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An Introduction to Statistical Programming Methods with R

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Introduction

This book is an early version of an ongoing project to equip students with the basic knowledge to master "statistical programming" with R.

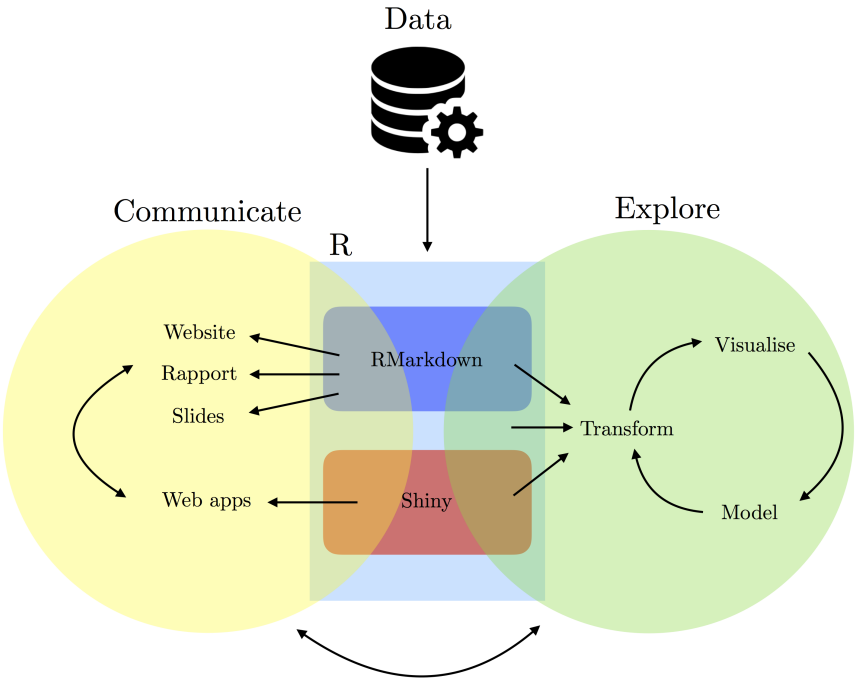
The statistical software `R` has come into prominence due to its flexibility as an efficient language that builds a bridge between software development and data analysis. For example, one strength of `R` is the facility to develop and quickly adapt to the different needs coming from the data management and analysis community while at the same time making use of other languages in order to deliver computationally efficient solutions. This book intends to present an approachable framework to statistical programming and software development using the wide variety of tools made available through `R`, from method-specific packages to version control programs. The general goals of the book are therefore the following:

- introduce tools and workflow for reproducible research (R/RStudio, Git/GitHub, etc.);
- introduce principles of tidy data and tools for data wrangling;
- exploit data structures to appropriately manage data, computer memory and computations;
- data manipulation through controls, instructions, and tailored functions;
- develop new software tools including functions, Shiny applications, and packages;
- manage software development process including version control, documentation (with embedded code), and dissemination for other users.

The rest of this introductory chapter will present the R software by explaining why it is used for this book and describing the basic

notations and tools that need to be known in order to better grasp its contents.

This document is **under development** and it is therefore preferable to always access the text online to be sure you are using the most up-to-date version. Due to its current development, you may encounter errors ranging from broken code to typos or poorly explained topics. If you do, please let us know! Simply add an issue to the GitHub repository used for this document (accessed here https://github.com/SMAC-Group/ds/issues) and we will make the changes as soon as possible. In addition, once you have learned RMarkdown and GitHub, feel free to make a pull request to offer bug fixes or corrections!



To demonstrate our goals, we will try to implement the process that is mentioned in the diagram above. In many cases, an input (e.g. data source) is provided, and then we process, explore, and/or manipulate the data with R. We then may communicate our findings

through websites, reports, slides, etc. using some combination of RMarkdown, R, and/or Shiny. This process is not always sequential as we often have new ideas or observations at any stage and begin exploring again.

0.1 R and RStudio

The statistical computing language R[1] has become commonplace for many applications in industry, government, and academia. Having started as an open-source language to make available different statistics and analytical tools to researchers and the public, it steadily developed into one of the major software languages which not only allows to develop up-to-date, sound, and flexible analytical tools, but also to include these tools within a framework which is well-integrated with other important tools. The latter is amplified thanks to the development of the RStudio[2] interface which provides a pleasant and functional user-interface for R as well as an efficient Integrated Development Environment (IDE) in which different programming languages, web-applications and other important tools are readily available to the user. In order to illustrate the relationship between R & RStudio in statistical programming, one might think of a car analogy in which R would be the drivetrain and chassis while RStudio adds comfortable seats and air conditioning. R is doing most of the work, and the user can basically get where they want to go using R without RStudio. RStudio is generally is making you more comfortable while you use R, but you won't get very far using RStudio without R.

[1] https://cran.r-project.org/
[2] https://www.rstudio.com/

0.1.1 Getting started with R

Since R is a free and open-source software, you may simply download it from the following link:

- R: https://cran.r-project.org/[3]

While R certainly can be used "as is" for many purposes, we strongly recommend using an IDE called RStudio. There are several versions of RStudio for different users (RStudio Desktop, Commercial, Server, etc.). The free RStudio Desktop version is sufficient for our purposes. RStudio can downloaded from the following link:

- RStudio: https://www.rstudio.com/[4]

You cannot use RStudio without having installed R on your computer.

0.1.2 Why R?

There are many reasons to use R. Two compelling reasons are that R is both free as in "free pizza", and free as in "free speech". Free–like "free pizza"–means that there is never a need to pay for any part of the R software, or contributed packages (i.e. add-on modules). Free–like "free speech"–means that there are very few restrictions on how R can be used or barriers to those who would like to contribute packages (i.e. add-on modules).

The fact that is a free and open-source software does not necessarily imply that it is a good software (although it is also that). The reason why this is an important feature consists in the fact that the results of any code or program developed in the R environment can easily be replicated therefore ensuring accessibility and transparency for the general user. More importantly however, this replicability of results is also accompanied by a wide variety of packages that are

[3] https://cran.r-project.org/
[4] https://www.rstudio.com/

made available through the R environment in which users can find a diversity of codes, functions, and features that are designed to tackle a large amount of programming and analytical tasks. Moreover, new packages are relatively simple to create and are extremely useful for code-sharing purposes since they enclose the codes, functions, and external dependencies that allow anyone to easily and efficiently install these features. Additionally, these accessibility and code-sharing features have established R as a platform for development and dissemination of cutting-edge tools directly from the developer to the end-user.

0.1.3 About RStudio

RStudio is a customizable IDE for the R enviornment where the user can have easy access to plots, data, help, files, objects and many other features that are useful to work efficiently with R. For the most part, RStudio provides nearly everything the R user will need in a self-contained, and well-organized environment. Moreover, it is possible to create "projects" in which it is possible to create a dedicated environment space for sets of specific functions and files aimed to deal with various tasks.

Below is short video demonstrating a basic introduction of RStudio and some of its elements.

In addition, RStudio provides embedded functionality to utilize collaborative version-control software including GitHub & Subversion as well as a set of powerful tools to save and communicate results (whether they be simulations, data analysis, or presenting and making available a new package to other users). Some examples of these tools are Rmarkdown which can be used respectively to integrate written narrative with embedded R code and other content, as well as and Shiny Web Apps which can provide an interactive user-friendly interface that permits a user to actively engage with a wide variety of tools built in R without the need to encounter raw R code. GitHub and Rmarkdown will be the object of a more in-depth description in the first chapters of this book in order to

provide the reader with the version-control and annotation tools that can be useful for the following chapters of this book.

0.1.4 Conventions

Throughout this book, `R` code will be typeset using a `monospace` font which is syntax highlighted. For example:

```
a <- pi
b <- 0.5
sin(a*b)
```

Similarly, `R` output lines (that usally appear in your Console) will begin with `##` and will not be syntax highlighted. The output of the above example is the following:

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

Aside from `R` code and output, this book will also insert boxes in order to draw the reader's attention to important, curious, or otherwise informative details. An example of these boxes was seen at the beginning of this introduction where an important aspect was pointed out to the reader regarding the "under construction" nature of this book. Therefore the following boxes and symbols can be used to represent information of different nature:

This is a **note** that could be interesting or useful to the reader.

This is a **tip** for implementing content from this book.

This highlights **important information**.

This is a **caution** to help the reader avoid minor problems.

This is a **warning** to help the reader avoid significant problems.

0.1.5 Getting help

In the previous section we presented some examples on how R can be used as a calculator and we have already seen several functions such as `sqrt()` or `log()`. To obtain documentation about a function in R, simply put a question mark in front of the function name (or just type `help()` around the function name), or use the search bar on the "Help" tab in your RStudio window, and its documentation will be displayed. For example, if you are interested in learning about the function `log()` you could simply type:

```
?log
```

which will display something similar to:

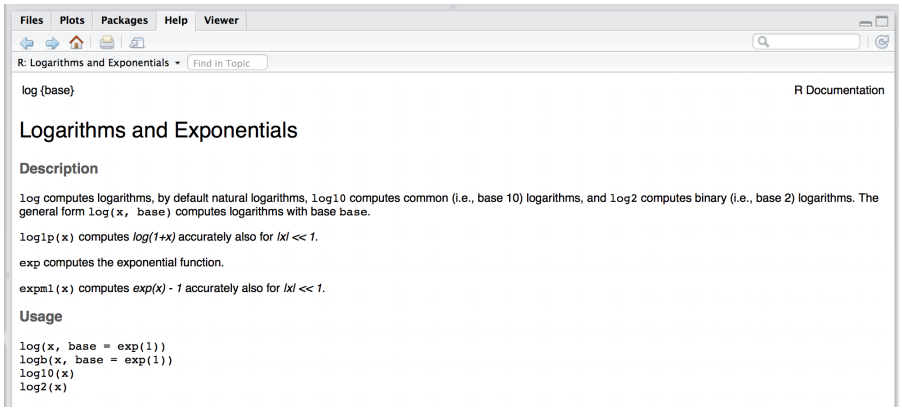


FIGURE 1

The R documentation is written by the author of the package. For mainstream packages in widespread use, the documentation is almost always quite good, but in some cases it can be quite technical, difficult to interpret, and possibly incomplete. In these cases, the best solution to understand a function is to search for

help on any search engine. Often a simple search like "side by side boxplots in R" or "side by side boxplots in ggplot2" will produce many useful results. The search results often include user forums such as "CrossValidated" or "StackExchange" in which the questions you have about a function have probably already been asked and answered by many other users.

You can often use the error message to search for answers about a problem you may have with a function.

0.1.6 Installing packages

`R` comes with a number of built-in functions but one of its main strengths is that there is a large number of packages on an ever-increasing range of subjects available for you to install. These packages provide additional functions, features and data to the R environement. If you want to do something in `R` that is not available by default, there is a good chance that there are packages that will respond to your needs. In this case, an appropriate way to find a package in `R` is to use the search option in the CRAN repository which is the official network of file-transfer protocols and web-servers that store updated versions of code and documentation for `R` (see CRAN website). Another general approach to find a package in `R` is simply to use a search engine in which to type the keywords of the tools you are looking for followed by "R package".

`R` packages can be installed in various ways but the most widely used approach is through the `install.packages()` function. Another way is to use the "Tools -> Install Packages. . . " path from the dropdown menus in `RStudio` or clicking on the "install" button in the "Packages" pane in the RStudio environment. The `install.packages()` function is very straight-forward and transcends any platform for the `R` environment. It is noteworthy that this approach assumes that the desired package(s) are available within the CRAN repository. This is very often the case, but there is a growing number of packages that are under-development or

completed and are made available through other repositories. In the latter setting, Chapter 02 will show other ways of installing packages from a commonly used repository called "GitHub".

Sticking momentarily to the packages available in the CRAN repository, the use of the `install.packages()` is quite simple. For example, if you want to install the package `devtools` you can simply write:

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

Once a package is installed it is not directly usable within your `R` session. To do so you will have to "load" the package into your current `R` session which is generally done through the function `library()`. For example, after having installed the `devtools` package, in order to use it within your session you would write:

```
library(devtools)
```

Once this is done, all the functions and documentation of this package are available and can be used within your current session. However, once you close your `R` session, all loaded packages will be closed and you will have to load them again if you want to use them in a new `R` session.

Please notice that although packages need to be loaded at each session if you want to use them, they need to be installed only once. The only exception to this rule is when you need to update the package or reinstall it for some reason.

One of the main packages that is required for this class would be our STAT 297 package, that contains all the necessary packages and functions that will be utilized in this book. Run the following code to install the package directly from GitHub.

```
install_github("SMAC-Group/stat297")
```

The STAT 297 package is required for use of many features in this book.

0.1.7 Additional References

There are many more elements in RStudio, and we encourage you to use the RStudio Cheatsheet[5] as a reference.

0.2 Basic Probability and Statistics with R

The R environment provides an up-to-date and efficient programming language to develop different tools and applications. Nevertheless, its main functionality lies in the core statistical framework and tools that consistute the basis of this language. Indeed, this book aims at introducing and describing the methods and approaches of statistical programming which therefore require a basic knowledge of Probability and Statistics in order to grasp the logic and usefulness of the features presented in this book.

For this reason, we will briefly take the reader through some of the basic functions that are available within R to obtain probabilities based on parametric distributions, compute summary statistics and understand basic data structures. The latter is just an introduction and a more in-depth description of different data structures will be given in a future chapter.

[5] https://www.rstudio.com/wp-content/uploads/2016/01/rstudio-IDE-cheatsheet.pdf

0.2.1 Simple calculations

Since the R environment can serve as an advanced calculator, it is worth noting this also allows for simple calculations. In the table below we show a few examples of such calculations where the first column gives a mathematical expression (calculation), the second gives the equivalent of this expression in R and finally in the third column we can find the result that is output from R.

Math.	R	Result
$2+2$	`2+2`	`4`
$\frac{4}{2}$	`4/2`	`2`
$3 \cdot 2^{-0.8}$	`3*2^(-0.8)`	`1.723048`
$\sqrt{2}$	`sqrt(2)`	`1.414214`
π	`pi`	`3.141593`
$\ln(2)$	`log(2)`	`0.6931472`
$\log_3(9)$	`log(9, base = 3)`	`2`
$e^{1.1}$	`exp(1.1)`	`3.004166`
$\cos(\sqrt{0.9})$	`cos(sqrt(0.9))`	`0.5827536`

0.2.2 Probability Distributions

Probability distributions can be uniquely characterized by different functions such as, for example, their density or distribution functions. Based on these it is possible to compute theoretical quantiles and also randomly sample observations from them. Replacing the R syntax for a given probability distribution with the general syntax `name`, all these functions and calculations are made available in R through the built-in functions:

- `dname` calculates the value of the density function (pdf);
- `pname` calculates the value of the distribution function (cdf);
- `qname` calculates the value of the theoretical quantile;
- `rname` generates a random sample from a particular distribution.

Note that, when using these functions in practice, `name` is replaced with the syntax used in R to denote a specific probability distribu-

tion. For example, if we wish to deal with a Uniform probability distribution, then the syntax `name` is replaced by `unif` and, furthering the example, to randomly generate observations from a uniform distribution the function to use will be therefore `runif`. `R` allows to make use of these functions for a wide variety of probability distributions that include, but are not limited to: Gaussian (or Normal), Binomial, Chi-square, Exponential, F-distribution, Geometric, Poisson, Student-t and Uniform. In order to get an idea of how these functions can be used, below is an example of a problem that can be solved using them.

0.2.2.1 Example: Normal Test Scores of College Entrance Exam

Assume that the test scores of a college entrance exam follows a Normal distribution. Furthermore, suppose that the mean test score is 70 and that the standard deviation is 15. How would we find the percentage of students scoring 90 or more in this exam?

In this case, we consider a random variable X that is normally distributed as follows: $X \sim N(\mu = 70, \sigma^2 = 225)$ where μ and σ^2 represent the mean and variance of the distribution respectively. Since we are looking for the probability of students scoring higher than 90, we are interested in finding $\mathbb{P}(X > x = 90)$ and therefore we look at the upper tail of the Normal distribution. To find this probability we need the distribution function (`pname`) for which we therefore replace `name` with the `R` syntax for the Normal distribution: `norm`. The distribution function in `R` has various parameters to be specified in order to compute a probability which, at least for the Normal distribution, can be found by typing `?pnorm` in the Console and are:

- `q`: the quantile we are interested in (e.g. 90);
- `mean`: the mean of the distribution (e.g. 70);
- `sd`: the standard deviation of the distribution (e.g. 15);
- `lower.tail`: a boolean determining whether to compute the probability of being smaller than the given quantile (i.e. $\mathbb{P}(X \leq x)$) which requires the default argument `TRUE` or larger (i.e. $\mathbb{P}(X > x)$) which requires to specify the argument `FALSE`.

Knowing these arguments, it is now possible to compute the probability we are interested in as follows:

```
pnorm(q = 90, mean = 70, sd = 15, lower.tail = FALSE)
```

```
## [1] 0.09121122
```

As we can see from the output, there is roughly a 9% probability of students scoring 90 or more on the exam.

0.2.3 Summary Statistics

While the previous functions deal with theoretical distributions, it is also necessary to deal with real data from which we would like to extract information. Supposing–as is often the case in applied statistics–we don't know from which distribution it is generated, we would be interested in understanding the behavior of the data in order to eventually identify a distribution and estimate its parameters.

The use of certain functions varies according to the nature of the inputs since these can be, for example, numerical or factors.

0.2.3.1 Numerical Input

A first step in analysing numerical inputs is given by computing summary statistics of the data which, in this section, we can generally denote as `x` (we will discuss the structure of this data more in detail in the following chapters). For central tendency or spread statistics of a numerical input, we can use the following `R` built-in functions:

- `mean` calculates the mean of an input `x`;
- `median` calculates the median of an input `x`;
- `var` calculates the variance of an input `x`;
- `sd` calculates the standard deviation of an input `x`;
- `IQR` calculates the interquartile range of an input `x`;
- `min` calculates the minimum value of an input `x`;

- `max` calculates the maximum value of an input `x`;
- `range` returns a vector containing the minimum and maximum of all given arguments;
- `summary` returns a vector containing a mixture of the above functions (i.e. mean, median, first and third quartile, minimum, maximum).

0.2.3.2 Factor Input

If the data of interest is a factor with different categories or levels, then different summaries are more appropriate. For example, for a factor input we can extract counts and percentages to summarize the variable by using `table`. Using functions and data structures that will be described in the following chapters, below we create an example dataset with 90 observations of three different colors: 20 being `Yellow`, 10 being `Green` and 50 being `Blue`. We then apply the `table` function to it:

```
table(as.factor(c(rep("Yellow", 20), rep("Green", 10), rep("Blue", 50))))
```

```
##
##   Blue  Green Yellow
##     50     10     20
```

By doing so we obtain a frequency (count) table of the colors.

0.2.3.3 Dataset Inputs

In many cases, when dealing with data we are actually dealing with datasets (see Chapter 03) where variables of different nature are aligned together (usually in columns). For datasets there is another convenient way to get simple summary statistics which consists in applying the function `summary` to the dataset itself (instead of simply a numerical input as seen earlier).

As an example, let us explore the Iris[6] flower dataset contained in

[6] https://en.wikipedia.org/wiki/Iris_flower_data_set

the R built-in `datasets` package. The data set consists of 50 samples from each of three species of Iris (Setosa, Virginica and Versicolor). Four features were measured from each sample consisting in the length and the width (in centimeters) of the both sepals and petals. This dataset is widely used as an example since it was used by Fisher to develop a linear discriminant model based on which he intended to distinguish the three species from each other using combinations of these four features.

Using this dataset, let us use the `summary` function on it to output the minimum, first quartile and thrid quartile, median, mean and maximum statistics (for the numerical variables in the dataset) and frequency counts (for factor inputs).

```
summary(iris)
```

```
##   Sepal.Length    Sepal.Width     Petal.Length    Petal.Width
##  Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100
##  1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300
##  Median :5.800   Median :3.000   Median :4.350   Median :1.300
##  Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199
##  3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800
##  Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500
##        Species
##  setosa    :50
##  versicolor:50
##  virginica :50
##
##
##
```

0.3 Main References

This is not the first (or the last) book that has been written explaining and describing statistical programming in `R`. Indeed, this can be seen as a book that brings together and reorganizes information and material from other sources structuring and tailoring it to a course in basic statistical programming. The main references (which are far from being an exhaustive review of literature) that can be used to have a more in-depth view of different aspects treated in this book are:

- **?** : a more technical and advanced introduction to `R`;
- **?** : basic building blocks of building packages in `R`;
- **?** : an overview of document generation in `R`;

0.4 License

Part I

Foundation

0

RMarkdown

RMarkdown is a framework that provides a literate programming format for data science. It can be used to save and execute R code within RStudio and also as a simple formatting syntax for authoring HTML, PDF, ODT, RTF, and MS Word documents as well as seamless transitions between available formats. The name "markdown" is an intentional contrast to other "markup" languages–e.g., hypertext markup language (HTML)–which require syntax that can be quite difficult to decipher for the uninitiated. One aim of the markdown paradigm is a syntax that is as human-readable as possible. "RMarkdown" is an implementation of the "markdown" language designed to accommodate embedded `R` code.

What is literate programming ?

Literate programming is the notion for programmers of adding narrative context with code to produce documentation for the program simultaneously. Consequently, it is possible to read through the code with explanations so that any viewer can follow through the presentation. RMarkdown offers a simple tool that allows to create reports or presentation slides in a reproducible manner with collateral advantages such as avoiding repetitive tasks by, for example, changing all figures when data are updated.

What is reproducible research ?

Reproducible research or reproducible analysis is the notion that an experiment's whole process, including collecting data, performing analysis and producing output, can be reproduced the same way

by someone else. Building non-reproducible experiments has been a problem both in research and in the industry, and having such an issue highly decreases the credibility of the authors' findings and, potentially, the authors themselves. In essence, allowing for reproducible research implies that anyone could run the code (knit the document, etc.) and obtain the same exact results as the original research and RMarkdown is commonly used to address this issue.

Below is a short video showing a basic overview of RMarkdown.

Below, we have created a framework application that you can use to test out different RMarkdown functions. Experiment with different R Markdown elements and utilize it to practice building and knitting HTML output.

You can access the online versions here:

- RMarkdown Web[7]
- RMarkdown Mobile[8]

or simply run it within the `stat297` package by using either

```
# RMarkdown Web
stat297::runShiny('rmd')

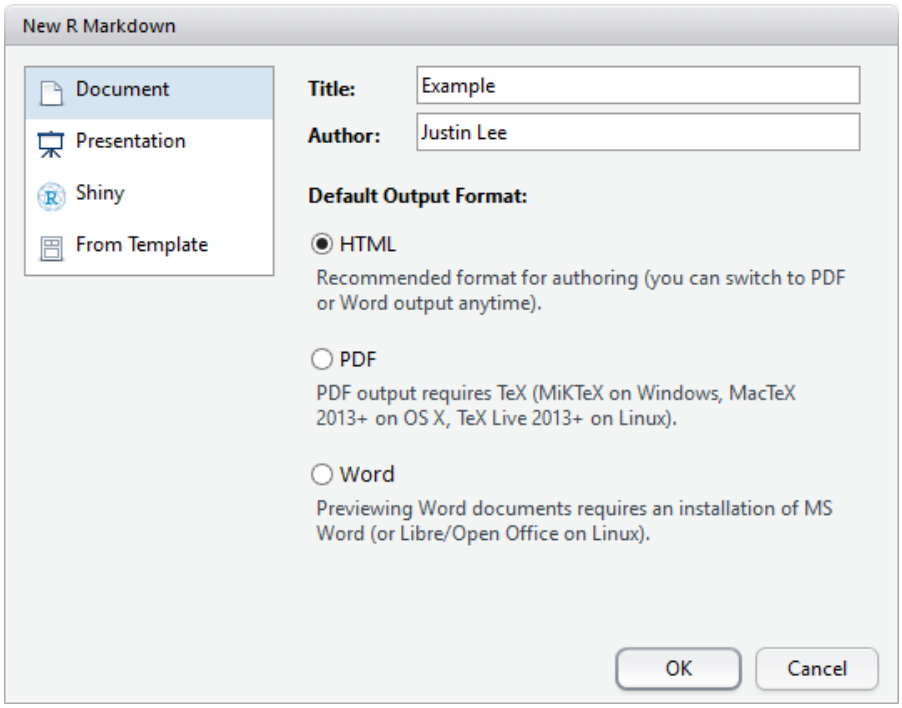
# RMarkdown Mobile
stat297::runShiny('rmd_mini')
```

0.5 Create an R Markdown file in RStudio

Within RStudio, click `File` → `New File` → `R Markdown`. Give the file a title and the author (your name) and select the default output,

[7] http://shiny.science.psu.edu/szg279/rmd/
[8] http://shiny.science.psu.edu/szg279/rmd_mini/

HTML. We can change this later so don't worry about it for the moment.



An RMarkdown is a plain text file that contains three different aspects:

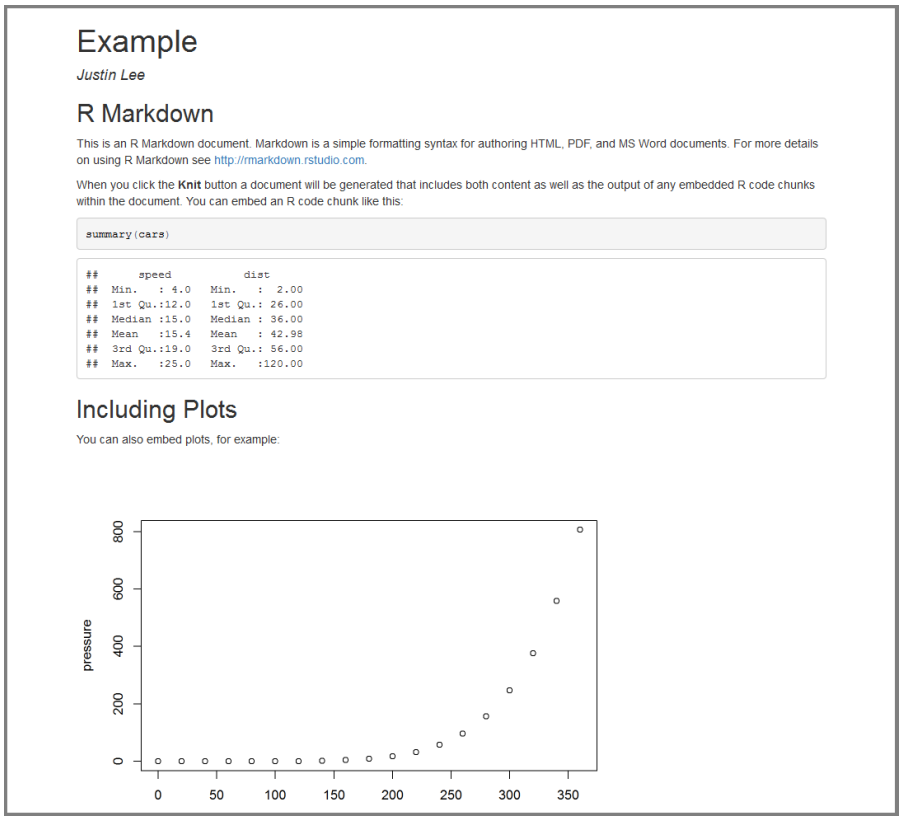
- YAML metadata
- Text
- Code Chunks

0.6 YAML Metadata

YAML stands for *YAML Ain't Markup Language* and is used to specify document configurations and properties such as name, date, output format, etc. The (optional) YAML header is surrounded before and after by "—" on a dedicated line.

You can also include additional formatting options[9] such as a table of contents or even a custom CSS style template which can be used to further enhance the presentation. For the purpose of this book, the default options should be sufficient. Below is an example knit output of the above RMarkdown file.

[9] http://RMarkdown.rstudio.com/html_document_format.html



The default output above is an html_document format but this format can be modified using, for example, `pdf_document` to output a pdf. However, the pdf format requires additional installation and configuration of a TeX distribution such as MikTeX[10]. Once available, the user can also include raw LaTeX and even define LaTeX macros in the RMarkdown document if necessary (we'll discuss more about LaTeX further on).

0.6.1 Subsections

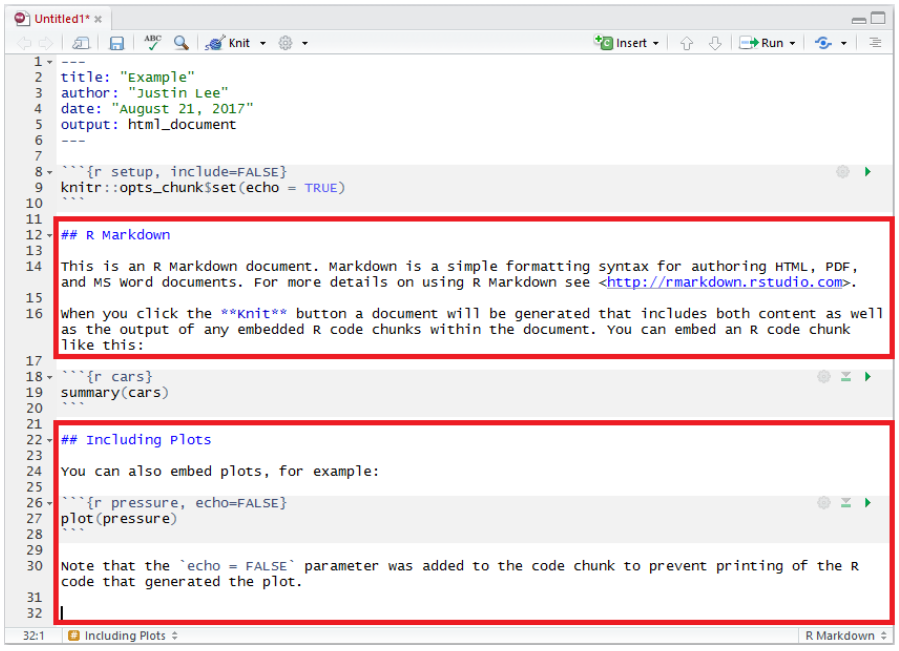
To make your sections numbered as sections and subsections, make sure you specify `number_sections: yes` as part of the YAML Metadata as shown below.

[10] https://miktex.org/2.9/setup

0.7 Text

Due to its literate nature, text will be an essential part in explaining your analysis. With RMarkdown, we can specify custom text formatting with emphases such as *italics*, **bold**, or `code style`. To understand how to format text, our previous sentence would be typed out as follows in RMarkdown:

```
With RMarkdown, we can specify custom text formatting with emphases such as *
```



0.7.1 Headers

As seen above, headers are preceded by a #. A single `#` produces the largest heading text while, to produce smaller headings, you simply need to add more `#`s! Heading level also impacts section and subsection nesting in documents and tables of contents, as well as slide breaks in presentation formats.

0.7.2 Lists

Lists can be extremely convenient to make text more readable or to take course notes during class. RMarkdown allows to create different list structures as shown in the code below:

```
* You can create bullet points by using symbols such as *, +, or -.
+ simply add an indent or four preceding spaces to indent a list.
    + You can manipulate the number of spaces or indents to your liking.
        - Like this.
    * Here we go back to the first indent.
1. To make the list ordered, use numbers.
1. We can use one again to continue our ordered list.
2. Or we can add the next consecutive number.
```

which delivers the following list structure:

- You can create bullet points by using symbols such as *, +, or -.
- simply add an indent or four preceding spaces to indent a list.
  - You can manipulate the number of spaces or indents to your liking.
    - Like this.
  - Here we go back to the first indent.

1. To make the list ordered, use numbers.
2. We can use one again to continue our ordered list.
3. Or we can add the next consecutive number.

0.7.3 Hyperlinks

To add hyperlinks with the full link, (ex: https://google.com/) you can follow the syntax below:

```
<https://google.com/>
```

whereas to add hyperlinks with a custom link title, (ex: Google[11]) follow the syntax below:

```
[Google](https://google.com)
```

0.7.4 Blockquotes

Use the > character in front of a line, *just like in email* to produce blockquotes which styles the text in a way to use if we quote a person, a song or another entity.

> "To grow taller, you should shave your head. Remember to bring the towels!"
>
> Justin Lee

0.7.5 Pictures

To add a picture with captions, follow the syntax below:

```
![Eberly College of Science Banner](http://science.psu.edu/psu_eberly_blue.pr
```

which will produce:

[11] https://google.com

Otherwise, to add a picture without any captions, follow the syntax below:

```
![](http://www.alumni.psu.edu/s/1218/16/images/logo.png)
```

which delivers:

0.7.6 LaTeX

LaTeX is a document preparation system that uses plain text as opposed to formatted text that is used for applications such as Microsoft Word. It is widely used in academia as a standard for the publication of scientific documents. It has control over large documents containing sectioning, cross-references, tables and figures.

0.7.6.1 LaTeX in RMarkdown

Unlike a highly formatted word processor, we cannot produce equations by clicking on symbols. As data scientists there is often the need to explain distributions and equations that are behind the methods we present. Within the text section of an RMarkdown document you can include LaTeX format text to output different forms of text, mainly equations and mathematical expressions.

Inline mathematical expressions can be added using the syntax: `$math expression$`. For example, if we want to write "where α is in degrees" we would write:

```
"where $\alpha$ is in degrees".
```

Using a slightly different syntax (i.e. `$$math expression$$`) we can obtain centered mathematical expressions. For example, the binomial probability distribution in LaTeX is written as

```
$$f(y|N,p) = \frac{N!}{y!(N-y)!}\cdot p^y \cdot
(1-p)^{N-y} = {{N}\choose{y}} \cdot p^y \cdot
(1-p)^{N-y}$$
```

which is output as:

$$f(y|N,p) = \frac{N!}{y!(N-y)!} \cdot p^y \cdot (1-p)^{N-y} = \binom{N}{y} \cdot p^y \cdot (1-p)^{N-y}$$

An introduction to the LaTeX format can be found here[12] if you want to learn more about the basics. An alternative can be to insert custom LaTeX formulas using a graphical interface such as codecogs[13].

0.7.7 Cross-referencing Sections

You can also use the same syntax `\@ref(label)` to reference sections, where label is the section identifier (ID). By default, Pandoc will generate IDs for all section headers, e.g., `# Hello World` will have an ID `hello-world`. To call header `hello-world` as a header, we type `\@ref(hello-world)` to cross-reference the section. In order to avoid forgetting to update the reference label after you change the section header, you may also manually assign an ID to a section header by appending {#id} to it.

0.7.8 Citations and Bibliography

Citations and bibliographies can automatically be generated with RMarkdown. In order to use this feature we first need to create

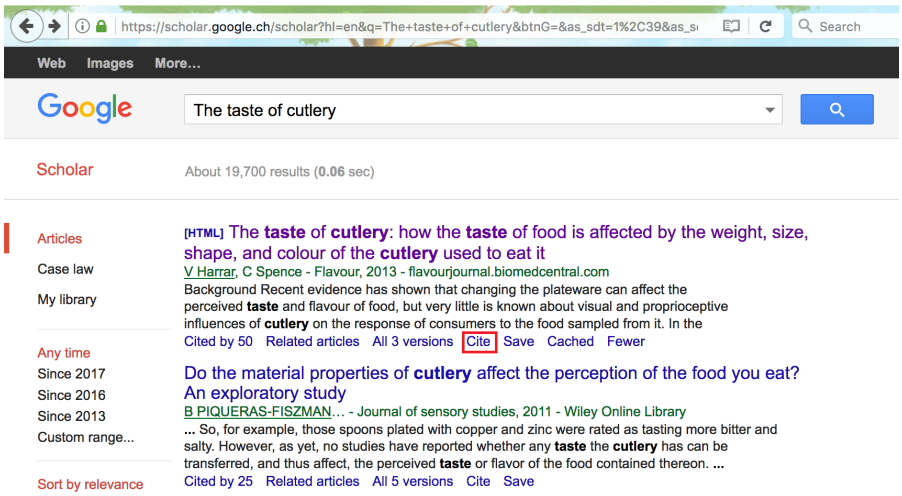
[12] http://www.math.harvard.edu/texman/
[13] https://www.codecogs.com/latex/eqneditor.php

a "BibTex" database which is a simple plain text file (with the extension ".bib") where each reference you would like to cite is entered in a specific manner.

