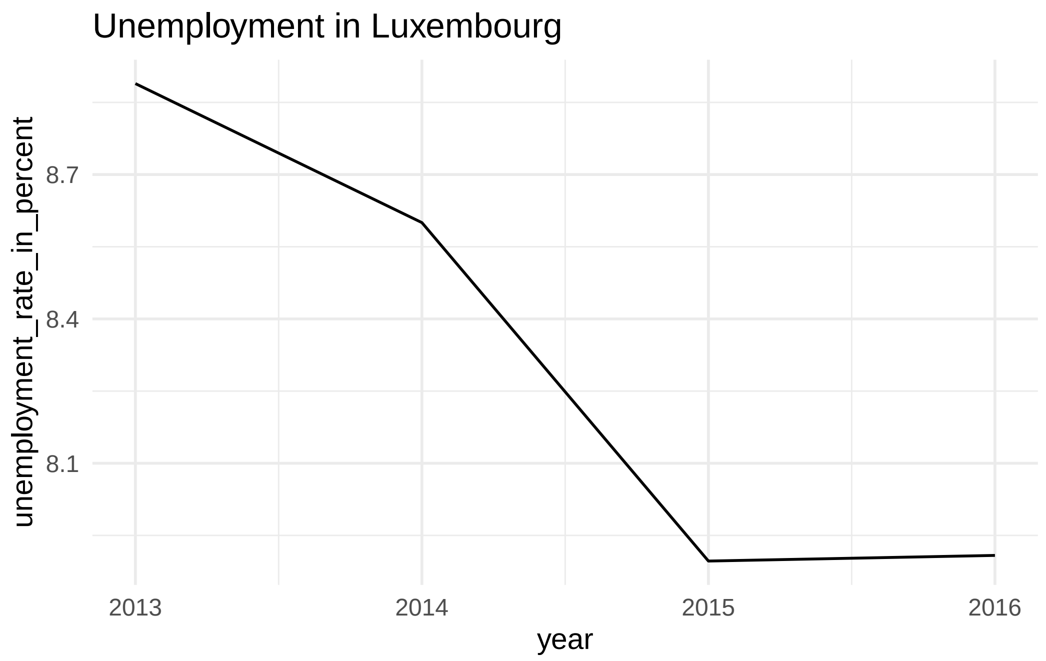
We could also have used an anonymous function:

```
nested_unemp %>%
  mutate(plots2 = map2(
    .x = data,
    .y = place_name,
    .f = \(.x,.y)(
                ggplot(data = .x) +
                  theme_minimal() +
                  geom_line(
                    aes(year, unemployment_rate_in_percent, group = 1)
                   ) +
                  labs(title = paste("Unemployment in", .y))
                  )
           )
         ) %>%
  pull(plots2)
```

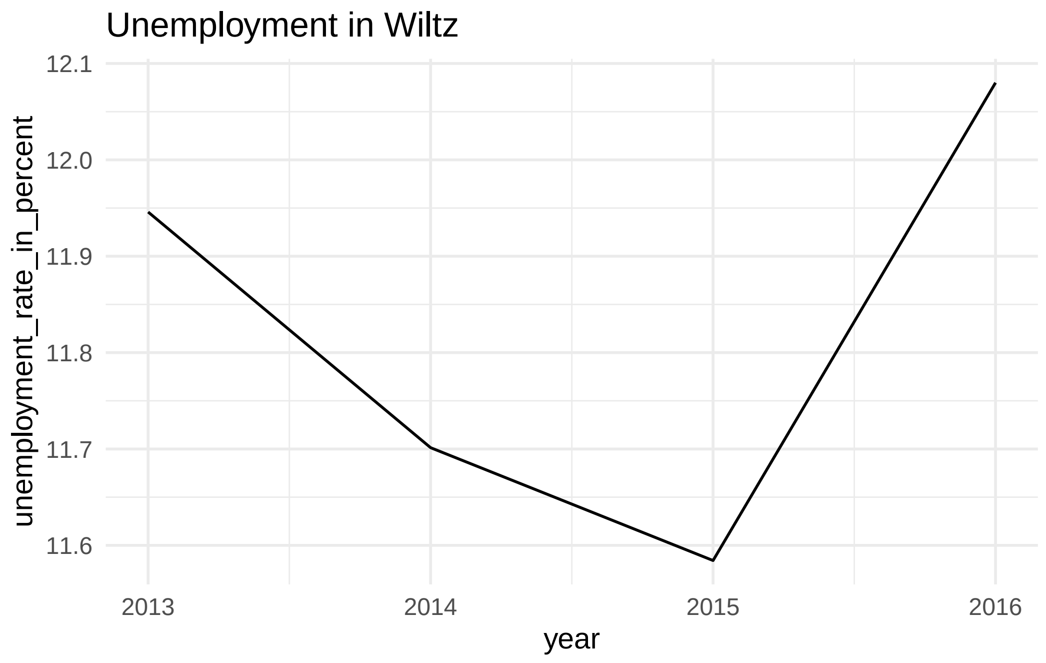
```
[[1]]
```



```
[[2]]
```


Unemployment in Luxembourg
unemployment_rate_in_percent
8.7
8.4
8.1
2013
2014
2015
2016
year

```
[[3]]
```


Unemployment in Wiltz
unemployment_rate_in_percent
12.1
12.0
11.9
11.8
11.7
11.6
2013
2014
2015
2016
year

This column-list based workflow is extremely powerful and I highly advise you to take the required time to master it.

4.4 Functional programming in R

Up until now we focused more on concepts than on specificities of the R programming language when it comes to functional programming. In the section, we will be focusing entirely on R-specific capabilities and packages for functional programming.

4.4.1 Base capabilities

R is a functional programming language, as already stated, and as such it comes with many functions out of the box to write functional code. We have already discussed `lapply()` and `Reduce()`. You should know that depending on what you want to achieve, there are other functions that are similar to `lapply()`: `apply()`, `sapply()`, `vapply()`, `mapply()` and `tapply()`. There's also `Map()` which is a wrapper around `mapply()`. Each function performs the same basic task of applying a function over all the elements of a list or list-like structure, but it can be hard to keep them apart. This is why `{purrr}`, which we will discuss in the next section, is quite an interesting alternative to base R's offering.

Another one of the quintessential functional programming functions (alongside `Reduce()` and `Map()`) that ships with R is `Filter()`. If you know `dplyr::filter()` you should be familiar with the concept of filtering rows of a data frame where the elements of one particular column satisfy a predicate. `Filter()` works the same way, but focusing on lists instead of data frame:

```r
Filter(is.character,
       list(
         seq(1:5),
         "Hey")
       )
```

```
[[1]]
[1] "Hey"
```

The call above only returns the elements where `is.character()` evaluates to `TRUE`.

Another useful function is `Negate()` which is a function factory that takes a boolean function as an input and returns the opposite boolean function. As an illustration, suppose that in the example above we wanted to get everything *but* the character:

```r
Filter(Negate(is.character),
       list(
         seq(1:5),
         "Hey")
       )
```

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

There are some other functions like this that you might want to check out: type `?Negate` in console to read more about them.

