

# **Deep R Programming**

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Weird is the world we live in, but the following had to be written.

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Anyway, any bug reports/corrections/feature requests are welcome. To make this textbook even better, please file them at <https://github.com/gagolews/deepr>.

Typeset with Xe<sub>La</sub>TeX. Please be understanding: it was an algorithmic process. Hence, the results are  $\in$  [good enough, perfect).

Homepage: <https://deepr.gagolewski.com/>

Datasets: <https://github.com/gagolews/teaching-data>

Release: v0.9.0 (draft) (2023-05-19T16:56:49+1000)

ISBN: 978-0-6455719-2-9 (v1.0; 2023; Melbourne: Marek Gagolewski)

DOI: [10.5281/zenodo.7490464](https://doi.org/10.5281/zenodo.7490464) (Zenodo)

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*Deep R Programming* by Marek Gagolewski<sup>1</sup> is a **comprehensive course on one of the most popular languages for data science** (statistical computing, graphics, machine learning, data wrangling and analytics). It **introduces the base language** in-depth. It is aimed at ambitious students, practitioners, and researchers who want to become **independent users** of this powerful environment.

Although available online, this is a whole course. It should be read from the beginning to the end. In particular, refer to the *Preface* for general introductory remarks.

**This early draft is distributed in the hope that it will be useful.**

For many students around the world, educational resources are hardly affordable. Therefore, I have decided that this book should **remain an independent, non-profit, open-access project** (available both in [PDF](#)<sup>2</sup> and [HTML](#)<sup>3</sup> forms). Whilst, for some people, the presence of a “designer tag” from a major publisher might still be a proxy for quality, it is my hope that this publication will prove useful to those seeking knowledge for knowledge’s sake.

**Please spread the news** about it by sharing the above URLs with your mates, peers, or students. Thank you.

Also, check out my other book, *Minimalist data wrangling with Python*<sup>4</sup> [26].

Any bug/typo reports/fixes are appreciated: please submit them via this project’s [Git-Hub repository](#)<sup>5</sup>.

Consider citing this book as: Gagolewski M. (2023), *Deep R Programming*, Zenodo, Melbourne, DOI: [10.5281/zenodo.7490464](https://doi.org/10.5281/zenodo.7490464)<sup>6</sup>, ISBN: 978-0-6455719-2-9, URL: <https://deepr.gagolewski.com/>.

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<sup>1</sup> <https://www.gagolewski.com>

<sup>2</sup> <https://deepr.gagolewski.com/deepr.pdf>

<sup>3</sup> <https://deepr.gagolewski.com/>

<sup>4</sup> <https://datawranglingpy.gagolewski.com/>

<sup>5</sup> <https://github.com/gagolews/deepr/issues>

<sup>6</sup> <https://dx.doi.org/10.5281/zenodo.7490464>



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## Preface

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### 0.1 To R, or not to R

R [67] has been named the eleventh most dreaded programming language in the 2022 StackOverflow Developer Survey<sup>7</sup>.

Also, it is a free app, so there must be something wrong with it, right?

But whatever, R is deprecated anyway; the “modern” way is to use **tidyverse**.

Or we should all just **switch to Python**<sup>8</sup>.

Well, not really<sup>9</sup>.

---

### 0.2 R (GNU S) as a language and an environment

Let us get one thing straight: R is *not* just a *statistical package*. It is a general-purpose, high-level programming language that happens to be very powerful for numerical, data-intense computing activities of any kind. It offers extensive support for statistical, machine learning, data analysis, data wrangling, and data visualisation applications, but there is much more.

Initially, R<sup>10</sup> was written for statisticians, by statisticians. Therefore, it is a free, yet more capable alternative to Stata, SAS, SPSS, Statistica, Minitab, Weka, etc. (and without any strings attached). Unlike in some of them, in R, a spreadsheet-like GUI is not the main gateway for performing computations on data. Here, a user must *write code* to get things done. Despite the learning curve’s being a little steeper for non-programmers, in the long run, it empowers their users because they are not limited only to the most common scenarios. If some functionality is missing or does not suit their needs, they can easily implement everything themselves.

It is thus very convenient for rapid prototyping. It helps turn our ideas into operational

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<sup>7</sup> <https://survey.stackoverflow.co/2022/>

<sup>8</sup> <https://datawranglingpy.gagolewski.com/>

<sup>9</sup> Or, as Aussies would say, *yeah, nah*.