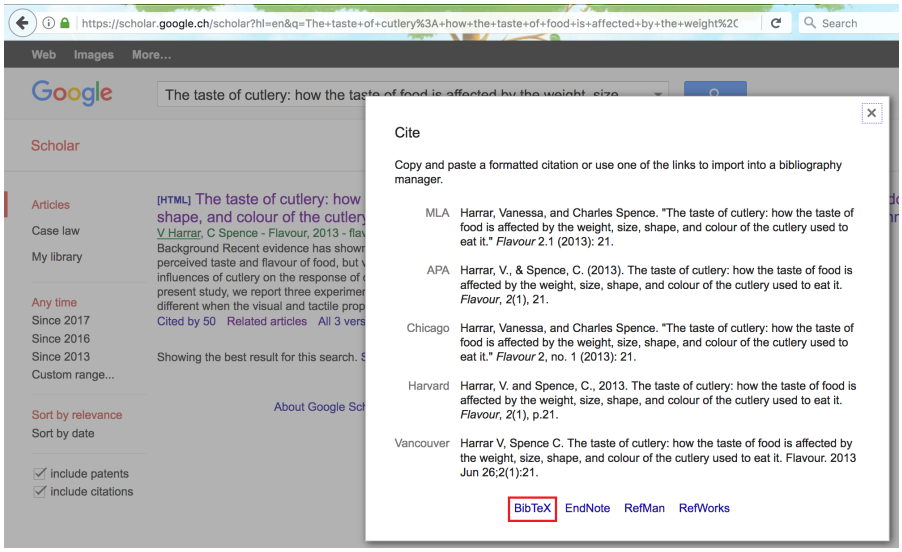
To illustrate how this is done, let us take the example of a recent paper where two researchers from Oxford University investigated the connection between the taste of food and various features of cutlery such as weight and color (calling this phenomenon the "taste of cutlery"). The BibTeX "entry" for this paper is given below:

```
@article{harrar2013taste,
  title={The taste of cutlery: how the taste of food is affected by the weigh
   shape, and colour of the cutlery used to eat it},
  author={Harrar, Vanessa and Spence, Charles},
  journal={Flavour},
  volume={2},
  number={1},
  pages={21},
  year={2013},
  publisher={BioMed Central}
}
```

This may look like a complicated format to save a reference but there is an easy way to obtain this format without having to manually fill in the different slots. To do so, go online and search for "Google Scholar" which is a search engine specifically dedicated to academic or other types of publications. In the latter search engine you can insert keywords or the title and/or authors of the publication you are interested in and find it in the list of results. In our example we search for "The taste of cutlery" and the publication we are interested in is the first in the results list.

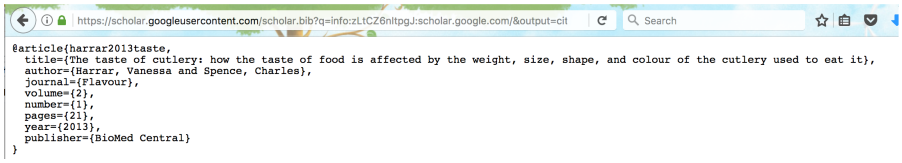


Below every publication in the list there is a set of options among which the one we are interested in is the "Cite" option that should open a window in which a series of reference options are available. Aside from different reference formats that can be copied and pasted into your document, at the bottom of the window you can find another set of options (with related links) that refer to different bibliography managers.

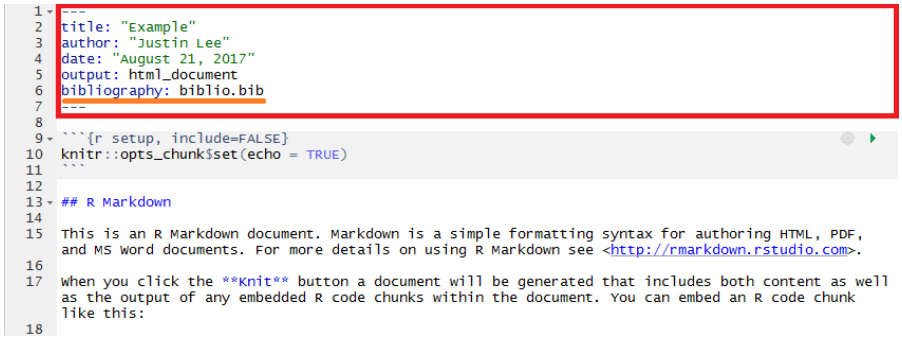


For ".bib" files we are interested in the "BibTeX" option and by

clicking on it we will be taken to another tab in which the format of the reference we want is provided. All that needs to be done at this point is to copy this format (that we saw earlier in this section) and paste in the ".bib" file you created and save the changes.



However, your RMarkdown document does not know about the existence of this bibliography file and therefore we need to insert this information in the YAML metadata at the start of our document. To do so, let us suppose that you named this file "biblio.bib" (saved in the same location as your RMarkdown document). All that needs to be done is to add another line in the YAML metadata with `bibliography: biblio.bib` and your RMarkdown will now be able to recognize the references within your ".bib" file.



There are also a series of other options that can be specified for the bibliography such as its format or the way references can be used within the text (see links at the end of this section).

Once the ".bib" file has been created and has been linked to your RMarkdown document through the details in the YAML metadata, you can now start using the references you have collected in the ".bib" file. To insert these references within your document at any point of your text you need to use the name that starts the reference field in your ".bib" file and place it immediately after the `@` symbol (without spaces). So, for example, say that we wanted to cite the

publication on the "taste of cutlery": in your RMarkdown all you have to do is to type `@harrar2013taste` at the point where you want this citation in the text and you will obtain: **?**. Moreover, it is often useful to put a citation in braces and for example if you want to obtain (see e.g. **?**) you can simply write `[see e.g. @harrar2013taste]`.

The user can also change the name that is used to call the desired reference as long as the same name is used to cite it in the RMarkdown document and that this name is not the same as another reference.

The references in the ".bib" file will not appear in the references that are output from the RMarkdown compiling procedure unless they are specifically used within the RMarkdown document.

Additional information on BibTeX and reference in RMarkdown can be found in the links below:

- Introduction to bibtex[14]
- Reference in RMarkdown[15]

0.7.9 Tables

For simple tables, we can be manually insert values as such follows:

```
+---------------+---------------+--------------------+
| Fruit         | Price         | Advantages         |
+===============+===============+====================+
| *Bananas*     | $1.34         | - built-in wrapper |
|               |               | - bright color     |
+---------------+---------------+--------------------+
| Oranges       | $2.10         | - cures scurvy     |
```

[14] https://www.economics.utoronto.ca/osborne/latex/BIBTEX.HTM
[15] http://RMarkdown.rstudio.com/authoring_bibliographies_and_citations.html

```
|               |               | - **tasty**        |
+---------------+---------------+--------------------+
```

to produce:

Fruit	Price	Advantages
Bananas	$1.34	• built-in wrapper • bright color
Oranges	$2.10	• cures scurvy • **tasty**

As an alternative we can use the simple graphical user interface online[16]. For more extensive tables, we create dataframe objects and project them using `knitr::kable()` which we will explain later on this book.

0.7.10 Additional References

There are many more elements to creating a useful report using RMarkdown, and we encourage you to use the RMarkdown Cheatsheet[17] as a reference.

0.8 Code Chunks

Code chunks are those parts of the RMarkdown document where it is possible to embed R code within your output. To insert these

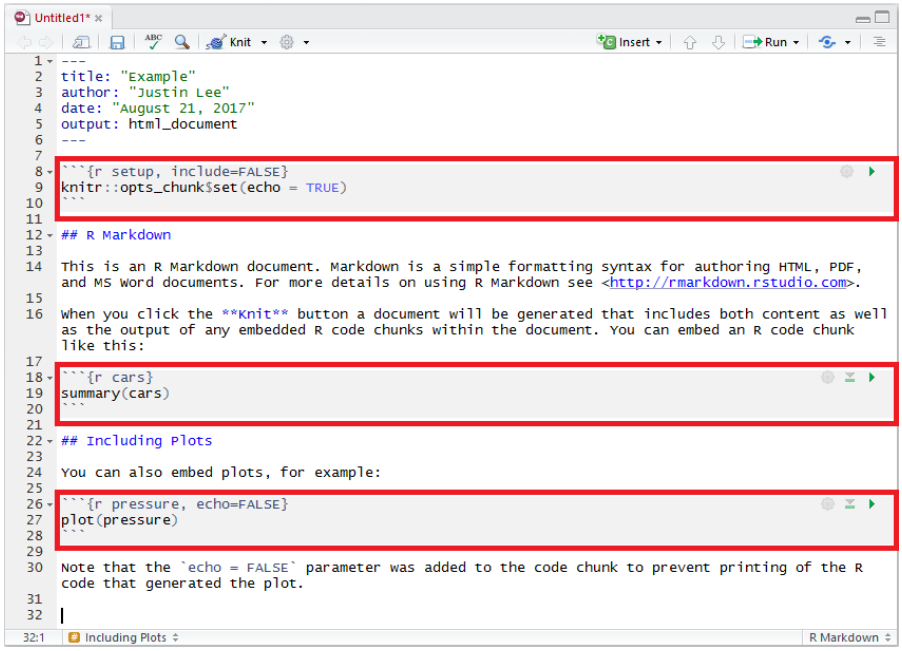
[16] http://www.tablesgenerator.com/markdown_tables

[17] https://www.rstudio.com/wp-content/uploads/2015/02/rmarkdown-cheatsheet.pdf

chunks within your RMarkdown file you can use the following shortcuts:

- the keyboard shortcut Ctrl + Alt + I (OS X: Cmd + Option + I)
- the Add Chunk command in the editor toolbar
- by typing the chunk delimiters ```{} and ```.

The following example highlights the code chunks in the example RMarkdown document we saw at the start of this chapter:



0.8.1 Code Chunk Options

A variety of options can be specified to manage the code chunks contained in the document. For example, as can be seen in the third code chunk in the example above, we specify an argument that reads `echo = FALSE` which is a parameter that was added to the code chunk to prevent printing the R code that generated the plot. This is a useful way to embed figures. More options can be

found from the RMarkdown Cheatsheet[18] and Yihui's notes on knitr options[19]. Here are some explanations of the most commonly used chunk options taken from these references:

- `eval`: (TRUE; logical) whether to evaluate the code chunk;
- `echo`: (TRUE; logical or numeric) whether to include R source code in the output file;
- `warning`: (TRUE; logical) whether to preserve warnings (produced by warning()) in the output like we run R code in a terminal (if FALSE, all warnings will be printed in the console instead of the output document);
- `cache`: (FALSE; logical) whether to "*cache*" a code chunk. This option is particularly important in practice and is discussed in more details in Section 0.8.4.

Plot figure options:

- `fig.path`: ('figure/'; character) prefix to be used for figure filenames (fig.path and chunk labels are concatenated to make filenames);
- `fig.show`: ('asis'; character) how to show/arrange the plots;
- `fig.width`, `fig.height`: (both are 7; numeric) width and height of the plot, to be used in the graphics device (in inches) and have to be numeric;
- `fig.align`: ('default'; character) alignment of figures in the output document (possible values are left, right and center;
- `fig.cap`: (NULL; character) figure caption to be used in a figure environment.

0.8.2 Comments

Adding comments to describe the code is extremely useful (if not essential) during every coding and programming process. It helps **you** take notes and remember what is going on and why you made use of these functions, as well as helping others understand your

[18] https://www.rstudio.com/wp-content/uploads/2015/02/rmarkdown-cheatsheet.pdf

[19] https://yihui.name/knitr/options/

code. Forgetting to comment or document your code often becomes a larger problem in the future when, among numerous lines of code, you have forgotten the reason for using certain functions or algorithms.

> "Don't document bad code – rewrite it." The Elements of Programming Style, Kernighan & Plauger

---

```
# Comment your code by preceding text with a #
# Keep it brief but comprehensible, so you can return to it
```

0.8.3 In-line R

The variables we store in an RMarkdown document will stay within the environment they were created in. This means that we can call and manipulate them anywhere within the document. For example, supposing we have a variable called `x` to which we assign a specific value, then in RMarkdown we can reference this variable by using `r x`: this will affix the value of the variable directly in a sentence. Here is a practical example:

```
a <- 2
```

where we have stored the value 2 in a variable called `a`. We can use the value of `a` as follows:

```
The value of $a$ is `r a`.
```

This translates in R Markdown to "The value of a is 2."

0.8.4 Cache

Depending on the complexity of calculations in your embedded R code, it may be convenient to avoid re-running the computations (which could be lengthy) each time you knit the document together. For this purpose, it possible to specify an additional argument for your embedded R code which is the `cache` argument. By default this argument is assigned the value `FALSE` and therefore the R code is run every time your document is compiled. However, if you specify this argument as `cache = TRUE`, then the code is only run the first time the document is compiled while the following times it simply stores and presents the results of the computations when the document was first compiled.

Below is a short video introducing caching in R Markdown.

The RMarkdown file used for this particular example can be found here: caching.Rmd[20].

Let us consider an example where we want to embed an R code with a very simple operation such as assigning the value of 2 to an object that we call `a` (that we saw earlier). This is clearly not the best example since this operation runs extremely quickly and there is no visible loss in document compilation time. However, we will use it just to highlight how the `cache` argument works. Therefore, if we want to avoid running this operation each time the document is compiled, then we just embed our R code as follows:

```
a <- 2
```

which would be written in RMarkdown as:

````
```{r computeA, cache = TRUE}
a <- 2
```
````

You will notice that we called this chunk of embedded R code

[20] code_examples/caching.Rmd

`computeA` and the reason for this will become apparent further on. Once we have done this we can compile the document that will run this operation and store its result. Now, if we compile the document again (independently from whether we made changes to the rest of the document or not) this operation will not be run and the result of the previous (first) compiling will be presented. However, if changes are made to the R code which has been "cached", then the code will be run again and this time its new result will be stored for all the following compilings until it is changed again.

This argument can therefore be very useful when computationally intensive R code is embedded within your document. Nevertheless it can suffer from a drawback which consists in dependencies of your "cached" R code with other chunks within the document. In this case, the other chunks of R code can be modified thereby outputting different results but these will not be considered by your "cached" R code. As an example, suppose we have another chunk of R code that we can "cache" and that takes the value of `a` from the previous chunk:

```
(d <- 2*a)
```

```
## [1] 4
```

which would be written in RMarkdown as:

````
```{r, cache = TRUE}
(d <- 2*a)
```
````

In this case, the output of this chunk will be `## 4` since `a <- 2` (from the previous chunk). What happens however if we modify the value of `a` in the previous chunk? In this case, the previous chunk will be recomputed but the value of `d` (in the following chunk) will not be updated since it has stored the value of 4 and it is not recomputed since this chunk has not been modified. To avoid this, a solution is to specify the chunks of code that the "cached" code depends on. This is why we initially gave a name to the first chunk

of code ("computeA") so as to refer to it in following chunks of "cached" code that depend on it. To refer to this code you need to use the option `dependson` as follows:

```
(d <- 2*a)
```

```
## [1] 4
```

which we would write as:

```
```{r, cache = TRUE, dependson = "computeA"}
(d <- 2*a)
```
```

In this manner, if the value of `a` changes in the first chunk, the value of `d` will also change but will be stored until either the `computeA` chunk or the latter chunk is modified.

0.9 Render Output

After you are done, run `RMarkdown::render()` or click the `Knit` button at the top of the RStudio scripts pane to save the output in your working directory.

FIGURE 2

The use of RMarkdown makes it possible to generate any file

format such as HTML, pdf and Word processor formats using `pandoc`. Pandoc is a free software that understands and converts useful markdown syntax, such as the code mentioned above, into a readable and clean format.

0.10 Addition Information

Click on the links below for more information on RMarkdown:

- RStudio RMarkdown tutorial[21]
- R-blogger's RMarkdown tutorial[22]
- RMarkdown Cheatsheet[23]

[21] http://RMarkdown.rstudio.com/authoring_quick_tour.html

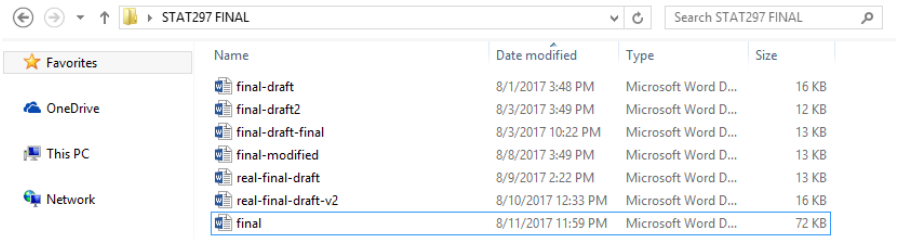
[22] https://www.r-bloggers.com/r-markdown-and-knitr-tutorial-part-1/

[23] https://www.rstudio.com/wp-content/uploads/2015/02/rmarkdown-cheatsheet.pdf

0

GitHub

When working on a report or a project, it is often the case that you keep separate versions either to keep track of the changes (in case you want to go back to a previous version) or to have a version for each person working on different parts of the project. As a result of this approach, you may have experienced a moment like this at least once in your life:



In these cases, after having modified and changed different parts of a report, you probably find yourself saving the same file over and over again while losing track of what changes you made. To respond to this problem, software has been developed to keep track of your changes by informing you on the saves you made and allowing you to go back to previous versions in order to revert those changes. This software is generally called "version control" and this chapter discusses the features of this software as well as introducing a specific version control platform called "GitHub". The latter includes a series of highly useful tools that can be extremely helpful, not only for the projects developed based on this book, but also for any personal or collaborative project you may undertake in the future.

0.11 Version Control

As mentioned above, *version control* is a system that records changes to a file or a set of files in order to keep track and possibly revert to or modify those changes over time. More specifically, it allows you to:

- record the entire history of a file;
- revert to a specific version of the file;
- collaborate on the same platform with other people;
- make changes without modifying the main file and add them once you feel comfortable with them.

All these features are highly important when projects start becoming more complex and/or different collaborators contribute to it. In the next section we present a version control platform called "GitHub" that is commonly used among programmers and software developers thereby allowing them also to make their work visible and available to the general public.

0.12 Git and GitHub

Among the different version control platforms, Git is a commonly used and powerful tool that is made more accessible through GitHub which is a commercial website. The latter uses the Git platform and stores local files into a flexible folder called a "repository". For the purposes of this course, we will be using this platform and in the following sections we will briefly describe how to install and get started with this version control platform.

Below is a video introducing GitHub.

0.12.1 Git Setup

To install Git, go to the website[24] and select the version which is compatible with the OS of your computer (e.g. Windows/Mac/Linux/Solaris). Once you've downloaded and installed Git, the first thing you should do is to configure it by setting your username and email address. This is important because each time you interact with the platform and upload (commit) your changes to Git, this information is used to synchronize versions and keep track of project evolution.

0.12.1.1 Tell Git Who You Are

Once you have installed Git, run the `Git Bash` software and type the following code below.

```
$ git config --global user.name "John Doe"
$ git config --global user.email johndoe@example.com
```

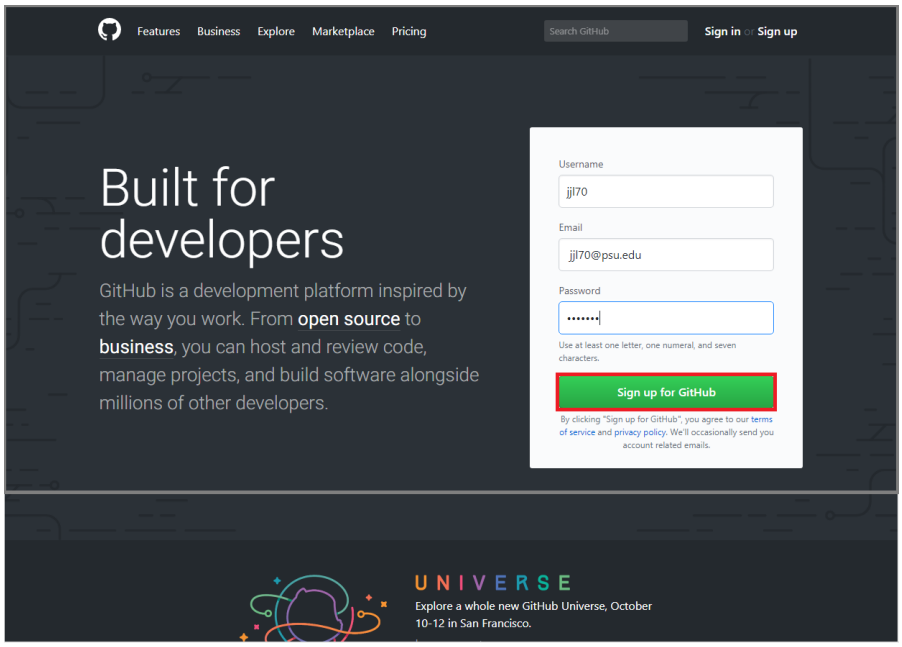
This is the initial configuration of your author name and email address for your commits. You may need to do this before you begin pushing and pulling with your current account information. This operation only needs to be done once when using the "–global" option because, in this case, Git will always use that information for anything you do on that system. If you want to override this with a different name or email address for specific projects, you can run the command without the "–global" option while working on those projects.

0.12.2 GitHub Setup

In order to set up GitHub, go to the GitHub website[25] and, for the purposes of the course, the first step is to sign up with your University email address.

[24] https://git-scm.com/downloads
[25] https://github.com/

Your username and email can be changed at any time so, if you want to change it, you can easily do so once this course is over.



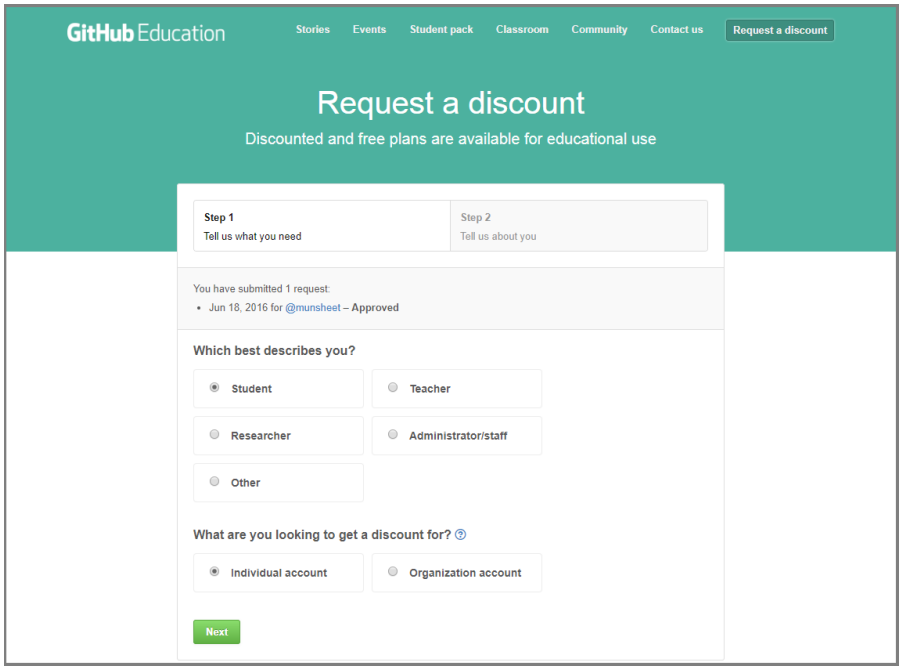
Once this is done, you reach `Step 2: Choose your plan` where you can choose the default plan ("Unlimited public repositories for free") and click `Continue`. The last (optional) step is `Step 3: Tailor your experience` which allows you to submit your information but this can also be skipped.

Your GitHub profile can also serve as a *resume* of your data science skills that will be highlighted by possible future projects that you save and commit.

0.12.3 Student Developer Pack

As a student, it is possible to benefit from specific advantages when using GitHub. Indeed, once you have set up your profile you can

go to this link[26] and follow the steps below to set up a "student developer pack" discount request to GitHub. Through this setup it will be possible for you not only to have free *public* repositories but also to make your own *private* repositories for free.



0.13 GitHub Workflow

Here is a video demonstrating the basic GitHub workflow in GitHub Desktop (initializing, committing, pushing and pulling) that we will follow for our assignments and projects.

In addition, here is a video demonstrating the basic GitHub workflow within RStudio.

While the main features and actions to manage the workflow in GitHub are desribed in the above videos, the following paragraphs

[26] https://education.github.com/discount_requests/new

give some extra details that can be helpful to consider when working with this version-control platform.

0.13.1 Branching

In the previous section we discussed the workflow as a means of directly making changes in the so-called *master* branch which is where our original and up-to-date work is stored. However, when working with different collaborators for example, it may be appropriate to create separate branches that will avoid modifying the original one until you're sure of the changes. In this perspective, *branching* is essentially creating an environment in which we can change anything without obstructing our original document. As mentioned, this idea is very useful for group-based activities where different people are working on the same files. Once we have made all our changes and are sure of the changes, we can merge the changes to the main `master` branch. You can learn more about branching here[27] and here[28].

0.13.2 Pull

Before starting (or continuing) to work on your project, make sure to always review changes that another collaborator has made. Once this is done you can make sure there are no merge conflicts and you can pull (or synchronize) your local branch with the most recent version of the repository. If merge conflicts were to happen, these can still be solved but it would be preferable to avoid them generating confusion.

[27] https://git-scm.com/book/en/v1/Git-Branching-Basic-Branching-and-Merging

[28] https://gist.github.com/vlandham/3b2b79c40bc7353ae95a

0.13.3 Commits

After we have created the branch, we can start modifying the documents (add, edit, or delete) within the repository. Once these changes are made, you need to `commit` them with an informative message, explaining why a particular change is being made. These specific messages allow you to backtrack on these changes later if you decide to look at the history of any of these files and find a bug. This information is extremely important since otherwise there's little point in using version control like GitHub. [29]

0.13.3.1 Pull Request

If you are directly working on the master branch, please disregard this section. Else, a `pull request` may be made by the person working on the branch, so that other collaborators can discuss about the commits made in the branch. Also, there are options for conversation in which they can review and comment directly onto the code as well.

[29] This scheme is inspired from diagrams by Prof. Bob Rudis and James Balamuta.

0.13.4 Push or Merge

Once you have either made the commits on your master branch or have the pull request confirmed by other collaborators, you can merge or push the changes into the remote master branch. This means that the version of the repository online will have your updated code and documents. This will be the final step to the cycle of the workflow after which we can clear and repeat the above procedure.

0.13.5 Merge Conflicts

Merge conflicts often occur when two different collaborators make different changes to the same line of a file, and also can happen when a file that is meant to be modified is deleted (although these may not be the only situations). To resolve these conflicts, we must directly edit the documents making sure potential conflicts are discussed before merging or pushing to the master branch, since merge conflicts often occur from miscommunication within groups.

0.14 GitHub Workflow on Command Line / Git Bash

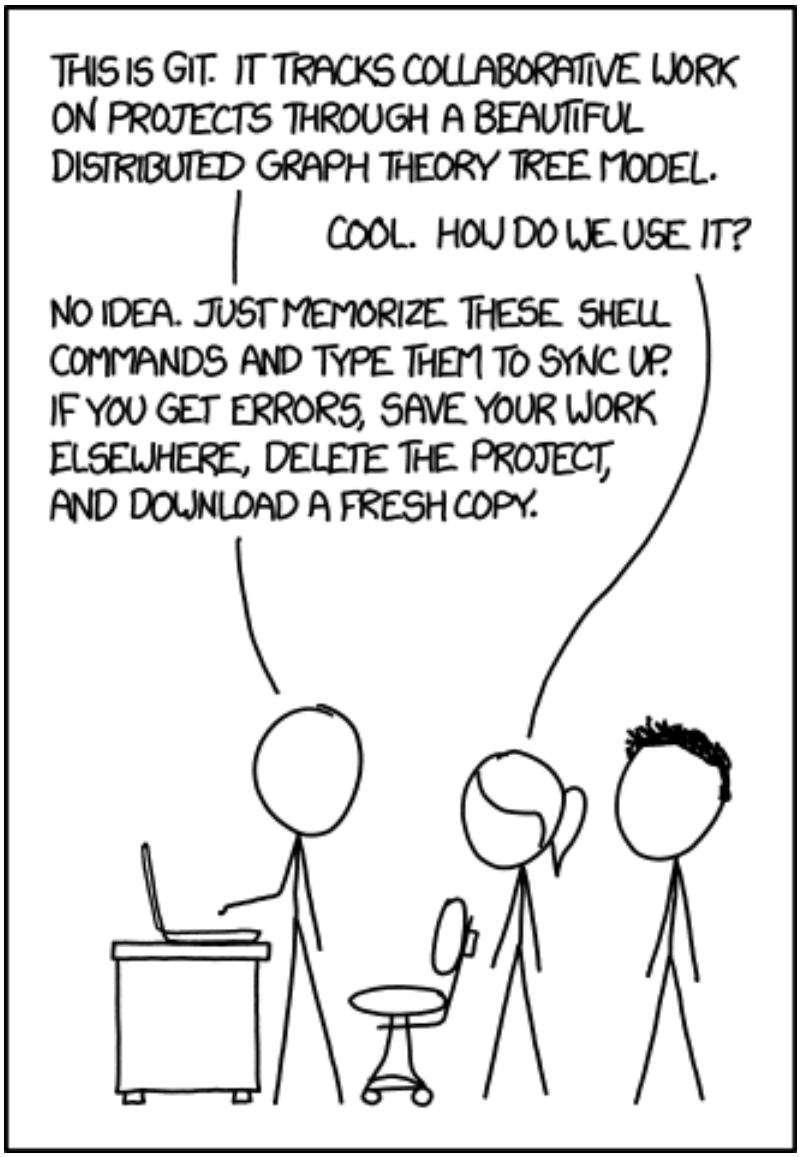
Here are commands that we can use within `Git Bash` if we are more comfortable working on the command line.

Command	Function
git init	Create a **local** repository
git branch “newbranch”	Create a new branch with given name
git checkout “newbranch”	Switch to specified branch
git status	List all the files that you have modified
git add -A	Add **all** files to staging
git commit -m “commit message”	Commit staged changes to **local** repository
git push	Commit saved changes to **remote** repository

Command	Function
git pull	Update changes from the **remote** repository

However, it is better for us to startby using more graphical user-interface options since they allow us to better understand what is going on. You **do not** want to follow this example[30]...

[30] https://xkcd.com/1597/



It is always important to know what is happening when we create, change, push, branch and pull from a repository.

0.15 Issues

Issues are a very good way to keep track of group tasks, bugs and announcements for your projects within GitHub. Below is a basic video introducing `issues` in GitHub.

0.16 Slack Integration

Slack is a platform created to communicate between group members, allowing for both direct individual messages as well as group messages. More information on how to use Slack can be found in this Slack Tutorial[31].

An added benefit of using Slack is that it can be integrated with GitHub in such a way that notifications will be posted to the group whenever someone pushes or makes a pull request. More information on GitHub integration with Slack can be found here[32].

A more detailed video providing a demonstration on the use of Slack in a real-life setting can be found below.

0.17 Additional References

Below are some supplemental references that can support you in a better use of GitHub.

[31] https://get.slack.help/hc/en-us/articles/218080037-Getting-started-for-new-members

[32] https://get.slack.help/hc/en-us/articles/232289568-Use-GitHub-with-Slack

- GitHub Introduction with RStudio[33]
- GitHub Workflow[34]
- GitHub on Command Line (video)[35]

[33] https://www.r-bloggers.com/rstudio-and-github/
[34] https://guides.github.com/introduction/flow/
[35] https://www.youtube.com/watch?v=oFYyTZwMyAg

Part II

Introduction to R

0

Data Structures

There are different data types that are commonly used in R among which the most important ones are the following:

- **Numeric** (or double): these are used to store real numbers. Examples: -4, 12.4532, 6.
- **Integer**: examples: 2L, 12L.
- **Logical** (or boolean): examples: `TRUE`, `FALSE`.
- **Character**: examples: `"a"`, `"Bonjour"`.

In R there are five types of data structures in which elements can be stored. A data structure is said to *homogeneous* if it only contains elements of the same type (for example it only contains character or only numeric values) and *heterogenous* if it contains elements of more than one type. The five types of data structures are commonly summarized in a table similar to the one below (see e.g. **?**):

TABLE 0.4: Five most common types of data structures used in R (**?**).

Dimension	Homogenous	Heterogeneous
1	Vector	List
2	Matrix	Data Frame
n	Array	

Consider a simple data set of the top five male single tennis players presented below:

TABLE 0.5: Five best male single tennis players as
ATP (07-15-2017).

Name	Date of Birth	Born	Country	ATP Ranking	P
Andy Murray	15 May 1987	Glasgow, Scotland	Great Britain	1	6
Rafael Nadal	3 June 1986	Manacor, Spain	Spain	2	8
Stan Wawrinka	28 March 1985	Lausanne, Switzerland	Switzerland	3	3
Novak Djokovic	22 May 1987	Belgrade, Serbia	Serbia	4	1
Roger Federer	8 August 1981	Basel, Switzerland	Switzerland	5	1

Notice that this data set contains a variety of data types; in the next sections we will use this data to illustrate how to work with five common data structures.

0.18 Vectors

A vector has three important properties:

- The **Type** of objects contained in the vector. The function `typeof()` returns a description of the type of objects in a vector.
- The **Length** of a vector indicates the number of elements in the vector. This information can be obtained using the function `length()`.
- **Attributes** are metadata attached to a vector. The functions `attr()` and `attributes()` can be used to store and retrieve attributes (more details can be found in Section 0.18.4).

`c()` is a generic function that combines arguments to form a vector. All arguments are coerced to a common type (which is the type of the returned value) and all attributes except names are removed.

For example, consider the number of grand slams won by the five players considered in the eighth column of Table 0.5:

```
grand_slam_win <- c(9, 15, 5, 12, 18)
```

To display the values stored in `grand_slam_win` we could simply enter the following in the R console:

```
grand_slam_win
```

```
## [1]  9 15  5 12 18
```

Alternatively, we could have created and displayed the value by using `()` around the definition of the object itself as follows:

```
(grand_slam_win <- c(9, 15, 5, 12, 18))
```

```
## [1]  9 15  5 12 18
```

Various forms of "nested concatenation" can be used to define vectors. For example, we could also define `grand_slam_win` as

```
(grand_slam_win <- c(9, c(15, 5, c(12, c(18)))))
```

```
## [1]  9 15  5 12 18
```

This approach is often used to assemble vectors in various ways.

It is also possible to define vectors with characters, for example we could define a vector with the player names as follows:

```
(players <- c("Andy Murray", "Rafael Nadal", "Stan Wawrinka",
              "Novak Djokovic", "Roger Federer"))
```

```
## [1] "Andy Murray"    "Rafael Nadal"   "Stan Wawrinka"  "Novak Djokovic"
## [5] "Roger Federer"
```

0.18.1 Type

We can evaluate the kind or type of elements that are stored in a vector using the function `typeof()`. For example, for the vectors we just created we obtain:

```
typeof(grand_slam_win)
```

```
## [1] "double"
```

```
typeof(players)
```

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

This is a little surprising since all the elements in `grand_slam_win` are integers and it would seem natural to expect this as an output of the function `typeof()`. This is because R considers any number as a "double" by default, except when adding the suffix `L` after an integer. For example:

```
typeof(1)
```

```
## [1] "double"
```

```
typeof(1L)
```

```
## [1] "integer"
```

Therefore, we could express `grand_slam_win` as follows:

```
(grand_slam_win_int <- c(9L, 15L, 5L, 12L, 18L))
```

```
## [1]  9 15  5 12 18
```

```
typeof(grand_slam_win_int)
```

```
## [1] "integer"
```

In general, the difference between the two is relatively unimportant.

0.18.2 Coercion

As indicated earlier, a vector has a homogeneous data structure meaning that it can only contain a single type among all the data types. Therefore, when more than one data type is provided, R will *coerce* the data into a "shared" type. To identify this "shared" type we can use this simple rule:

$$\text{logical} < \text{integer} < \text{numeric} < \text{character},$$

which simply means that if a vector has more than one data type, the "shared" type will be that of the "largest" type according to the progression shown above. For example:

```
# Logical + numeric
(mix_logic_int <- c(TRUE, 12, 0.5))
```

```
## [1]  1.0 12.0  0.5
```

```
typeof(mix_logic_int)
```

```
## [1] "double"
```

```
# Numeric + character
(mix_int_char <- c(14.3, "Hi"))
```

```
## [1] "14.3" "Hi"
```

```
typeof(mix_int_char)
```

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

0.18.3 Subsetting

Naturally, it is possible to "subset" the values of in our vector in many ways. Essentially, there are four main ways to subset a vector. Here we'll only discuss the first three:

- **Positive Index**: We can *access* or *subset* the i-th element of a vector by simply using `grand_slam_win[i]` where i is a positive number between 1 and the length of the vector.

```
# Accessing the first element
grand_slam_win[1]
```

```
## [1] 9
```

```
# Accessing the third and first value
grand_slam_win[c(3, 1)]
```

```
## [1] 5 9
```

```
# Duplicated indices yield duplicated values
grand_slam_win[c(1, 1, 2, 2, 3, 4)]
```

```
## [1]  9  9 15 15  5 12
```

- **Negative Index**: We *remove* elements in a vector using negative indices:

```
# Removing the second observation
grand_slam_win[-2]
```

```
## [1]  9  5 12 18
```

```
# Removing the first and fourth observations
grand_slam_win[c(-1, -4)]
```

```
## [1] 15  5 18
```

- **Logical Indices**: Another useful approach is based on *logical* operators:

```
# Access the first and fourth observations
grand_slam_win[c(TRUE, FALSE, FALSE, TRUE, FALSE)]
```

```
## [1]  9 12
```

Note that it is not permitted to "mix" positive and negative indices. For example, `grand_slam_win[c(-1, 2)]` would produce an error message.