Before continuing with R packages that extend R's functional programming capabilities it's also important to stress that just as R is a functional programming language, it is also an object oriented language. In fact, R is what John Chambers called a *functional OOP* language (Chambers (2014)). We won't delve too much into what this means (read Wickham (2019) for this), but as a short discussion, consider the `print()` function. Depending on what type of object the user gives it, it seems as if somehow `print()` knows what to do with it:

```r
print(5)
```

```
[1] 5
```

```r
print(head(mtcars))
```

```
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

```r
print(str(mtcars))
```

```
'data.frame':	32 obs. of  11 variables:
 $ mpg : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
 $ cyl : num  6 6 4 6 8 6 8 4 4 6 ...
 $ disp: num  160 160 108 258 360 ...
 $ hp  : num  110 110 93 110 175 105 245 62 95 123 ...
 $ drat: num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69 3.92 3.92 ...
 $ wt  : num  2.62 2.88 2.32 3.21 3.44 ...
 $ qsec: num  16.5 17 18.6 19.4 17 ...
 $ vs  : num  0 0 1 1 0 1 0 1 1 1 ...
 $ am  : num  1 1 1 0 0 0 0 0 0 0 ...
 $ gear: num  4 4 4 3 3 3 3 4 4 4 ...
 $ carb: num  4 4 1 1 2 1 4 2 2 4 ...
NULL
```

The way this works, is essentially a mixture of functional and object oriented programming, so functional OOP. Let's take a closer look at the source code of `print()` by simply typing `print` without brackets, into a console:

```
print
```

```
function (x, ...)
UseMethod("print")
<bytecode: 0x561ed4ac2450>
<environment: namespace:base>
```

Quite unexpectedly, the source code of `print()` is one line long and is just `UseMethod("print")`. So all `print()` does is use a generic method called "print". If your text editor has autocompletion enabled, you might see that there are actually quite a lot of `print()` functions. For example, type `print.data.frame` into a console:

```
print.data.frame
```

```
function (x, ..., digits = NULL, quote = FALSE, right = TRUE,
    row.names = TRUE, max = NULL)
{
    n <- length(row.names(x))
    if (length(x) == 0L) {
        cat(sprintf(ngettext(n, "data frame with 0 columns and %d row",
            "data frame with 0 columns and %d rows"), n), "\n",
            sep = "")
    }
    else if (n == 0L) {
        print.default(names(x), quote = FALSE)
        cat(gettext("<0 rows> (or 0-length row.names)\n"))
    }
    else {
        if (is.null(max))
            max <- getOption("max.print", 99999L)
        if (!is.finite(max))
            stop("invalid 'max' / getOption(\"max.print\"): ",
                max)
        omit <- (n0 <- max%/%length(x)) < n
        m <- as.matrix(format.data.frame(if (omit)
            x[seq_len(n0), , drop = FALSE]
        else x, digits = digits, na.encode = FALSE))
        if (!isTRUE(row.names))
            dimnames(m)[[1L]] <- if (isFALSE(row.names))
                rep.int("", if (omit)
                  n0
                else n)
            else row.names
        print(m, ..., quote = quote, right = right, max = max)
        if (omit)
            cat(" [ reached 'max' / getOption(\"max.print\") -- omitted",
                n - n0, "rows ]\n")
    }
    invisible(x)
}
<bytecode: 0x561ed5bdd0d0>
<environment: namespace:base>
```

This is the `print` function for `data.frame` objects. So what `print()` does is look at the class of its argument `x`, and then look for the right `print` function. In more traditional OOP languages, users would type something like:

```
mtcars.print()
```

In these languages, objects encapsulate method (the equivalent of our functions), so if `mtcars` is a data frame, it encapsulates a `print()` method that then does the printing. R is different, because classes and methods are kept separate. If a package developer creates a new class of object, then the developer also must implement the required methods. For example in the `{chronicler}` package, the `chronicler` class is defined and a `print.chronicler()` function is defined to print these objects.

All of this to say that if you want to extend R by writing packages, learning some OOP essentials is also important. But for data analysis, functional programming does the job perfectly. To learn more about R's different OOP systems (yes, R can do OOP in diffirent ways and the one I sketched here is the simplest, but probably the most used as well, one), take a look at Wickham (2019).

4.4.2 purrr

The `{purrr}` package, developed by Posit, contains many functions to make functional programming with R more smooth. In the previous section, we discussed the `apply()` family of function; they all do a very similar thing, which is looping over a list and applying a function to the elements of the list, but it is not quite easy to remember which one does what. Also, for some of these functions like `apply()`, the list comes first, and then the function, but in the case of `mapply()`, the function comes first. Another issue with these functions is that it is not always easy to know what type the output is going to be. List? Atomic vector? Something else?

`{purrr}` solves this issue by offering the `map()` family of functions, which behave in a very conistent way. The basic function is called `map()` and we've already used it:

```
map(seq(1:5), sqrt)
```

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

[[2]]
[1] 1.414214

[[3]]
[1] 1.732051

[[4]]
[1] 2

[[5]]
[1] 2.236068
```

But there are many interesting variants:

```
map_dbl(seq(1:5), sqrt)
```

```
[1] 1.000000 1.414214 1.732051 2.000000 2.236068
```

`map_dbl()` coerces the output to an atomic vector of doubles instead of a list of doubles. Then there's:

```
map_chr(letters, toupper)
```

```
 [1] "A" "B" "C" "D" "E" "F" "G" "H" "I" "J" "K" "L" "M" "N" "O" "P" "Q" "R" "S"
[20] "T" "U" "V" "W" "X" "Y" "Z"
```

for when the output needs to be an atomic vector of characters.

There are many others, so take a look at the document with `?map`. There's also `walk()` which is used if you're only interested in the side-effect of the function (for example if the function takes paths as input and saves something to disk).

`{purrr}` also has functions to replace `Reduce()`, simply called `reduce()` and `accumulate()`, and there are many, many other useful functions. Read through the documentation of the package and take the time to learn about all it has to offer.

4.4.3 withr

`{withr}` is a powerful package that makes it easy to "purify" functions that behave in a way that can cause problems. Remember the function from the introduction that randomly gave out a recipe Bruno liked? Here it is again:

```
h <- function(name, food_list = list()){

  food <- sample(c("lasagna", "cassoulet", "feijoada"), 1)

  food_list <- append(food_list, food)

  print(paste0(name, " likes ", food))

  food_list
}
```

Because this function returns results that are not consistent for a fixed input, this function is not referentially transparent. So we improved the function like this:

```
h2 <- function(name, food_list = list(), seed = 123){

  # We set the seed, making sure that we get the same selection of food for a given seed
  set.seed(seed)
  food <- sample(c("lasagna", "cassoulet", "feijoada"), 1)

  # We now need to unset the seed, because if we don't, guess what, the seed will stay set
  set.seed(NULL)

  food_list <- append(food_list, food)

  print(paste0(name, " likes ", food))

  food_list
}
```

The problem with this approach is that we need to modify our function. We can instead use `withr::with_seed()` to achieve the same effect:

```
withr::with_seed(seed = 123,
                 h("Bruno"))
```

```
[1] "Bruno likes feijoada"

[[1]]
[1] "feijoada"
```

It is also easier to create a wrapper if needed:

```
h3 <- function(..., seed){
  withr::with_seed(seed = seed,
                   h(...))
}
```

```
h3("Bruno", seed = 123)
```

```
[1] "Bruno likes feijoada"

[[1]]
[1] "feijoada"
```

Before we downloaded a dataset and loaded it into memory; we did so by first created a temporary file, then downloading it and then loading it. Suppose that instead of loading this data into our session, we simply wanted to test whether the link was still working. We wouldn't want to keep the loaded data in our session, so to avoid having to delete it again manually, we could use `with_tempfile()`:

```
withr::with_tempfile("unemp", {
  download.file("https://github.com/b-rodrigues/myPackage/raw/main/data/unemp.rda", destfi
  load(unemp)
  nrow(unemp)
  }
)
```

```
Warning in unlink(mget(new, envir = env), recursive = TRUE): expanded path length 35189 woul
list(year = c(2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 
2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 2013, 20
```

```
[1] 472
```

The data got downloaded, and then loaded, and then we computed the number of rows of the data, without touching the global environment, or state, of our current session.