0.18.4 Attributes

Let's suppose that we conduct an experiment under specific conditions, say a date and place that are stored as attributes of the object containing the results of this experiment. Indeed, objects can have arbitrary additional attributes that are used to store metadata on the object of interest. For example:

```
attr(grand_slam_win, "date") <- "07-15-2017"
attr(grand_slam_win, "type") <- "Men, Singles"
```

To display the vector with its attributes

```
grand_slam_win
```

```
## [1]  9 15  5 12 18
## attr(,"date")
## [1] "07-15-2017"
## attr(,"type")
## [1] "Men, Singles"
```

To only display the attributes we can use

```
attributes(grand_slam_win)
```

```
## $date
## [1] "07-15-2017"
##
## $type
## [1] "Men, Singles"
```

It is also possible to extract a specific attribute

```
attr(grand_slam_win, "date")
```

```
## [1] "07-15-2017"
```

0.18.5 Adding Labels

In some cases, it is useful to characterize vector elements with labels. For example, we could define the vector `grand_slam_win` and associate the name of each corresponding athlete as a label, i.e.

```
(grand_slam_win <- c("Andy Murray" = 9, "Rafael Nadal" = 15,
                     "Stan Wawrinka" = 5, "Novak Djokovic" = 12,
                     "Roger Federer" = 18))
```

```
##    Andy Murray   Rafael Nadal  Stan Wawrinka Novak Djokovic  Roger Federer
##              9             15              5             12             18
```

The main advantage of this approach is that the number of grand slams won can now be referred to by the player's name. For example:

```
grand_slam_win["Andy Murray"]
```

```
## Andy Murray
##           9
```

```
grand_slam_win[c("Andy Murray","Roger Federer")]
```

```
##   Andy Murray Roger Federer
##             9            18
```

All labels (athlete names in this case) can be obtained with the function `names()`, i.e.

```
names(grand_slam_win)
```

```
## [1] "Andy Murray"    "Rafael Nadal"   "Stan Wawrinka"  "Novak Djokovic"
## [5] "Roger Federer"
```

0.18.6 Working with Dates

When working with dates it is useful to treat them as real dates rather than character strings that *look* like dates (to a human) but don't otherwise *behave* like dates. For example, consider a vector of three dates: `c("03-21-2015", "12-13-2011", "06-27-2008")`.

The `sort()` function returns the elements of a vector in ascending order, but since these dates are actually just character strings that *look* like dates (to a human), R sorts them in alphanumeric order (for characters) rather than chronological order (for dates):

```
# The `sort()` function sorts elements in a vector in ascending order
sort(c("03-21-2015", "12-31-2011", "06-27-2008", "01-01-2012"))
```

```
## [1] "01-01-2012" "03-21-2015" "06-27-2008" "12-31-2011"
```

Converting the character strings to "yyyy-mm-dd" would solve our sorting problem, but perhaps we also want to calculate the number of days between two events that are several months or years apart.

The `as.Date()` function is one straight-forward method for converting character strings into dates that can be used as such. The typical syntax is of the form:

```
as.Dates(<vector of dates>, format = <your format>)
```

Considering the dates of birth presented in Table 0.5 we can save them in an appropriate format using:

```
(players_dob <- as.Date(c("15 May 1987", "3 Jun 1986", "28 Mar 1985",
                          "22 May 1987", "8 Aug 1981"),
                        format = "%d %b %Y"))
```

```
## [1] "1987-05-15" "1986-06-03" "1985-03-28" "1987-05-22" "1981-08-08"
```

Note the syntax of `format = "%d %b %Y"`. The following table shows common format elements for use with the `as.Date()` function:

TABLE 0.6: Common date formatting elements for use with `as.Date()` reproduced from statmethods.net.

Symbol	Meaning	Example
%d	day as a number (0-31)	01-31
%a	abbreviated weekday	Mon
%A	unabbreviated weekday	Monday
%m	month (00-12)	00-12
%b	abbreviated month	Jan
%B	unabbreviated month	January
%y	2-digit year	07
%Y	4-digit year	2007

There are many advantages to using the `as.Date()` format (in addition to proper sorting). For example, the subtraction between two dates becomes more meaningful and yields the difference in days between them. As an example, the number of days between Rafael Nadal's and Andy Murray's dates of birth can be obtained as

```
players_dob[1] - players_dob[2]
```

```
## Time difference of 346 days
```

In addition, subsetting becomes also more intuitive and, for example, to find the players born after 1 January 1986 we can simply run:

```
players[players_dob > "1986-01-01"]
```

```
## [1] "Andy Murray"    "Rafael Nadal"   "Novak Djokovic"
```

There are many other reasons for using this format (or other date formats). A more detailed discussion on this topic can, for example, be found in Cole Beck's notes[36].

0.18.7 Useful Functions with Vectors

The reason for extracting or creating vectors often lies in the need to collect information from them. For this purpose, a series of useful functions are available that allow to extract information or arrange the vector elements in a certain way which can be of interest to the user. Among the most commonly used functions we can find the following ones

`length()` `sum()` `mean()` `order()` and `sort()`

whose name is self-explanatory in most cases. For example we have

[36] http://biostat.mc.vanderbilt.edu/wiki/pub/Main/ColeBeck/datestimes.pdf

```
length(grand_slam_win)
```

```
## [1] 5
```

```
sum(grand_slam_win)
```

```
## [1] 59
```

```
mean(grand_slam_win)
```

```
## [1] 11.8
```

To sort the players by number of grand slam wins, we could use the function `order()` which returns the *position* of the elements of a vector sorted in an ascending order,

```
order(grand_slam_win)
```

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

Therefore, we can sort the players in ascending order of wins as follows

```
players[order(grand_slam_win)]
```

```
## [1] "Stan Wawrinka"  "Andy Murray"    "Novak Djokovic" "Rafael Nadal"
## [5] "Roger Federer"
```

which implies that Roger Federer won most grand slams. Another related function is `sort()` which simply sorts the elements of a vector in an ascending manner. For example,

```
sort(grand_slam_win)
```

```
##  Stan Wawrinka    Andy Murray Novak Djokovic   Rafael Nadal  Roger Federer
```

```
##             5             9            12            15            18
```

which is compact version of

```
grand_slam_win[order(grand_slam_win)]
```

```
##  Stan Wawrinka    Andy Murray Novak Djokovic   Rafael Nadal  Roger Federer
##             5             9            12            15            18
```

It is also possible to use the functions `sort()` and `order()` with characters and dates. For example, to sort the players' names alphabetically (by first name) we can use:

```
sort(players)
```

```
## [1] "Andy Murray"    "Novak Djokovic" "Rafael Nadal"   "Roger Federer"
## [5] "Stan Wawrinka"
```

Similarly, we can sort players by age (oldest first)

```
players[order(players_dob)]
```

```
## [1] "Roger Federer"  "Stan Wawrinka"  "Rafael Nadal"   "Andy Murray"
## [5] "Novak Djokovic"
```

or in an reversed manner (oldest last):

```
players[order(players_dob, decreasing = TRUE)]
```

```
## [1] "Novak Djokovic" "Andy Murray"    "Rafael Nadal"   "Stan Wawrinka"
## [5] "Roger Federer"
```

There are of course many other useful functions that allow to deal with vectors which we will not mention in this section but can be found in a variety of references (see e.g. **?**).

0.18.8 Creating sequences

When using R for statistical programming and data analysis it is very common to create sequences of numbers. Here are three common ways used to create such sequences:

- `from:to`: This method is quite intuitive and very compact. For example:

```
1:3
```

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

```
(x <- 3:1)
```

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

```
(y <- -1:-4)
```

```
## [1] -1 -2 -3 -4
```

```
(z <- 1.3:3)
```

```
## [1] 1.3 2.3
```

- `seq_len(n)`: This function provides a simple way to generate a sequence from 1 to an arbitrary number `n`. In general, `1:n` and `seq_len(n)` are equivalent with the notable exceptions where `n = 0` and `n < 0`. The reason for these exceptions will become clear in Section 0.24.3.1. Let's see a few examples:

```
n <- 3
1:n
```

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

```
seq_len(n)
```

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

```
n <- 0
1:n
```

```
## [1] 1 0
```

```
seq_len(n)
```

```
## integer(0)
```

- `seq(a, b, by/length.out = d)`: This function can be used to create more "complex" sequences. It can either be used to create a sequence from `a` to `b` by increments of `d` (using the option `by`) or of a total length of `d` (using the option `length.out`). A few examples:

```
(x <- seq(1, 2.8, by = 0.4))
```

```
## [1] 1.0 1.4 1.8 2.2 2.6
```

```
(y <- seq(1, 2.8, length.out = 6))
```

```
## [1] 1.00 1.36 1.72 2.08 2.44 2.80
```

This can be combined with the `rep()` function to create vectors with repeated values or sequences, for example:

```
rep(c(1,2), times = 3, each = 1)
```

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

```
rep(c(1,2), times = 1, each = 3)
```

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

```
rep(c(1,2), times = 2, each = 2)
```

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

where the option `times` allows to specify how many times the object needs to be repeated and `each` regulates how many times each element in the object is repeated.

It is also possible to generate sequences of dates using the function `seq()`. For example, to generate a sequence of 10 dates between the dates of birth of Andy Murray and Rafael Nadal we can use

```
seq(from = players_dob[1], to = players_dob[2], length.out = 10)
```

```
##  [1] "1987-05-15" "1987-04-06" "1987-02-27" "1987-01-19" "1986-12-12"
##  [6] "1986-11-03" "1986-09-26" "1986-08-18" "1986-07-11" "1986-06-03"
```

Similarly, we can create a sequence between the two dates by increments of one week (backwards)

```
seq(players_dob[1], players_dob[2], by = "-1 week")
```

```
##  [1] "1987-05-15" "1987-05-08" "1987-05-01" "1987-04-24" "1987-04-17"
##  [6] "1987-04-10" "1987-04-03" "1987-03-27" "1987-03-20" "1987-03-13"
## [11] "1987-03-06" "1987-02-27" "1987-02-20" "1987-02-13" "1987-02-06"
## [16] "1987-01-30" "1987-01-23" "1987-01-16" "1987-01-09" "1987-01-02"
## [21] "1986-12-26" "1986-12-19" "1986-12-12" "1986-12-05" "1986-11-28"
## [26] "1986-11-21" "1986-11-14" "1986-11-07" "1986-10-31" "1986-10-24"
## [31] "1986-10-17" "1986-10-10" "1986-10-03" "1986-09-26" "1986-09-19"
## [36] "1986-09-12" "1986-09-05" "1986-08-29" "1986-08-22" "1986-08-15"
## [41] "1986-08-08" "1986-08-01" "1986-07-25" "1986-07-18" "1986-07-11"
## [46] "1986-07-04" "1986-06-27" "1986-06-20" "1986-06-13" "1986-06-06"
```

or by increments of one month (forwards)

```
seq(players_dob[2], players_dob[1], by = "1 month")
```

```
##  [1] "1986-06-03" "1986-07-03" "1986-08-03" "1986-09-03" "1986-10-03"
##  [6] "1986-11-03" "1986-12-03" "1987-01-03" "1987-02-03" "1987-03-03"
## [11] "1987-04-03" "1987-05-03"
```

0.18.9 Example: Apple Stock Price

Suppose that someone is interested in analyzing the behavior of Apple's stock price over the last three months. The first thing needed to perform such analysis is to recover (automatically) today's date. In R, this can be obtained as follows

```
(today <- Sys.Date())
```

```
## [1] "2018-10-03"
```

Once this is done, we can obtain the date which is exactly three months ago by using

```
(three_months_ago <- seq(today, length = 2, by = "-3 months")[2])
```

```
## [1] "2018-07-03"
```

With this information, we can now download Apple's stock price and represent these stocks through a candlestick chart which summarizes information on daily opening and closing prices as well as minimum and maximum prices. These charts are often used with the hope of detecting trading patterns over a given period of time.

```
library(quantmod)
getSymbols("AAPL", from = three_months_ago, to = today)
candleChart(AAPL, theme = 'white', type = 'candles')
```

FIGURE 3: Candlestick chart for Apple's stock price for the last three months.

Using the price contained in the object we downloaded (i.e. `AAPL`), we can compute Apple's arithmetic returns which are defined as follows

$$R_t = \frac{S_t - S_{t-1}}{S_{t-1}}, \tag{0.1}$$

where R_t are the returns at time t and S_t is the stock price. This is implemented in the function `ClCl()` within the `quantmod` package. For example, we can create a vector of returns as follows

```
AAPL_returns <- na.omit(ClCl(AAPL))
```

where `na.omit()` is used to remove missing values in the stock prices vector since, if we have $n + 1$ stock prices, we will only have n returns and therefore the first return cannot be computed. We can now compute the mean and median of the returns over the considered period.

```
mean(AAPL_returns)
```

```
## [1] 0.003586873
```

```
median(AAPL_returns)
```

```
## [1] 0.002893129
```

However, a statistic that is of particular interest to financial operators is the Excess Kurtosis which, for a random variable that we denote as X, can be defined as

$$\text{Kurt} = \frac{\mathbb{E}\left[(X - \mathbb{E}[X])^4\right]}{\left(\mathbb{E}\left[(X - \mathbb{E}[X])^2\right]\right)^2} - 3. \tag{0.2}$$

The reason for defining this statistic as *Excess* Kurtosis lies in the fact that the standardized kurtosis is compared to that of a Gaussian distribution (whose kurtosis is equal to 3) which has exponentially decaying tails. Consequently, if the Excess Kurtosis is positive, this implies that the distribution has heavier tails than a Gaussian and therefore has higher probabilities of extreme events occurring. To understand why the Excess Kurtosis is equal to 0 for a Gaussian distribution click on the button below:

Excess Kurtosis Derivation

Assuming X to be Gaussian, we have $X \sim \mathcal{N}(\mu, \sigma^2)$. Then, we define Z as $Z \sim \mathcal{N}(0,1)$ and Y as $Y = Z^2 \sim \chi_1^2$. Remember that a random variable following a χ_1^2 distribution has the following properties: $\text{Var}[Y] = 2$ and $\mathbb{E}[Y] = 1$. Using these definitions and properties, we obtain:

$$\begin{aligned}\text{Kurt} &= \frac{\mathbb{E}\left[(X - \mathbb{E}[X])^4\right]}{\left(\mathbb{E}\left[(X - \mathbb{E}[X])^2\right]\right)^2} - 3 = \frac{\mathbb{E}\left[(X - \mathbb{E}[X])^4\right]}{\left[\text{Var}\left(X\right)\right]^2} - 3 = \frac{\mathbb{E}\left[(X - \mathbb{E}[X])^4\right]}{\sigma^4} - 3 \\ &= \mathbb{E}\left[\left(\frac{X - \mathbb{E}[X]}{\sigma}\right)^4\right] - 3 = \mathbb{E}\left[Z^4\right] - 3 = \text{Var}[Z^2] + \mathbb{E}^2\left[Z^2\right] - 3 \\ &= \text{Var}[Y] + \mathbb{E}^2\left[Y\right] - 3 = 0.\end{aligned} \tag{0.3}$$

This implies that the theoretical value of the excess Kurtosis for a normally distributed random variable is 0.

Given this statistic, it is useful to compute this on the observed data and for this purpose a common estimator of the excess Kurtosis is

$$k = \frac{\frac{1}{n}\sum_{t=1}^{n}\left(R_t - \bar{R}\right)^4}{\left(\frac{1}{n}\sum_{t=1}^{n}\left(R_t - \bar{R}\right)^2\right)^2} - 3, \tag{0.4}$$

where $\bar{R}$ denotes the sample average of the returns, i.e.

$$\bar{R} = \frac{1}{n}\sum_{i=1}^{n} R_i.$$

In R, this can simply be done as follows:

```
mu <- mean(AAPL_returns)
(k <- mean((AAPL_returns - mu)^4)/(mean((AAPL_returns - mu)^2))^2 - 3)
```

```
## [1] 4.014467
```

Therefore, we observe an estimated Excess Kurtosis of 4.01 which is quite high and tends to indicate that the returns have heavier tails than the normal distribution. In Chapter @ref(#control), we will revisit this example and investigate if there is **enough evidence** to conclude that Apple's stock has Excess Kurtosis larger than zero.

0.19 Matrices

Matrices are a common data structure in R which have two dimensions to store multiple vectors of the same length combined as a unified object. The `matrix()` function can be used to create a matrix from a vector:

```
(mat <- matrix(1:12, ncol = 4,  nrow = 3))
```

```
##      [,1] [,2] [,3] [,4]
```

```
## [1,]    1    4    7   10
## [2,]    2    5    8   11
## [3,]    3    6    9   12
```

Notice that the first argument to the function is a vector (in this case the sequence 1 to 12) which is then transformed into a matrix with four columns (`ncol = 4`) and three rows (`nrow = 3`).

By default, the vectors are transformed into matrices by placing the elements by column (i.e. top to the bottom of ech column in sequence until all columns are full). If you wish to fill the matrix by row, all you need to do is specify the argument `byrow = T`.

```
# Compare with the matrix above
matrix(1:12, ncol = 4,  nrow = 3, byrow = T)
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    2    3    4
## [2,]    5    6    7    8
## [3,]    9   10   11   12
```

Usually the length of the vector (i.e. number of elements in the vector) is the result of the multiplication between the number of columns and number of rows. What happens if the vector has fewer elements for the same matrix dimension? What happens if the vector has more elements?

It is often the case that we already have equi-dimensional vectors available and we wish to bundle them together as matrix. In these cases, two useful functions are `cbind()` to combine vectors as vertical **c**olumns side-by-side, and `rbind()` to combine vectors as horizontal **r**ows. An example of `cbind()` is shown here:

```
players <- c("Andy Murray", "Rafael Nadal", "Stan Wawrinka",
             "Novak Djokovic", "Roger Federer")
```

```
grand_slam_win <- c(9, 15, 5, 12, 18)
win_percentage <- c(78.07, 82.48, 63.96, 82.77, 81.80)
(mat <- cbind(grand_slam_win, win_percentage))
```

```
##      grand_slam_win win_percentage
## [1,]              9          78.07
## [2,]             15          82.48
## [3,]              5          63.96
## [4,]             12          82.77
## [5,]             18          81.80
```

The result in this case is a 5×2 matrix (with `rbind()` it would have been a 2×5 matrix). Once the matrix is defined, we can assign names to its rows and columns by using `rownames()` and `colnames()`, respectively. Of course, the number of names must match the corresponding matrix dimension. In the following example, each row corresponds to a specific player (thereby using the `players` vector) and each column corresponds to a specific statistic of the players.

```
rownames(mat) <- players
colnames(mat) <- c("GS win", "Win rate")
mat
```

```
##                GS win Win rate
## Andy Murray         9    78.07
## Rafael Nadal       15    82.48
## Stan Wawrinka       5    63.96
## Novak Djokovic     12    82.77
## Roger Federer      18    81.80
```

0.19.1 Subsetting

As with vectors, it is possible to subset the elements of a matrix. Since matrices are two-dimensional data structures, it is necessary to specify the position of the elements of interest in both dimensions.

For this purpose we can use `[ , ]` immediately following the named matrix. Note the use of `,` within the square brackets in order to specify both row and column position of desired elements within the matrix (e.g. `matrixName[row, column]`). Consider the following examples:

```
# Subset players "Stan Wawrinka" and "Roger Federer" in matrix named "mat"
mat[c("Stan Wawrinka", "Roger Federer"), ]
```

```
##                GS win Win rate
## Stan Wawrinka       5    63.96
## Roger Federer      18    81.80
```

```
# Subset includes row 1 and 3 for all columns
mat[c(1, 3), ]
```

```
##                GS win Win rate
## Andy Murray         9    78.07
## Stan Wawrinka       5    63.96
```

```
# Subset includes all rows for column 2
mat[ , 2]
```

```
##    Andy Murray   Rafael Nadal  Stan Wawrinka Novak Djokovic  Roger Federer
##          78.07          82.48          63.96          82.77          81.80
```

```
# Subset includes rows 1, 2, & 3 for column 1
mat[1:3, 1]
```

```
##   Andy Murray  Rafael Nadal Stan Wawrinka
##             9            15             5
```

It can be noticed that, when a space is left blank before or after the comma, this means that respectively all the rows or all the columns are considered.

0.19.2 Matrix Operators in R

As with vectors, there are some useful functions that can be used with matrices. A first example is the function `dim()` that allows to determine the dimension of a matrix. For example, consider the following 4×2 matrix

$$\mathbf{A} = \begin{bmatrix} 1 & 5 \\ 2 & 6 \\ 3 & 7 \\ 4 & 8 \end{bmatrix}$$

which can be created in R as follows:

```
(A <- matrix(1:8, 4, 2))
```

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

Therefore, we expect `dim(A)` to return the vector `c(4, 2)`. Indeed, we have

```
dim(A)
```

```
## [1] 4 2
```

Next, we consider the function `t()` that allows transpose a matrix. For example, $\mathbf{A}^T$ is equal to:

$$\mathbf{A}^T = \begin{bmatrix} 1 & 2 & 3 & 4 \\ 5 & 6 & 7 & 8 \end{bmatrix},$$

which is a 2×4 matrix. In R, we achieve this as follows

```
(At <- t(A))
```

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

```
dim(At)
```

```
## [1] 2 4
```

Aside from playing with matrix dimensions, matrix algebraic operations have specific commands. For example, the operator `%*%` is used in R to denote matrix multiplication while, as opposed to scalar objects, the regular product operator `*` performs the element by element product (or Hadamard product) when applied to matrices. For example, consider the following matrix product:

$$\mathbf{B} = \mathbf{A}^T\mathbf{A} = \begin{bmatrix} 30 & 70 \\ 70 & 174 \end{bmatrix},$$

which can be done in R as follows:

```
(B <- At %*% A)
```

```
##      [,1] [,2]
## [1,]   30   70
## [2,]   70  174
```

Other common matrix operations include finding the determinant of a matrix and finding its inverse. These are often used, for example, when computing the likelihood function for a variable following a Gaussian distribution or when simulating time series or spatial data. The functions that perform these operations are `det()` and `solve()` that respectively find the determinant and the inverse of a matrix (which necessarily has to be square). The function `det()` can be used to compute the determinant of a square matrix. In

the case of a 2×2 matrix, there exists a simple solution for the determinant which is

$$\det(\mathbf{D}) = \det\left(\begin{bmatrix} d_1 & d_2 \\ d_3 & d_4 \end{bmatrix}\right) = d_1 d_4 - d_2 d_3.$$

Consider the matrix $\mathbf{B}$, we have

$$\det(\mathbf{B}) = 30 \cdot 174 - 70^2 = 320.$$

In R, we can simply do

```
det(B)
```

```
## [1] 320
```

The function `solve()` is also an important function when working with matrices as it allows to inverse a matrix. It is worth remembering that a square matrix that is not invertible (i.e. $\mathbf{A}^{-1}$ doesn't exist) is called *singular* and the determinant offers a way to "check" if this is the case for a given matrix. Indeed, a square matrix is singular if and only if its determinant is 0. Therefore, in the case of $\mathbf{B}$, we should be able to compute its inverse. As for the determinant, there exists a formula to compute the inverse of 2×2 matrices, i.e.

$$\mathbf{D}^{-1} = \begin{bmatrix} d_1 & d_2 \\ d_3 & d_4 \end{bmatrix}^{-1} = \frac{1}{\det(\mathbf{D})} \begin{bmatrix} d_4 & -d_2 \\ -d_3 & d_1 \end{bmatrix}.$$

Considering the matrix $\mathbf{B}$, we obtain

$$\mathbf{B}^{-1} = \begin{bmatrix} 30 & 70 \\ 70 & 174 \end{bmatrix}^{-1} = \frac{1}{320} \begin{bmatrix} 174 & -70 \\ -70 & 30 \end{bmatrix} = \begin{bmatrix} 0.54375 & -0.21875 \\ -0.21875 & 0.09375 \end{bmatrix}$$

```
(B_inv <- solve(B))
```

```
##           [,1]     [,2]
## [1,]  0.54375 -0.21875
## [2,] -0.21875  0.09375
```

Finally, we can verify that

$$\mathbf{G} = \mathbf{B}\mathbf{B}^{-1},$$

should be equal to the identity matrix,

```
(G <- B %*% B_inv)
```

```
##      [,1]          [,2]
## [1,]    1 -8.881784e-16
## [2,]    0  1.000000e+00
```

The result is of course extremely close but $\mathbf{G}$ is not exactly equal to the identity matrix due to rounding and other numerical errors.

Another function of interest is the function `diag()` that can be used to extract the diagonal of a matrix. For example, we have

$$\text{diag}\left(\mathbf{B}\right) = \begin{bmatrix} 30 & 174 \end{bmatrix},$$

which can be done in R as follows:

```
diag(B)
```

```
## [1]  30 174
```

Therefore, the function `diag()` computes the trace of matrix (i.e. the sum of the diagonal elements). For example,

$$\text{tr}\left(\mathbf{B}\right) = 204,$$

or in R:

```
sum(diag(B))
```

```
## [1] 204
```

Another use of the function `diag()` is to create diagonal matrices. Indeed, if the argument of this function is a vector, its behavior is the following:

$$\text{diag}\left(\begin{bmatrix} a_1 & a_2 & \cdots & a_n \end{bmatrix}\right) = \begin{bmatrix} a_1 & 0 & \cdots & 0 \\ 0 & a_2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & a_n \end{bmatrix}.$$

Therefore, this provides a simple way of creating an identity matrix by combining the functions `diag()` and `rep()` (discussed in the previous section) as follows:

```
n <- 4
(ident <- diag(rep(1, n)))
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    0    0    0
## [2,]    0    1    0    0
## [3,]    0    0    1    0
## [4,]    0    0    0    1
```

0.19.3 Example: Summary Statistics with Matrix Notation

A simple example of the operations we discussed in the previous section is given by many common statistics that can be re-expressed using matrix notation. As an example, we will consider three common statistics that are the sample mean, variance and covariance. Let us consider the following two samples of size n

$$\mathbf{x} = [x_1 \;\; x_2 \;\; \cdots \;\; x_n]^T$$
$$\mathbf{y} = [y_1 \;\; y_2 \;\; \cdots \;\; y_n]^T .$$

The sample mean of $\mathbf{x}$ is

$$\bar{x} = \frac{1}{n}\sum_{i=1}^{n} x_i,$$

and its sample variance is

$$s_x^2 = \frac{1}{n}\sum_{i=1}^{n} (x_i - \bar{x})^2 .$$

The sample covariance between $\mathbf{x}$ and $\mathbf{y}$ is

$$s_{x,y} = \frac{1}{n}\sum_{i=1}^{n} (X_i - \bar{x})(Y_i - \bar{y}),$$

where $\bar{y}$ denotes the sample mean of $\mathbf{y}$.

Consider the sample mean, this statistic can be expressed in matrix notation as follows

$$\bar{x} = \frac{1}{n}\sum_{i=1}^{n} x_i = \frac{1}{n}\mathbf{x}^T\mathbf{1},$$

where $\mathbf{1}$ is a column vector of n ones.

$$\begin{aligned} s_x^2 &= \frac{1}{n}\sum_{i=1}^{n} (x_i - \bar{x})^2 = \frac{1}{n}\sum_{i=1}^{n} x_i^2 - \bar{x}^2 = \frac{1}{n}\mathbf{x}^T\mathbf{x} - \bar{x}^2 \\ &= \frac{1}{n}\mathbf{x}^T\mathbf{x} - \left(\frac{1}{n}\mathbf{x}^T\mathbf{1}\right)^2 = \frac{1}{n}\left(\mathbf{x}^T\mathbf{x} - \frac{1}{n}\mathbf{x}^T\mathbf{1}\mathbf{1}^T\mathbf{x}\right) \\ &= \frac{1}{n}\mathbf{x}^T\left(\mathbf{I} - \frac{1}{n}\mathbf{1}\mathbf{1}^T\right)\mathbf{x} = \frac{1}{n}\mathbf{x}^T\mathbf{H}\mathbf{x}, \end{aligned}$$

where $\mathbf{H} = \mathbf{I} - \frac{1}{n}\mathbf{1}\mathbf{1}^T$. This matrix is often called the *centering* matrix. Similarly, for the sample covariance we obtain

$$s_{x,y} = \frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y}) = \frac{1}{n}\mathbf{x}^T\mathbf{H}\mathbf{y}.$$

In the code below we verify the validity of these results through a simple simulated example where we compare the values of the three statistics based on the different formulas discussed above.

```
# Sample size
n <- 100

# Simulate random numbers from a zero mean normal distribution with
# variance equal to 4.
x <- rnorm(n, 0, sqrt(4))

# Simulate random numbers from normal distribution with mean 3 and
# variance equal to 1.
y <- rnorm(n, 3, 1)

# Note that x and y are independent.

# Sample mean
one <- rep(1, n)
x_bar <- 1/n*sum(x)
x_bar_mat <- 1/n*t(x)%*%one

# Sample variance of x
H <- diag(rep(1, n)) - 1/n * one %*% t(one)
s_x <- 1/n * sum((x - x_bar)^2)
s_x_mat <- 1/n*t(x) %*% H %*% x

# Sample covariance
y_bar <- 1/n*sum(y)
s_xy <- 1/n*sum((x - x_bar)*(y - y_bar))
s_xy_mat <- 1/n*t(x) %*% H %*% y
```

To compare, let's construct a matrix of all the results that we calculated.

```
cp_matrix <- matrix(c(x_bar, x_bar_mat, s_x, s_x_mat, s_xy, s_xy_mat), ncol =
row.names(cp_matrix) <- c("Sample Mean", "Sample Variance", "Sample Covarian
colnames(cp_matrix) <- c("Scalar", "Matrix")
cp_matrix
```

```
##                        Scalar     Matrix
## Sample Mean         0.1374096  0.1374096
## Sample Variance     4.4333314  4.4333314
## Sample Covariance -0.3624978 -0.3624978
```

Therefore, using the previously obtained results we can construct the following *empirical* covariance matrix

$$\widehat{\text{Cov}}(X, Y) = \begin{bmatrix} s_x^2 & s_{x,y} \\ s_{x,y} & s_y^2 \end{bmatrix}. \tag{0.5}$$

In R, this can be done as

```
# Sample variance of y
s_y_mat <- 1/n*t(y) %*% H %*% y

# Covariance matrix
(V <- matrix(c(s_x_mat, s_xy_mat, s_xy_mat, s_y_mat), 2, 2))
```

```
##            [,1]       [,2]
## [1,]  4.4333314 -0.3624978
## [2,] -0.3624978  1.1356772
```

This result can now be compared to

```
cov(cbind(x, y))
```

```
##            x          y
## x  4.4781125 -0.3661594
## y -0.3661594  1.1471486
```

We can see that the results are slightly different from what we

expected. This is because the calculation of `cov()` within the default R `stats` package is based on an unbiased estimator which is not the one we used. To obtain the same result, we can go back to our estimation by calculating via the below method

```
(n-1)/n*cov(cbind(x, y))
```

```
##            x          y
## x  4.4333314 -0.3624978
## y -0.3624978  1.1356772
```

0.19.4 Example: Portfolio Optimization

Suppose that you are interested in investing your money in two stocks, say Apple and Netflix. However, you are wondering how much of each stock you should buy. To make it simple let us assume that you will invest ωW in Apple (AAPL) and $(1-\omega)W$ in Netflix (NFLX), where W denotes the amount of money you would like to invest, and $\omega \in [0, 1]$ dictates the proportion allocated to each investment. Let R_A and R_N denote, respectively, the daily return (see Equation (0.1) if you don't remember what returns are) of Apple and Netflix. To make things simple we assume that the returns R_A and R_N are jointly normally distributed so we can write

$$\mathbf{R} \overset{iid}{\sim} \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Sigma}),$$

where

$$\mathbf{R} = \begin{bmatrix} R_A \\ R_N \end{bmatrix}, \quad \boldsymbol{\mu} = \begin{bmatrix} \mu_A \\ \mu_N \end{bmatrix}, \text{ and } \boldsymbol{\Sigma} = \begin{bmatrix} \sigma_A^2 & \sigma_{AN} \\ \sigma_{AN} & \sigma_N^2 \end{bmatrix}.$$

Using these assumptions, the classical portfolio optimization problem, which would allow you to determine a "good" value of ω, can be stated as follows: Given our initial wealth W, the investment problem is to decide how much should be invested in our first asset

(Apple) and in our second asset (Netflix). As mentioned earlier, we assume that $\omega \in [0, 1]$, implying that it is only possible to buy the two assets (i.e. *short positions* are not allowed). Therefore, to solve our investment problem we must choose the value of ω which would maximize your personal *utility*. Informally speaking, the utility represents a measurement of the "usefulness" that is obtained from your investment. To consider a simple case, we will assume that you are a particularly *risk averse* individual (i.e. you are looking for an investment that is as sure and safe as possible) and as such you want to pick the value of ω providing you with the smallest investment risk. We can then determine the optimal value of ω as follows. First, we construct a new random variable, say Y, which denotes the return of your portfolio. Since you invest ωW in Apple and $(1-\omega)W$ in Netflix, it is easy to see that

$$Y = [\omega R_A + (1-\omega)R_N]\, W.$$

In general the risk and variance of an investment are two different things but in our case we assume that the return $\mathbf{R}$ is normally distributed and in this case the variance can perfectly characterize the risk of our investment. Therefore, we can define the risk of our investment as the following function of ω

$$f(\omega) = \text{Risk}(Y) = \text{Var}(Y) = \left[\omega^2\sigma_A^2 + (1-\omega)^2\sigma_N^2 + 2\omega(1-\omega)\sigma_{AN}\right] W^2.$$

The function $f(\omega)$ is minimized for the value ω^* which is given by

$$\omega^* = \frac{\sigma_N^2 - \sigma_{AN}}{\sigma_A^2 + \sigma_N^2 - 2\sigma_{AN}}. \tag{0.6}$$

If you are interested in understanding how Equation (0.6) was obtained, click on the button below:

Minimum Variance Portfolio Derivation

To obtain ω^* we first differentiate the function $f(\omega)$ with respect to ω, which gives

$$\frac{\partial}{\partial \omega} f(\omega) = \left[2\omega\sigma_A^2 - 2(1-\omega)\sigma_N^2 + 2(1-2\omega)\sigma_{AN}\right] W^2 \tag{0.7}$$

Then, we define ω^* as

$$\omega^* \ : \frac{\partial}{\partial \omega} f(\omega) = 0. \tag{0.8}$$

Therefore, we obtain

$$\omega^* \left(\sigma_A^2 + \sigma_N^2 - 2\sigma_{AN}\right) = \sigma_N^2 - \sigma_{AN}, \tag{0.9}$$

which simplifies to

$$\omega^* = \frac{\sigma_N^2 - \sigma_{AN}}{\sigma_A^2 + \sigma_N^2 - 2\sigma_{AN}}. \tag{0.10}$$

Finally, we verify that our result is a minimum by considering the second derivative, i.e.

$$\frac{\partial^2}{\partial \omega^2} f(\omega) = 2W \left[\sigma_A^2 + \sigma_N^2 - 2\sigma_{AN}\sigma_{AN}\right]. \tag{0.11}$$

Since W is strictly positive, all that remains to conclude our derivation is to verify that $\sigma_A^2 + \sigma_N^2 - 2\sigma_{AN}\sigma_{AN} \leq 0$. In fact, this is a well known inequality which is a direct consequence of the Tchebychev inequality. However, here is a simpler argument to understand why this is the case. Indeed, it is obvious that $\mathrm{Var}(R_A - R_N) \leq 0$ and we also have $\mathrm{Var}(R_A - R_N) = \sigma_A^2 + \sigma_N^2 - 2\sigma_{AN}$. Thus, we obtain

$$\mathrm{Var}(R_A - R_N) = \sigma_A^2 + \sigma_N^2 - 2\sigma_{AN} \leq 0,$$

which verifies that our result is a minimum.

Using (0.6), we obtain that the expected value and variance of our investment are given by

$$\text{Expected Value Investment} = \left[\omega^* \mu_A + (1-\omega^*)\mu_N\right] W,$$
$$\text{Variance Investment} = \left[(\omega^*)^2\sigma_A^2 + (1-\omega^*)^2\sigma_N^2 + 2\omega^*(1-\omega^*)\sigma_{AN}\right] W^2.$$

In practice, the vector $\boldsymbol{\mu}$ and the matrix $\boldsymbol{\Sigma}$ are unknown and must be estimated using historical data. In the code below, we compute the optimal value of ω based on (0.6) by using the last five years of historical data for the two stocks considered. For simplicity we set W to one but note that W plays no role in determining ω^*.

```
# Load quantmod
library(quantmod)

# Download data
today <- Sys.Date()
five_years_ago <- seq(today, length = 2, by = "-5 year")[2]
getSymbols("AAPL", from = five_years_ago, to = today)
getSymbols("NFLX", from = five_years_ago, to = today)

# Compute returns
Ra <- na.omit(ClCl(AAPL))
Rn <- na.omit(ClCl(NFLX))

# Estimation of mu and Sigma
Sigma <- cov(cbind(Ra, Rn))
mu <- c(mean(Ra), mean(Rn))

# Compute omega^*
omega_star <- (Sigma[2, 2] - Sigma[1, 2])/(Sigma[1, 1] + Sigma[2, 2] - 2*Sig

# Compute investment expected value and variance
mu_investment <- omega_star*mu[1] + (1 - omega_star)*mu[2]
var_investment <- omega_star^2*Sigma[1,1] + (1 - omega_star)^2*Sigma[2,2] +
  2*omega_star*(1 - omega_star)*Sigma[1,2]
```

From this code, we obtain $\omega^* \approx 85.59\%$. In the table below we

TABLE 0.7: Expected value and variance of stocks and our investment

	Apple	Netflix	Investment
Expected value	0.0010546	0.0020199	0.0011937
Variance	0.0002009	0.0006986	0.0001864

compare the empirical expected values and variances of the stocks as well as those of our investment:

```
investment_summary <- matrix(NA, 2, 3)
dimnames(investment_summary)[[1]] <- c("Expected value", "Variance")
dimnames(investment_summary)[[2]] <- c("Apple", "Netflix", "Investment")
investment_summary[1, ] <- c(mu, mu_investment)
investment_summary[2, ] <- c(diag(Sigma), var_investment)
knitr::kable(investment_summary)
```

In Table 0.7 and the plot below we can observe that Netflix has high risk and high return. Apple seems like a safer investment in terms of risk but lower in expected return. Our portfolio optimization investment, however, seems to be in a good area, meaning that it has low risk and a return that is between the two stocks mentioned above. Finally, we provide a graphical representation of the obtained results in the figure below.

FIGURE 4: Graphical representation of Apple, Netflix and min-variance portfolio based on these two assets.

0.20 Array

Arrays allow to construct **multidimensional** objects. Indeed, vectors and matrices are respectively objects in one and two dimensions while arrays can in be in an arbitrary n dimension. Essentially,

matrices are a special case of arrays which is only in two dimensions. Matrices are commonly used in Statistics while arrays are much rarer but nevertheless worth being aware of. To consider a simple using arrays we will revisit an example presented in the previous section where we constructed a matrix containing the number of Grand Slam won and the win rate of the five players considered in Table 0.5. This matrix was constructed as follows:

```
players <- c("Andy Murray", "Rafael Nadal", "Stan Wawrinka",
             "Novak Djokovic", "Roger Federer")
grand_slam_win <- c(9, 15, 5, 12, 18)
win_percentage <- c(78.07, 82.48, 63.96, 82.77, 81.80)
mat <- cbind(grand_slam_win, win_percentage)
rownames(mat) <- players
colnames(mat) <- c("GS win", "Win rate")
mat
```

```
##                GS win Win rate
## Andy Murray         9    78.07
## Rafael Nadal       15    82.48
## Stan Wawrinka       5    63.96
## Novak Djokovic     12    82.77
## Roger Federer      18    81.80
```

The data used to construct this matrix we collected in mid-July 2017 and suppose that we now would like to add to this existing the object the updated numbers from mid-September 2017. This can be done by constructing an array as shown in the example below.

```
# Constuct "empty" array
my_array <- array(NA, dim = c(5, 2, 2))
dimnames(my_array)[[1]] <- players
dimnames(my_array)[[2]] <- c("GS win", "Win rate")
dimnames(my_array)[[3]] <- c("07-15-2017", "09-13-2017")

# Construct matrix
```

```
my_array[,,1] <- mat
my_array[,,2] <- cbind(c(9, 16, 5, 12, 19),
                       c(78.07, 82.49, 63.96, 82.77, 81.80))
my_array
```

```
## , , 07-15-2017
##
##                GS win Win rate
## Andy Murray         9    78.07
## Rafael Nadal       15    82.48
## Stan Wawrinka       5    63.96
## Novak Djokovic     12    82.77
## Roger Federer      18    81.80
##
## , , 09-13-2017
##
##                GS win Win rate
## Andy Murray         9    78.07
## Rafael Nadal       16    82.49
## Stan Wawrinka       5    63.96
## Novak Djokovic     12    82.77
## Roger Federer      19    81.80
```

Like what we experimented with matrices, we can extract and manipulate information.

```
length(my_array)    # length is 20, i.e. 5x2x2 = 20
```

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

```
dim(my_array)       # dimensions are 5x2x2
```

```
## [1] 5 2 2
```

```
is.array(my_array)  # yes it is an array!
```

```
## [1] TRUE
```

Subsetting the elements of an array works similarly to what we already discussed with matrices. Below are a few examples:

```
my_array[,,1]
```

```
##                GS win Win rate
## Andy Murray         9    78.07
## Rafael Nadal       15    82.48
## Stan Wawrinka       5    63.96
## Novak Djokovic     12    82.77
## Roger Federer      18    81.80
```

```
my_array[1,,2]
```

```
##   GS win Win rate
##     9.00    78.07
```

```
my_array[,1,]
```

```
##                07-15-2017 09-13-2017
## Andy Murray             9          9
## Rafael Nadal           15         16
## Stan Wawrinka           5          5
## Novak Djokovic         12         12
## Roger Federer          18         19
```

Finally, we can assess if some our five won any Grand Slam between mid-July and mid-September 2017 by using the code below:

```
players[my_array[,1,2] > my_array[,1,1]]
```

```
## [1] "Rafael Nadal"  "Roger Federer"
```

0.21 List

A list is one of the commonly used **heterogeneous** data structures, which depicts a generic "vector" containing other object types. For example, we can create a list containing numeric character and logical vectors as well as matrices. Here we can create a list that contains different element types. (numeric, character, logical, matrix)

```
# List elements
num_vec <- c(188, 140)
char_vec <- c("Height", "Weight", "Length")
logic_vec <- rep(TRUE, 8)
my_mat <- matrix(0, nrow = 5, ncol = 5)

# List initialization
(my_list <- list(num_vec, char_vec, logic_vec, my_mat))
```

```
## [[1]]
## [1] 188 140
##
## [[2]]
## [1] "Height" "Weight" "Length"
##
## [[3]]
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
##
## [[4]]
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    0    0    0    0    0
## [2,]    0    0    0    0    0
## [3,]    0    0    0    0    0
```

```
## [4,]    0    0    0    0    0
## [5,]    0    0    0    0    0
```

Alternatively, it is possible to add named labels to the elements of your list. For example,

```
# List initialization with custom names
(my_list <- list(number = num_vec, character = char_vec,
                 logic = logic_vec, matrix = my_mat))
```

```
## $number
## [1] 188 140
##
## $character
## [1] "Height" "Weight" "Length"
##
## $logic
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
##
## $matrix
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    0    0    0    0    0
## [2,]    0    0    0    0    0
## [3,]    0    0    0    0    0
## [4,]    0    0    0    0    0
## [5,]    0    0    0    0    0
```

Subsetting is very similar to what we have already discussed. Indeed, we have

```
# Extract the first and third element
my_list[c(1, 3)]
```

```
## $number
## [1] 188 140
##
## $logic
```

```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

```
# Compare these two subsets
my_list[1]
```

```
## $number
## [1] 188 140
```

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

```
## [1] 188 140
```

```
# Using labels to subset
my_list$number
```

```
## [1] 188 140
```

```
my_list$matrix
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    0    0    0    0    0
## [2,]    0    0    0    0    0
## [3,]    0    0    0    0    0
## [4,]    0    0    0    0    0
## [5,]    0    0    0    0    0
```

```
my_list$matrix[,3] # Extract third column of matrix
```

```
## [1] 0 0 0 0 0
```

It is interesting to notice the difference between `my_list[1]` and `my_list[[1]]`. To understand this difference suppose that we are interested in retrieving the second element of the vector `num_vec` which is stored in list `my_list`. In general most people use of the two ways presented below:

```
# These mean the same thing!
my_list[[1]][2]
```

```
## [1] 140
```

```
my_list$number[2]
```

```
## [1] 140
```

Simply including one bracket like `my_list[1]` will return the first element of the list, but will retain the `list` structure. `my_list` is a list, and `my_list[1]` is also a list. In other words, one bracket retains the class information, while using two brackets simplifies the list into a numeric vector.

```
# type of object
typeof(my_list)
```

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

```
typeof(my_list[1])
```

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

Therefore, `my_list[1][2]` **does not work** and if you wish to use `my_list[1]` you will have to a syntax similar to the ones presented below:

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

```
## [1] 140
```

```
my_list[1]$number[2]
```

```
## [1] 140
```

Most people generally uses `[[` to select any single element, whereas `[` returns a list of the selected elements.

0.22 Dataframe

A data frame is a **heterogeneous** data structure used for storing data tables. A data frame is the most common way of storing data in R, and it has a 2D structure and shares properties of both the matrix and the list. The table contains lists of equal-length, same-type vectors, and most datasets will have a data frame format.

We can create a data frame using data.frame()

```
### Creation

players <- c("Andy Murray", "Rafael Nadal", "Stan Wawrinka",
             "Novak Djokovic", "Roger Federer")

grand_slam_win <- c(9, 15, 5, 12, 18)

date_of_birth <- c("15 May 1987", "3 June 1986", "28 March 1985",
                   "22 May 1981", "8 August 1981")

country <- c("Great Britain", "Spain", "Switzerland",
             "Serbia", "Switzerland")
ATP_ranking <- c(1, 2, 3, 4, 5)

prize_money <- c(60449649, 85920132, 30577981, 109447408, 104445185)

tennis <- data.frame(date_of_birth, grand_slam_win, country,
                     ATP_ranking, prize_money)

dimnames(tennis)[[1]] <- players
tennis
```

```
##                date_of_birth grand_slam_win       country ATP_ranking
## Andy Murray      15 May 1987              9 Great Britain           1
## Rafael Nadal      3 June 1986             15         Spain           2
## Stan Wawrinka   28 March 1985              5   Switzerland           3
## Novak Djokovic    22 May 1981             12        Serbia           4
## Roger Federer   8 August 1981             18   Switzerland           5
##                prize_money
## Andy Murray       60449649
## Rafael Nadal      85920132
## Stan Wawrinka     30577981
## Novak Djokovic   109447408
## Roger Federer    104445185
```

Notice that each column has its own type. We can check if we have achieved our goal by using:

```
is.data.frame(tennis)
```

```
## [1] TRUE
```

0.22.1 Combination

Data frames can also be combined. Let say we want to add some information to the table above (e.g. the player's height) and if he is right-handed or left-handed.

We can do so by using `cbind()` - column bind and `rbind()` - row bind:

```
height <- c(1.90, 1.85, 1.83, 1.88, 1.85)
hand <- c("R","L","R","R","R")

(tennis <- cbind(tennis, data.frame(height, hand)))
```

```
##                date_of_birth grand_slam_win       country ATP_ranking
## Andy Murray      15 May 1987              9 Great Britain           1
## Rafael Nadal      3 June 1986             15         Spain           2
```

```
## Stan Wawrinka  28 March 1985              5   Switzerland           3
## Novak Djokovic   22 May 1981             12        Serbia           4
## Roger Federer  8 August 1981             18   Switzerland           5
##                prize_money height hand
## Andy Murray       60449649   1.90    R
## Rafael Nadal      85920132   1.85    L
## Stan Wawrinka     30577981   1.83    R
## Novak Djokovic   109447408   1.88    R
## Roger Federer    104445185   1.85    R
```

0.22.2 Subsetting

Like for vectors, it is also possible to subset the values that we have stored in our data frames. Since data frames possess the characteristics of both lists and matrices: if you subset with a single vector, they behave like lists; if you subset with two vectors, they behave like matrices.

Let us say we want only want to know the country and date of birth of the players.

```
# There are two ways to select columns from a data frame
# Like a list:
tennis[c("country", "date_of_birth")]
```

```
##                      country date_of_birth
## Andy Murray    Great Britain   15 May 1987
## Rafael Nadal           Spain   3 June 1986
## Stan Wawrinka    Switzerland 28 March 1985
## Novak Djokovic        Serbia   22 May 1981
## Roger Federer    Switzerland 8 August 1981
```

```
# Like a matrix
tennis[, c("country", "date_of_birth")]
```

```
##                      country date_of_birth
```

```
## Andy Murray    Great Britain   15 May 1987
## Rafael Nadal           Spain   3 June 1986
## Stan Wawrinka    Switzerland 28 March 1985
## Novak Djokovic        Serbia   22 May 1981
## Roger Federer    Switzerland 8 August 1981
```

We can extract column names of dataframes by using `names`.

```
names(tennis)
```

```
## [1] "date_of_birth"  "grand_slam_win" "country"        "ATP_ranking"
## [5] "prize_money"    "height"         "hand"
```

```
# To access a single element, let say the date of birth,
# you can also use:
tennis$date_of_birth
```

```
## [1] 15 May 1987   3 June 1986   28 March 1985 22 May 1981   8 August 1981
## 5 Levels: 15 May 1987 22 May 1981 28 March 1985 ... 8 August 1981
```

We can change the ordering of the columns outputted by simply changing the order within the `c()` subsetting.

```
# Note the difference between
tennis[, c(1, 3)]
```

```
##                date_of_birth       country
## Andy Murray      15 May 1987 Great Britain
## Rafael Nadal     3 June 1986         Spain
## Stan Wawrinka  28 March 1985   Switzerland
## Novak Djokovic   22 May 1981        Serbia
## Roger Federer  8 August 1981   Switzerland
```

```
# and
tennis[, c(3, 1)]
```

```
##                       country date_of_birth
```

```
## Andy Murray    Great Britain   15 May 1987
## Rafael Nadal           Spain   3 June 1986
## Stan Wawrinka    Switzerland 28 March 1985
## Novak Djokovic        Serbia   22 May 1981
## Roger Federer    Switzerland 8 August 1981
```

Let us say we want only want to know right-handed players. We can subset `rows` using similar syntax as above.

```
# We will talk more about == in the next chapter
# This represents all players with hand equal to "R"
tennis[hand=="R",]
```

```
##                date_of_birth grand_slam_win       country ATP_ranking
## Andy Murray      15 May 1987              9 Great Britain           1
## Stan Wawrinka  28 March 1985              5   Switzerland           3
## Novak Djokovic   22 May 1981             12        Serbia           4
## Roger Federer  8 August 1981             18   Switzerland           5
##                prize_money height hand
## Andy Murray       60449649   1.90    R
## Stan Wawrinka     30577981   1.83    R
## Novak Djokovic   109447408   1.88    R
## Roger Federer    104445185   1.85    R
```

```
# Note what this returns
hand=="R"
```

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

Often data are better view when it is sorted. The function `order` helps do this, which can be utilized with subsetting to output a custom sorted dataframe based on a column(s).

Below we will order the tennis players by the number of grand slam wins. Set `decreasing=TRUE` to order the rows in descreasing order.

```
# increasing order
tennis[order(tennis[,"grand_slam_win"]),]
```

```
##                date_of_birth grand_slam_win       country ATP_ranking
## Stan Wawrinka  28 March 1985              5   Switzerland           3
## Andy Murray      15 May 1987              9 Great Britain           1
## Novak Djokovic   22 May 1981             12        Serbia           4
## Rafael Nadal     3 June 1986             15         Spain           2
## Roger Federer  8 August 1981             18   Switzerland           5
##                prize_money height hand
## Stan Wawrinka     30577981   1.83    R
## Andy Murray       60449649   1.90    R
## Novak Djokovic   109447408   1.88    R
## Rafael Nadal      85920132   1.85    L
## Roger Federer    104445185   1.85    R
```

```
# descreasing order
tennis[order(tennis[,"grand_slam_win"], decreasing = TRUE),]
```

```
##                date_of_birth grand_slam_win       country ATP_ranking
## Roger Federer  8 August 1981             18   Switzerland           5
## Rafael Nadal     3 June 1986             15         Spain           2
## Novak Djokovic   22 May 1981             12        Serbia           4
## Andy Murray      15 May 1987              9 Great Britain           1
## Stan Wawrinka  28 March 1985              5   Switzerland           3
##                prize_money height hand
## Roger Federer    104445185   1.85    R
## Rafael Nadal      85920132   1.85    L
## Novak Djokovic   109447408   1.88    R
## Andy Murray       60449649   1.90    R
## Stan Wawrinka     30577981   1.83    R
```

0.22.3 Example: Maps

Dataframe objects can be optimized for different applications, as many packages use dataframes as input or output objects. For example, we will use a package, `ggmap` to map simple cities. We will talk more about the functionality of the package later. We can extract the latitude - longitude information of the specific cities of the tennis players using `geocode` within `ggmap`.

```
library(ggmap)
birth_place <- c("Glasgow, Scotland", "Manacor, Spain", "Lausanne, Switzerla
                 "Belgrade, Serbia", "Basel, Switzerland")
birth_coord <- geocode(birth_place, source = "dsk")
```

Furthermore, we can create new columns of dataframes using vectors that we created before.

```
birth_coord$Players <- players
birth_coord$GS <- grand_slam_win
birth_coord
```

```
##         lon      lat        Players GS
## 1 -4.249989 55.86115    Andy Murray  9
## 2  3.209550 39.56964   Rafael Nadal 15
## 3  6.632820 46.51600  Stan Wawrinka  5
## 4 20.465130 44.80401 Novak Djokovic 12
## 5  7.573270 47.55840  Roger Federer 18
```

```
is.data.frame(birth_coord)
```

```
## [1] TRUE
```

Let's represent this information graphically. We haven't seen how to make graph yet so don't worry too much about the details of how this graph is made.

```
library(mapproj)
map <- get_map(location = 'Switzerland', zoom = 4)
ggmap(map) + geom_point(data = birth_coord,
             aes(lon, lat, col = Players, size = GS)) +
             scale_size(name="Grand Slam Wins") +
             xlab("Longitude") + ylab("Latitude")
```

As we see, we can produce various output using dataframe objects.

0

Control Structures

0.23 Introduction

When you're building a larger or more complex program than the examples we considered previously, we need to use various **control structures** to control the "flow" of our actions. Essentially, a control structure is a "block" of code that analyzes variables and chooses a direction in which to go based on given parameters. These pieces of code represent the most basic decision-making processes in computing.

There exist essentially two kinds of control structures.

- The first one allows to determine whether a given condition is satisfied and select an appropriate response. A simple analogy to our day-to-day life would be "**if** it's raining outside, **then** take an umbrella" (we will come back to this example in the next section).
- The second kind of control structure allows to repeat of a block of code multiple times. For example, such an approach can be used to convert a color image to a gray-scale by applying the same operation(s) (i.e. same code) to each pixel of the image. In this chapter, we will first discuss the two kinds of control structures previously mentioned and then present various examples to help build our intuition.

0.24 Selection control statements

Suppose that we are interested in creating a simple code to check if it rained over the last hour and, if this is the case, lead us to decide whether we should take an umbrella today. To write such a code we essentially need three things:

1) Find out how much it rained in the last hour at our location. Such information is now easily accessible through various websites and we can for example used the R package `rwunderground` to access this information. Note that you will need to create an account and request an API key before being able to use it (see package documentation[37] for more details). Then, the amount of precipitation (in inches) in the last hour can be retrieved using the code below:

```
library(rwunderground)
(rain <- conditions(set_location(zip_code = "16802"), message = FALSE)$preci
```

```
## [1] 0
```

2) Construct a logical (or Boolean) variable created from the variable `rain` to assess whether or not an umbrella is needed. For example, we can say that if we see signs of rain in the last hour, then we should take an umbrella. This can be done using the code below and in Section @ref(logical_operators) we will discuss how to construct logical variables in more detail.

[37] https://cran.r-project.org/web/packages/rwunderground/rwunderground.pdf

```
(umbrella <- rain > 0)
```

```
## [1] FALSE
```

3) Finally, we need to select operators based on the logical variables constructed in the previous step to bring everything together. For example, we could use the `if/else` statement presented below. This simple code will print "*You should probably take an umbrella*" if the logical variable `umbrella` is `TRUE` and print "*An umbrella is probably not necessary*", otherwise.

```
if (umbrella){
  print("You should probably take an umbrella")
}else{
  print("An umbrella is probably not necessary")
}
```

```
## [1] "An umbrella is probably not necessary"
```

0.24.1 Logical Operators

Logical operators are very commonly used in programming to create (or return) logical (boolean) variables. In general, logical operations take place by comparing one or more variables following specific rules. The table below summarizes the commonly used logical operators:

Command	Description	Example	Result
x > y	x greater than y	`4 > 3`	TRUE
x >= y	x greater or equals to y	`1 >= 1`	TRUE
x < y	x less than y	`c(12 < 20, 1 < 1)`	TRUE, FALSE
x <= y	x less than or equals to y	`12 <= 1`	FALSE
x == y	x equal to y	`c(2 == 2, 1 == 2)`	TRUE, FALSE
x != y	x not equal to y	`c(2 != 2, F != T)`	FALSE, TRUE

Command	Description	Example	Result
`!`x	Not x	`c(!(2 > 1), !FALSE)`	FALSE, TRUE
x `||`y	x or y (not vectorized)	`(1 > 1) || (2 < 3)`	TRUE
x `|`y	x or y (vectorized)	`c(1 > 1, F) || c(T, 2 < 3)`	TRUE
x `&&` y	x and y (not vectorized)	`TRUE && TRUE`	TRUE
x `&` y	x and y (vectorized)	`c(TRUE, T) & c(TRUE, F)`	TRUE, FALSE
xor(x,y)	test if only one is TRUE	`xor(TRUE, TRUE)`	FALSE
`all`(x)	test if all are TRUE	`all(c(T, F, F))`	FALSE
`any`(x)	test if one or more is TRUE	`any(c(T, F, F))`	TRUE

There is a subtle difference between `||`and `|` (or `&&` and `&`). Indeed, when using `x && y` or `x || y` it implicitly assumes that `x` and `y`are of length 1 and when these are applied to vectors **only the first elements** of each vector will be considered. For example, `c(TRUE,FALSE) || c(FALSE, FALSE)` is equivalent to `TRUE || FALSE` and will only return `TRUE`. On the other hand, `&` and `|` can be applied to vectors and `c(TRUE,FALSE) || c(FALSE, FALSE)` is equivalent to `c(TRUE || FALSE, FALSE || FALSE)` and will return `TRUE FALSE`. It is also worth mentioning that `TRUE | c(FALSE, FALSE)` is equivalent to `c(TRUE || FALSE, TRUE || FALSE)` (i.e. the `TRUE` is used twice) and will return `TRUE TRUE`. These differences are a common source of bugs.

When using `&` or `|` to create/return logical variables we have to be aware of something called **short-circuit evaluation** which can create bugs that may be difficult to find. Indeed, suppose that we interested in using an expression such as `x & y` and that if the variable `x` is `FALSE` then `y` will not be evaluated. The idea behind this evaluation is that, regardless of the value of `y`, the expression `x & y` should be `TRUE`. However, this implicitly assumes that `y` does not contain any mistakes and if this were indeed to be the case, this could create bugs that would be hard to find. For example, consider the expression `y = x && 2 == NULL`, then if `x` is `FALSE` `y` will be `FALSE` while if `x` is `TRUE` `y` will be `NA`, which

obviously is likely to be problematic. Similarly, when considering an expression such as `x | y`, the variable `y` will only be evaluated if `x` is `FALSE`.

0.24.2 Selection Operators

Selection operators govern the flow of code. We can observe if/else statements everywhere, no matter what language.

0.24.2.1 `if` Statements

The most basic selection operator is called an `if` statement. Essentially, an `if` statement tells R to do a certain task for a certain case. In plain English it would correspond to something like, "If this is true, do that" or as in our motivating example "If it rains take an umbrella". In R, you would say:

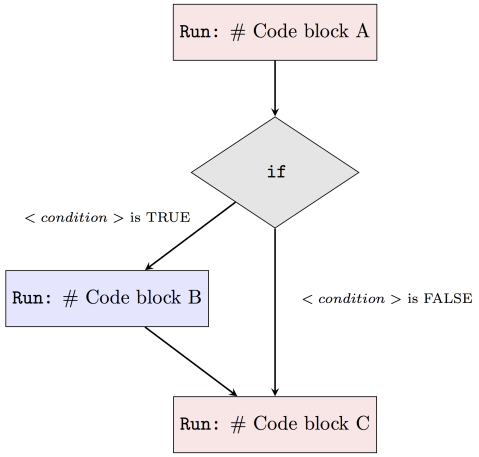
```
if (<this is TRUE>){
  <do that>
}
```

or

```
if (<it rains>){
  <take an umbrella>
}
```

In general, we can represent an `if` statement using the following diagram:

```
# Code block A
if (< condition >){
    # Code block B
}
# Code block C
```



The `<conditon>` denotes a **logical** variable that is used determine if the code inside of `{ }` will be evaluated. For example, if `<condition>` is `FALSE` then our program will run `Code block A` and then `Code block C`. On the other hand, if `<condition>` is `TRUE` our program will run `Code block A`, `Code block B` and finally `Code block C`.

Below we present two examples where two `if` statements are used. In the first example, we use an `if` statement to compute the absolute value of a variable called `x`:

```
x <- 4

if (x < 0){
  x <- -x
}

x
```

```
## [1] 4
```

Now we change `x` to a negative value:

```
x <- -4

if (x < 0){
  x <- -x
}

x
```

```
## [1] 4
```

In the second example, we use an `if` statement to assess if `x` is an even number and, if this is the case, we print a simple message.

```
if (x %% 2 == 0){
  print(paste(x, "is an even number"))
}
```

```
## [1] "4 is an even number"
```

```
x <- 3

if (x %% 2 == 0){
  print(paste(x, "is an even number"))
}
```

0.24.2.2 `if/else` Statements

Often when we write a program we want to tell R what to do when our condition is `TRUE` and also what to do when it is `FALSE`. Of course, we could do something like:

```
if (condition){
  plan A
}
```

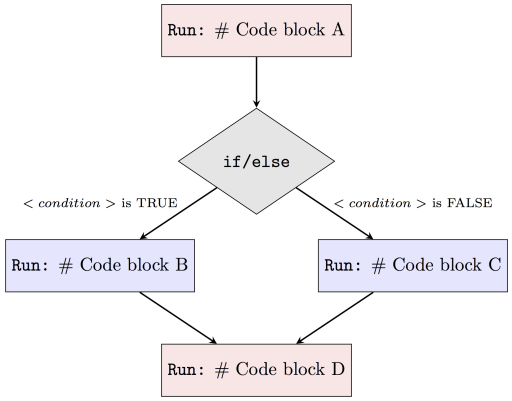
```
if (!condition){
  plan B
}
```

However, the above syntax is somewhat clumsy and one generally would prefer to use an `if/else` statement. In plain English it would correspond to something like, "If this is true, then do plan A otherwise do plan B". In R we would write:

```
if (condition){
  plan A
}else{
  plan B
}
```

Similarly to an `if` statement, we can represent an `if/else` statement using the diagram below:

```
# Code block A
if (< condition >){
    # Code block B
}else{
    # Code block C
}
# Code block D
```



Therefore, when `<condition>` is `TRUE` our program will run `Code block A`, `Code block B` and then `Code block D` while when `<condition>` is `FALSE` it will run `Code block A`, `Code block B` and finally `Code block D`. Using this new tool we can revisit our previous example on even numbers to include a custom message in the case of an odd number. This can be done as follows:

```
x <- 2

if (x %% 2 == 0){
  print(paste(x, "is an even number"))
}else{
  print(paste(x, "is an odd number"))
}
```

```
## [1] "2 is an even number"
```

```
x <- 3

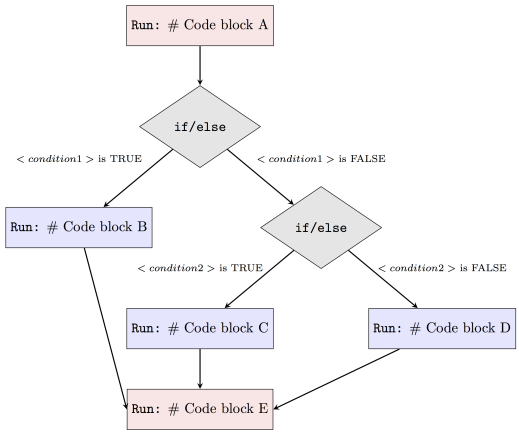
if (x %% 2 == 0){
  print(paste(x, "is an even number"))
}else{
  print(paste(x, "is an odd number"))
}
```

```
## [1] "3 is an odd number"
```

0.24.2.3 `if/elseif/else` Statements

We can also control the flow of statements with multiple if/else statements, depending on the number of cases we consider. Typically, the more cases we have, the more else if statements. An example visualization is provided below.

```
# Code block A
if (< condition1 >){
    # Code block B
}else if (< condition2 >){
    # Code block C
}else{
    # Code block D
}
# Code block E
```



0.24.2.4 `switch` Statement

Earlier we mentioned that if/elseif/else statements allow us to choose between TRUE and FALSE when there are two options. With the above idea, when there are more than two options we can simply use nested if/else statements. What about when we have roughly 20 options to choose from? In this case, if we stick to using nested if/else statements, the programming logic will be very difficult to understand. The switch statement option in R programming can help us handle this type of problems more effectively.

Before we put switch statements into the case study, let's first start to understand the basic switch statement syntax in R.

```
switch (Expression,
        "Option 1" = Execute this statement when the expression result matche
        "Option 2" = Execute this statement when the expression result matche
        "Option 3" = Execute this statement when the expression result matche
        ....
        ....
        "Option N" = Execute this statement when the expression result matche
        Default Statements
)
```

- The `expression` value is the condition which R will evaluate. This should be either integer or character.
- When the `expression` value matches more than one option, the first matching statement will be returned.
- Besides the conditional statement, R also allows us to add the `default statement`, which will be returned when none of the listed options are matched.

With the above syntax in mind, let's now check a simple case study with R switch statements.

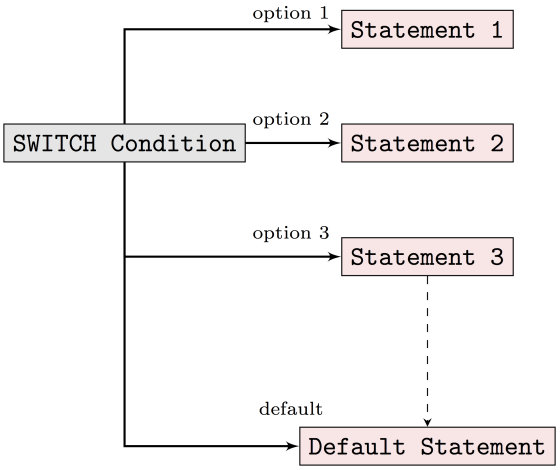
```
number1 <- 20
number2 <- 5
operator = readline(prompt="Please enter any ARITHMETIC OPERATOR: ")

switch(operator,
       "+" = print(paste("Addition of two numbers is: ", number1 + number2))
       "-" = print(paste("Subtraction of two numbers is: ", number1 - number
       "*" = print(paste("Multiplication of two numbers is: ", number1 * num
       "/" = print(paste("Division of two numbers is: ", number1 / number2))
)
```

When running the above code in R, we can expect results like:

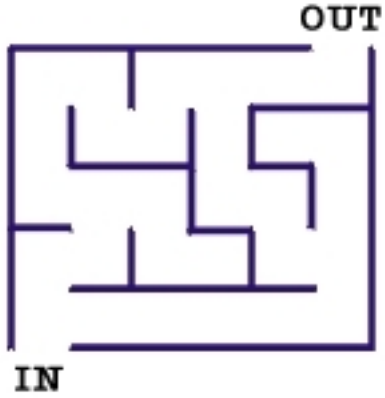
```
> number1 = 20
> number2 = 5
> operator = readline(prompt="Please enter any ARITHMETIC OPERATOR: ")
Please enter any ARITHMETIC OPERATOR: +
>
> switch(operator,
+        "+" = print(paste("Addition of two numbers is: ", number1 + number2)),
+        "-" = print(paste("Subtraction of two numbers is: ", number1 - number2)),
+        "*" = print(paste("Multiplication of two numbers is: ", number1 * number2)),
+        "/" = print(paste("Division of two numbers is: ", number1 / number2))
+ )
[1] "Addition of two numbers is:  25"
> operator = readline(prompt="Please enter any ARITHMETIC OPERATOR: ")
Please enter any ARITHMETIC OPERATOR: *
> switch(operator,
+        "+" = print(paste("Addition of two numbers is: ", number1 + number2)),
+        "-" = print(paste("Subtraction of two numbers is: ", number1 - number2)),
+        "*" = print(paste("Multiplication of two numbers is: ", number1 * number2)),
+        "/" = print(paste("Division of two numbers is: ", number1 / number2))
+ )
[1] "Multiplication of two numbers is:  100"
```

In conclusion, we can visualize the R switch statement as follows:



0.24.3 Iterative Control Statements

Iterative control statements are an extremly useful R method for repeating a task multiple times. For example, pretend we are trying to build a program that solves a simple maze like the one below.



It would be pretty easy to simply draw out the possible solutions with the naked eye. However, if you were actually inside the maze, you would need to narrow your perspective and think of a strategy,

like marking paths you have already visited. Suppose that we have a strategy in mind to solve this problem. For example, we could consider the following approach at any given point in time:

- if there is space in front of you, go forward
- else, if there is space on your right, turn right
- else, if there is space on your left, turn left
- else, [all three sides (forward, left, right) are closed] turn around

This strategy could easily be programmed using the methods discussed in Section 0.24 but to actually program it you would need to repeat this strategy until you escaped the maze. Your strategy could for example be written as:

```
repeat (until "you are free"){
  if ("space in front of you"){
    go forward
  }else if ("space on your right"){
    turn right
  }else if ("space on your left"){
    turn left
  }else{
    turn around
  }
}
```

Try to develop an algorithm to exit the maze presented above. Could you escape? Though it might take some time (and probably would not correspond to the fastest strategy) one can show that this method can solve any maze (assuming of course that a solution exists). In this section we discuss the elements necessary to actually program the "`repeat (until "you are free")`" part of our algorithm.

0.24.3.1 `for` Loops

Let's consider the following situation:

```
print(1)
print(2)
print(3)
print(4)
print(5)
print(6)
```

This seems feasible when we only need to print out the numbers from 1 to 6. What if we want to print out the numbers from 1 to 100? It is such a clumsy and tedious approach if we keep repeating `print()` line by line to do so.

For loops in R help us solve this type of problems much more effectively in only a couple lines of codes. It allows us to repeat the same part of code, or say a sequence of same instructions, under certain conditions without explicitly writing out the code everytime. For example, to do exactly the same as the above example with for loops, all we need is:

```
for (number in 1:6){
  print(number)
}
```

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

To interpret the above for loops in plain English, we can read it as "When the number is in the sequence {1,2,3,4,5,6}, we will print this number until we exhaust all numbers in the sequence". As we can see obviously, this approach simplifies our code so much more as we only need to write the code chunk (`print()` in this case) once, not six times, not to mention when we want to print out all

the numbers from 1 to 100 compared to repeating `print()` line by line for 100 times.

The basic syntax of for loops in R is as follows:

```
for (some specified sequence to loop over){
  execute this statement when we still haven not reached the last item in the
}
```

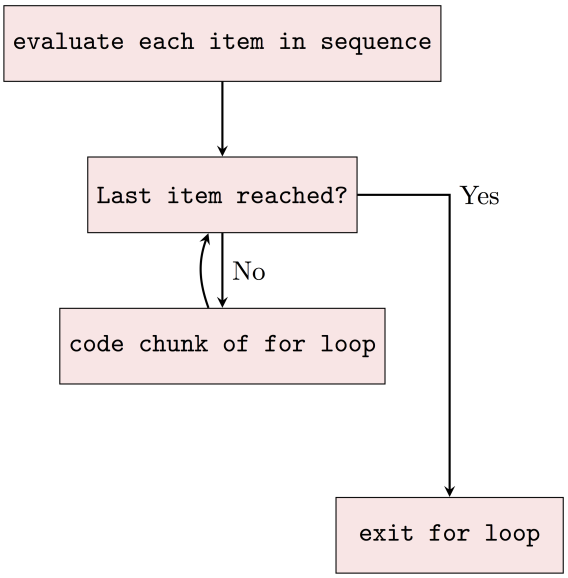
`Next` also helps when you want to skip for some cases in which you don't want the statement to be executed. To see how `next` works together with for loops in R, let's consider the following more mathematical example when you want to print out all the odd numbers between 1 to 10.

```
for (i in 1:10) {
  if (!i %% 2){
    next
  }
  print(i)
}
```

```
## [1] 1
## [1] 3
## [1] 5
## [1] 7
## [1] 9
```

From the results, we notice that R automatically skip to run `print(i)` when `!i %%2` is TRUE. To interpret the above in plain English, we can read it as "if the number i cannot be divided by 2, we skip the below and consider the NEXT number in the sequence". In this case, we can still use for loops when we have some exceptional cases.

In conclusion, we can visualize the R for loops as follows:



Up till now, we can see that for loops can simplify our work a lot when we need to execute a sequence of same instructions for multiple times. However, there are still disadvantages to use for loops in R. We may hardly notice now with only a few simple iterations to run. But indeed, R can be very slow when running iteration, especially when we need to do a lot of big iterations with big data. Sometimes we may prefer to avoid using for loops in R by using other approaches since R supports vectorization, which will allow for much faster calculations. For example, solutions that make use of loops are less efficient than vectorized solutions that make use of apply functions, such as lapply and sapply. It's often better to use the latter.

Apply methods are often used to make operations on some structured data. For example, let's simulate a matrix of some random samples.