Just like for `{purrr}`, `{withr}` has many useful functions which I encourage you to familiarize yourself with.

4.5 Conclusion

If there is only one thing that you should remember from this chapter, it would be pure functions. This is in my opinion not very difficult to do and comes with many benefits. But, avoiding loops and replacing them with higher-order functions (`lapply()`, `Reduce()`, `purrr::map()` – and its variants –) also pays off. While this chapter stresses the advantages of functional programming, you should not forget that R is not a pure, and solely, functional programming language and that other paradigms, like object oriented programming, are also available to you, and if your goal is to master the language (instead of "just" using it to solve data analysis problems), then you also need to know about R's OOP capabilities.

5 Testing your code

5.1 Assertive testing (and defenvise programming?)

The analysis is still in Quarto, so how could the readers of this book test their code? Copying here what Miles wrote on the subject:

'Assertive programming' is a topic that might be missing from the book. I think of it as a kind of dual of unit testing. Unit testing is for more generally applicable packaged code. But when you have functions in your analysis pipeline that operate on a very specific kind of input data, unit testing becomes kind of nonsensical because you're left to dream up endless variations of your input dataset that may never occur. It's a bit easier to flip the effort to validating the assumptions you have about your input and output data, which you can do in the pipeline functions themselves rather than separate unit testing ones. This is nice because it ensures the validation is performed in the pipeline run, and so is backed by the same reproducibility guarantees.

I think at the end of the chapter we should hint at unit testing, but leave it as a subsection of the next chapter that deals with packaging code.

6 Keeping it DRY with literate programming

In order to build a reproducible pipeline, we will be working together on a project. The project itself will be quite simple and will simply consist in getting some data "trapped" inside a Microsoft Excel Workbook into a data frame, and then creating a plot. The point of this book is not to teach you data analysis no data visualization, but instead, engineering the project in such a way that it is:

- Documented;
- Tested;
- Reproducible.

We will start our project like someone with time constraints does, and see how we can reach our goal of having a nice reproducible project as painlessly as possible. There is only one catch; to make the whole process as easy as possible, we will be using literate programming, and not simply programming.

By the way, you might want to create a new repository and use it for the example documents that we are going to work on together in this chapter. But since the goal of this chapter is to teach you about literate programming, we won't tell you when to commit an push, just try to do it from time to time, and especially once you're done with an example!

6.1 Literate programming

In literate programming, we mix code and prose together, in a way that makes it easy for both non-technical users and programmers to understand what is going on. Scripts written this way are also very easy to compile, or render, into a variety of document formats like `html` and `docx`. R supports several ways of doing literate programming: Sweave, knitr and Quarto.

Sweave was the first tool available to R (and S) users, and allowed the mixing of R and LaTeX code to create a document. Friedrich Leisch developed Sweave in 2002 and described it in his 2002 paper (Leisch (2002)). As Leisch argues, *the traditional way of writing a report as part of a statistical data analysis project uses two separate steps*: running the analysis using some software, and then copy and pasting the results into a word processing tool. The problem with this approach is that much time is wasted copy and pasting things, so experimenting with different layouts or data analysis techniques is very time consuming. Copy and paste mistakes will also happen (it's not a question of if, but when) and updating reports (for example, when new data comes in) means that someone will have, again, to copy and paste the updated results into a new document.

Sweave provided (and still provides, as it is still well functioning!) a way to embed the analysis in the document itself, in this case a LaTeX source file, and R code was executed whenever the document was compiled. This gave researchers considerable time savings when it was time to update a report or drafting a research paper.

The snippet below shows the example from Leisch's paper:

```
\documentclass[a4paper]{article}

\begin{document}

In this example we embed parts of the examples from the
\texttt{kruskal.test} help page into a LaTeX document:

<<>>=
data (airquality)
kruskal.test(Ozone ~ Month, data = airquality)
@

which shows that the location parameter of the Ozone
distribution varies significantly from month to month.
Finally we include a boxplot of the data:

\begin{center}
<<fig=TRUE,echo=FALSE>>=
boxplot(Ozone ~ Month, data = airquality)
@
\end{center}

\end{document}
```

Even if you've never seen a LaTeX source file, you should be able to figure out what's going on. The first line states what type of document we're writing. Then comes `\begin{document}` which tells the compiler where the document starts. Then comes the content. You can see that it's a mixture of plain English with R code defined inside chunks starting with `<<>>=` and ending with `@`. Finally, the documents ends with `\end{document}`. Getting a human readable PDF from this source is a two-step process: first this source gets converted into a `.tex` file and then this `.tex` file into a PDF. Sweave is included with every R installation since version 1.5.0, and still works to this day. For example, we can test that our Sweave installation works just fine by compiling the example above. This is what the final output looks like:

In this example we embed parts of the examples from the `kruskal.test` help page into a LaTeX document:

```
> data (airquality)
> kruskal.test(Ozone ~ Month, data = airquality)

        Kruskal-Wallis rank sum test

data:  Ozone by Month
Kruskal-Wallis chi-squared = 29.267, df = 4, p-value = 6.901e-06
```

which shows that the location parameter of the Ozone distribution varies significantly from month to month. Finally we include a boxplot of the data:

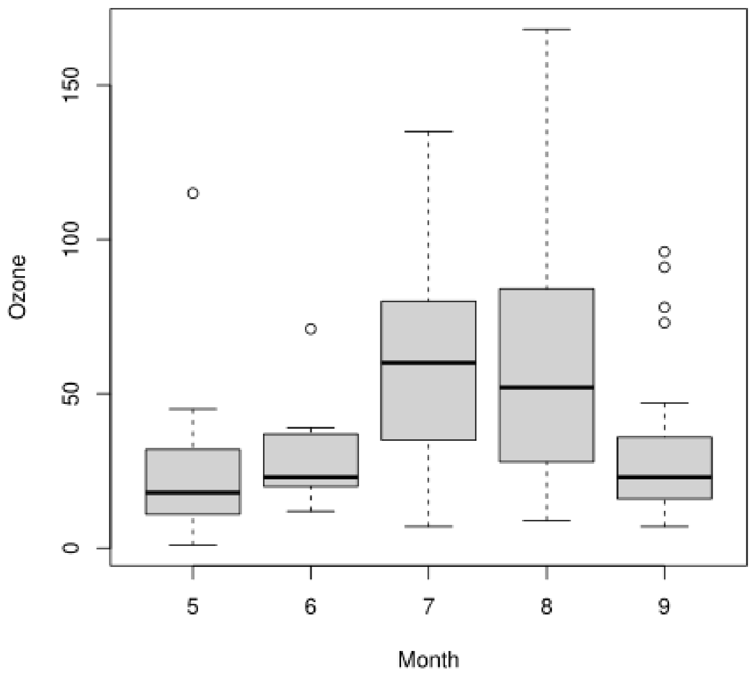


Figure 6.1: More than 20 years later, the output is still the same

Let us just state that the fact that it is still possible to compile this example more than 20 years later is an incredible testament to how mature and stable this software is (both R, Sweave, and LaTeX). But as impressive as this is, LaTeX has a steep learning curve, and Leisch even advocated the use of the Emacs text editor to edit Sweave files, which also has a very steep learning curve (but this is entirely optional; for example we edited and compiled the example on the Rstudio IDE).