```
(exp_mat = matrix(rnorm(60),ncol = 3))
```

```
##              [,1]        [,2]        [,3]
##  [1,]  0.94264912  0.97129400  1.68529946
```

```
##  [2,] -1.54433424 -0.12059055  1.22173473
##  [3,]  1.92951252 -1.04643002  0.61444018
##  [4,] -0.75991686  0.20699467  0.86218858
##  [5,]  1.08951791 -0.06078078 -1.06752316
##  [6,] -0.35065936 -0.57768288  1.03731534
##  [7,] -0.18588595 -0.40293968  0.38930071
##  [8,]  0.26631478 -2.22241120  0.19439612
##  [9,]  0.07945905 -1.08220515 -0.47541793
## [10,]  0.62391283  1.88244921  0.26669057
## [11,] -1.37242333  0.22497235 -0.52147618
## [12,] -0.22614800  0.08530340  0.20213233
## [13,] -0.15417994 -0.70940862  0.37684181
## [14,] -0.28688260  1.12938605 -1.35845137
## [15,] -1.14549570  0.46605330  1.11646689
## [16,] -0.57833306  0.29616826 -1.24839644
## [17,]  1.20423147  0.69292618 -1.84019251
## [18,]  0.77388894 -0.11523996  1.53426210
## [19,]  1.79602743 -0.18210614 -1.66679156
## [20,] -0.54578433  0.08785389 -0.04871862
```

To get the mean of each column, we can calculate each column mean separately or use a for loop.

```
# Observe what this does
mean(exp_mat)
```

```
## [1] 0.03921963
```

```
# Calculate separately
mean(exp_mat[,1])
```

```
## [1] 0.07777353
```

```
mean(exp_mat[,2])
```

```
## [1] -0.02381968
```

```
mean(exp_mat[,3])
```

```
## [1] 0.06370505
```

```
# Using a for loop
for(i in 1:3){
  print(mean(exp_mat[,i]))
}
```

```
## [1] 0.07777353
## [1] -0.02381968
## [1] 0.06370505
```

However, using `apply`, we can do this in a very simple manner.

```
apply(exp_mat, 2, mean)
```

```
## [1]  0.07777353 -0.02381968  0.06370505
```

```
# The 2 indicates operations on columns and not rows
```

We will see how these approaches can help accelerate our work later.

0.24.3.2 `while` Statements

As an alternative of for loops, while statement in R is another approach that can help us repeat the code chunk only when specific conditions are satisfied. For example, we can use while statement to do exactly the same as above to print out all numbers from 1 to 6 as followings:

```
i = 1
while (i <= 6){
```

```
  print(i)
  i = i+1
}
```

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

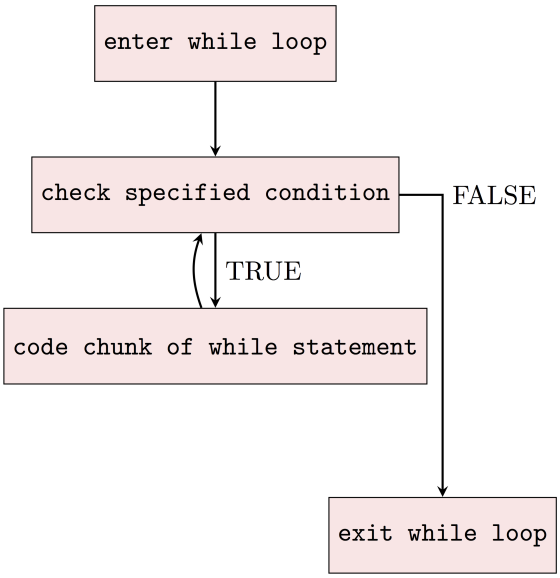
The above code can be interprented in plain English as: "Let's start with number 1. When the number i is still smaller than or equal to 6, we print it out. Then we consider the next integer of it and stop when we finish all the numbers smaller than or equal to 6."

As we can see, while statement is used to iterate until a specific condition is met. To make use of while statement in R, we introduce the basic syntax of it as following:

```
while (some specified condition)
{
   statement to execute when the above condition is satisfied
}
```

Here we evaluate the condition and if it is `TRUE`, then we execute the statement inside the code chunk. Once we finish running the statement, we evaluate the condition again and exit the loops when the condition is evaluated as `FALSE`.

In conclusion, we can visualize how the while statement works in R as following:



0.25 Example: The Bootstrap

The (non-parametric) bootstrap was introduced by **?** as a numerical method to provide a simple estimator of the distribution of an estimator. This method became rapidly very popular since it is completely automatic, requires no theoretical derivation and is (almost) always available no matter how complicated our estimator of interest is. Moreover, most statistical methods are based on various asymptotic approximations (often through the central limit theorem) that can however deliver poor results in finite sample settings. Bootstrap techniques generally enjoy better finite sample performance while paying a price in terms of computation burden. A formal discussion of the properties of (non-parametric) bootstrap techniques is far beyond the scope of this textbook but it's actually quite simple to understand its algorithm. To motivate this discussion, suppose that we ask 10 students how much time they work at

home for their STAT 297 class. Say we obtain the following results (in hours):

```
student_work <- c(0, 0, 0, 0, 0, 0.25, 0.75, 0.75, 1, 1.25, 6)
```

We can compute the mean time spent

```
mean_hour <- mean(student_work)
```

Moreover, we compute a simple confidence interval of the **average number** of hours spent by a student enrolled in STAT 297. Since we have no reason to believe that the number of hours spent working at home for this class is not Gaussian, we can construct an asymtotic confidence interval using:

$$\bar{x} \pm z_{1-\alpha/2} \frac{\hat{\sigma}}{\sqrt{n}},$$

where $\bar{x}$ is the sample mean, α is the significance level which delivers $z_{1-\alpha/2}$ quantile of standard Gaussian distribution and $\hat{\sigma}$ is the sample standard deviation (we assume that estimating the standard deviation has no impact on the distribution of $\bar{x}$). In R, this interval can therefore be computed as follows:

```
alpha <- 0.05
n <- length(student_work)
sd_hour <- sd(student_work)
z <- qnorm(1 - alpha/2)
mean_hour + c(-1, 1)*z*sd_hour/sqrt(n)
```

```
## [1] -0.1256494  1.9438313
```

Based on this confidence interval your instructor is very disappointed since the confidence interval includes 0, indicating that it is possible that the students study on average zero hours. But does this interval makes sense? The lower bound of the interval is negative implying that students can also have negative hours

of study. This of course makes no sense indicating that with this sample size the asymptotic Gaussian approximation makes little sense.

To solve this issue, the (non-parametric) bootstrap is a convenient and appropriate tool to compute more adequate finite sample confidence intervals. Letting $\mathbf{X} = [X_1 \ \ldots \ X_n]$ denote the sample (in our case `student_work`), the way the bootstrap works is as follows:

- **Step 1:** Let $i = 1$.
- **Step 2:** Construct a new sample, say $\mathbf{X}^*$, by sampling **with replacement** n observations from $\mathbf{X}$.
- **Step 3:** Compute the average of $\mathbf{X}^*$ which we will denote as $\bar{X}_i$. Let $i = i + 1$ and if $i < B$ go to **Step 2** otherwise go to **Step 4**.
- **Step 4**: Compute the empirical quantiles of $\bar{X}_i$.

Here is a simple function to implement this approach:

```
# Number of boostrap replications
B <- 500

# Compute the length of vector
n <- length(student_work)

# Confidence level
alpha <- 0.05

# Initialisation of
boot_mean <- rep(NA, B)

# Step 1
for (i in 1:B){
  # Step 2
  student_work_star <- student_work[sample(1:n, replace = TRUE)]

  # Step 3
  boot_mean[i] <- mean(student_work_star)
```

```
}

# Step 4
quantile(boot_mean, c(alpha/2, 1 - alpha/2))
```

```
##      2.5%     97.5%
## 0.2045455 2.0801136
```

Based on this result your instructor is relieved since they know that, at a level of confidence of 95%, you are spending at least more than 10 minutes on your course work.

How would you modify the above code to obtain the same output using the `while` control?

A researcher developed a new drug to help patients recover after a surgery. To investigate if her drug is working as expected, she starts by creating a simple test experiment on mice. In this experiment, the researcher records the survival times of 14 mice after a test surgery. Out of the 14 mice, 8 of them are given the new drug while the remaining ones are used as a control group (where no treatement is given). Her results (in days) are the following:

- **Treatement** group: 38, 76, 121, 86, 52, 69, 41 and 171;
- **Control** group: 18, 12, 52, 82, 102 and 25.

She believes that the median survival time is a "good" way to measure effectiveness of her drug. Based on this experiment, she obtains that the median survival time for the control group is 38.5 days while it is 72.5 days for the treatement group. She wonders if you could help her to find an approriate (bootstrap) confidence interval for the difference of the medians. Using this result, do you believe that the drug increases the median survial time of mice after the test surgery?

0.26 Example: Random Walk

The term *random walk* was first introduced by Karl Pearson in the early nineteen-hundreds. There exist a large range of random walk processes. For example, one of the simplest forms of a random walk process can be explained as follows: suppose that you are walking on campus and your next step can either be to your left, your right, forward or backward (each with equal probability). The code illustrates how to program such a random process:

```
# Control seed
set.seed(1992)

# Number of steps
steps <- 10^5

# Direction probability (i.e. all direction are equally likely)
probs <- c(0.25, 0.5, 0.75)

# Initial matrix
step_direction <- matrix(0, steps+1, 2)

# Start random walk
for (i in seq(2, steps+1)){
  # Draw a random number from U(0,1)
  rn = runif(1)

  # Go right if rn \in [0,prob[1])
  if (rn < probs[1]) {step_direction[i,1] = 1}

  # Go left if rn \in [probs[1], probs[2])
  if (rn >= probs[1] && rn < probs[2]) {step_direction[i,1] = -1}

  # Go forward if rn \in [probs[2], probs[3])
```

```
  if (rn >= probs[2] && rn < probs[3]) {step_direction[i,2] = 1}

  # Go backward if rn \in [probs[3],1]
  if (rn >= probs[3]) {step_direction[i,2] = -1}
}

# Cumulative steps
position = data.frame(x = cumsum(step_direction[, 1]),
                      y = cumsum(step_direction[, 2]))

# Let's make a nice graph...
# Graph parameters
color = "blue4"
xlab = "X-position"
ylab = "Y-position"
pt_pch = 16
pt.cex = 2
main = paste("Simulated 2D RW with", steps, "steps", sep = " ")
hues = seq(15, 375, length = 3)
pt_col = hcl(h = hues, l = 65, c = 100)[1:2]
par(mar = c(5.1, 5.1, 1, 2.1))

# Main plot
plot(NA,  xlim = range(position[,1]),
          ylim = range(range(position[,2])),
          xlab = xlab, ylab = ylab, xaxt = 'n',
          yaxt = 'n', bty = "n", ann = FALSE)
win_dim = par("usr")

par(new = TRUE)
plot(NA, xlim = range(position[,1]), ylim = c(win_dim[3], win_dim[4] + 0.09*
       xlab = xlab, ylab = ylab, xaxt = 'n', yaxt = 'n', bty = "n")
  win_dim = par("usr")

# Add grid
grid(NULL, NULL, lty = 1, col = "grey95")
```

```
# Add title
x_vec = c(win_dim[1], win_dim[2], win_dim[2], win_dim[1])
y_vec = c(win_dim[4], win_dim[4],
            win_dim[4] - 0.09*(win_dim[4] - win_dim[3]),
            win_dim[4] - 0.09*(win_dim[4] - win_dim[3]))
polygon(x_vec, y_vec, col = "grey95", border = NA)
text(x = mean(c(win_dim[1], win_dim[2])), y = (win_dim[4] - 0.09/2*(win_dim[

# Add axes and box
lines(x_vec[1:2], rep((win_dim[4] - 0.09*(win_dim[4] - win_dim[3])),2), col
box()
axis(1, padj = 0.3)
y_axis = axis(2, labels = FALSE, tick = FALSE)
y_axis = y_axis[y_axis < (win_dim[4] - 0.09*(win_dim[4] - win_dim[3]))]
axis(2, padj = -0.2, at = y_axis)

# Add trajectory
lines(position, type = "l", col = color, pch = 16)

# Start and end points
points(c(0,position[steps+1,1]), c(0,position[steps+1,2]), cex = pt.cex, col

# Legend
leg_pos = c(min(position[,1]), max(position[,2]))
legend(leg_pos[1], leg_pos[2], c("Start","End"),
      col = pt_col, pch = pt_pch, pt.cex = pt.cex, bty = "n")
```

Such processes inspired Karl Pearson's famous quote that

> "*the most likely place to find a drunken walker is somewhere near his starting point.*"

Empirical evidence of this phenomenon is not too hard to find on a Friday night.

0.27 Example: Monte-Carlo Integration

0.27.1 Introduction

Monte Carlo integration is a powerful technique for numerical integration. It is particularly useful to evaluate integrals of "high-dimension". A detailed (and formal) discussion of this method is clearly beyond the scope of this class and we shall restrict our attention to the most basic form(s) of Monte Carlo integration and briefly discuss the rational behind this method.

Originally, such Monte Carlo methods were known under various names among which *statistical sampling* was probably the most commonly used. In fact, the name *Monte Carlo* was popularized by several researchers in Physics, including Stanislaw Ulam, Enrico Fermi and John von Neumann. The name is believed to be a reference to a famous casino in Monaco where Stanislaw Ulam's uncle would borrow money to gamble. Enrico Fermi was one of the first to use this technique which he employed to study the properties of a newly-discovered neutron in the 1930s. Later for example, these methods played a central role in many of the simulations required for the Manhattan project.

With this in mind, let us give an idea of this approach by supposing we are interested in computing the following integral:

$$I = \int_a^b f(x)dx.$$

Of course, this integral can be approximated by a Riemann sum:

$$I \approx \Delta x \sum_{i=1}^{n} f(a + (i-1)\Delta x),$$

where $\Delta x = \frac{b-a}{n}$ and the idea behind this approximation is that as the number of partitions n increases, the Riemann sum will become closer and closer to I. Also (under some technical conditions), we have that

$$I = \lim_{n\to\infty} \Delta x \sum_{i=1}^{n} f(a + (i-1)\Delta x).$$

In fact, the rational of a Monte Carlo integral is quite close to the Riemann sum since, in its most basic form, we approximate I by averaging samples of the function $f(x)$ at uniform random points within the interval $[a, b]$. Therefore, the Monte Carlo *estimator* of I is given by

$$\hat{I} = \frac{b-a}{B} \sum_{i=1}^{B} f(X_i), \tag{0.12}$$

where $X_i = a + U_i(b-a)$ and $U_i \sim \mathcal{U}(0,1)$. In fact, (0.12) is quite intuitive since $\frac{1}{B}\sum_{i=1}^{B} f(X_i)$ represents an estimation of the average value of $f(x)$ in the interval $[a, b]$ and thus $\hat{I}$ is simply the average value times the length of the interval, i.e. $(b-a)$. If you would like to learn more about the properties of Monte-Carlo integrals, click on the button below:

Properties

A more formal argument on the validity of this approach can be found in analyzing the statistical properties of the estimator $\hat{I}$. In order to do so, we start by considering its expected value

$$\mathbb{E}\left[\hat{I}\right] = \frac{b-a}{B} \sum_{i=1}^{B} \mathbb{E}\left[f(X_i)\right] = \frac{b-a}{B} \sum_{i=1}^{B} \int f(x)g(x)dx,$$

where $g(x)$ denotes the pdf of X_i. Since $X_i \sim \mathcal{U}(a, b)$ it follows that

$$g(x) = \begin{cases} \frac{1}{b-a} & \text{if } x \in [a, b] \\ 0 & \text{if } x \notin [a, b] \end{cases}$$

Therefore, we have

$$\mathbb{E}\left[\hat{I}\right] = \frac{b-a}{B}\sum_{i=1}^{B}\int_a^b \frac{f(x)}{b-a}dx = \int_a^b f(x)dx = I,$$

Since X_i are iid, the same can be said about $f(X_i)$ and therefore by the **Strong Law of Large Numbers** we have that $\hat{I}$ converges *almost surely* to I, which means that

$$\mathbb{P}\left(\lim_{B\to\infty}\hat{I} = I\right) = 1.$$

This result implies that as the number of simulations B goes to infinity we can guarantee that the solution will be exact.

Unfortunately, this result doesn't give us any information on how quickly this estimate converges to a "sufficiently accurate" solution for the problem at hand. This can be done by studying the variance of $\hat{I}$ and its *rate of convergence*. Indeed, we have

$$\begin{aligned}
\text{var}\left(\hat{I}\right) &= \left(\frac{b-a}{B}\right)^2 \sum_{i=1}^{B}\left\{\mathbb{E}\left[f^2(X_i)\right] - \mathbb{E}^2\left[f(X_i)\right]\right\} \\
&= \frac{1}{B^2}\sum_{i=1}^{B}\left\{(b-a)\int_a^b f^2(x)dx - \left(\int_a^b f(x)dx\right)^2\right\} \\
&= \frac{(b-a)I_2 - I^2}{B}
\end{aligned}$$

where $I_2 = \int_a^b f^2(x)dx$. A simple estimator of this quantity is given by

$$\hat{I}_2 = \frac{b-a}{B}\sum_{i=1}^{B} f^2(X_i),$$

and therefore using $\hat{I}$ we obtain:

$$\widehat{\text{var}}\left(\hat{I}\right) = \frac{(b-a)\hat{I}_2 - \hat{I}^2}{B} = \frac{b-a}{B^2}\sum_{i=1}^{B}\left[(b-a)f^2(X_i) - f(X_i)\right]$$

Thus, it is easy to see that the rate of convergence of $\widehat{\text{var}}\left(\hat{I}\right)$ is B^{-1} and we may write $\text{var}\left(\hat{I}\right) = \mathcal{O}(B)$. This implies that if we wish to reduce the error (or standard deviation) by half, we need to quadruple B. Such a phenomon is very common in many fields of research such as Statistics where this is often called the *curse of dimensionality*.

0.27.2 Implementation

The function `mc_int()`, which is available in the `stat297` package, implements the above method. This functions has four inputs:

- `x_range`: A vector containing the integration domain, i.e. a and b,
- `fun`: A string containing the function you wish to integrate where x is used to indicate the variable of integration,
- `B`: A numeric value to denote the number of Monte-Carlo replications,
- `seed`: A numeric value to control the seed of the random number generator.

For example, if you want to estimate

$$\int_1^3 \frac{\exp\left(\sin(x)\right)}{x}dx,$$

using 10^4 Monte-Carlo replications, you can use the following command:

```
library(stat297)
mc_int(x_range = c(1,3), fun = "exp(sin(x))/x", B = 10^5)
```

```
## $I
## [1] 2.558104
##
## $var
## [1] 1.401222e-05
##
## $fun
## [1] "exp(sin(x))/x"
##
## $x_range
## [1] 1 3
##
## $B
## [1] 1e+05
##
## attr(,"class")
## [1] "MCI"
```

At this point, it is probably a good idea to try to programm this yourself and to compare your results (and code!) with the function `mc_int()`. This should be rather easy to implement but one thing that may be a little delicate is how to pass the function you wish to integrate as an input. A possible way of doing this is to use a string so that, for example, if we have to integrate the function $\sin(x)$ you could simply write `fun = sin(x)` when calling your function. This implies that we should be able to "transform" a string into a function that we can evaluate, which is something that we can achieve by combining the functions `eval` and `parse`. An example is provided below:

```
my_fun = "x^2"
x = 0:3
eval(parse(text = my_fun))
```

```
## [1] 0 1 4 9
```

If you're having trouble understanding what these functions are doing have a look at their help files by writing `?eval` and `?parse`.

0.27.3 Application to the Normal Distribution

Suppose that $X \sim \mathcal{N}(4, 1.25^2)$ and that we are interested in computing the following probability $\mathbb{P}(1 < X < 4.5)$. The probability density of the normal distribution for a random variable with mean μ and variance σ^2 is given by:

$$f(x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(x-\mu)^2}{2\sigma^2}\right).$$

Therefore, the probability we are interested in can be written as the following integral

$$\mathbb{P}(1 < X < 4.5) = \int_1^{4.5} \frac{1}{\sqrt{3.125\pi}} \exp\left(-\frac{(x-4)^2}{3.125}\right).$$

Analytically, this is not an easy problem and of course there are many ways to solve it. However, we could try to use a Monte-Carlo integral to solve it. For example:

```
my_fun = "1/sqrt(3.125*pi)*exp(-((x - 4)^2)/3.125)"
(prob = mc_int(x_range = c(1, 4.5), fun = my_fun, B = 10^7))
```

```
## $I
## [1] 0.6471691
##
## $var
## [1] 1.449985e-08
##
## $fun
## [1] "1/sqrt(3.125*pi)*exp(-((x - 4)^2)/3.125)"
##
## $x_range
## [1] 1.0 4.5
##
## $B
## [1] 1e+07
```

```
##
## attr(,"class")
## [1] "MCI"
```

Based on this result, we can write $\mathbb{P}(1 < X < 4.5) \approx 64.72\%$ with a standard error of about 0.01%. We can compare our results with what we would obtain with the function `pnorm` which provides a nearly exact result:

```
pnorm(4.5, 4, 1.25) - pnorm(1, 4, 1.25)
```

```
## [1] 0.6472242
```

This shows that our estimation is within one standard error of a near perfect result.

0.27.4 Application to Nonelementary Integrals

In layman's terms, a nonelementary integral of a given (elementary) function is an integral that cannot be expressed as an elementary function. The French mathematicien Joseph Liouville was the first to prove the existance of such a nonelementary integral. A well-known example of such integrals are the Fresnel integrals that have been used for a very wide range of applications going from the computation of electromagnetic field intensity to roller roster design. These integrals are defined as:

$$S(y) = \int_0^t \sin\left(x^2\right) dx \qquad \text{and} \qquad C(y) = \int_0^y \cos\left(x^2\right) dx.$$

In this example, we will only consider $S(y)$. In general it is believed that the most convenient way of evaluating these functions up to an arbitrary level of precision is to use a power series representation that converges for all y:

$$S(y) = \sum_{i=1}^{\infty} (-1)^n \, \frac{y^{4i+1}}{(2i+1)\,!\,(4i+3)}.$$

In this example, we will study the estimation of $S(\pi)$ as well as the *precision* of this estimation.

```
B = 4^(4:13)
results = matrix(NA, length(B), 2)
for (i in 1:length(B)){
  mc_res = mc_int(c(0, 2), "sin(x^2)", B = B[i], seed = i+12)
  results[i, ] = c(mc_res$I, sqrt(mc_res$var))
}


trans_blue = hcl(h = seq(15, 375, length = 3), l = 65, c = 100, alpha = 0.15)
plot(NA, xlim = range(B), ylim = range(cbind(results[, 1] + results[,2],
      results[, 1] -results[,2])), log = "x", ylab = "Estimated Integral",
      xlab = "Number of Simulations B", xaxt = 'n')
grid()
axis(1, at = B, labels = parse(text = paste("4^", 4:13, sep = "")))
polygon(c(B, rev(B)), c(results[, 1] + results[, 2],
                        rev(results[, 1] - results[, 2])), border = NA, col =
lines(B, results[, 1], type = "b", col = "blue4", pch = 16)
abline(h = 0.8048208, col = "red4", lty = 2)
legend("topright", c("Estimated value", "Standard error interval", "Good appr
       pch = c(16, 15, NA), lwd = c(1, NA, 1), lty = c(1, NA, 2),
       pt.cex = c(1, 2, NA), col = c("blue4", trans_blue, "red4"))
```

0

Functions

This chapter aims at highlighting the main advantages, characteristics, arguments and structure of functions in R. As you might already know, a function is a collection of logically connected commands and operations that allow the user to input some arguments and obtain a desired output (based on the given arguments) without having to rewrite the mentioned code each time that specific output is needed. Indeed, a common task in statistical research for example consists in running some simulation studies which give support (or not) to the use of a certain method of inference. In this case, it's not efficient to rewrite the code each time it is needed within a simulation study because it would lead to lengthy code and increased risk of miss-coding.

In the following paragraphs, we will describe an example for which we will build a function that allows to respond to the related research question. Following from the previous chapter where we discussed matrix algebra in R, at the end of this chapter we will therefore implement a function that allows us to perform least-squares regression and inference using these notions of matrix algebra. Indeed, it may be interesting to understand the behavior of this estimator in different simulation settings and it would not be practical to rewrite the series of commands to obtain the least-squares estimator in each setting. For this reason, a function that implements this estimator would be more appropriate and, in fact, this function already exists in the base R functions and is called `lm()`. However, we will learn how to build our own least-squares regression function and compare its results with those of `lm()` to check if they're the same. To do so, we will consider a dataset in which linear regression is used to study the age of the universe.

Example: The Hubble Constant

The example dataset we will study is taken from **?** which discusses data collected from the Hubble Space Telescope key project containing information on the velocity and relative distance of 24 galaxies. This information has been used to compute the "Hubble constant" which is a fixed parameter that links velocity and distance of celestial bodies through which it is possible to compute the age of the universe based on the "Big Bang" theory. The link is given by this simple linear relationship

$$y = \beta x,$$

where y represents the velocity while x is the distance between galaxies. Once the Hubble constant is known, its inverse (i.e. β^{-1}) gives the age of the universe based on the big bang theory.

Therefore we will use the abovementioned dataset to estimate Hubble's constant to then get an estimate of the age of the universe. This dataset can be found in the `gamair` package under the name `hubble` and when plotting the two variables of interest in a scatterplot there appears to be a positive linear relationship between the two variables.

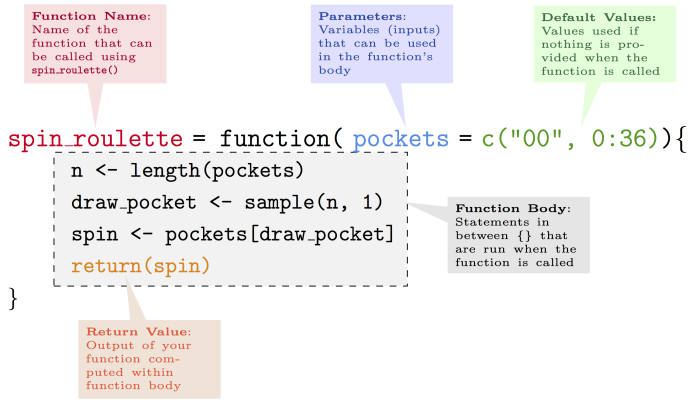
```
# Load gamair library and retrieve Hubble dataset
library(gamair)
data(hubble)

# Plot data
plot(y = hubble$y, x = hubble$x, col="darkblue", pch = 20, main="Distance vs
     ylab = "Velocity (in km/s)", xlab = "Distance (in Megaparsecs)")
grid()
```

By the end of this chapter we will therefore be able to build a function to obtain an estimate of β and, consequently, an estimate of the age of the universe based on the big bang theory (as well as a means of testing whether a Creationist hypothesis on the age of the universe is reasonable based on the latter theory).

0.28 R functions

In order to build our own functions, the next sections will present the main features of functions in R by studying their main components. The following annotated example gives a brief overview of a simple function that draws a random number issued from the "spin" of an American roulette [38]:



As can be noticed, we first define the name we want to give to the function.

It is important to make sure that the function name is specific and does not correspond to other functions that may need to be used within your work session. If two functions have the same

[38] This scheme is inspired from diagrams by Prof. Bob Rudis and James Balamuta.

name, just as with other R objects, the function that will be used is the last one that has been defined within the R working session.

Once we have defined the name, we then attribute a function to this name by using the `function` syntax to which we assign some parameters (or attributes). The latter are the values or data that the user will input in order for the function to deliver the desired output. The latter is subsequently obtained through the code constituting the *body* of the function. Once the code has made the necessary computations, the function needs to know which results are to be given as an output. This can be done, for example, using the `return` syntax.

A couple of simple examples can be functions that compute the sample mean:

```
my_mean <- function (x) {
  average <- sum(x, na.rm = T)/sum(!is.na(x))
  return(average)
}
```

or multiplies two numbers:

```
my_prod <- function (a, b) {
  prod <- a*b
  return(prod)
}
```

Using these functions, we can compute the sample mean of the annual precipitation in US cities (that can be found in the base R dataset `precip`):

```
my_mean(precip)
```

```
## [1] 34.88571
```

or the product of 265 and 83:

```
my_prod(265, 83)
```

```
## [1] 21995
```

A particular case of function building are so-called "infix" functions that allow to create new operators that carry out specific types of computations. So, instead of defining the name of a function, you can define the symbol to be used in order to make use of that function. For example, to sum two numbers in R you can do as follows:

```
1 + 2
```

```
## [1] 3
```

which is simply a predefined infix function that can also be used as follows:

```
`+`(1, 2)
```

```
## [1] 3
```

Therefore the `+` operator is the result of a predefined infix function in R. However, all user-defined infix functions must start and end with the `%` symbol. For example, using an operator that we define as `%^%`, we can deliver the product of two numbers that is zero if the product is actually negative:

```
`%^%` <- function(a, b) {
  prod = a*b
  (prod > 0)*prod
}
```

This infix function can now be used through the operator as follows:

```
2 %^% 2
```

```
## [1] 4
```

```
2 %^% -1
```

```
## [1] 0
```

Having described the general structure of an R function, let us go more into detail by analysing the three main components to R functions:

- **body**: the code lines containing the commands and operations which deliver the desired output;
- **arguments**: the inputs the user gives to the function which will determine the value or type of output of a function;
- **environment**: every R function is built within an enviroment of reference from which to source possible input values and/or other functions necessary for it to work.

The next sections will therefore go more into detail regarding these components and describe how they contribute to the correct building of a function in R.

0.29 Creating functions in R

As an example for the following sections, let us implement a function that takes two arguments and multiplies them according to the type of object they are (i.e. scalar, vector or matrix). To do so, we will first build a skeleton for this function:

```
gen_prod <- function (...) {
  ...
}
```

As you can see, we find a name for the function we want to build, which in this case is `gen_prod`, and specify that we are going to attribute a `function` to this name. Following this assignment, we find a set of curved brackets `(...)` followed by a set of curly brackets `{...}` which should include the *arguments* and *body* of the function respectively. The next two sections will describe these two components and then discuss the third component which is the function *environment*.

0.29.1 Function arguments

Before implementing a function, we first need to ask ourselves what is the basic information that we need in order to obtain the desired output. In the case of a general product, as mentioned above, the only information that is essential to perform the operation is the first element and the second element we wish to multiply. These will therefore have to be the elements we need to provide to our function in order for it to deliver the desired product and, in R, we can provide the names we want for them (say `first_arg` and `second_arg`):

```
gen_prod <- function (first_arg, second_arg) {
  ...
}
```

We will build this function such that the first argument has a higher (or equal) dimension than the second (e.g. the first is a vector while the second is another vector or a scalar). Let us suppose that `a = matrix(1:8, 4, 2)` is a 4×2 matrix and `b = matrix(8:1, 2, 4)` is a 2×4 matrix. Given that this is a matrix multiplication,

these arguments need to be entered in the correct order (such that the dimensions correspond):

```
gen_prod(a, b)
```

In the above syntax, we used so-called *positional matching* where arguments to the function must be entered in the same order as they are defined in the function itself. If these are entered in the wrong order the function will either give the incorrect output or give errors since the format of the input could be incompatible with the body of the function. In general, it is therefore possible to use positional matching for the first and most important arguments of a function, but it is generally suggested to use names for the arguments. For our function, we could consequently define the arguments as follows:

```
gen_prod <- function (first_arg = matrix(rnorm(9), 3, 3),
                      second_arg = matrix(rnorm(9), 3, 3)) {
  ...
}
```

You can notice that we assigned the value `matrix(rnorm(9), 3, 3)` to both of these variables. This is their "default" value which, if not specified otherwise, is used as input for the function (which in this case would deliver a 3×3 matrix result of the product of the two matrices whose elements are generated randomly from a standard normal distribution).

Supposing that we leave the arguments of the functions defined as above, there are different ways to specify these arguments. When calling a function, R first matches the arguments through *perfect matching*, meaning that it searches for the arguments matching the exact name (in our case "first_arg" and "second_arg"). Failing to match the arguments by their exact name, R then searches for the arguments through *prefix matching*, meaning that it uses the first letters of the argument names to match them. For example, we could call the function in the following manner:

```
gen_prod(second_arg = b, first_arg = a)
```

or even

```
gen_prod(fi = a, second = b)
```

So, as long we correctly specify the beginning of the argument's name and as long as it's not ambigiuous (meaning that its name cannot be confused with that of another argument), then it is possible to provide only part of the argument's name and R will recognise and correctly associate the provided value with the corresponding variable.

Finally, failing to match arguments in any of the above cases, R uses positional matching and therefore assigns values to the variables based on the order they have been entered when calling the function. We could therefore go back to using the function like we did at the start by specifying `gen_prod(a, b)`.

It is possible to also specify arguments in terms of the default value of other arguments. For example, we could define the arguments as follows `a = matrix(rnorm(9), 3, 3), b = 2*a`. There are many other interesting ways of specifying argument values and they can be seen, for example, in `?` .

A special framework in which to specify arguments for a general function is the case where the arguments are objects that belong to a specific class for which a base function can be used. A simple example is the "`ts`" class of objects in R for which a function exists such that the user simply needs to call the `plot()` function (without needing to know that the function behind is the `plot.ts()` function). Let us for example suppose that some function has created a matrix whose elements represent pixel intensities of an image and that this function has assigned a class to this matrix called `"pixel"`. In the following code we therefore simply assign this class to an object called `image`.

```
image <- matrix(rgamma(100, shape = 2), 10, 10)
class(image) = "pixel"
```

If we were to plot this, we would obtain the following plot:

```
plot(image)
```

which simply plots the values for given coordinates. Given that this is not what we want, let us create a function that allows the user to simply use the `plot()` function which automatically recognises the object and plots a heatmap of the pixel intensity:

```
plot.pixel <- function (mat) {
  suppressWarnings(heatmap(mat, Colv=NA, Rowv=NA, labRow=NA, labCol=NA, scal
}
```

If we use the `plot()` function now, we obtain the following:

```
plot(image)
```

which produces the desired output simply using the general-purpose function `plot()`.

To conclude, additional arguments can be left to be specified by

the user. This is the case, for example, when there is the possibility of specifying arguments for other functions that are used within the function itself. This can be done by using the argument `...` which can be added to any function and will match user-specified arguments that do not match the predefined ones in the function. An example of this type of argument is again given by the base `plot()` function in R where the predefined arguments are `x` and `y` (representing the coordinates of the points in the plot) while other optional arguments, such as graphical parameters, can be added taking advantage of the `...` argument (e.g. the user could specify the argument `type = "l"` even though this is not included among the specified arguments of the function `plot()`). This argument is particularly useful when you want to obtain values for other function arguments but don't want to specify their names in advance.

0.29.2 Function body

The body of a function is simply the set of instructions and (possible) other functions that use the arguments provided by the user and computes the desired output. In our case, we need to put into practice a series of tools we learned in the previous chapter (e.g. matrix operations) in order to implement a function that delivers multiplication of objects of different nature. Let us start by delivering the product of the objects `first_arg` and `second_arg`:

```
gen_prod <- function (first_arg = matrix(rnorm(9), 3, 3),
                      second_arg = matrix(rnorm(9), 3, 3)) {
  first_arg%*%second_arg
}
```

If the user doesn't provide any arguments to the function, this will automatically return a 3×3 matrix (product of two 3×3 matrices built using randomly generated observations from a standard normal). Otherwise, the user can enter the elements of multiplication to obtain their output of interest. For this reason, it would be appropriate that the first and second argument given by

the user had compatible dimensions. But what if the latter isn't the case? When building a function body it is important to consider the possible problems ("bugs") that could arise if the inputs the user has given cannot be managed by the body of code you have written. For example, let us suppose that the user provides two 3 $\times$ 2 matrices as the first and second arguments:

```
gen_prod(matrix(rnorm(6), 3, 2), matrix(rnorm(6), 3, 2))
```

```
## Error in first_arg %*% second_arg: non-conformable arguments
```

In this case we see that the function outputs an error and it would be appropriate to insert a checking procedure at the start of our function in order to consider all possible objects that can be multiplied and issue explanations that are useful to the user in order for them to realise what the problem is. We could therefore add a check procedure before we perform the multiplication:

```
gen_prod <- function (first_arg = matrix(rnorm(9), 3, 3),
                      second_arg = matrix(rnorm(9), 3, 3)) {
  if (dim(first_arg)[2] == dim(second_arg)[1]) {
    first_arg%*%second_arg
  } else {
    stop("Object dimensions are not compatible")
  }
}
```

As you can see in the example above, we have used a control statement in which we check whether the dimensions for matrix multiplication are respected. If they are, then the function returns the desired product while it returns an error message if this is not the case. The latter is done via the use of the `stop()` function which outputs the text `Error in ...: Object dimensions are not compatible` if the dimensions are not compatible:

```
gen_prod(matrix(rnorm(9),3,3), matrix(rnorm(12),4,3))
```

```
## Error in gen_prod(matrix(rnorm(9), 3, 3), matrix(rnorm(12), 4, 3)): Object
```

When a problem is detected in the body of a function, there may not necessarily be the need to interrupt the execution of the function with an error message. Indeed, in the above example, we could allow the function to check if the number of columns in the second object is compatible with that of the first and, if so, transpose the second matrix in order to obtain the correct multiplication with a warning message notifying the user that this has been done:

```
gen_prod <- function (first_arg = matrix(rnorm(9), 3, 3),
                      second_arg = matrix(rnorm(9), 3, 3)) {
  if (dim(first_arg)[2] == dim(second_arg)[1]) {
    first_arg%*%second_arg
  } else {
    if (dim(first_arg)[2] == dim(second_arg)[2]) {
      warning("Second object has been transposed")
      first_arg%*%t(second_arg)
    } else {
      stop("Object dimensions are not compatible")
    }
  }
}
```

The function `warning()` therefore allows to output a result even though there can be some errors in the inputs, notifying the user of the steps made to achieve this output (please type `?message` to understand what this function allows you to do to communicate with the user). However, let us suppose that the second object entered in this function is a vector. Given our current body in the function we would get the following output:

```
gen_prod(matrix(rnorm(9),3,3), rnorm(3))
```

```
## Error in if (dim(first_arg)[2] == dim(second_arg)[1]) {: argument is of le
```

We obtain this error because the function `dim()` only works on matrices (not vectors or scalars), therefore we can anticipate this problem by making sure that all objects are considered as matrices:

```
gen_prod <- function (first_arg = matrix(rnorm(9), 3, 3),
                      second_arg = matrix(rnorm(9), 3, 3)) {
  first_arg <- as.matrix(first_arg)
  second_arg <- as.matrix(second_arg)

  if (dim(first_arg)[2] == dim(second_arg)[1]) {
    first_arg%*%second_arg
  } else {
    if (dim(first_arg)[2] == dim(second_arg)[2]) {
      warning("Second object has been transposed")
      first_arg%*%t(second_arg)
    } else {
      stop("Object dimensions are not compatible")
    }
  }
}
```

which consequently gives us

```
gen_prod(matrix(rnorm(9),3,3), rnorm(3))
```

```
##            [,1]
## [1,]  2.1907865
## [2,] -0.1400335
## [3,] -4.6557412
```

Finally, a last check that can be made is whether the second

argument is a scalar. Indeed, if the first argument is not scalar, our function would not perform a multiplication:

```
gen_prod(matrix(rnorm(9),3,3), rnorm(1))
```

```
## Error in gen_prod(matrix(rnorm(9), 3, 3), rnorm(1)): Object dimensions are
```

although we can always multiply a scalar by a matrix or a vector. Therefore we can add one last control statement:

```
gen_prod <- function (first_arg = matrix(rnorm(9), 3, 3),
                      second_arg = matrix(rnorm(9), 3, 3)) {
  first_arg <- as.matrix(first_arg)
  second_arg <- as.matrix(second_arg)

  if(dim(second_arg)[1]==1 & dim(second_arg)[2]==1) {
    first_arg*second_arg[1]
  } else {
    if (dim(first_arg)[2] == dim(second_arg)[1]) {
      first_arg%*%second_arg
    } else {
      if (dim(first_arg)[2] == dim(second_arg)[2]) {
        warning("Second object has been transposed")
        first_arg%*%t(second_arg)
      } else {
        stop("Object dimensions are not compatible")
      }
    }
  }
}
```

which allows us to have

```
gen_prod(matrix(rnorm(9),3,3), rnorm(1))
```

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

```
## [1,]  2.480805 4.2744753 -0.4074524
## [2,] -4.480960 0.4466988  1.7753060
## [3,] -1.806759 0.5300720 -1.4009631
```

Additional check procedures should be carried out in order to understand if the first object has equal or higher dimensions compared to the second (although the user should be made aware of this in the description of the function). However we leave this exercise to the reader since it would simply be redundant in the message conveyed on programming the body of a function.

As you can see, the body of a function can rapidly become lengthy and complex when adding control statements and computations to it. This can become an issue if you program a complex function and then have to share it with a collaborator or modify it after some time you haven't used it. It is therefore good practice to comment your functions and make sure that the objects consisting in the output of your function are clear to someone who reads the function. In the latter case, the `return()` function makes sure that only the objects that you're interested in are returned to the user (avoiding that eventual unassigned and unimportant values are returned).

```
gen_prod <- function (first_arg = matrix(rnorm(9), 3, 3),
                      second_arg = matrix(rnorm(9), 3, 3)) {

  # Make sure that all objects are considered as matrices
  first_arg <- as.matrix(first_arg)
  second_arg <- as.matrix(second_arg)

  # Check if second argument is a scalar and, if so, return product (prod)
  if(dim(second_arg)[1]==1 & dim(second_arg)[2]==1) {
    prod <- first_arg*second_arg[1]
  }else{
    # Check if the objects have compatible dimensions and, if so, return pr
    if (dim(first_arg)[2] == dim(second_arg)[1]) {
```

```
      prod <- first_arg%*%second_arg
    }else{
      # Check if other dimensions are compatible if the initial
      # ones are not and, if so, transpose the second object and return
      # product (prod) with warning for the user
      if (dim(first_arg)[2] == dim(second_arg)[2]) {
        warning("Second object has been transposed")
        prod <- first_arg%*%t(second_arg)
      } else {
        # Output an error message if none of the dimensions are compatible
        stop("Object dimensions are not compatible")
      }
    }
  }
  return(prod)
}
```

0.30 Function environment

Generally speaking, an environment is a virtual space in which certain names are associated to specific objects and values. The main characterstics of an environment are the following (see Wickham: Environments[39]):

- Every name in an environment is unique
- Every environment has a parent

The second characteristic means that when working within a given environment, you're also working in an environment (parent) which includes that environment. For example, in R the usual environment one works in is the "global environment" and its parent is the last package that has been loaded in the R session while the "base

[39] http://adv-r.had.co.nz/Environments.html

environment" is a special case of the global environment and is the environment of the base package (whose parent is the empty environment).

Within this structure, also functions have their own types of environments. Based on this structure, functions will look for the names of objects (and associated values) through scoping methods that start within the function's environment and then, if these are not found, proceed to looking for the names in the parent environments. The types of environments for R functions are the following:

- Enclosing: this is the environment in which the function was created (usually the global environment) and each function only has one enclosing environment
- Binding: this is the environment in which the function is associated to a given name (usually the enclosing and binding environment are the same)
- Execution: this environment is created each time a function is called and in which the objects created by this function during execution are stored
- Calling: this environment is associated with the execution environment and reports the environment in which a function was called

First of all, the enclosing environment of a function can be found by using the `environment()` function:

```
environment(gen_prod)
```

```
## <environment: R_GlobalEnv>
```

With this function therefore informs the user on the enclosing environment and its main difference with the binding environment consists in the fact that the first determines how to find values (lexical scoping) while the second determines how to find the function. The reason for this separation (at least one of the main reasons) lies in the need to separate package namespaces. By the latter we mean, for example, the case where packages have the same names for different functions, allowing to preserve the name of the function in

the enclosing environment unless otherwise specified. An example can be given with the `var()` function (to compute the variance) which uses the `missing()` function (in the base package) to check if a value is specified as an argument to a function (check with `?missing`). Let us suppose we compute the variance of a vector:

```
x <- c(2,4,5,3,7,9)
var(x)
```

```
## [1] 6.8
```

Let us now create another function called `missing` in the global environment which takes `x` as an argument but only returns 100. After this, we execute the code above again:

```
missing = function (x) 100
x <- c(2,4,5,3,7,9)
var(x)
```

```
## [1] 6.8
```

The result is always the same although the `var()` function would have halted execution if it had considered our own `missing()` function. This is possible thanks the to the package namespace which keeps packages independent through the separate use of enclosing and binding environments.

Finally, the execution environment allows to create a temporary environment in which the function can create its objects without affecting the environment in which it is created and called. For example, suppose that we call our `gen_prod` function but, before doing so, we define an object called `prod` and assign a value to it:

```
prod <- 1
```

We know that our `gen_prod()` function creates an object with the same name and, according to standard R programming rules, the new object with the same name should overwrite the previous one:

```
output <- gen_prod(matrix(rnorm(100), 10, 10), matrix(rnorm(100), 10, 10))
prod
```

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

As can be seen, although our `gen_prod()` function defines the object `prod`, this quantity remains in the execution environment and does not affect or modify the environment in which is it called (calling environment) and is removed once the function has completed execution.

0.31 Example (continued): Least-squares function

To implement our linear regression function we need to understand the algebra behind least squares and make use of the matrix operations in R explained in the previous chapter. Based on the linear algebra behind least-squares regression, let us implement a function that delivers inference on the parameter vector $\boldsymbol{\beta}$ and therefore define the skeleton of this R function:

```
my_lm <- function (...) {

  ...

}
```

As you can see, we find a name for the function we want to build, which in this case is `my_lm`, and specify that we are going to attribute a `function` to this name. Following this assignment, we find a set of curved brackets `(...)` followed by a set of curly brackets `{...}` which should include the *arguments* and *body* of the function respectively. While the *body* of a function simply corresponds to all the command lines (and other functions) that are used to deliver an

output, the next sections will tackle function arguments as well as other important aspects such as their environment and attributes.

In the framework of linear regression the goal is to explain an $n \times 1$ vector of observations $\mathbf{y}$ (representing the response variable) through a linear combination of p explanatory variables (or predictors or covariates) that are stored in an $n \times p$ matrix $\mathbf{X}$. More specifically, the framework is the following:

$$\mathbf{y} = \mathbf{X}^T \boldsymbol{\beta} + \epsilon,$$

where $\boldsymbol{\beta}$ is the $p \times 1$ parameter vector of interest that links the covariates with the response variable while ϵ is the $n \times 1$ random error vector with null expectation and variance σ^2.

When we collect data for the purpose of linear regression, the unknown terms in the above setting are the parameter vector $\boldsymbol{\beta}$ and the variance parameter σ^2. In order to estimate $\boldsymbol{\beta}$, assuming that the matrix $\left(\mathbf{X}^T\mathbf{X}\right)^{-1}$ exists, the least-squares estimator for it is given by:

$$\hat{\boldsymbol{\beta}} = \left(\mathbf{X}^T\mathbf{X}\right)^{-1} \mathbf{X}^T\mathbf{y} \tag{0.13}$$

If you are interested in understanding how Eq. (0.13) is derived, click on the button. If you're not familiar with such calculations we suggest you read some introduction to linear regression (see for example **?**).

Derivation of Least-Squares Estimator

The least-square estimator $\hat{\boldsymbol{\beta}}$ is given by

$$\hat{\boldsymbol{\beta}} = \text{argmin}_\beta \ (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})$$

The first step of this derivation is to reexpress the term $(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})$ as follows:

$$(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) = \mathbf{y}^T\mathbf{y} + \boldsymbol{\beta}^T\mathbf{X}^T\mathbf{X}\boldsymbol{\beta} - 2\boldsymbol{\beta}^T\mathbf{X}^T\mathbf{y}.$$

In case you were surprised by the term $2\boldsymbol{\beta}^T\mathbf{X}^T\mathbf{y}$ remember that a scalar can always be transposed without changing its value and therefore we have that $\boldsymbol{\beta}^T\mathbf{X}^T\mathbf{y} = \mathbf{y}^T\mathbf{X}\boldsymbol{\beta}$. Now, our next step is to the following derivative

$$\frac{\partial}{\partial\, \boldsymbol{\beta}}\ (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})\,.$$

To do this we should keep in mind the following results

$$\frac{\partial}{\partial\, \boldsymbol{\beta}}\ \boldsymbol{\beta}^T\mathbf{X}^T\mathbf{y} = \mathbf{y}^T\mathbf{X},$$

and

$$\frac{\partial}{\partial\, \boldsymbol{\beta}}\ \boldsymbol{\beta}^T\mathbf{X}^T\mathbf{X}\boldsymbol{\beta} = 2\boldsymbol{\beta}^T\mathbf{X}^T\mathbf{X}.$$

The proof of these two results can for example be found in Propositions 7 and 9 of Prof. Barnes' notes[40]. Using these two results we obtain

$$\frac{\partial}{\partial\, \boldsymbol{\beta}}\ (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) = 2\boldsymbol{\beta}^T\mathbf{X}^T\mathbf{X} - 2\mathbf{y}^T\mathbf{X}.$$

By solving for the first order condition (and under some technical assumptions not discussed here) we can redefine $\hat{\boldsymbol{\beta}}$ through the follwing equation

$$\hat{\boldsymbol{\beta}}^T\mathbf{X}^T\mathbf{X} = \mathbf{y}^T\mathbf{X},$$

which is equivalent to

$$\mathbf{X}^T\mathbf{X}\hat{\boldsymbol{\beta}} = \mathbf{X}^T\mathbf{y}.$$

If $\left(\mathbf{X}^T\mathbf{X}\right)^{-1}$ exists, $\hat{\boldsymbol{\beta}}$ is therefore given by

$$\hat{\boldsymbol{\beta}} = \left(\mathbf{X}^T\mathbf{X}\right)^{-1}\mathbf{X}^T\mathbf{y},$$

which verifies Eq. (0.13).

The variance of $\hat{\boldsymbol{\beta}}$ is given by

$$\text{Var}\left(\hat{\boldsymbol{\beta}}\right) = \sigma^2\left(\mathbf{X}^T\mathbf{X}\right)^{-1}, \tag{0.14}$$

and if you are interested, you can click on the button below to see how this formula was derived.

Derivation - Variance of Least-Squares Estimator

If we let $\mathbf{A} = \left(\mathbf{X}^T\mathbf{X}\right)^{-1}\mathbf{X}^T$, then we have

$$\begin{aligned}\text{Var}\left(\hat{\boldsymbol{\beta}}\right) &= \text{Var}\left(\mathbf{A}\mathbf{y}\right) = \mathbf{A}\text{Var}\left(\mathbf{y}\right)\mathbf{A}^T = \sigma^2\mathbf{A}\mathbf{A}^T \\ &= \sigma^2\left(\mathbf{X}^T\mathbf{X}\right)^{-1}\mathbf{X}^T\mathbf{X}\left(\mathbf{X}^T\mathbf{X}\right)^{-1} = \sigma^2\left(\mathbf{X}^T\mathbf{X}\right)^{-1},\end{aligned}$$

which verifies Eq. (0.14). To understand the above derivation it may be useful to remind and point out a few things:

- $\text{Var}\left(\mathbf{A}\mathbf{y}\right) = \mathbf{A}\text{Var}\left(\mathbf{y}\right)\mathbf{A}^T$ since $\mathbf{A}$ is not a random variable.
- $\mathbf{A}\text{Var}\left(\mathbf{y}\right)\mathbf{A}^T = \sigma^2\mathbf{A}\mathbf{A}^T$ since$\text{Var}\left(\mathbf{y}\right) = \sigma^2\mathbf{I}$ and therefore we have $\mathbf{A}\text{Var}\left(\mathbf{y}\right)\mathbf{A}^T = \sigma^2\mathbf{A}\mathbf{I}\mathbf{A}^T = \sigma^2\mathbf{A}\mathbf{A}^T$.
- The result $\mathbf{A}\mathbf{A}^T = (\mathbf{X}^T\mathbf{X})^{-1}$ is based on the fact that $(\mathbf{X}^T\mathbf{X})^{-1}$ is symmetric but this is not necessarily intuitive. Indeed, this follows from the fact that any square and invertible matrix $\mathbf{B}$ is such that the inverse and transpose operator commute, meaning that $(\mathbf{B}^T)^{-1} = (\mathbf{B}^{-1})^T$. Therefore since the matrix $\mathbf{X}^T\mathbf{X}$ is square and (by assumption) invertible we have $[(\mathbf{X}^T\mathbf{X})^{-1}]^T = [(\mathbf{X}^T\mathbf{X})^T]^{-1} = (\mathbf{X}^T\mathbf{X})^{-1}$.

In general, the residual variance is unknown and needs to be estimated. A common and unbiased estimator of σ^2 is given by

$$\hat{\sigma}^2 = \frac{1}{n-p}\left(\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}}\right)^T\left(\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}}\right) \tag{0.15}$$

The rest of this section aims at implementing Eq. (0.13) to (0.15).

Putting aside possible problems with the data that would require a more in-depth knowledge and discussion of linear regression theory, we can proceed to estimate the Hubble constant by using the velocity as the response variable y and the distance as the explanatory variable x. Let us therefore start by implementing Eq. (0.13) within our function in order to get an estimate of β.

```
my_lm = function(response, covariates) {

  # Define parameters
  n <- length(response)
  p <- dim(covariates)[2]
  df <- n - p

  # Estimate beta through Eq. (6.1)
  beta.hat <- solve(t(covariates)%*%covariates)%*%t(covariates)%*%response

  # Return the estimated value of beta
  beta.hat
}
```

Before discussing the body and output of this function, we can first underline an important aspect of programming. Indeed, we defined the number of covariates (and length of the vector $\boldsymbol{\beta}$) as `p <- dim(covariates)[2]` where the function `dim()` presupposes that the object `covariates` is a matrix. Nevertheless, in our case the object `covariates` would correspond to `hubble$x` which is a vector and therefore this operation would return `NULL` as an

output. When programming it is therefore important to think ahead and understand if there are any particular cases where parts of the body of your function may not work.

Taking into account the above note, it would be appropriate to make sure that the code in the body of the function works also in particular cases (e.g. the `covariates` object is a vector and not a matrix). In our case we therefore use the function `as.matrix()` which forces an object to be considered as a matrix in order for it to be used within matrix opeations.

```
my_lm = function(response, covariates) {

  # Make sure data formats are appropriate
  response <- as.vector(response)
  covariates <- as.matrix(covariates)

  # Define parameters
  n <- length(response)
  p <- dim(covariates)[2]
  df <- n - p

  # Estimate beta through Eq. (6.1)
  beta.hat <- solve(t(covariates)%*%covariates)%*%t(covariates)%*%response

  # Return the estimated value of beta
  beta.hat
}
```

Other checks can be introduced at the beginning of the function to make sure that the function is used correctly and obtain an appropriate output. In our case, for example, we could even introduce a check to understand if `response` and `covariates` have the same number of rows and interrupt the function execution

and output an error message if this is not the case, making the user aware of this probem.

As you may notice, using the matrix operators we obtain an object we decide to call `beta.hat` and, to tell the function to return this value, we simply specify it without any other commands after it has been computed. A more appropriate way of defining the outputs of a function would however be the `return()` function that avoids ambiguous outputs due to mistakes in coding or others within the function body. By using `return()` we make sure the desired outputs are given and it improves readability of the function for other users (see the next example further on).

With the `my_lm()` function we can now estimate the value for β that we denote as $\hat{\beta}$. However, we don't have an estimate of its variance for which we would need to implement Equations (0.14) and (0.15). We can therefore add these equations to the body of our `my_lm()` function:

```
my_lm = function(response, covariates) {

  # Make sure data formats are appropriate
  response <- as.vector(response)
  covariates <- as.matrix(covariates)

  # Define parameters
  n <- length(response)
  p <- dim(covariates)[2]
  df <- n - p

  # Estimate beta through Eq. (6.1)
  beta.hat <- solve(t(covariates)%*%covariates)%*%t(covariates)%*%response

  # Estimate of the residual variance (sigma2) from Eq. (6.3)
  # Compute residuals
  resid <- response - covariates%*%as.matrix(beta.hat)
```

```
  sigma2.hat <- (1/df)*t(resid)%*%resid

  # Estimate of the variance of the estimated beta from Eq. (1.2)
  var.beta <- sigma2.hat*solve(t(covariates)%*%covariates)

  # Return all estimated values
  return(list(beta = beta.hat, sigma2 = sigma2.hat, variance_beta = var.beta
}
```

There are a couple of things to underline in the above function. Firstly, when defining the `resid` object we also used `as.matrix()` for the object `beta.hat`: this is because it can happen (as in our example) that the dimension of $\boldsymbol{\beta}$ could be equal to one (i.e. a scalar) and the matrix multiplication would not work and output an error. By using the `as.matrix()` function, we ensure that this multiplication will work also when $\boldsymbol{\beta}$ is a scalar (i.e. when there is only one covariate). A second aspect to underline is the way in which we return multiple function outputs. Indeed, in our case we decide to return not only the estimate of β but also the estimated residual variance as well as the variance of $\hat{\beta}$. To do so, we use the `list()` function that allows to store objects of different nature (e.g. scalars, vectors, matrices) as elements of a single object while assigning names to them. For example, the estimated parameter β will be accessible through the element name `beta` (we'll see how this done further on).

Nevertheless, in order to answer the question of our example on the Hubble constant, we would need to obtain a confidence interval for our estimated paramter $\hat{\beta}$. Although the information needed for this purpose is available to the user through the current output, it may be useful to directly provide the confidence interval since it is a piece of information which is almost always required to deliver inference on the true parameter β. Let us therefore build a confidence interval within our function for which we will assume that the estimated variance of $\hat{\beta}$ is actually the true variance (otherwise we would need to build a confidence interval based on

the Student-t distribution which we will not deal with at this stage of our course). Assuming therefore that

$$\hat{\beta} \sim \mathcal{N}\left(\beta, \hat{\sigma}^2 (X^T X)^{-1}\right),$$

we consequently have that the confidence interval is given by

$$\left[\hat{\beta} - z_{1-\alpha/2}\sqrt{\hat{\sigma}^2 (X^T X)^{-1}}\,,\; \hat{\beta} + z_{1-\alpha/2}\sqrt{\hat{\sigma}^2 (X^T X)^{-1}}\right], \quad (0.16)$$

where $z_{1-\alpha/2}$ is the $(1-\alpha/2)^{th}$ quantile of the standard normal distribution.

Let us therefore add this output to our function which would require an extra argument: the confidence level. The most common confidence level used is the 95% level which is obtained by defining the significance level $\alpha = 0.05$. We could therefore add the latter argument to our function and set its default value to 0.05.

```
my_lm = function(response, covariates, alpha = 0.05) {

  # Make sure data formats are appropriate
  response <- as.vector(response)
  covariates <- as.matrix(covariates)

  # Define parameters
  n <- length(response)
  p <- dim(covariates)[2]
  df <- n - p

  # Estimate beta through Eq. (6.1)
  beta.hat <- solve(t(covariates)%*%covariates)%*%t(covariates)%*%response

  # Estimate of the residual variance (sigma2) from Eq. (6.3)
  # Compute residuals
  resid <- response - covariates%*%as.matrix(beta.hat)
  sigma2.hat <- (1/df)*t(resid)%*%resid
```

```
  # Estimate of the variance of the estimated beta from Eq. (6.2)
  var.beta <- sigma2.hat*solve(t(covariates)%*%covariates)

  # Estimate of the confidence interval based on alpha
  quant <- 1 - alpha/2
  ci.beta <- c(beta.hat - qnorm(p = quant)*sqrt(var.beta), beta.hat +
                 qnorm(p = quant)*sqrt(var.beta))

  # Return all estimated values
  return(list(beta = beta.hat, sigma2 = sigma2.hat,
              variance_beta = var.beta, ci = ci.beta))
}
```

We now have now a general function to perform linear regression which has a series of scalar outputs as well as a vector (i.e. the confidence interval). Let us now complete this chapter by investigating how the `my_lm()` function performs compared to the base `lm()` function.

```
# Linear regression with lm() function
fit_lm = lm(hubble$y~hubble$x-1)

# Linear regression with my_lm() function
fit_my_lm = my_lm(hubble$y, hubble$x)

# Compare outputs
manual_results = c(fit_my_lm$beta, fit_my_lm$sigma2)
base_results = c(fit_lm$coefficients,
                    (1/fit_lm$df.residual)*t(fit_lm$residuals)%*%fit_lm$res
results = cbind(manual_results, base_results)
row.names(results) = c("Beta", "Sigma")
results
```

```
##       manual_results base_results
## Beta        76.58117     76.58117
```

```
## Sigma    67046.33165  67046.33165
```

As one can notice, the two procedures give the same outputs indicating that our `my_lm()` function well implements the linear regression method. We can now proceed to use our function in order to test the Creationist hypothesis on the age of the universe assuming the validity of the big bang theory. First of all, due to different measurement units we perform a unit transformation and then compute the age in years (which requires an additional transformation since the previous one gives a unit of s^{-1}).

```
# Estimated Hubble's constant
hubble_const <- fit_my_lm$beta/3.09e19
# Note: The estimated Hubble's constant in inverse seconds, [s^(-1)]

# Age of the universe in seconds
age_sec <- 1/hubble_const

# Age of the universe in years
age_sec/(60^2*24*365)
```

Based on this estimation, the age of the universe appears to be almost 13 billion years. However, we know that $\hat{\beta}$ is a random variable that therefore follows a distribution which, based on asymptotic statistical theory, is a normal distribution with expectaton β and variance $\sigma^2(X^TX)^{-1}$.

Now, let's suppose that we have a hypothesis on the age of the universe, for example that of Creation Scientists who claim that the universe is 6000 years old based on a reading from the Bible. Assuming the validity of the big bang theory, which is not the case for Creation Scientists, let us nevertheless test if their claim appears to be reasonable within this postulated framework. For this purpose we can build a 95% confidence interval for the true Hubble constant β and understand if the Hubble constant implied by the postulated age of the universe falls within this interval. Firstly, we can determine this constant under the null hypothesis which can be defined as follows

$$H_0 \ : \ \beta = 163 \times 10^6,$$

since this value of β would imply that the universe is roughly 6000 years old. The alternative hypothesis is that the true β is not equal to the above quantity (i.e. $H_A \ : \ \beta \neq 163 \times 10^6$). . . . Let us therefore replace the values in Eq. (0.16):

```
# 95% confidence interval for the Hubble constant
fit_my_lm$ci
```

```
## [1] 68.81032 84.35203
```

The confidence interval lies between 68 and 84 which clearly does not contain the value implied by the age of the universe postulated by the Creation Scientists. Hence, assuming the validity of the big bang theory, we can reject this hypothesis at a 95% level.

Part III

Extending

0

Shiny Web Applications

Shiny is an R package that makes it easy to build interactive web apps through R. It made avaialble directly through RStudio and can be employed loading the corresponding library (i.e. `library(shiny)`).

0.32 Introduction

In order to build an application, we first need to understand its structure as well as the elements it needs to work. The idea is to take some input (such as parameters) and produce an output based on some code that will not be visible to the user and will connect the input and output. In this chapter we will describe how to build a Shiny application for which a brief tutorial can be found below.

In the following paragraphs, we will provide more details on how a Shiny app can be built using the example illustrated in the tutorial.

0.33 Step 1. Defining the R Code in the backend of the Shiny app

Before we build the interface of the web application, we need to focus on the R code which, in the framework of Shiny app development, is also commonly known as the "backend" of the application. To make sure that all the intended operations work

within the application, we need to make sure that the R code that serves as the skeleton of this app works smoothly.

For instance, based on the tutorial example, we may intend to build an application that creates a histogram based on the waiting time between eruptions of the Old Faithful geyser in Yellowstone National Park (that can be found in the R dataset `faithful`), allowing the user to specify the number of bins. Using the second column in the dataset (representing the waiting times), if we were to use the default values for the histogram function in R we would obtain the following plot.

```
x <- faithful[, 2]
hist(x)
```

However, the representation and interpretation of the data can sometimes change considerably if using different visualization parameters. Indeed, among others, the `hist()` function includes an option called `breaks` that allows the user to specify a vector giving the number of breakpoints between histogram cells. An example of how this is used and changes the representation of the data can be found below.

```
par(mfrow = c(1,2))

# Histogram with 9 bins
bins <- seq(min(x), max(x), length.out = 10)
hist(x, breaks = bins)

# Histogram with 19 bins
```

```
bins <- seq(min(x), max(x), length.out = 20)
hist(x, breaks = bins)
```

As you may notice, the number of bins created by using this option is always one unit less than the length of the specified vector (i.e. 9 and 19). Therefore, if we intend to deliver an app that allows the user to directly specify the number of bins, we should take this into account and add one unit to the input that the user has given within the `length.out` option. Ideally, we would be looking to implement a function which includes the following steps:

```
input <- 10

# Histogram with input bins
bins <- seq(min(x), max(x), length.out = input + 1)
hist(x, breaks = bins)
```

where the value given to the `input` object (which is 10 in the above example) is the only value required and can be assigned by the user through the app interface. The next step will explain how to do so.

0.34 Step 2: User Interface (UI) / Frontend

Once we have determined the structure of the code we can now start creating the Shiny app by firstly developing the UI (or frontend) with which the user will interact. To address this part, let us take the tutorial example as a guide and inspect the part of the code related to the UI.

```
# Define UI for application that draws a histogram
ui <- fluidPage(

   # Application title
   titlePanel("Old Faithful Geyser Data"),

   # Sidebar with a slider input for number of bins
   sidebarLayout(
      sidebarPanel(
         sliderInput("bins",
                     "Number of bins:",
                     min = 1,
                     max = 50,
                     value = 30)
      ),

      # Show a plot of the generated distribution
      mainPanel(
         plotOutput("distPlot")
      )
   )
)
```

As can be seen, all the code that will be dedicated to creating the UI is assigned to an object called `ui` through a function called `fluidPage()` (see `?fluidPage` for more information). The two main elements of this function are the panel dedicated to the title

that will appear for the app (`titlePanel()`) and the layout to give to web page which in this example is a layout with a sidebar for the user to enter their inputs and a main panel in which the outputs will be visualized (`sidebarLayout()`). In the next paragraphs we will provide more details on the possible contents to be presented in the app interface, as well as the options that can be employed to allow the user to enter the needed inputs and the options for visualizing the outputs.

Content Creation

We want to design the application in the way that it is comprehensive and also easy to interpret. Below are some often-used options of content creation that will be beneficial to know.

Function	Description
titlePanel()	The title of the application
sidebarLayout()	Creates a sidebar layout for fluidPage()
sidebarPanel()	Makes a sidebar menu
mainPanel()	Main content area for different outputs

Input Controls

We also want to provide spaces so that the client can change any desired parameter. For example, in the above example, this would be the number of bins. Below are some input controls the developer can use.

Function	Description
numericInput()	Number entry input
radioButtons()	Radio button selection
selectInput()	Dropdown menu
sliderInput()	Range slider (1/2 values)
submitButton()	Submission button
textInput()	Text input box

Function	Description
checkboxInput()	Single checkbox input
dateInput()	Date Selection input
fileInput()	Upload a file to Shiny
helpText()	Describe input field

Output Render Controls

The different type of output that is shown can be designed depending on what the developer intends it to be. Examples of these options are shown below. We advise you to follow the videos and research different options that fit the desired output.

Function	Description
plotOutput()	Display a rendered plot
tableOutput()	Display in Table
textOutput()	Formatted Text Output
uiOutput()	Dynamic UI Elements
verbatimTextOutput()	“as is”" Text Output“
imageOutput()	Render an Image
htmlOutput()	Render Pure HTML

0.35 Step 3: Implementing the backend (server)

This step consists in adapting the structure of the code seen in Step 1 to the requirements of the Shiny app structure. This is done by creating a function which, as arguments, has an `input` and an `output` as can be seen below always using the example given in the tutorial.

```
server <- function(input, output) {

   output$distPlot <- renderPlot({
      # generate bins based on input$bins from ui.R
      x    <- faithful[, 2]
      bins <- seq(min(x), max(x), length.out = input$bins + 1)

      # draw the histogram with the specified number of bins
      hist(x, breaks = bins, col = 'darkgray', border = 'white')
   })
}
```

In this example, the function is called `server()` and contains only one object called `output` with a corresponding element called `distPlot` (`output$distPlot`). It must be underlined that the latter name must correspond to the name given for the output in the UI setup (i.e. the `distPlot` name inserted in `plotOutput("distPlot")`, see Step 2). The content of the output in this example is a plot and we therefore use the `renderPlot()` function in which we can include the code that we developed in Step 1 (with some added graphical parameters for the color of the bins and their borders). Of course, this output will depend on the input provided by the user which is used when defining the `bins` object (i.e. `bins <- seq(min(x), max(x), length.out = input$bins + 1)`). Just like for the `output` object, also in this case the `input` object has an element whose name must correspond to the name given for the input when building the UI (i.e. `sliderInput("bins",...)`).

0.36 Step 4: Connecting frontend and backend

Once we have developed the structure and defined the functions and objects for the UI (frontend) and backend environments, all

that needs to be done is to ensure that they can communicate with each other. Using the Shiny environment, this can be quickly and easily done by using the `shinyApp()` function which takes the object defining the UI interface (`ui` in our example, see Step 2) and the function that takes the input and delivers the output (`server` in our example, see Step 3).