The next generation of literate programming tools was provided by a package called `{knitr}` in 2012. From the perspective of the user, the biggest change from Sweave is that `{knitr}` is able to use many different formats as source files. The one that became very likely the most widely used format is a flavour of the Markdown markup language, R Markdown (Rmd). But `{knitr}` can also run code chunks for other languages, such as Python, Perl, Awk, Haskell, bash and more (Xie (2014)). Since version 1.18, `{knitr}` uses the `{reticulate}` package to provide a Python engine for the Rmd format. To illustrate the Rmd format, let's rewrite the example from Leisch's Sweave paper into it:

~~~
---
output: pdf_document
---

In this example we embed parts of the examples from the
\texttt{kruskal.test} help page into a LaTeX document:

```{r}
data (airquality)
kruskal.test(Ozone ~ Month, data = airquality)
```



which shows that the location parameter of the Ozone
distribution varies significantly from month to month.
Finally we include a boxplot of the data:

```{r, echo = FALSE}
boxplot(Ozone ~ Month, data = airquality)
```
~~~

This is what the output looks like:

Just like in a Sweave document, an Rmd source file also has a header in which authors can define a number of options. Here we only specified that we wanted a pdf document as an output file. We then copy and pasted the contents from the Sweave source, but changed the chunk delimiters from `<<>>=` and `@` to ` ```{r} ` to start an R chunk and ` ``` ` to end it. Remember; we

In this example we embed parts of the examples from the `kruskal.test` help page into a LaTeX document:

```
data (airquality)
kruskal.test(Ozone ~ Month, data = airquality)
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  Ozone by Month
## Kruskal-Wallis chi-squared = 29.267, df = 4, p-value = 6.901e-06
```

which shows that the location parameter of the Ozone distribution varies significantly from month to month. Finally we include a boxplot of the data:

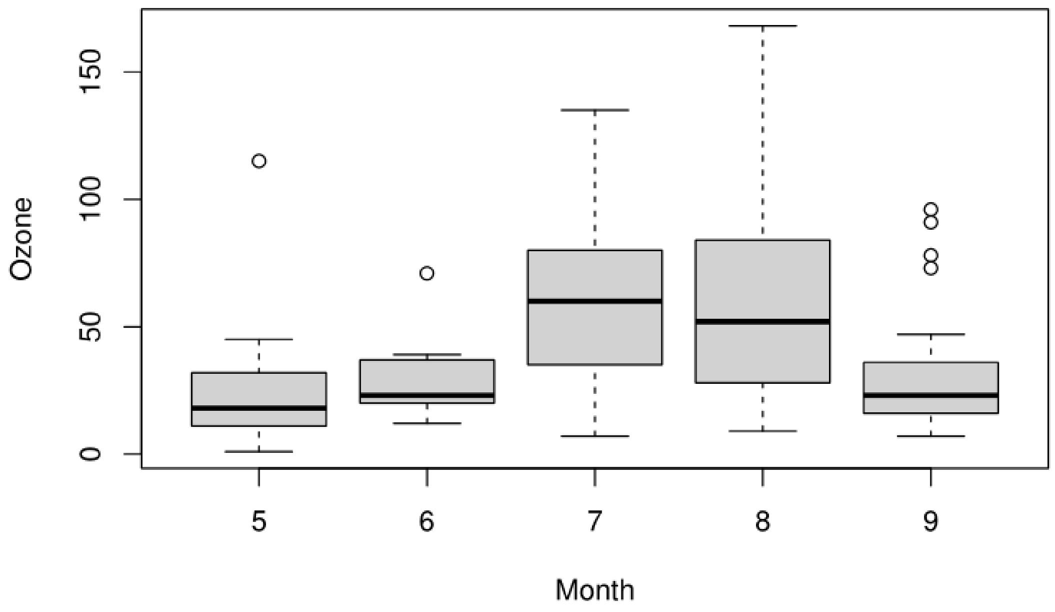


Figure 6.2: It's very close to the Sweave output

need to specify the engine in the chunk because `{knitr}` supports many engines. For example, it is possible to run a bash command by adding this chunk to the source:

~~~
---
output: pdf_document
---

In this example we embed parts of the examples from the
\texttt{kruskal.test} help page into a LaTeX document:

```{r}
data (airquality)
kruskal.test(Ozone ~ Month, data = airquality)
```

which shows that the location parameter of the Ozone
distribution varies significantly from month to month.
Finally we include a boxplot of the data:

```{r, echo = FALSE}
boxplot(Ozone ~ Month, data = airquality)
```

```{bash}
pwd
```
~~~

(bash's `pwd` command shows the current working directory). You may have noticed that we also keep two LaTeX commands in the source Rmd, `\texttt{}` and `LaTeX`. This is because Rmd files get first converted into `LaTeX` files and then into a PDF. If you're using RStudio, this document can be compiled by clicking a button or using a keyboard shortcut, but you can also use the `rmarkdown::render()` function. This function does two things transparently: it first converts the Rmd file into a source LaTeX file, and then converts it into a PDF. It is of course possible to convert the document to a Word document as well however, LaTeX commands will be ignored. Html is another widely used output format.

If you're a researcher and prefer working with LaTeX directly instead of having to switch to Markdown, you can either use Sweave, or use `{knitr}` but instead of writing your documents using the R Markdown format, you can use the `Rnw` format which is basically the same as Sweave, but uses `{knitr}` for compilation. Take a look at this example from the `{knitr}` github repository for example.

You should know that `{knitr}` makes it possible to author many, many different types of documents. It is possible to write books, blogs, package documentation (and even entire packages, as we shall see later in this book), Powerpoint slides… It is extremely powerful because we can use the same general R Markdown knowledge to build many different outputs:

Finally, the latest in literate programming for R is a new tool developed by Posit, called Quarto. If you're an R user and already know `{knitr}` and the Rmd format, you should be able to immediately use Quarto. So what's the difference? In practice and for R users not much. There are many things that Quarto is able to do out of the box that you can't, without extensions, do with `{knitr}`. Quarto has some nice defaults; in fact this book is written in Quarto instead of `{knitr}` because the default Quarto output looks nicer than the default `{knitr}` output. However, there may even be things that Quarto can't do at all (at least for now) when compared to `{knitr}`. So why bother switching? Well, Quarto provides sane defaults and some nice features out of the box, and the cost of switching from the Rmd format to Quarto's Qmd format is basically 0. Also, and this is probably the biggest reason to use Quarto, is that Quarto is not tied to R. Quarto is actually a standalone tool that needs to be installed alongside your R installation, and works completely independently. In fact, you can use Quarto without having R installed at all, as Quarto, just like `{knitr}` supports many engines. This means that if you're primarily using Python, you can author documents with Quarto. Quarto also supports the Julia programming language and Observable JS, making it possible to include interactive visualisations into an Html document. Let's take a look at how the example from Leisch's paper looks as a Qmd file:

~~~
---
output: pdf
---

In this example we embed parts of the examples from the
\texttt{kruskal.test} help page into a LaTeX document:

```{r}
data (airquality)
kruskal.test(Ozone ~ Month, data = airquality)
```



which shows that the location parameter of the Ozone
distribution varies significantly from month to month.
Finally we include a boxplot of the data:

```{r, echo = FALSE}
boxplot(Ozone ~ Month, data = airquality)
```
~~~

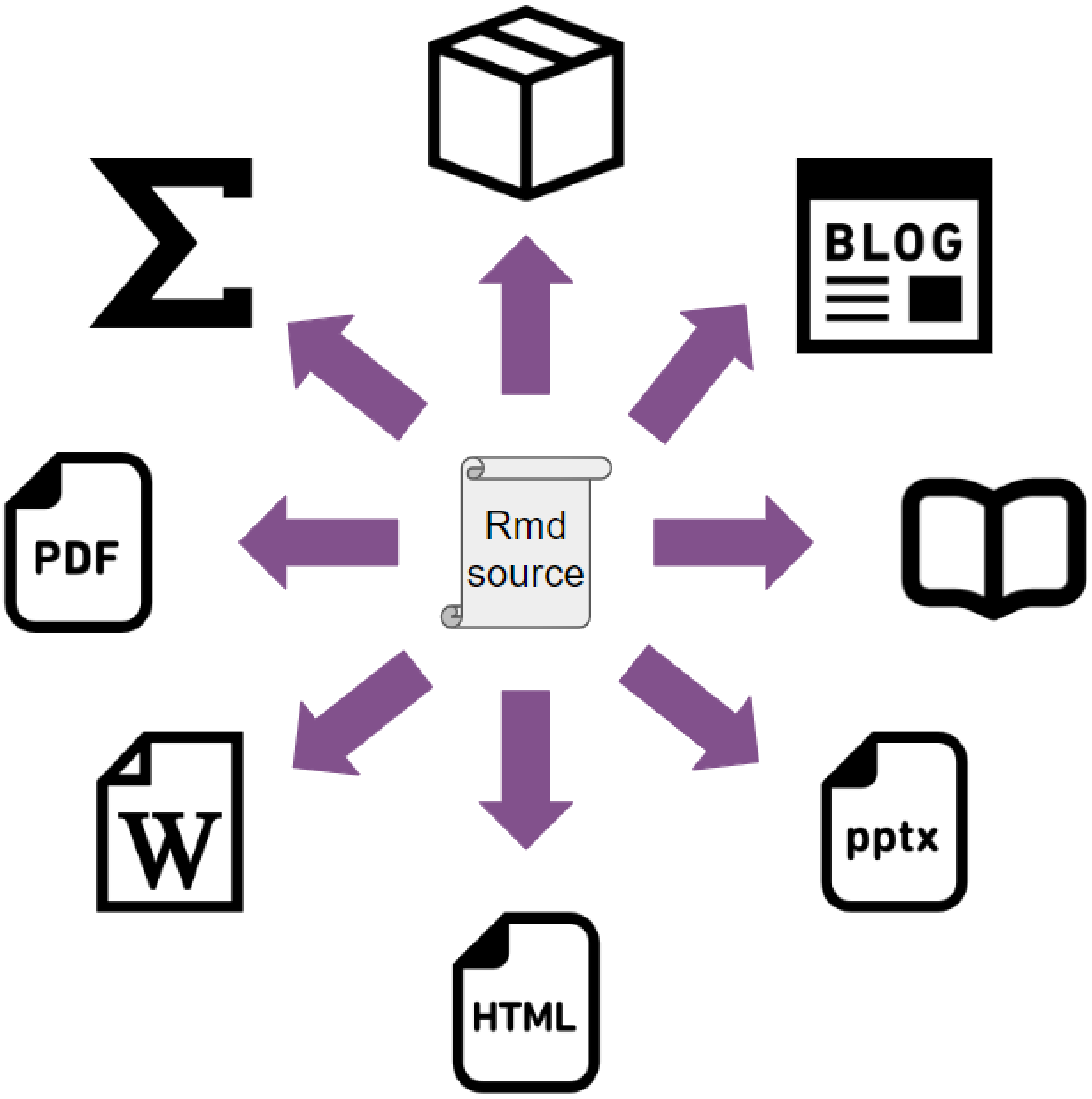


Figure 6.3: One format to rule them all

(I've omitted the bash chunk from before, not because Quarto does not support it, but to keep close to the original example from the paper.)

As you can see, it's exactly the same as the Rmd file from before. The only difference is in the header. In the Rmd file we specified the output format as:

```
---
output: pdf_document
---
```

whereas in the Qmd file we changed it to:

```
---
output: pdf
---
```

While Quarto is the latest option in literate programming, it is quite recent, and as such, we feel it might be better to stick with `{knitr}` and the Rmd format for now, so that's what we're going to use going forward. Also, the `{knitr}` and the Rmd format are here to stay, so there's little risk in keeping using it, and anyways, as already stated, if switching to Quarto becomes a necessity, the cost of switch would be very, very low. In what follows, we won't be focused on anything really `{knitr}` or Rmd specific, so should you want to use Quarto instead, you should be able to follow along without any problems at all, since the Rmd and Qmd formats have so much overlap (but whenever there would be major differences between the two formats, we will highlight them).

In the next two sections, we will discuss how to set up and use `{knitr}` as well as give you a quick overview of the R Markdown syntax. However, we will very quickly focus on the templating capabilities of `{knitr}`: expanding text, using child documents, and parameterised reports. These are advanced topics and not easy to tackle if you're not comfortable with R already. Just as functions and higher-order functions like `lapply()` avoid having to repeat yourself, so does templating, but for literate programming. The goal is to write functions that returns literal R Markdown code, so that you can loop over these functions to build entire sections of your documents. However, difficult these features are to master, they are also extremely powerful, as they help you focus on what really matters.

6.2 {knitr} basics

This section will be a very small intro to {knitr}. We are going to teach you just enough to get started, and we are going to focus on the Rmd format. There are many resources out there that you can use if you want to dig deeper, for instance the R Markdown website from Posit, or the R Markdown: The Definitive Guide and R Markdown Cookbook eBooks. We will also not assume that you are using the RStudio IDE and give you instead the lower level commands to render documents. If you use RStudio and want to know how to use it effectively to author Rmd documents, you should take a look at Quick Tour page. In fact, this section will basically focus on the same topics, but without focusing on how to use RStudio.

6.2.1 Set up

The first step is to install the {knitr} and the {rmarkdown} packages. Simple type:

```
install.packages("rmarkdown")
```

in an R console. Since {knitr} is required to install {rmarkdown}, it gets installed automatically. If you want to compile PDF documents, you should also have a working LaTeX distribution. You can skip this next part if you're only interested in generating PDF and Word files. For what follows, we will only be rendering Html documents, so no need to install LaTeX (by the way, you do not need a working Word installation to compile documents to the docx format). However, if you already have a working LaTeX installation, you shouldn't have to do anything else to generate PDF documents. If you don't have a working LaTeX distribution, then Yihui Xie, the creator of {knitr} created an R package called {tinytex} that makes it extremely easy to install a LaTeX distribution. In fact, this is the way we recommend installing LaTeX even if you're not an R user (it is possible to use the tinytex distribution without R; it's just that the {tinytex} R package provides many functions that makes installing and maintaining it very easy). Simply run these commands in an R console to get started:

```
install.packages("tinytex")
tinytex::install_tinytex()
```

and that's it! If you need to install specific LaTeX packages, then refer to the **Maintenance** section on tinytex's website. For example, to compile the example from Leisch's article on Sweave discussed previously, we had to install the grfext LaTeX package (as explained by the error output in the console when we tried compiling). So, we simply needed to run the following command to get it:

```
tlmgr_install("grfext")
```

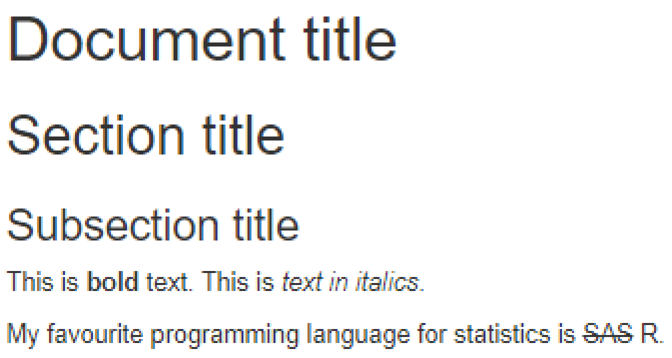
After you've installed {knitr}, {rmarkdown} and, optionally, {tinytex}, simply try to compile the following document:

```
---
output: html_document
---

# Document title

## Section title

### Subsection title

This is **bold** text. This is *text in italics*.

My favourite programming language for statistics is ~~SAS~~ R.
```

save this document into a file called `rmd_intro.rmd` using you're favourite text editor. Then render it into an Html file by running the following command in the R console:

```
rmarkdown::render("path/to/rmd_test.rmd")
```

This should create a file called `rmd_test.html`; open it with your web browser and you should see the following:



Document title

Section title

Subsection title

This is **bold** text. This is *text in italics*.

My favourite programming language for statistics is ~~SAS~~ R.

Figure 6.4: It's very close to the Sweave output

Congratulations, you just *knitted* your first Rmd document!

6.2.2 Markdown ultrabasics

R Markdown is a flavour of Markdown, which means that you should know some Markdown to really take full advantage of R Markdown. The document from before should have already shown you some basics: titles, sections and subsections all start with a `#` and the depth level is determined by the number of `#`s. For bold text, simply put the words in between `**` and for italics use only one `*`. If you want ***bold and italics***, use `***`. The original designer of Markdown did not think that underlining text was important, so there is no *easy* way of doing it unfortunately. For this, you need to use a somewhat hidden feature; without going into too much technical details, the program that converts Rmd files to the final output format is called Pandoc, and it's possible to use some of Pandoc's features to format text. For example, for underlining:

```
[This is some underlined text in a R Markdown document]{.underline}
```

This will underline the text between square brackets.[1]

The next step is actually to mix code and prose. As you've seen from Leisch's canonical example, this is quite easily achieved by using R code chunks. The R Markdown example below shows various code chunks alongside some options. For example, a code chunk that uses the `echo = FALSE` option will not appear (but the output of the computation will):

~~~~
---
title: "Document title"
output: html_document
date: "2023-01-28"
---

# R code chunks

This below is an R code chunk:

```{r}
data(mtcars)

plot(mtcars)
```




The code chunk above will appear in the final output. The code chunk below will be hidden:
~~~~

[1]https://stackoverflow.com/a/68690065/1298051

~~~
```{r, echo = FALSE}
data(iris)

plot(iris)
```



This next code chunk will not be evaluated:

```{r, eval = FALSE}
data(titanic)

str(titanic)
```



The last one runs, but code and output from the code is not shown in the final document.
This is useful for loading libraries and hiding startup messages:

```{r, include = FALSE}
library(dplyr)
```
~~~

If you use RStudio and create a new R Markdown file from the menu, a new R Markdown file is generated for you to fill out. The first R chunk is this one:

~~~
```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
```
~~~

This is an R chunk named `setup` and with the option `include = FALSE`. Naming chunks is optional, but we are going to make use of this later on. What this chunk runs is one line of code that defines a global option to show all chunks by default (which is the default behaviour). You can change `TRUE` to `FALSE` if you want to hide every code chunk instead (if you're using Quarto, global options are set differently).

Something else you might have noticed in the previous example, is that we've added some more content in the header:

```
---
title: "Document title"
output: html_document
date: "2023-01-28"
---
```

There are several other options available that you can define in the header. Later on, when we'll be building our project together, we will provide some more options (like having a table of contents).

The finish this part on code chunks, you should know about inline code chunks. Take a look at the following example:

~~~
---
title: "Document title"
output: html_document
date: "2023-01-28"
---

# R code chunks

```{r, echo = FALSE}
data(iris)
```




The iris dataset has `r nrow(iris)` rows.
~~~

The last sentence from this example has an inline code chunk. This quite useful, as it allows to parameterise sentences and paragraphs, and thus avoids needing to copy and paste (and we will go quite far into how to avoid copy and pasting, thanks to more advanced features we will shortly discuss).

To finish this crash course, you should know that to use footnotes you need to write the following:

```
This sentence has a footnote.[^1]

[^1]: This is the footnote.
```

and that you can write LaTeX formulas as well. For example, add the following into the the example from before and render either a PDF or a html document (don't put the LaTeX formula below inside a chunk, simply paste it as if it were normal text. This doesn't work for Word output because Word does not support LaTeX equations):

```
\begin{align*}
S(\omega)
&= \frac{\alpha g^2}{\omega^5} e^{[ -0.74\bigl\{\frac{\omega U_\omega 19.5}{g}\bigr\}^{\!-
&= \frac{\alpha g^2}{\omega^5} \exp\Bigl[ -0.74\Bigl\{\frac{\omega U_\omega 19.5}{g}\Bigr\
\end{align*}
```

6.3 Keeping it DRY

We're now coming to why this chapter is titled as it is.

Whatever you're doing, you should keep it DRY - DRY stands for *don't repeat yourself*. Repeating yourself by, say, copy and pasting, leads to errors and makes reading and understanding your code more difficult. This can be avoided by using functions, as we discussed in the previous chapter, but what if you need to write a document that has the following structure:

- A title
- A section
- A table inside this section
- Another section
- Another table inside this section
- Yet another section
- Yet another table inside this section

Is there a way to automate the creation of such a document by taking advantage of the repeating structure? Of course there is. The question is not, *is it possible to do X?*, but *how to do X?*.

6.3.1 Generating R Markdown code from code

The example below is a fully working minimal example of this. Copy it inside a document titled something like `rmd_templating.Rmd` and render it. You will see that the output contains more sections than defined in the source. This is because we use templating at the end. Take some time to read the document, as the text inside explains what is going on:

```
---
title: "Templating"
output: html_document
date: "2023-01-27"
```

~~~
---

```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
```


## A function that creates tables

```{r}
create_table <- function(dataset, var){
  table(dataset[var]) |>
    knitr::kable()
}
```


The function above uses the `table()` function to create frequency tables,
and then this gets passed to the `knitr::kable()` function that produces a
good looking table for our rendered document:

```{r}
create_table(mtcars, "am")
```


Let' suppose that we want to generate a document that would look like this:

- first a section title, with the name of the variable of interest
- then the table

So it would look like this:

## Frequency table for variable: "am"

```{r}
create_table(mtcars, "am")
```
~~~

~~~
We don’t want to create these sections for every variable by hand.

Instead, we can define a function that returns the R markdown code required
to create this. This is this function:

```{r}
return_section <- function(dataset, var){
  a <- knitr::knit_expand(text = c("## Frequency table for variable: {{variable}}",
                                   create_table(dataset, var)),
                          variable = var)
  cat(a, sep = "\n")
}
~~~

This new function, `return_section()` uses `knitr::knit_expand()` to generate
R Markdown code. Words between `{{}}` get replaced by the provided `var` argument
to the function. So when we call `return_section("am")`, `{{variable}}` is replaced
by `"am"`. `"am"` then gets passed down to `create_table()` and the frequency
table gets generated. We can now generate all the section by simply applying
our function to a list of column names:

```{r, results = "asis"}
invisible(lapply(colnames(mtcars), return_section, dataset = mtcars))
```
```

The last function, named `return_section()` uses `knitr::knit_expdand()`, which is the one that does the heavy lifting. This function returns literal R Markdown code. It returns `## Frequency table for variable: {{variable}}` which creates a level 2 section title with the text *Frequency table for variable: xxx* where the `xxx` will get replaced by the variable passed to `return_section()`. So calling `return_section(mtcars, "am")` will print the following in your console:

```
## Frequency table for variable: am
|am | Freq|
|:--|----:|
|0  |   19|
|1  |   13|
```

We now simply need to find a clever way to apply this function to each variable in the `mtcars`
```

dataset. For this, we are going to use `lapply()` which implements a for loop (you could use `purrr::map()` just as well for this):