```
shinyApp(ui = ui, server = server)
```

Therefore, having completed the UI and backend code, to launch the Shiny Web app you simply need to execute this code (or push the "Run App" button at the top of your Shiny app code).

0.37 Step 5: Customize

We can confidently say that shiny can be heavily customized, like how webpage applications are customized, even without explicitly using complex javascript or HTML elements.

One of such examples are a `submitButton(...)`, in which we can run responsive output from input data using a button to initiate. More can be read from here[41].

Another of such example is controlling the content creation process other than the default.

[41] https://shiny.rstudio.com/reference/shiny/1.0.4/submitButton.html

0.38 Example: Monte-Carlo Integration

0.39 Example: Buffon's needle

In 1777, the French nobleman Georges-Louis Leclerc, Compte de Buffon (Count of Buffon) posed the following problem to the Royal Academy of Sciences in Paris (**?**):

> Suppose that you drop a needle of unit length on a plane ruled by the lines $y = m$ ($m = 0, \pm 1, \pm 2, ...$) - what is then the probability that the needle comes to lie in a position where it crosses one of the lines?

Compte de Buffon also provided the answer and showed that the needle will intersect lines with a predictable probability. In mathematical terms, his solution (still known today as the Buffon principle) can be stated as follows:

$$\mathbb{P}(\text{intersection}) = \frac{2}{\pi}. \tag{0.17}$$

If you are curious about the derivation of this result, click on the button below.

Derivation - Equation (7.1)

This proof is based on the solution of Example 4.5.8 of **?**. We start by letting (X, Y) denote the coordinates of the point at the center of the needle and let Θ be the angle, modulo π, that lies between the needle and the horizontal lines. Next, we define the

distance from the needle's center to the nearest line beneath it as $Z = Y - \lfloor Y \rfloor$, where $\lfloor Y \rfloor$ denotes the "floor" of Y, i.e. the greatest integer not greater than Y. Since the needle is randomly casted, we have that the joint density of (Z, Θ) is given by:

$$f_{Z,\Theta}(z, \theta) = f_Z(z) f_\Theta(\theta) = \frac{1}{\pi},$$

for $0 \leq z \leq 1$ and $0 \leq \theta \leq \pi$. By drawing a diagram one can see that an interception occurs if and only if $(Z, \Theta) \in \mathcal{B}$, where

$$\mathcal{B} = \left\{ (z, \theta) \ : \ \ z \leq \frac{1}{2}\sin(\theta) \ \text{ or } \ 1 - z \leq \frac{1}{2}\sin(\theta) \right\}.$$

Therefore, we obtain

$$\mathbb{P}(\text{intersection}) = \iint_{\mathcal{B}} f_{Z,\Theta}(z, \theta)\, dz\, d\theta = \frac{1}{\pi} \int_0^\pi \left(\int_0^{\frac{1}{2}\sin(\theta)} dz + \int_{1-\frac{1}{2}\sin(\theta)}^1 dz \right) d\theta = \frac{2}{\pi},$$

which verifies Equation (0.17) and concludes the proof.

Georges-Louis Leclerc's motivation behind this problem was to design an experiment to estimate the value of π. Indeed, if you fling a needle a large number B times onto a ruled plane and count the number of times S_B that the needle intersects a line, we might be able to approximate $\mathbb{P}(\text{intersection})$ and therefore π. From Equation (0.17), we know that the proportion S_B/B will be "close" to the probability $\mathbb{P}(\text{intersection})$. In fact the (weak) law of large number garantees that S_B/B converges (in probability) to $2/\pi$, i.e. for any given $\varepsilon > 0$,

$$\lim_{B \to \infty} \ \mathbb{P}\left(\left| \frac{S_B}{B} - \frac{2}{\pi} \right| > \varepsilon \right) = 0.$$

Thus, the estimator

$$\hat{\pi}_B = \frac{2B}{S_B},$$

is a plausible estimator of π. The Continous Mapping Theorem (see e.g. Theorem 1.14 of **?**) can (among others) be used to show that $\hat{\pi}$ is a **consistent** estimator of π (i.e. $\hat{\pi}$ converges in probability to π). In 1777, Georges-Louis Leclerc investigated this problem and computed $\hat{\pi}_B$ by flinging a needle 2084 times, which may consitute the first recorded example of a Monte-Carlo method (simulation?) in use.

To illustrate the convergence of our estimator we could fling a needle B times and compute the following estimators:

$$\hat{\pi}_j = \frac{2j}{S_j}, \;\; j = k, \ldots, B$$

where $k \ll B$. Once this is done, we could create a graph with j on the horizontal axis and $\hat{\pi}_j$ on the vertical axis. Since $\hat{\pi}_B$ is a consistent estimator we should see that $\hat{\pi}_j$ tends to get closer and closer to π as j increases. In this graph we could also superimpose several experiments (recasting the needle B times several times) to reinforce our argument.

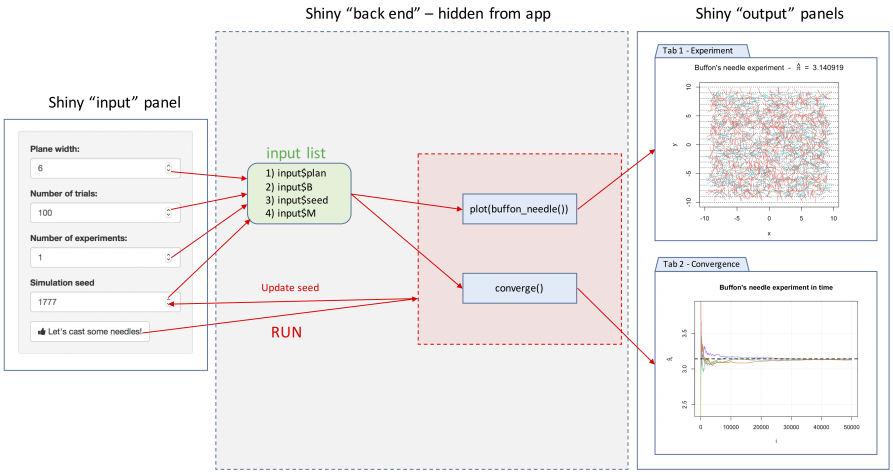
The goal of this example is to create a Shiny app to visualize and illustrate Buffon's needle experiment. For this purpose, we will use the following steps:

1) **Step 1: Backend**: Create all the functions needed for the backend of our app. A possible approach is to create the following functions:
   a) `cast_needle()`: this function randomly casts a needle on plane and returns its coordinates as well as a binary variable to indicate if the needle crossed a line;
   b) `buffon_experiment()`: this function performs a Monte-Carlo experiment by flinging a large number of needles using the function `cast_needle()`;
   c) `plot.buffon_experiment()`: to visualize the experiment (i.e. show all the needles randomly dropped) and compute the estimator $\hat{\pi}_B$ for the experiment at hand;

d) `converge()`: to illustrate the convergence of the estimator by creating the graph mentioned at the end of the previous paragraph.

2) **Step 2: Frontend**: Create widgets to collect all inputs needed by the backend:
   a) dimension of the plane on which the needles are dropped;
   b) the number of needles being used, i.e. B;
   c) number of experiments which is needed to illustrate the convergence of the estimator;
   d) the seed to allow "replicable" experiments. Aside from allowing the user to enter these variables, we will need to create two output "tabs". In the first one, we will "print" the result(s) of the experiment and in the second one we will illustrate the convergence of the estimator. Finally, we will need a button to "run" a new experiment.
3) **Step 3: Connecting frontend and backend**: In this third step we will need to connect the inputs with the outputs. Indeed, we will use the `input` list created by the widget defined in the previous step (Step 2) to create the graphs to be displayed in the two output tabs. We will also need to "activate" the button (i.e. connect the inputs to the appropriate functions) in order to run a new experiment and update the "seed" after every new experiment.

To summarize, our approach should follow the steps presented in the chart below:



In the next sections, we will discuss in detail how to program each step.

0.39.1 Step 1: Backend

Let us start with the function `cast_needle()`. This function has a single input, i.e. the width of the (square) plane on which the needle is cast and returns a `list` containing:

- `$start`: the coordinates of one end of the needle;
- `$end`: the coordinates of the other end of the needle;
- `$cross`: a binary variable to indicate if the needle intercepts a line.

An additional input could be added consisting in the length of the needle. However, in this example we only consider needles of unit length.

A possible implementation of this function is given below:

```
cast_needle <- function(plane_width = 20){
  available_range <- plane_width/2 - 1 # where 1 is the length of the needle
```

```
  x_start <- runif(2, -available_range, available_range)
  angle <- runif(1, 0, 2*pi)
  x_end <- c(cos(angle), sin(angle)) + x_start # where the angles are multip
  cross <- floor(x_start[2]) != floor(x_end[2])
  out <- list(start = x_start, end = x_end, cross = cross)
  out
}
```

Here is an example of the output of this function:

```
needle <- cast_needle(plane_width = 4)
needle
```

```
## $start
## [1] 0.1307334 0.3302562
##
## $end
## [1] 0.1470854 1.3301225
##
## $cross
## [1] TRUE
```

and we could now for example provide the following graphical representation of this random cast:

```
plot(NA, xlim = c(-2, 2), ylim = c(-2, 2), xlab = "x", ylab = "y")
abline(h = -2:2, lty = 3)
lines(c(needle$start[1], needle$end[1]), c(needle$start[2], needle$end[2]))
```

Next, we consider the function `buffon_experiment()`. This function is based on the previous function and contains the following inputs:

- `B`: the number of needles being casted;

- `plane_width`: the width of the (square) plane on which the needles are casted;
- `seed`: the "seed" used by the random number generator (allows to replicate results);

and returns a `list` containing:

- `$start`: a $B \times 2$ matrix containing the coordinates of one end of the B needles;
- `$end`: a $B \times 2$ matrix containing the coordinates of the other end of the B needles;
- `$cross`: a vector of length B containing boolean variables to indicate whether a needle crosses a line or not;
- `$plane`: the width of the (square) plane.

A possible implementation of this function is provided below:

```
buffon_experiment <- function(B = 2084, plane_width = 10, seed = NULL){

  if (!is.null(seed)){
    set.seed(seed)
  }

  X_start <- X_end <- matrix(NA, B, 2)
  cross <- rep(NA, B)

  for (i in 1:B){
    inter <- cast_needle(plane_width = plane_width)
    X_start[i, ] <- inter$start
    X_end[i, ] <- inter$end
    cross[i] <- inter$cross
  }

  out <- list(start = X_start, end = X_end, cross = cross, plane = plane_wid
  class(out) <- "buffon_experiment"
  out
}
```

For example, if we consider an experiment where four needles are cast, we could obtain:

```
experiment <- buffon_experiment(B = 4, plane_width = 4)
experiment
```

```
## $start
##             [,1]         [,2]
## [1,]  0.5668833 -0.719905025
## [2,]  0.7966649  0.304674088
## [3,] -0.7692311 -0.007315481
## [4,]  0.2704636 -0.262152664
##
## $end
##              [,1]       [,2]
## [1,] -0.24968864 -0.1426613
## [2,] -0.17226155  0.5520232
## [3,] -0.05723734 -0.7095013
## [4,]  0.16782619  0.7325662
##
## $cross
## [1] FALSE FALSE FALSE  TRUE
##
## $plane
## [1] 4
##
## attr(,"class")
## [1] "buffon_experiment"
```

which could be represented as

```
plot(NA, xlim = c(-2, 2), ylim = c(-2, 2), xlab = "x", ylab = "y")
abline(h = -2:2, lty = 3)
for (i in 1:4){
  lines(c(experiment$start[i,1], experiment$end[i,1]),
```

```
        c(experiment$start[i,2], experiment$end[i,2]))
}
```

We can now write a custom `plot()` function for the output of the function `buffon_experiment()`. This function will provide a way to visualize the experiment and will compute $\hat{\pi}_B$, which will be shown in the title. A possible function is provided below:

```
plot.buffon_experiment <- function(obj){
  cross <- obj$cross
  X_start <- obj$start
  X_end <- obj$end
  B <- length(cross)
  cols <- rev(hcl(h = seq(15, 375, length = 3), l = 65, c = 100)[1:2])

  title_part1 <- 'Buffon\'s needle experiment  -  '
  title_part2 <- ' = '
  pi_hat <- round(2/mean(obj$cross), 6)

  title <- bquote(.(title_part1) ~ hat(pi)[B] ~ .(title_part2) ~ .(pi_hat))

  plot(NA, xlab = "x", ylab = "y", xlim = c(-obj$plane/2, obj$plane/2),
       ylim = c(-obj$plan/2, obj$plan/2),
       main = title)
  abline(h = (-obj$plan):obj$plan, lty = 3)

  for (i in 1:B){
    lines(c(X_start[i,1], X_end[i,1]), c(X_start[i,2], X_end[i,2]),
          col = cols[cross[i] + 1])
  }
}
```

Therefore, we could now run the same experiment as Georges-Louis

Leclerc by flinging 2084 needles almost instanteously (which is the default value in the `buffon_experiment()` function we created):

```
experiment <- buffon_experiment(B = 2084)
plot(experiment)
```

Finally, we can consider the function `converge()`. Similarly to `buffon_experiment()`, the function `converge()` has the following inputs:

- `B`: the number of needles being cast;
- `plane_width`: the width of the (square) plane on which the needles are cast;
- `seed`: the "seed" used by the random number generator (allows to replicate results);
- `M`: the number of experiments.

The function returns the graph mentioned at the end of the previous section. A possible implementation of this function is provided below:

```
converge <- function(B = 2084, plane_width = 10, seed = 1777, M = 12){

  if (B < 10){
    warning("B was changed to 10")
    B <- 10
  }

  pi_hat <- matrix(NA, B, M)
  trials <- 1:B
  cols <- rev(hcl(h = seq(15, 375, length = (M+1)),
                  l = 65, c = 100, alpha = 1)[1:M])
  set.seed(seed)

  for (i in 1:M){
```

```
    cross <- buffon_experiment(B = B, plane_width = plane_width)$cross
    pi_hat[,i] <- 2*trials/cumsum(cross)
  }

  plot(NA, xlim = c(1,B), ylim = pi + c(-3/4, 3/4), type = "l", col = "darkb
       ylab = bquote(hat(pi)[j]),
       xlab = "j", main = "Buffon\'s needle experiment")
  grid()

  for (i in 1:M){
    lines(trials, pi_hat[,i], col = cols[i])
  }

  abline(h = pi, lwd = 2, lty = 2)
}
```

Therefore, if we were to repeat the original experiment of Georges-Louis Leclerc 20 times and compute $\hat{\pi}_j$ for each experiment we would obtain:

```
converge(B = 2084, M = 20, seed = 10)
```

which provides some illustrations on the convergence of the estimator.

0.39.2 Step 2: Frontend

We start by constructing an "empty" Shiny app, i.e.

```
# Define UI for application
ui <- fluidPage(

  # Application title
```

```
  titlePanel(h4("Buffon\'s needle experiment - Inputs:")),

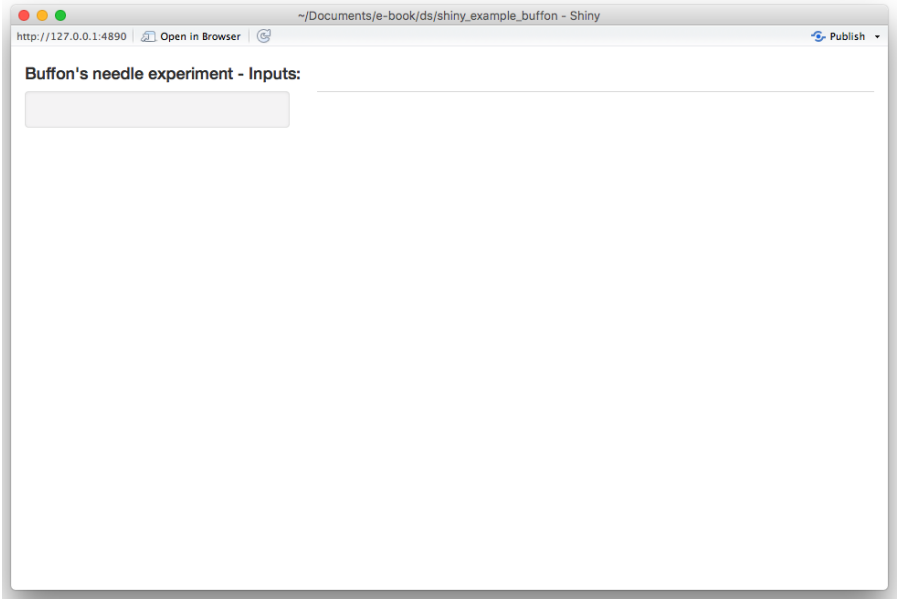
  sidebarLayout(
    sidebarPanel(
      # Add inputs here!
    ),

    mainPanel(
      tabsetPanel(
        # Add tabs here!
      )
    )
  )
)

# Define server
server <- function(input, output) {
}

# Run the application
shinyApp(ui = ui, server = server)
```

If you run this empty app you should obtain the result below:



We will start by adding the required input widgets by modifying the `ui` function as follows:

```
# Define UI for application
ui <- fluidPage(

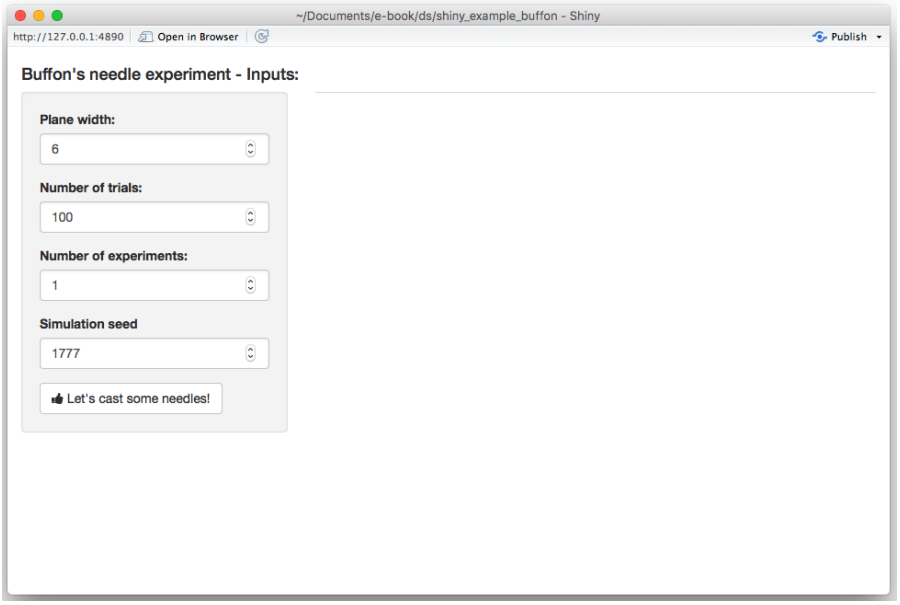
  # Application title
  titlePanel(h4("Buffon\'s needle experiment - Inputs:")),

  sidebarLayout(
    sidebarPanel(
      numericInput("plane", "Plane width:", 10, 6, 100),
      numericInput("B", "Number of trials:", 100, 20, 10^6),
      numericInput("M", "Number of experiments:", 1, 1, 100),
      numericInput("seed", "Simulation seed", 1777, 1, 1000000),
      actionButton("cast", "Let's cast some needles!", icon = icon("thumbs-u
    ),

    mainPanel(
      tabsetPanel(
```

```
        # Add tabs here!
      )
    )
  )
)
```

By running this update you should now obtain:



Next, we create two output tabs in which we will find the previously mentioned graphs. This can be done by again modifying the `ui`function as follows:

```
# Define UI for application
ui <- fluidPage(

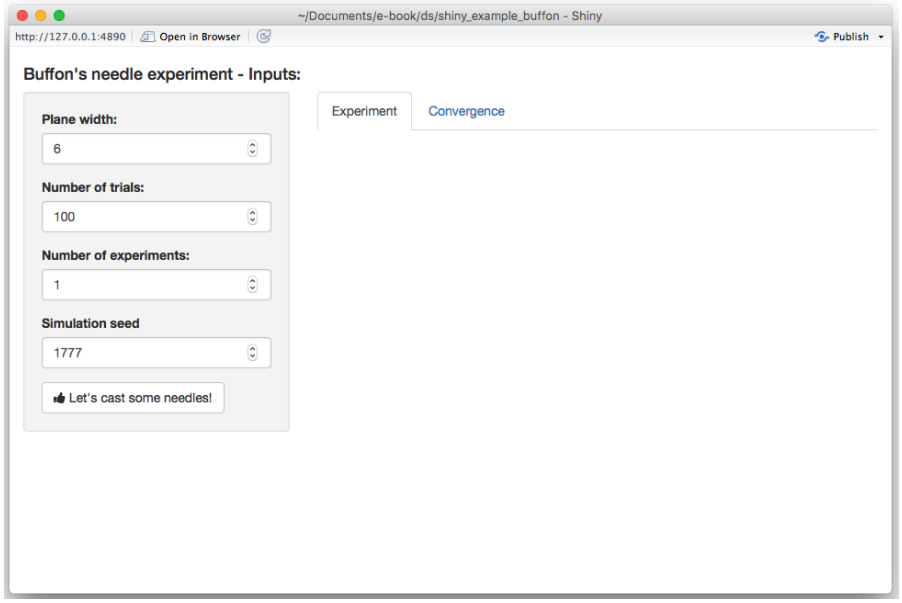
  # Application title
  titlePanel(h4("Buffon\'s needle experiment - Inputs:")),

  sidebarLayout(
    sidebarPanel(
```

```
      numericInput("plane", "Plane width:", 10, 6, 100),
      numericInput("B", "Number of trials:", 100, 20, 10^6),
      numericInput("M", "Number of experiments:", 1, 1, 100),
      numericInput("seed", "Simulation seed", 1777, 1, 1000000),
      actionButton("cast", "Let's cast some needles!", icon = icon("thumbs-u
    ),

    mainPanel(
      tabsetPanel(
        tabPanel("Experiment", plotOutput("exp")),
        tabPanel("Convergence", plotOutput("conv"))
      )
    )
  )
)
```

The app should now look like this:



At this point, we have completed the `ui` function and will modify the `server` in the next section.

0.39.3 Step 3: Connecting frontend and backend

In this section, we will focus on the `server` function to produce the desired output. Let us start by "connecting" our output tabs defined in the `ui` function with the output in the server function. Since both outputs are graphs, we will use the function `renderPlot()` as follows:

```
server <- function(input, output) {
  output$exp <- renderPlot({
    # Add graph 1 here!
  }, height = 620)

  output$conv <- renderPlot({
    # Add graph 2 here!
  }, height = 620)
}
```

If you re-run the app at this point our changes will have no visible effect. Next, we will focus on the first graph based on the functions `buffon_experiment()` and `plot.buffon_experiment()`. The first thing we will need is to (re-)run the `buffon_experiment()` when the user clicks on the "action" button. This can be done by adding the following lines to the `server` function:

```
cast <- eventReactive(input$cast, {
    buffon_experiment(B = input$B, plane_width = input$plane,
                      seed = input$seed)
  })
```

When this function is (re-)evaluated we want to update/create the first plot, which can be done by replacing the following part of the `server` function

```
output$exp <- renderPlot({
```

```
    # Add graph 1 here!
}, height = 620)
```

with

```
output$exp <- renderPlot({
    plot(cast())
}, height = 620)
```

Therefore, your `server` function should now be:

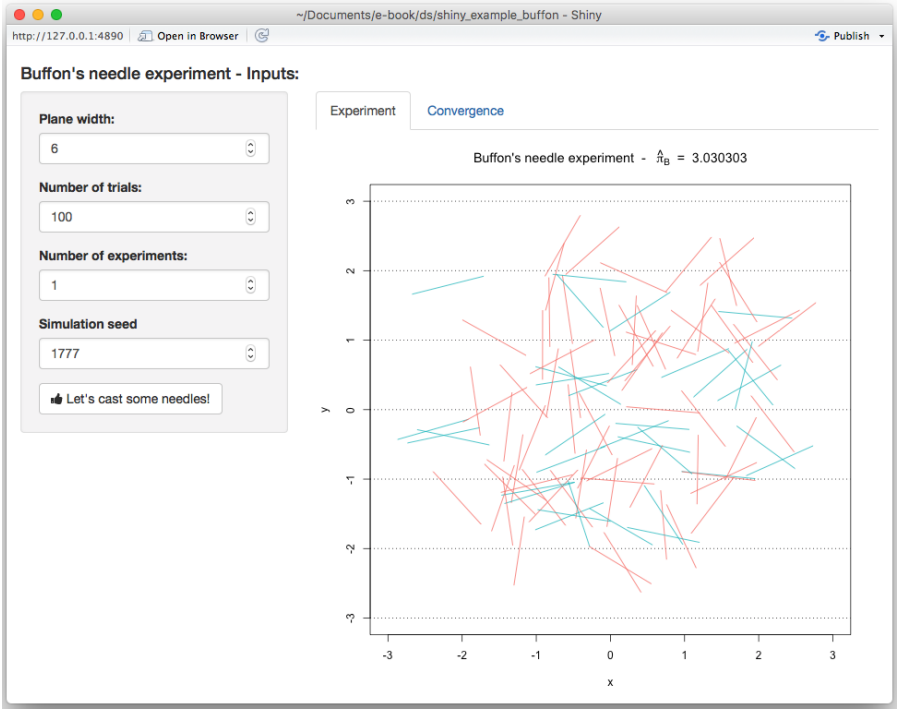
```
server <- function(input, output) {

  # Fling some needles!
  cast <- eventReactive(input$cast, {
    buffon_experiment(B = input$B, plane_width = input$plane,
                      seed = input$seed)
  })

  output$exp <- renderPlot({
    plot(cast())
  }, height = 620)

  output$conv <- renderPlot({
    # Add graph 2 here!
  }, height = 620)
}
```

and when reloading the app you should now see:



Similarly, we do the same thing for the second graph by adding the following lines to our `server` function:

```
conv <- eventReactive(input$cast, {
    converge(B = input$B, plane_width = input$plane,
             seed = input$seed, M = input$M)
})
```

and replacing

```
output$conv <- renderPlot({
    # Add graph 2 here!
}, height = 620)
```

with

```
output$conv <- renderPlot({
    conv()
}, height = 620)
```

After these changes, your `server` function should look like this:

```
server <- function(input, output) {

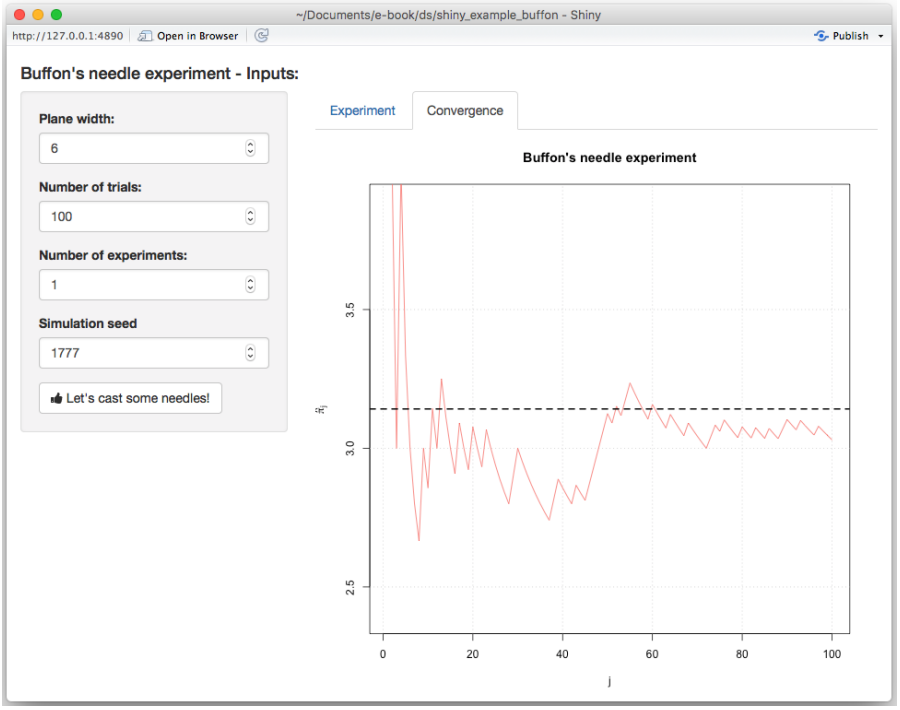
  # Fling some needles!
  cast <- eventReactive(input$cast, {
    buffon_experiment(B = input$B, plane_width = input$plane,
                      seed = input$seed)
  })

  conv <- eventReactive(input$cast, {
    converge(B = input$B, plane_width = input$plane,
             seed = input$seed, M = input$M)
  })

  output$exp <- renderPlot({
    plot(cast())
  }, height = 620)

  output$conv <- renderPlot({
    conv()
  }, height = 620)
}
```

and when reloading the app you should now see on the second tab:



Our next step is now to update the seed every time the "action" button is pushed. To do so, we will first need to add an additional input to the `server` function called `session` which will allow us to **dynamically** update the input directly from the `server` function. Therefore, in order to randomly generate a new seed each time the user clicks on the "action" button, we can do the following:

```
observeEvent(input$cast,{
    updateNumericInput(session, "seed",
                       value = round(runif(1, 1, 10^4)))
})
```

Therefore, your final `server` function is now:

```
server <- function(input, output, session) {

  observeEvent(input$cast,{
```

```
    updateNumericInput(session, "seed",
                       value = round(runif(1, 1, 10^4)))
  })

  # Fling some needles!
  cast = eventReactive(input$cast, {
    buffon_experiment(B = input$B, plane_width = input$plane,
                      seed = input$seed)
  })

  conv = eventReactive(input$cast, {
    converge(B = input$B, plane_width = input$plane,
             seed = input$seed, M = input$M)
  })

  output$exp <- renderPlot({
    plot(cast())
  }, height = 620)

  output$conv <- renderPlot({
    conv()
  }, height = 620)
}
```

With this change, you will now observe that the seed is updated each time the "action" button is clicked. The final version of the app we have just created can be found here[42].

[42] http://shiny.science.psu.edu/szg279/buffon/

0

R Packages

In this chapter we introduce one of the most useful tools for R programming as well as for statistical programming in general. Indeed, one of the main goals for statistical programming is to then be able to share all the code and functions that have been implemented in order to respond to a specific task. The latter may often be quite *messy* to do given that different files and functions can be present in various directories or repositories and, for example, some codes may use functions from other codes but do not load the same libraries, thereby producing execution errors.

In order to avoid the above complications (and to program in a healthy and organized manner), R allows you to create *packages* that are software platforms that collect functions as well as other files which, among others, describe these functions and provide users with documentation that allow them to understand and efficiently use these functions. Moreover, when sharing a package (or making it available within a repository) all the user needs to do is to install and load the package within an R session which then makes available the entire environment needed for all the functions included in the package to work. In a nutshell, whenever creating functions to answer a specific research interest or professional task, it is always good to do so by first creating a package within which these functions can be stored and documented.

In this chapter we will describe and explain the steps necessary to create an R package using RStudio. There are other ways and other procedures to produce an R package but in this chapter we will describe one possible way which is consistent with the approach to statistical programming that is presented in this book. As in the previous chapters, we will make use of an example to guide the

reader through the different aspects of package building and, for this purpose, let us assume we want to build a package that allows a user to perform Monte-Carlo integration for any user-specificed function as well as produce plots that represent these functions as well as the integrated area. In this case, we have an extremely simple setting where, based on code used in the previous chapters, we only have the following two functions to be included in the package:

```
mc_int = function(x_range, fun, B, seed = 1291){
  # A few checks
  # Check x_range
  if (length(x_range) != 2 || x_range[1] >= x_range[2]){
    stop("x_range is incorrectly specified")
  }

  # Check fun
  if (class(fun) != "character"){
    stop("fun is incorrectly specified and should be a character")
  }

  x = mean(x_range)
  test_fun = try(eval(parse(text = fun)), silent = TRUE)
  if (class(test_fun) == "try-error"){
    stop("fun cannot be evaluated")
  }

  # Check B
  if (B < 1){
    error("B is incorrectly specified")
  }

  # Set seed
  set.seed(seed)

  # Compute the length of the interval, i.e. (b-a)
```

```
  interval_length = diff(x_range)

  # Let's draw some uniforms to get Ui and Xi
  Ui = runif(B)
  Xi = x_range[1] + Ui*interval_length

  # Compute \hat{I}
  x = Xi
  I_hat = interval_length*mean(eval(parse(text = fun)))

  # Compute \hat{I}_2
  I2_hat = interval_length*mean((eval(parse(text = fun)))^2)
  var_I_hat = (interval_length*I2_hat - I_hat^2)/B

  # Output list
  out = list(I = I_hat, var = var_I_hat,
             fun = fun, x_range = x_range, B = B)
  class(out) = "MCI"
  out
}

plot.MCI = function(x, ...){
  obj = x
  x_range = obj$x_range
  fun = obj$fun

  Delta = diff(x_range)
  x_range_graph = c(x_range[2] - 1.15*Delta, x_range[1] + 1.15*Delta)
  x = seq(from = x_range_graph[1], to = x_range_graph[2], length.out = 10^3)
  f_x = eval(parse(text = fun))
  plot(NA, xlim = range(x), ylim = range(f_x), xlab = "x", ylab = "f(x)")
  grid()
  title(paste("Estimated integral: ", round(obj$I,4),
              " (", round(sqrt(obj$var),4),")", sep = ""))
  lines(x, f_x)
  x = seq(from = x_range[1], to = x_range[2], length.out = 10^3)
```

```
  f_x = eval(parse(text = fun))
  cols = hcl(h = seq(15, 375, length = 3), l = 65, c = 100, alpha = 0.4)[1:3]
  polygon(c(x, rev(x)), c(rep(0, length(x)), rev(f_x)),
          border = NA, col = cols[1])
  abline(v = x_range[1], lty = 2)
  abline(v = x_range[2], lty = 2)
}
```

Hence, the package will contain:

- the `mc_int()` function: that computes an approximation of the integral of the function `fun` with respect to `x` within the range `x_range` via Monte-Carlo integration using uniform sampling;
- the `plot.MCI()` function: a class function that will plot the object that is created as an output of the `mc_int()` function.

An example of use of these functions and their output is the following:

```
obj = mc_int(x_range = c(0,1), fun = "x^2*sin(x^2/pi)", B = 10^3)
plot(obj)
```

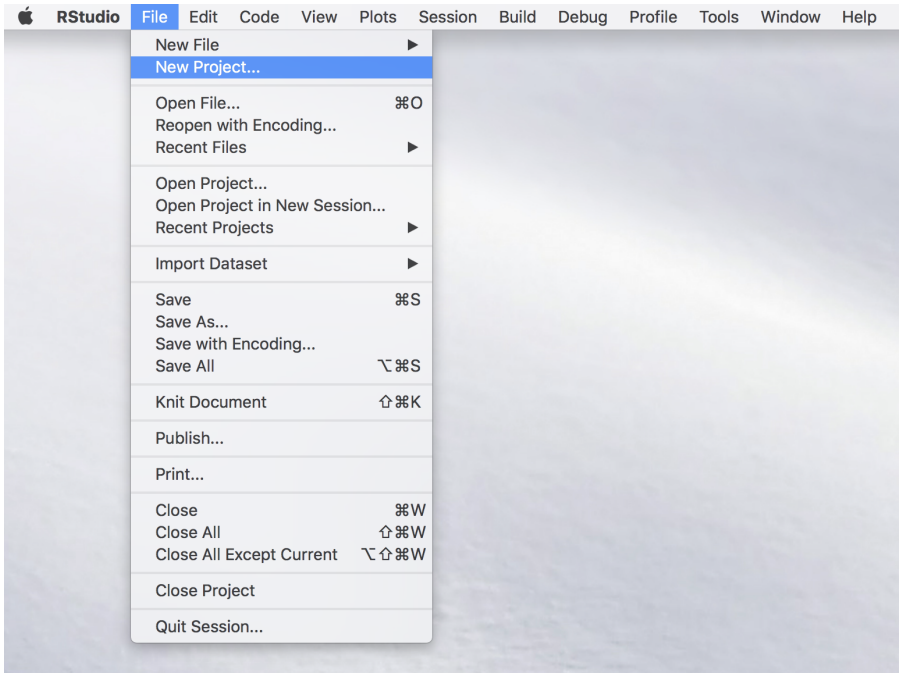
Now let us suppose that we want to make these functions available to the general user who may be looking for tools that allow them to perform Monte-Carlo intergration. Although we only have two functions, it would be appropriate to provide a single platform containing these functions along with documentation that describes the contents and use of these functions. Therefore, in the following sections we will describe the process to develop an R package for these functions which is consquently valid for any collection of functions needed to perform a specific task.

0.40 Basic steps

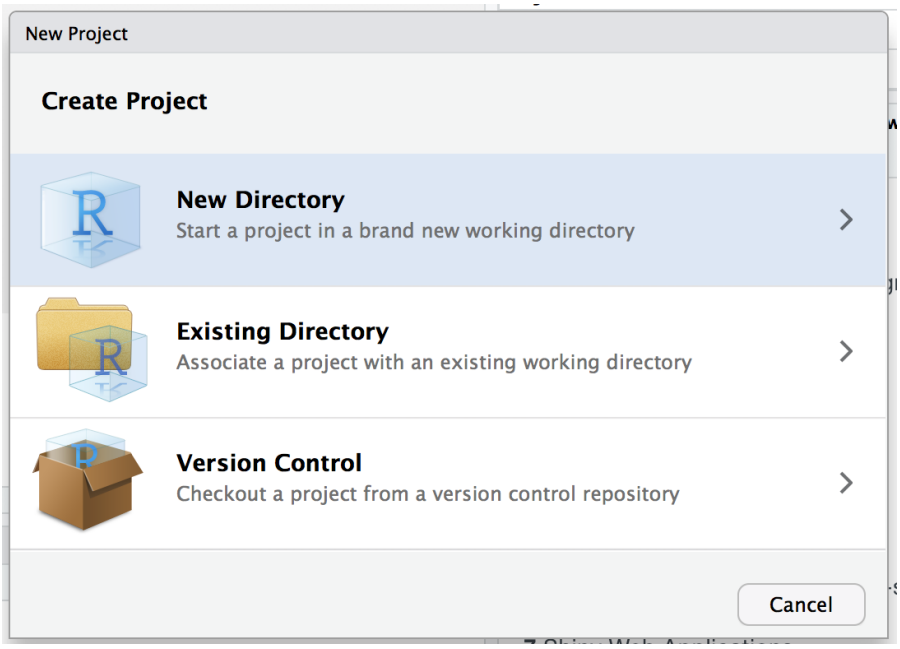
As mentioned earlier, the process to develop an R package that is described in this chapter is not strict or unique since there are many different ways of structuring and building them. However, in this book we will describe one way of building a package which is consistent with the approach to statistical programming that has been described thus far. Keeping this in mind, below the reader can find the basic steps to build an R package.

0.40.1 Step 1: Create an "empty" R package

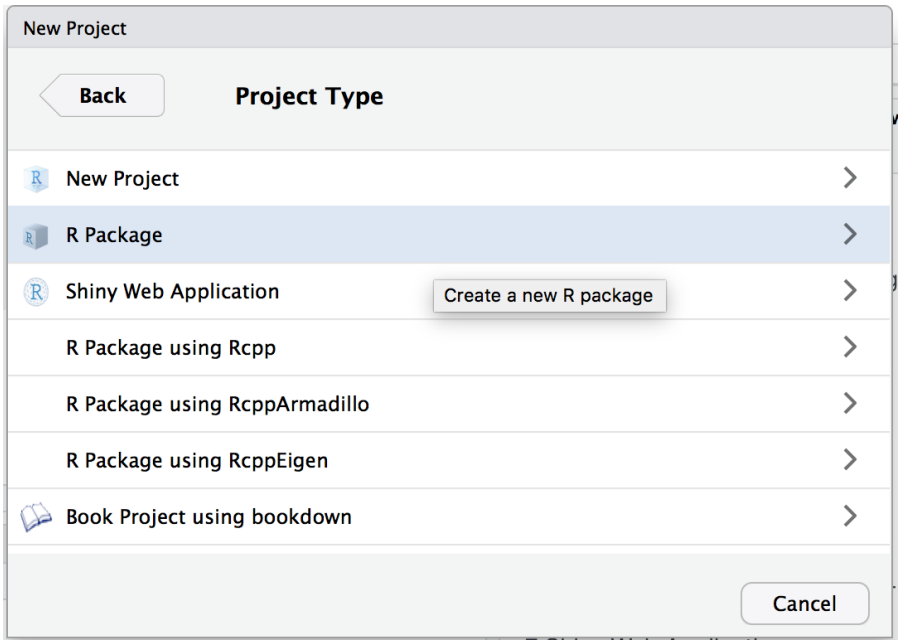
The first step to create an R package using RStudio is to build the *skeleton* of the package which contains the basic folders and files that are needed. To do so, within RStudio you should select to create a "New Project..." from the File menu within RStudio as shown below.



Once this is done you will see a new window with different options (see image below) among which you select "New Directory" (unless you wish to create the package within an existing directory which is usually not convenient for purpose of organization).

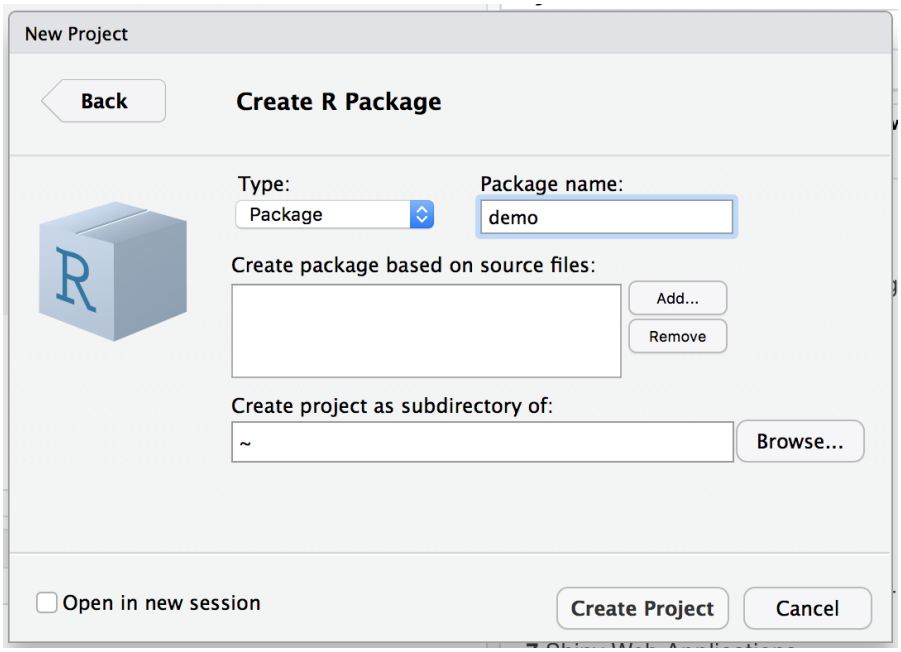


Again, another window will appear in which RStudio asks you for the type of project you wish to create and, quite intuitively, you should select the "R Package" option as shown below.

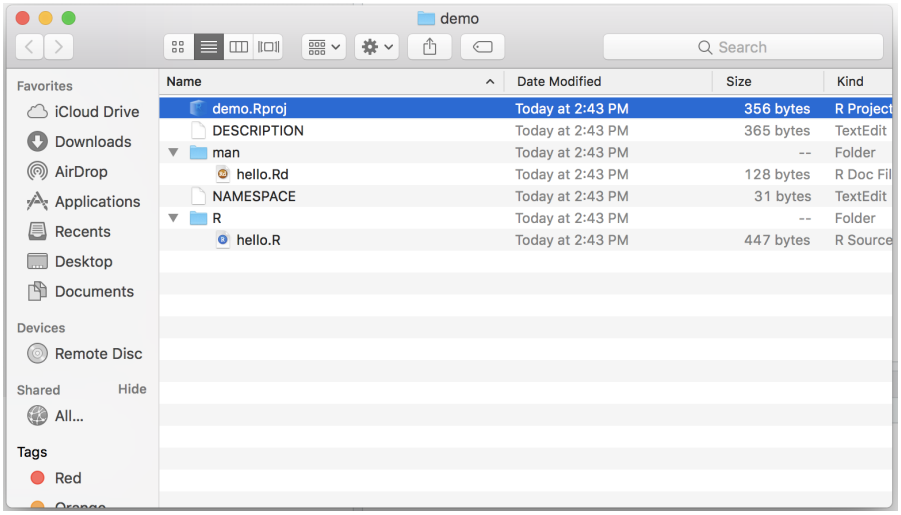


By doing so you prompt a successive window in which it is possible to name our package which, in the example below, will be `demo`. In the context of this chapter we will not consider the other options that are made available to the user (for more details you can check this link[43]).

[43] http://r-pkgs.had.co.nz/



Once the package has been named, you can select "Create Project" and another window will be prompted in which the basic files and folders needed for a package will be visualized within an overall repository with the same name as the package (i.e. "demo") as shown below.



Within the logic of this chapter which provides one possible pro-

cedure (out of various) to build an R package, we will proceed to removing the following files from this folder:

- NAMESPACE
- man/hello.Rd
- R/hello.R

These files are default functions and documentation that are created to provide a basis for the user who can then modify them using their own descriptions and functions. However, for the procedure described in this chapter their presence is redundant (as seen further on) and consequently we invite the reader to remove them if they decide to follow the steps described in this chapter.

0.40.2 Step 2: Edit description file

This first step hence creates the skeleton of the package and, in the following steps, we can focus on giving body to this skeleton, starting from the file which contains a summary description of the structure and contents of the package which is to be found in the "DESCRIPTION" file. Once this is opened the user will notice different parts to this file in which various information on the package is contained such as the package name, author information, license and imports. Although there are other pieces of information (see this link[44]), we will quickly discuss the latter three in the following paragraphs.

Author Roles

One of the lines of information in the description file corresponds to the authors of the package. This therefore corresponds to the list of persons who have actively contributed to the development of code and functions that are included in the package. When there is more than author, the line corresponding to the author can be replaced by a format like the following:

[44] http://r-pkgs.had.co.nz/description.html