```
invisible(lapply(colnames(mtcars),
                 return_section,
                 dataset = mtcars))
```

This will create, for each variable in `mtcars`, the same R Markdown code as above. Notice that the R Markdown chunk where the call to `lapply()` is has the option `results = "asis"`. This is because the function returns literal Markdown code, and we don't want the parser to have to parse it again. We tell the parser "don't worry about this bit of code, it's already good". As you see, the call to `lapply()` is wrapped inside `invisible()`. This is because `return_section()` does not return anything, it just prints something to the console. No object is returned. So if you don't wrap the call to `lapply()` inside `invisible()`, then a bunch of `NULL`s will also get printed. To avoid this, use `invisible()` (and use `purrr::walk()` rather than `purrr::map()`).

Click here to see the output.

This is not an easy topic, so take the time to play around with the example above. Try to print a plot instead of a table, try to generate more complex Markdown code, remove the call to `invisible()` and knit the document and see what happens with the output, replace the call to `lapply()` with `purrr::walk()` or `purrr::map()`. Really take the time to understand what is going on.

While extremely powerful, this approach using `knitr::knit_expand()` only works if your template only contains text. If you need to print something more complicated in the document, you need to use child documents instead. For example, suppose that instead of a table we wanted to show a plot made using `{ggplot2}`. This would not work, because a ggplot object is not made of text, but is a list with many elements. The `print()` method for ggplot object then does the fancy printing into a graph. But if you want to show plots using `knitr::knit_expand()`, then the contents of the list will be shown, not the plot itself. This is where child documents come in. Child documents are exactly what you think they are: they're smaller documents that get knitted and then embedded into the parent document. You can define anything within these child documents, and as such you can even use them to print more complex objects, like a ggplot object. Let's go back to the example from before and make use of a child document (for ease of presentation, we will not use a separate Rmd file, but will inline the child document into the main document). Read the Rmd example below carefully, as all the steps are explained:

```
---
title: "Templating with child documents"
output: html_document
date: "2023-01-27"
```

~~~
---

```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
library(ggplot2)
```

## A function that creates ggplots

```{r}
create_plot <- function(dataset, aesthetic){

  ggplot(dataset) +
    geom_point(aesthetic)

}
```

The function above takes a dataset and an aesthetic made using `ggplot2::aes()` to
create a plot:

```{r}
create_plot(mtcars, aes(y = mpg, x = hp))
```

Let's suppose that we want to generate a document that would look like this:

- first a section title, with the dataset used;
- then a plot

So it would look like this:

## Dataset used: "mtcars"

```{r}
create_plot(mtcars, aes(y = mpg, x = hp))
```

We don't want to create these sections for every aesthetic by hand.

Instead, we can make use of a child document that gets knitted separately
and then embedded in the parent document. The chunk below makes use of this trick:
~~~

~~~
```{r, results = "asis"}

x <- list(aes(y = mpg, x = hp),
          aes(y = mpg, x = hp, size = am))

res <- lapply(x,
              function(dataset, x){

  knitr::knit_child(text = c(

    '\n',
    '## Dataset used: `r deparse(substitute(dataset))`',
    '\n',
    '```{r, echo = F}',
    'print(create_plot(dataset, x))',
    '```'

     ),
     envir = environment(),
     quiet = TRUE)

}, dataset = mtcars)


cat(unlist(res), sep = "\n")
```

The child document is the `text` argument to the `knit_child()` function.
`text` is literal R Markdown code: we define a level 2 header, and then
an R chunk. This child document gets knitted, so we need to specify the
environment in which it should get knitted. This means that the child
document will get knitted in the same environment as the parent document
(our current global environment). This way, every package that get loaded
and every function or variable that got defined in the parent document
will also be available to the child document.

To get the dataset name as a string, we use the
`deparse(substitute(dataset))` trick; this substitutes "dataset" by its
bound value, so `mtcars`. But `mtcars` is an expression and we don’t
want it to get evaluated, or the contents of the entire dataset would
be used in the title of the section. So we use `deparse()` which turns
~~~

```
unevaluated expressions into strings.

We then use `lapply()` to loop over two aesthetics with an anonymous function
that encapsulates the child document. So we get two child documents that get
knitted, one per aesthetic. This gets saved into variable `res`. This is thus
a list of knitted Markdown.

Finally, we need unlist `res` to actually merge the Markdown code from the
child documents into the parent document.
```

Click here to take a look at the output.

Here again, take some time to play with the above example. Change the child document, try to print other types of output, really take your time to understand this. To know more about child documents, take a look at this section of the R Markdown Cookbook (Xie, Dervieux, and Riederer (2020)).

6.3.2 Tables in R Markdown documents

Getting tables right in Rmd documents is not always an easy task. There are several packages specifically made just for this task.

In this short section, we want to point you towards two packages that check the following boxes:

- Work the same way regardless of output format we want to knit our document into:
- Work for any type of table: summary tables, regression tables, two-way tables, etc.

Let's start with the simplest type of table, which would be showing the head of a dataset for example. `{knitr}` comes with the `kable()` function, but this function generates a very plain looking output. For something publication-worthy, we recommend the `{flextable}` package, developed by Gohel and Skintzos (2023):

```
library(flextable)

my_table <- head(mtcars)

flextable(my_table) |>
  set_caption(caption = "Head of the mtcars dataset") |>
  theme_booktabs()
```

mpg	cyl	disp	hp	drat	wt	qsec	vs	am	ge
21.0	6	160	110	3.90	2.620	16.46	0	1	
21.0	6	160	110	3.90	2.875	17.02	0	1	
22.8	4	108	93	3.85	2.320	18.61	1	1	
21.4	6	258	110	3.08	3.215	19.44	1	0	
18.7	8	360	175	3.15	3.440	17.02	0	0	
18.1	6	225	105	2.76	3.460	20.22	1	0	

We won't go into much detail on how `{flextable}` works, but it is very powerful, and the fact that it works for PDF, Html, Word and Powerpoint outputs is really a massive plus. If you want to learn more about `{flextable}`, there's a whole, free, ebook on it. `{flextable}` can create very complicated tables, so really take the time to dig in!

The next package is `{modelsummary}`, by Arel-Bundock (2022), and this one focuses on regression and summary tables. It is extremely powerful as well, and just like `{flextable}`, works for any type of output. It is very simple to get started:

```r
library(modelsummary)

model_1 <- lm(mpg ~ hp + am, data = mtcars)
model_2 <- lm(mpg ~ hp, data = mtcars)

models <- list("Model 1" = model_1,
               "Model 2" = model_2)

modelsummary(models)
```

Here again, we won't got into much detail, but recommend instead that you read the package's website which has very detailed documentation.

These packages can help you keeping it DRY, so take some time to learn them.

6.3.3 Parametrized reports

Templating and child documents are very powerful, but sometimes you don't want to have one section dedicated to each unit of analysis within the same report, but rather, you want a complete separate report by unit of analysis. This is also possible thanks to parameterised reports.

	Model 1	Model 2
(Intercept)	26.585	30.099
	(1.425)	(1.634)
hp	−0.059	−0.068
	(0.008)	(0.010)
am	5.277	
	(1.080)	
Num.Obs.	32	32
R2	0.782	0.602
R2 Adj.	0.767	0.589
AIC	164.0	181.2
BIC	169.9	185.6
Log.Lik.	−78.003	−87.619
RMSE	2.77	3.74

Let's modify the example from before, which consisted in creating one section per column of the `mtcars` dataset and a frequency table, and make it now one separate report for each column. The R Markdown file will look like this:

~~~
---
title: "Report for column `r params$var` of dataset `r params$dataset`"
output: html_document
date: "2023-01-27"
params:
  dataset: mtcars
  var: "am"
---

```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
```