```
Authors@R: c(
    person("Justin", "Lee", email = "justinlee@psu.edu", role = c("aut","cre
    person("Stephane", "Guerrier", role = "aut"),
    person("Roberto", "Molinari", role = "aut"),
    person("Matthew", "Beckman", role = "aut")
    )
```

This information is important also because it will impact how it is displayed later in the rendered package website (see further on). As you can notice it possible to also specify the role that the author has in relation to the package using the option `role =`, followed by codes for the type of role. In the above examples we can see two types of role that correspond to `aut` which indicates an *author* of the package while `cre` stands for *creator* who is the person in charge of maintaining the package and receiving information as well as bug reports or suggestions. There are other two possible roles available which are `ctb` and `cph` that correspond to *contributor* and *copyright holder* respectively, where the contributor is a person who has provided some minor contributions to the package while the copyright holder is the person or company who holds the copyright of the package.

License

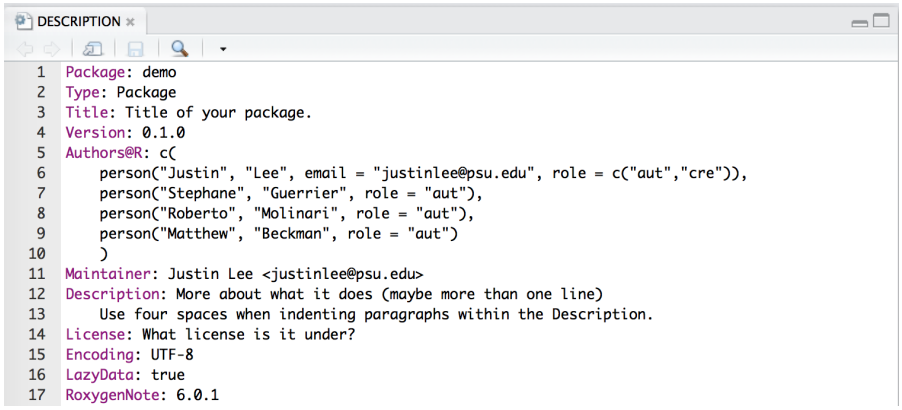
The package license determines to what extent and under what conditions the package (and its contents) can be shared and accessed by users. The most common license is the GNU General Public License which is a widely used free software license that guarantees end-users the possibility to run, study, share and modify the software. A complete list of all the possible licenses can be found at this link[45] and you are free to choose the license that best fits your requirements.

[45] https://cran.r-project.org/web/licenses/

Imports

It is often the case that your code and functions will depend on functions that are made available from other packages in R. In order to make sure that these packages are available to the user when they install your package, it is important to specify on which external packages yours relies on. In this sense, the `Imports` line in the DESCRIPTION file allows you to do just this so it is important to remember to check whether external packages are correctly specified in this section of the file.

Our example on Monte-Carlo integration only depends on the base functions in R and therefore there is no need to specify external packages for this case. Therefore, our "demo" package DESCRIPTION file ends up looking as follows:

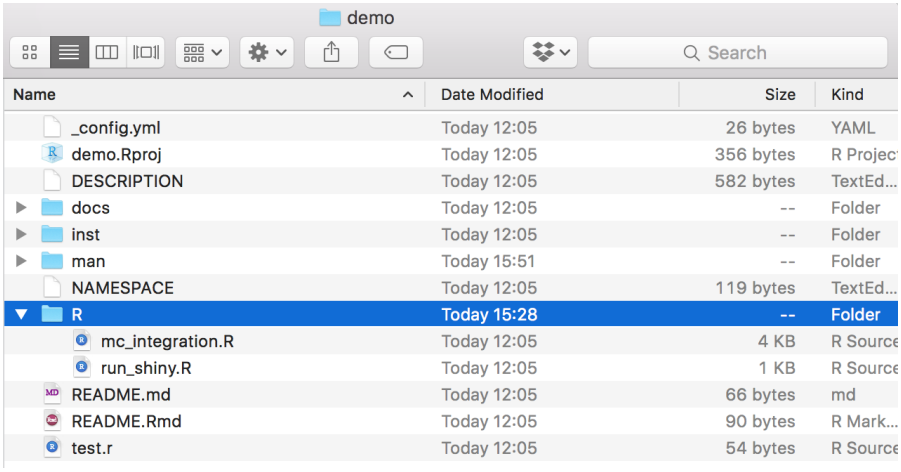


0.40.3 Step 3: Move your R scripts into the R folder

Having completed the description of the package we can now focus on adding the truly essential part of the package: the functions that deliver the outputs required by the user. In order for the functions to be considered as part of the package, the scripts containing these functions need to be moved into the R folder that is created as part of the package skeleton as seen earlier (therefore replacing the "hello.R" script that we chose to delete).

The organization of the code that collects the functions is subjective and can be included all in one single R script or in various scripts. It is usually suggested to group these functions into separate scripts according to their relative themes or specific tasks they are created for, especially when there is a considerable number of functions in the package. This approach allows to more easily find and fix any errors that are present in the functions as opposed to going through thousands of lines of code to find the function you're interested in.

In our example we only have two functions so there is no need to separate them and, consequently, we include them in a single R script that we call "mc_integration.R" which is included in the R folder for our demo package.



As you may notice, there is another file called "run_shiny.R" which, as we will see later, contains the code to create a Shiny app that is part of the package.

0.40.4 Step 4: Documentation

The next essential component of a package is its documentation which enables users to know how to use it. Indeed, when users access the `demo` package, they should essentially know how to use its functions by gaining access to help files through the use of commands like `?mc_int` for example. A possible (and efficient) way

of creating package documentation is by using a specific syntax before each function in your R scripts which will then be used to automatically generate the necessary `.Rd` files by using the commands `devtools::document()` or `roxygen2::roxygenize`.

We will use the `mc_int()` function from our demo package as an example to show the syntax that can be used before each function which is intended for the user:

```
#' @title Simple Monte-Carlo integration
#'
#' @description Compute an approximation of the integral of the function f(
#' with respect to dx in the range [a, b] by Monte-Carlo integration using
#' uniform sampling.
#' @param x_range A \code{vector} of dimension 2 used to denote the integra
#' region of interest, i.e. [a, b].
#' @param fun A \code{string} containing the function to be integrated. It
#' is assumed that \code{x} is used as the variable of interest.
#' @param B A \code{numeric} (integer) used to denote the number of simulat
#' @param seed A \code{numeric} used to control the seed of the random numb
#' generator used by this function.
#' @return A \code{list} containing the following attributes:
#' \describe{
#'      \item{I}{Estimated value of the integral}
#'      \item{var}{Estimated variance of the estimator}
#' }
#' @author Stephane Guerrier
#' @importFrom stats runif
#' @export
#' @examples
#' mc_int(x_range = c(0,1), fun = "x^2", B = 10^5)
#' mc_int(x_range = c(0,1), fun = "x^2*sin(x^2/pi)", B = 10^5)
mc_int = function(x_range, fun, B, seed = 1291){
  # A few checks
  # Check x_range
  if (length(x_range) != 2 || x_range[1] >= x_range[2]){
    stop("x_range is incorrectly specified")
```

```
}

# Check fun
if (class(fun) != "character"){
  stop("fun is incorrectly specified and should be a character")
}

x = mean(x_range)
test_fun = try(eval(parse(text = fun)), silent = TRUE)
if (class(test_fun) == "try-error"){
  stop("fun cannot be evaluated")
}

# Check B
if (B < 1){
  error("B is incorrectly specified")
}

# Set seed
set.seed(seed)

# Compute the length of the interval, i.e. (b-a)
interval_length = diff(x_range)

# Let's draw some uniforms to get Ui and Xi
Ui = runif(B)
Xi = x_range[1] + Ui*interval_length

# Compute \hat{I}
x = Xi
I_hat = interval_length*mean(eval(parse(text = fun)))

# Compute \hat{I}_2
I2_hat = interval_length*mean((eval(parse(text = fun)))^2)
var_I_hat = (interval_length*I2_hat - I_hat^2)/B
```

```
  # Output list
  out = list(I = I_hat, var = var_I_hat,
             fun = fun, x_range = x_range, B = B)
  class(out) = "MCI"
  out
}
```

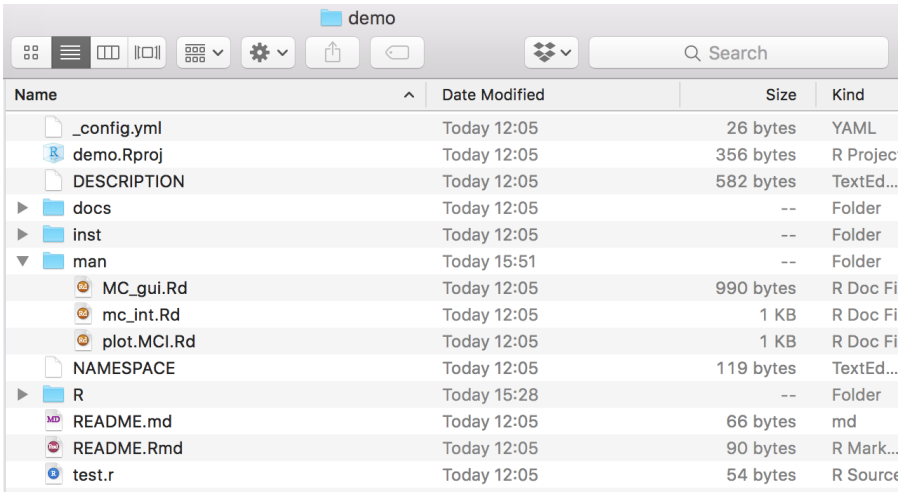
As can be seen, all the syntax which contributes to the documentation of the function is preceded by the syntax `#'` and is immediately followed (with no spacing) by the code of the function itself. Focussing on the contents of this documentation, the `@title` and `@description` entries will constitute respectively the title describing the function in a succint manner and the text providing a more detailed description of what the function does. We then find the `@param` syntax that is repeated for each parameter considered by the function in which a brief description of what the parameter is and what type of input is needed for it from the user. Finally we find the `@return` section where there is a description of the outputs of the function and eventual indications as to how these should be interpreted. Additional information can be provided such as the author(s) who specifically contributed to creating the function (`@author`), the packages or functions needed for the function to be employed (`@importFrom`) and examples that can show the user how to use this function in practice (`@examples`).

A final note should be given to the `@export` syntax which MUST absolutely be specified if you want the function you're documenting to be made available to the user. Indeed, there may be functions that are simply created to be used within other functions that are made available to the user and these therefore don't need to have this option specified. However, if the function needs to be made available to the user, then it is essential that this option is specified within the function documentation. Additional information on package documentation can be found here[46].

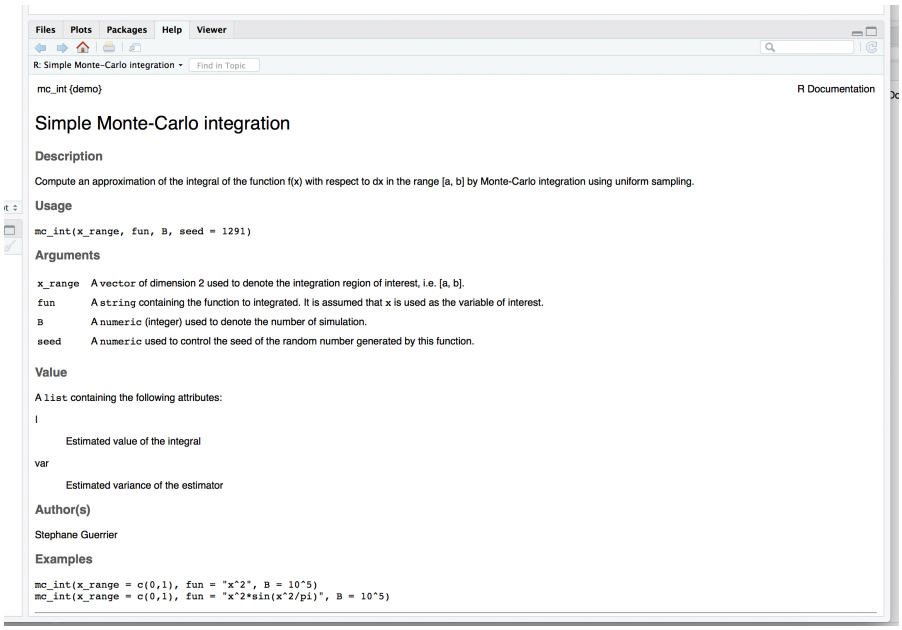
Once all the necessary functions have been documented, it is

[46] http://r-pkgs.had.co.nz/man.html#man-functions

possible to compile this documentation by using the commands `devtools::document()` or `roxygen2::roxygenize` (as mentioned earlier) or by directly building the package. Having done so, an `.Rd` file for each function will appear in the "man" folder (from which we earlier deleted the `hello.Rd` file). Below is an example of the `.Rd` files created for the functions in our example (with an added documentation for a function called `MC_gui` which is related to the code created for the Shiny app).

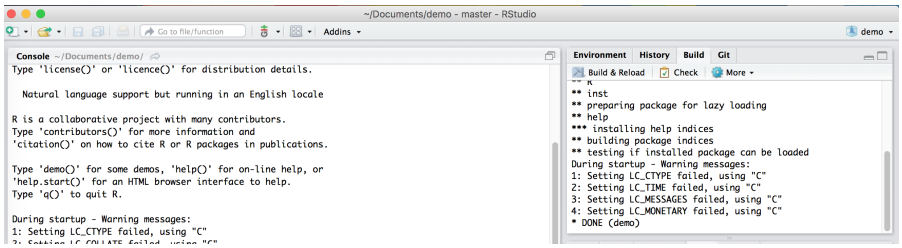


It is possible to check whether the documentation has been correctly compiled by using the command `?yourfunction`. Indeed, if we compiled our example documentation properly, this is what we get by using `?mc_int`:

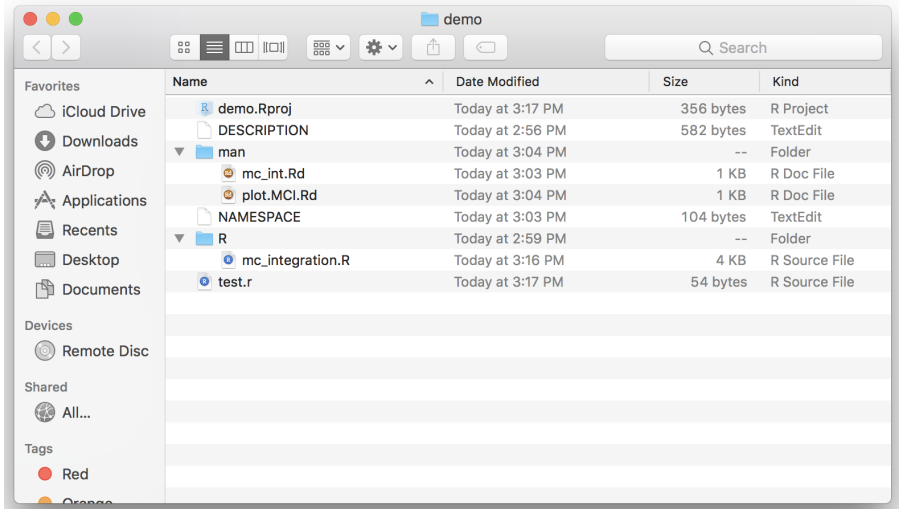


0.40.5 Step 5: Test your package

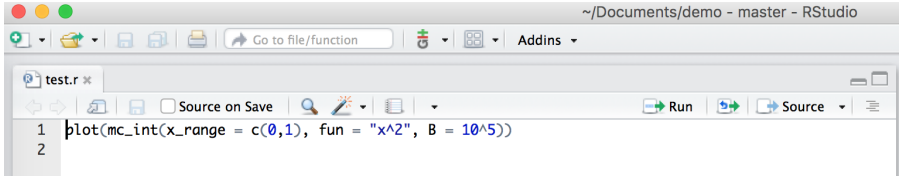
The previous steps are all that is necessary to complete the main components that are essential for an R package. Once these have correctly been completed, it is possible to build your package, meaning that you can combine all functions and documentation into a single software platform which can then be made available to the user. This can be done directly through the RStudio IDE where the "Environment, History, . . . " pane contains a label named "Build". When selecting this label different options will appear just beneath it, including one called "Build & Reload" which, if selected, will allow you to build the package and load it in your work session. If everything has worked smoothly, then the mentioned pane should report some logs that end with `* DONE (nameofpackage)` (see example below).



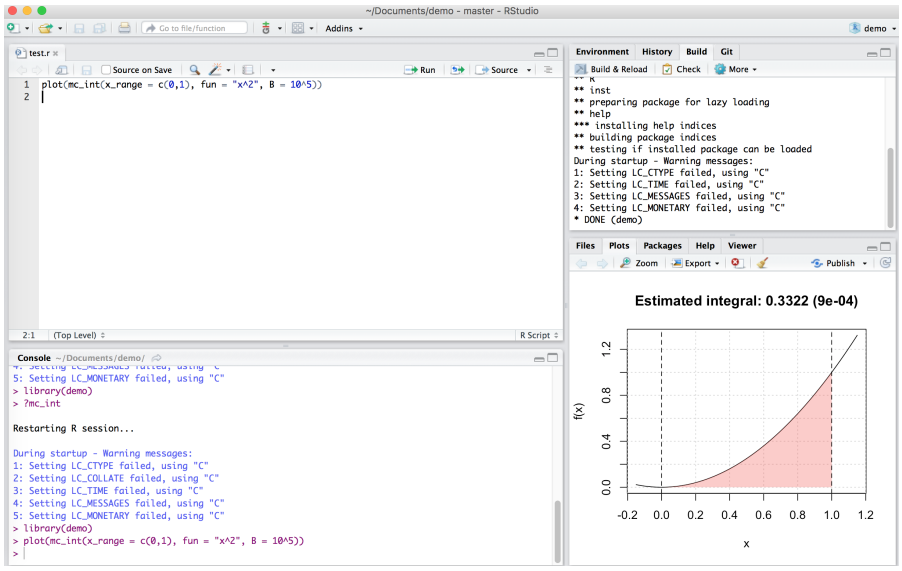
It is at this point that you can start testing whether the documentation and the functions work as they are supposed to. For this reason, it is always appropriate to create a test script to be placed in the main directory of the package folder that can be run to check if the functions behave the same and that no errors are output after some major changes are made to the package.



In our example, given that we can check both functions with one command, our test file can be as follows:



After making possible changes to the functions, we can run the test script and always expect to obtain the following output:



If this output is not the same or does not appear at all, then we need to go back to the functions to find where an error was made.

0.40.6 Step 6: Add a "README.Rmd" file

It is always helpful to create additional material to ensure that your package can be understood and used in the widest manner possible. For this purpose it is possible to create an additional "README.Rmd" file which, as an RMarkdown document, can be used to add descriptions, examples and videos that showcase the usage of your package through a web-page. An example of how to structure this file is given below:

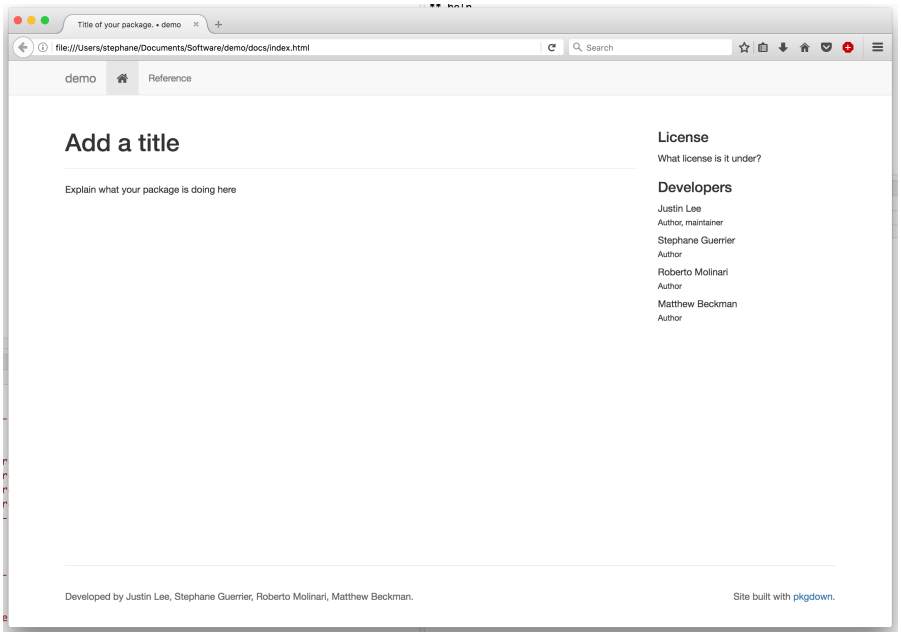
```
---
output: github_document
---

# Add a title

Explain what your package is doing here
```

Having saved this file within the main folder of your package, you

can compile this document using the `pkgdown` package (this can be installed by executing the following command in your console: `devtools::install_github("hadley/pkgdown")`). When the latter package is installed and loaded, all you need to do is execute the command `pkgdown::build_site()` to obtain the following web-page:



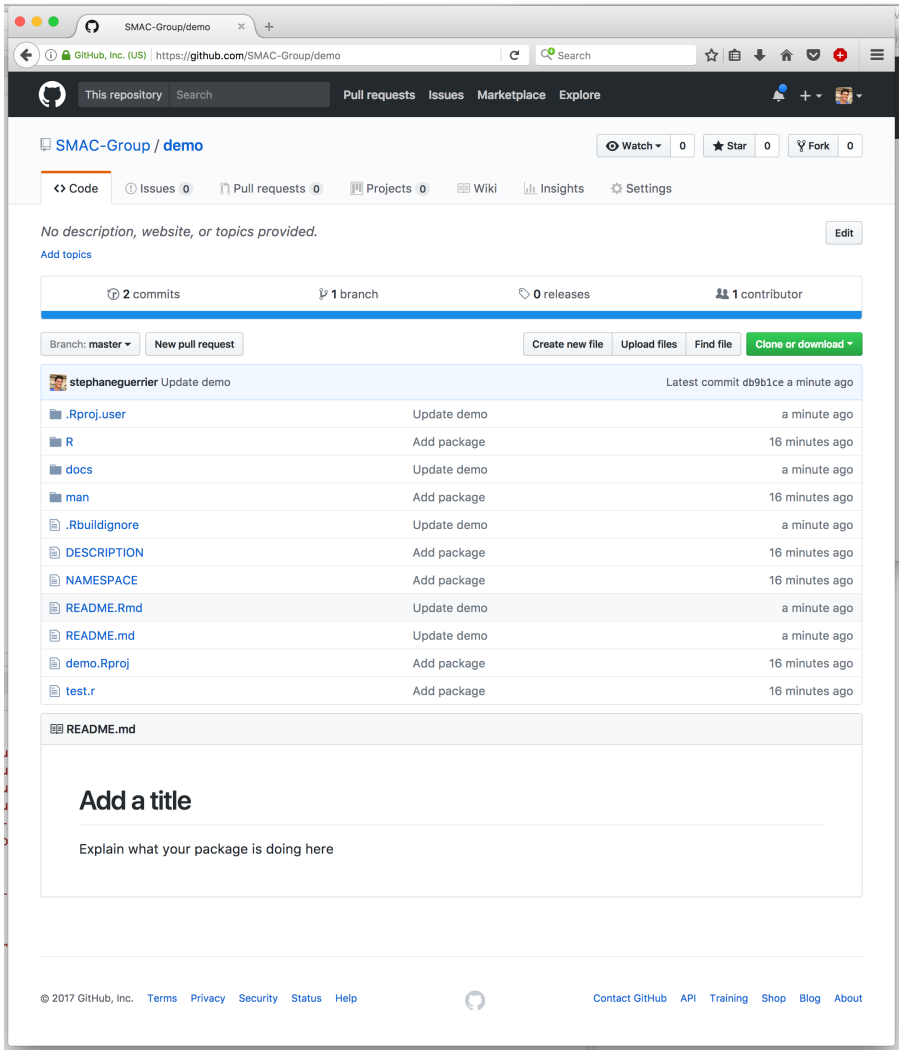
In order to publish this web-page, it is possible to do so by creating a GitHub repository dedicated to your package which constitutes the final basic step.

0.40.7 Step 7: Create a github repo - possibly with the same name as package

The basic idea of creating a package is to share a set of functions with collaborators and users. As we saw in Chapter 2, a convenient tool to share code and projects is GitHub and, in this case as well, you can create a repository dedicated to your package. In this case, it would be convenient to name the repository with the same name

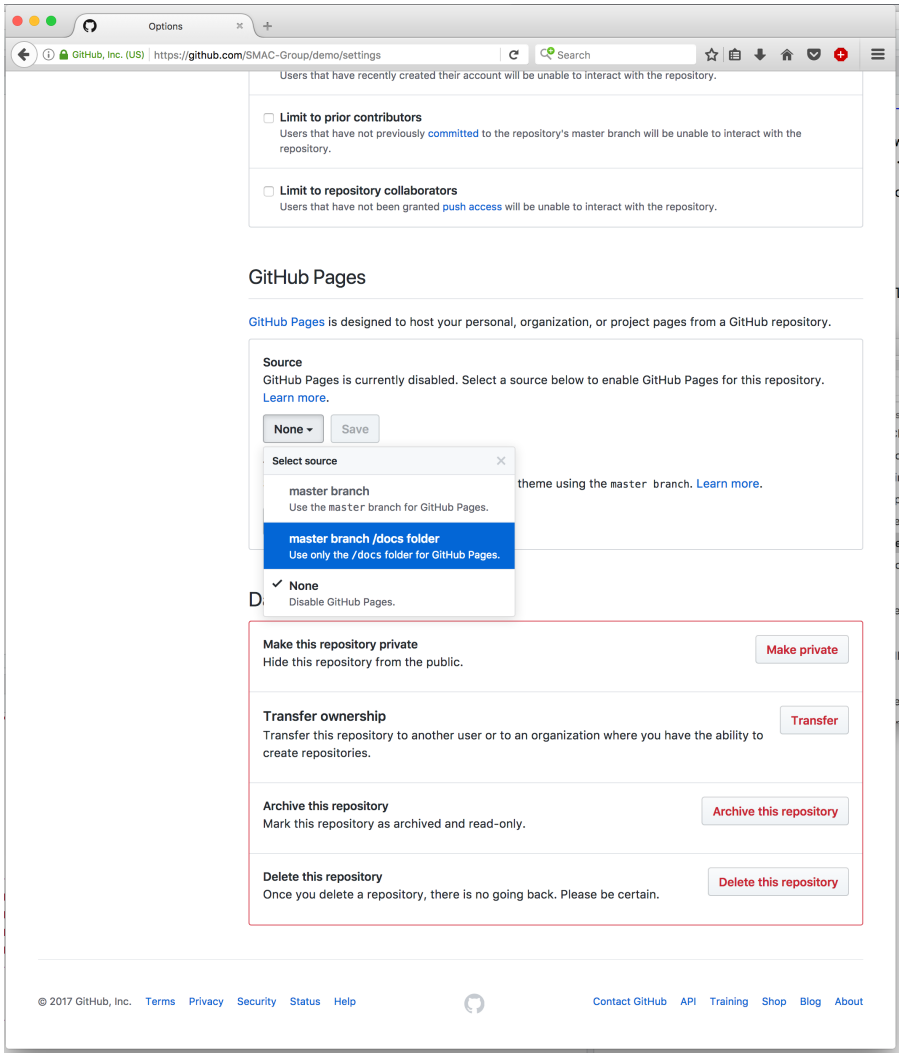
of your package so that users can more easily find and access the package that you make available through GitHub.

Once you have created a repository and loaded your package on GitHub, for our example you should obtain something similar to the following case:



As you can see, the GitHub repository takes the content of the .Rmd file and presents its content just below the list of folders and files that compose the package. However, it is possible to also

create a separate and dedicated web-page (using the contents of the .Rmd file) by using GitHub Pages. To do so, select the "Settings" label within your GitHub repository and scroll down to the GitHub Pages section where you can select the "master branch/docs folder" option under the "Source" area (as can be seen below).



Once this is done, you can eventually personalize the web-page a little more by selecting a particular theme for it (more details further on). Having done so, the page is already made available through the following address: `https://<your github`

id>.github.io/<your repo name>/. For our example, this is available at https://smac-group.github.io/demo/.

0.41 Advanced

Up to now we have described the basic steps that are necessary to build, share and describe an R package. However, it is always possible to add features to the package itself or to the documentation used to explain and promote it. In the following paragraphs we just describe a few of them to allow the reader to get a further idea of the extent to which one can develop packages.

0.41.1 Adding a shiny app

A feature which can be useful to make your package accessible to the general user (as well as to promote it) can be the possibility of including a Shiny app as an interface to your package. To do so, you will have to include a new folder called "inst" within your package main folder and in which an additional folder is then included with a name of your choice (let us say "MC_int" for the example we have used throughout this chapter). Within the latter you can then include the R script(s) to run the Shiny app (say "app.R") which makes use of the functions made available within the package. An example of the content of such a script is the following:

```
# Define UI for application that draws a plot of the approximate integral
ui <- fluidPage(

   # Application title
   titlePanel("Monte-Carlo Integration"),

   # Sidebar with text input for the function to integrate, numeric inputs
   sidebarLayout(
```

```
      sidebarPanel(
        textInput("fun", "Function to integrate:","sin(10*x)*exp(cos(x))"),
        numericInput("low", "Integral lower bound:", 0, min = -100, max = 10
        numericInput("up", "Integral upper bound:", 1, min = -100, max = 100
        numericInput("B", "Number of Monte-Carlo replications:", 10^5,
                     min = 100, max = 10^9),
        actionButton("button", "Compute Integral")
      ),

      # Show a plot of the integrated area under the function
      mainPanel(
         plotOutput("distPlot")
      )
   )
)

# Define server logic required to draw the integration plot
server <- function(input, output) {

  a <- eventReactive(input$button, {
    mc_int(x_range = c(input$low, input$up),
           fun = input$fun, B = input$B)
  })

  output$distPlot <- renderPlot({
      plot(a())
  })

}

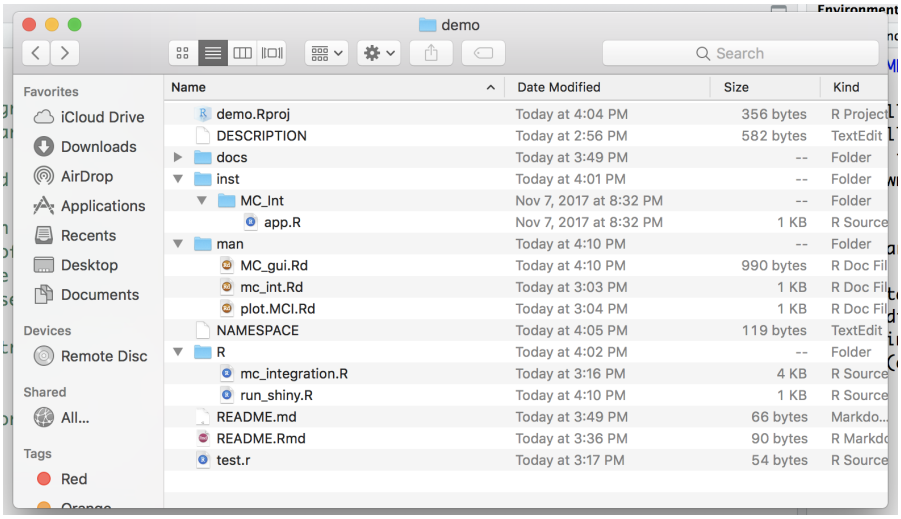
# Run the application
shinyApp(ui = ui, server = server)
```

Once this is done, an additional R script needs to included within the "R" folder. This R script will contain a function that allows the user to generate a Shiny app (based on the contents of "app.R" for

example) and consequently to use the app interface to make use of the package functions. Following from our example, suppose that the latter script, which we will call "run_shiny.r" for this example, contains the following function:

```
#' @export
MC_gui = function(){
  appDir = system.file("MC_int", package = "demo")
  shiny::runApp(appDir, display.mode = "normal")
}
```

Given these steps, our main package folder should look like this:



After having created the above mentioned folders and correctly written and placed the functions within these folders, all you need to do to make this feature available to the user is to execute the command `devtools::document()` and successively build the package again. Having done so, the only command that the user needs to use to access the Shiny app is to run the function `MC_gui()` in the console.

0.41.2 Custom website

Below is a video about customizing the website.

EXAMPLE: smac-group/demo

0

High performance computing

(coming soon)

0

Website creation

(coming soon)