## Frequency table for `r params$var`

```{r, echo = F}
create_table <- function(dataset, var){

  dataset <- get(dataset)
~~~

~~~
  table(dataset[var]) |>
    knitr::kable()
}
```



The table below is for variable `r params$var` of dataset `r params$dataset`.

```{r}
create_table(params$dataset, params$var)
```

```{r, eval = FALSE, echo = FALSE}
# Run these lines to compile the document
# Set eval and echo to FALSE, so that this does not appear
# in the output, and does not get evaluated when knitting
rmarkdown::render(
             input = "param_report_example.Rmd",
             params = list(
               dataset = "mtcars",
               var = "cyl"
             )
           )

```
~~~

Save the code above into an Rmd file title something like `param_report_example.Rmd` (preferably inside its own folder). At the end of the document, we wrote the lines to render this document inside a chunk that does not get shown to the reader, nor gets evaluated:

~~~
```{r, eval = F, echo = FALSE}
rmarkdown::render(
             input = "param_report_example.Rmd",
             params = list(
               dataset = "mtcars",
               var = "cyl"
             )
           )
```
~~~

You need to run these lines yourself to knit the document.

This will pass the list `params` with elements "mtcars" and "cyl" down to the report. Every `params$dataset` and `params$var` in the report gets replaced by "mtcars" and "cyl" respectively. Also, notice that in the header of the document, we defined default values for the params. Something else you need to be aware of, is that the function `create_table()` inside the report is slightly different than before. It now starts with the following line:

```
dataset <- get(dataset)
```

Let's break this down. `params$dataset` contains the string "mtcars". I made the decision to pass the dataset as a string, so that I could use it in the title of the document. But then, inside the `create_table()` function, I have the following code:

```
dataset[var]
```

`dataset` can't be a string here, but needs to be a variable name, so `mtcars` and not "mtcars". This means that I need to *convert* that string into a name. `get()` searches an object by name, and then makes it possible to save it to a new variable called `dataset`. The rest of the function is then the same as before. This little difficulty can be avoided by hard-coding the dataset inside the R Markdown file, or by passing the dataset as the `params$dataset` and not the string, in the render function. However, if you pass down the name of the dataset as a variable instead of the dataset name as a string, then you need to covert it to a string if you want to use it in the text (so `mtcars` to "mtcars", using `deparse(substitute(dataset))` as in child documents example).

If you instead want to create one report per variable, you could compile all the documents at once with:

~~~
```{r, eval = F, echo = F}
columns <- colnames(mtcars)

lapply(columns,
  (\(x)rmarkdown::render(
                    input = "param_report_example.Rmd",
                    output_file = paste0("param_report_example_", x, ".html"),
                    params = list(
                      dataset = "mtcars",
                      var = x
                    )
                  )
  )
)
```
~~~

By now, this should not intimidate you anymore; we use `lapply()` to loop over a list of column names (that we get using `colnames()`). Because we don't want to overwrite the report we need to change the name of the output file. We do so by using `paste0()` which creates a new string that contains the variable name, so each report gets its own name. `x` inside the `paste0()` function is each element, one after the other, of the `columns` variable we defined first. Think of it as the `i` in a for loop. We then must also pass this to the `params` list, hence the `var = x`. The complete call to `rmarkdown::render()` is wrapped inside an anonymous function, because we need to use the argument `x` (which is each column defined in the columns list) in different places.

Before continuing, we highly recommend that you try running this yourself, and also that you try to build your own little parameterised reports. Maybe start by replacing "mtcars" by "iris" in the code to compile the reports and see what happens, and then when you're comfortable with parameterised reports, try templating inside a parameterised report!

It is important to not fall to the temptation of copy and pasting sections of your report, or parts of your script, instead of using these more advanced features provided by the language. It is tempting, especially under time pressure, to just copy and paste bits of code and get things done instead of writing what seems to be unnecessary code to finally achieve the same thing. The problem however, is that in practice copy and pasting code to simply get things done will come bite you sooner rather than later. Especially when you're still in the exploration/drafting phase of the project. It make take more time to set up, but once you're done, it is much easier to experiment with different parameters, test the code or even re-use the code for other projects. Not only that, but forcing you to actually think about how to set up your code in a way that avoids repeating yourself also helps with truly understanding the problem at hand. What part of the problem is constant and does not change? What does change? How often, and why? Can you also fix these parts or not? What if instead of five sections that I need to copy and paste, I had 50 sections? How could I scale that up?

Asking yourself these questions, and solving them, will ultimately make you better programmer.

Remember: keep it DRY.

Part II

Part 2

7 Packaging your code

In this chapter you're going to learn how to create your own package.

We should make clear that this does not mean publishing the package on CRAN.

7.1 Benefits of packages

7.2 Intro to packge dev

This is where fusen comes into play I guess; so we start from the Qmd file that was written before, containing the functions an the analysis, and see how we can now create a package from it, and use that file as a vignette? Copying here what Sébastien said on the matter

7.3 Document your package (?)

I guess fusen makes this process easy and leverages roxygen?

7.4 Managing package dependencies (?)

Discuss NAMESPACE and DESCRIPTION and all that. I think it's important to also discuss here how to define dependencies from remotes, not just CRAN.

7.5 Unit testing

This is where I think we should discuss unit testing

7.6 pkgdown

8 Build automation

Why build automation: removes cognitive load, is a form of documentation in and of itself, as Miles said

It is possible to communicate a great deal of domain knowledge in code, such that it is illuminating beyond the mere mechanical number crunching. To do this well the author needs to make use of certain styles and structures that produce code that has layers of domain specific abstraction a reader can traverse up and down as they build their understanding of the project. Functional programming style, coupled with a dependency graph as per {targets} are useful tools in this regard.

9 Introduction to reproducibility

Since we said in the intro to the book that reproducibility is on a continuum, I think that this chapter should focus on the bare minimum, which would culminate with renv

Then at the end, explain why renv is not enough (does nothing for R itself, nor the environment the code is running on)

10 Advanced topics in reproducibility

Now that the readers are familiar with renv, but also its shortcomings, we can go a step further and introduce Docker. I think some primer on the Linux command line could be included here

10.1 First steps with Docker

To write your own Dockerfile, you need some familiarity with the Linux cli, so here's...

10.2 A primer on the Linux command line

10.3 Dockrizing your project

11 Continuous integration and continuous deployment/delivery

References

Arel-Bundock, Vincent. 2022. "modelsummary: Data and Model Summaries in R." *Journal of Statistical Software* 103 (1): 1–23. https://doi.org/10.18637/jss.v103.i01.

Chambers, John M. 2014. "Object-Oriented Programming, Functional Programming and R." *Statistical Science* 29 (2): 167–80. https://doi.org/10.1214/13-STS452.

Gohel, David, and Panagiotis Skintzos. 2023. *Flextable: Functions for Tabular Reporting*.

Leisch, Friedrich. 2002. "Sweave: Dynamic Generation of Statistical Reports Using Literate Data Analysis." In *Compstat*, edited by Wolfgang Härdle and Bernd Rönz, 575–80. Physica-Verlag HD.

Wickham, Hadley. 2019. *Advanced r*. CRC press.

Xie, Yihui. 2014. "Knitr: A Comprehensive Tool for Reproducible Research in R." In *Implementing Reproducible Computational Research*, edited by Victoria Stodden, Friedrich Leisch, and Roger D. Peng. Chapman; Hall/CRC. http://www.crcpress.com/product/isbn/9781466561595.

Xie, Yihui, Christophe Dervieux, and Emily Riederer. 2020. *R Markdown Cookbook*. Chapman; Hall/CRC.