<sup>10</sup> Or we should rather say: S, whose open-source reimplementation/dialect R is; see below for historical notes. Credit must be given where credit is due.

code that can be tested, extended, polished, run in production, and otherwise enjoyed. As an interpreted language, it can not only be executed in an interactive read-eval-print loop (command–result, question–answer, ...), but also in batch mode (running whole, standalone scripts).

Thus, we would rather position R amongst such tools/languages for numerical or scientific computing as Python with the NumPy ecosystem, Julia, GNU Octave, Scilab, MATLAB, etc. However, it is more *specialised* in data science applications than any of them. Hence, it provides a much smoother experience. This is why, over the years, R has become the de facto standard in statistics and many other related fields.

---

**Important** R is a whole ecosystem (environment). It not only consists of the R language interpreter, but also features advanced:

- graphics capabilities (see [Chapter 13](#)),
  - a consistent, well-integrated help system ([Section 1.4](#)),
  - ways for convenient interfacing with compiled code ([Chapter 14](#)),
  - a package system and centralised package repositories (such as CRAN and Bioconductor; [Section 7.3.1](#)),
  - a lively community of users and developers – curious and passionate people, like you and me.
- 

---

**Note** R is a free, open-source (licensed under the GNU General Public License v2) variation or dialect of the very popular S system designed in the mid-1970s by Rick A. Becker, John M. Chambers, and Allan R. Wilks at Bell Labs; see [3, 4, 5, 6] and its later revisions [7, 9, 13, 55].

Quoting [4]:

---

*The design goal for S is, most broadly stated, to enable and encourage good data analysis, that is, to provide users with specific facilities and a general environment that helps them quickly and conveniently look at many displays, summaries, and models for their data, and to follow the kind of iterative, exploratory path that most often leads to a thorough analysis. The system is designed for interactive use with simple but general expressions for the user to type, and immediate, informative feedback from the system, including graphic output on any of a variety of graphical devices.*

---

S became popular because it offered greater flexibility than the standalone statistical packages. It was praised for its high interactivity and array orientation that was known from APL, the familiar syntax of the C language that involves the use of {curly braces}, the ability to treat code as data known from Lisp (Chapter 15), the notion of lazy arguments (Chapter 17), and the ease of calling external C and Fortran routines (Chapter 14). Its newer versions were also somewhat object-oriented (Chapter 10).

However, S was a commercial system. To address this, R (GNU S) was developed in the mid-1990s<sup>11</sup> by Robert Gentleman and Ross Ihaka of the Statistics Department, University of Auckland, and many contributors; see [12, 37] for some historical notes. In essence, R was supposed to be backwards-compatible with S, but some design choices led to their evaluation models' being slightly different: its design was heavily inspired by Scheme (with its environment model of evaluation; see [1] and Chapter 16 for more details)

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### 0.3 Aims, scope, and design philosophy

Many users were introduced to R by means of some very advanced operations involving data frames, formulae, and functions that rely on nonstandard evaluation (metaprogramming), like:

```
lm(
  Ozone~Solar.R+Temp,
  data=subset(airquality, Temp>60, select=-(Month:Day))
) |> summary()
```

This is horrible.

Another group was isolated from the base R through a thick layer of third-party packages that feature an overwhelming number of functions (every operation, regardless of its complexity, has a different name), often duplicate the core functionality, and sometimes are quite incompatible with our traditional system.

Both user families ought to be fine, as long as they limit themselves to solving only the simplest and most common data processing problems.

But we yearn for more. We do not want hundreds of prefabricated *recipes* for popular dishes that we can mindlessly apply without much understanding.

Our aim is to learn *base R*, which is *supposed to be* the common language (lingua franca)

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<sup>11</sup> R version 0.49 released in April 1997 (the first for which *source code*<sup>2</sup> is available on CRAN), was already quite feature-rich (e.g., implemented S3 methods, formulae, and data frames introduced in the 1991 version of S [13]).

<sup>11</sup> <https://cloud.r-project.org/src/base/R-0/>

for all R users. We want to be able to indite code that everybody *should* understand; code that will work without modifications ten years from now (no slang!).

We want to be able to tackle *any* data-intense problem. Furthermore, we want to develop *transferable* skills so that learning new tools such as Python with NumPy and Pandas (e.g., [26]) or Julia will be much easier later: R is not the only notable environment out there.

Anyway, enough preaching. This graduate<sup>12</sup>-level textbook is for independent readers who:

- do not mind a slightly steeper learning curve at the beginning,
- can appreciate a more cohesively and comprehensively<sup>13</sup> organised material,
- would like to experience the joy of solving problems by programming,
- do not want to be made obsolete by artificial “intelligence” in the future.

Some will benefit from it as a first introduction to R (yet, without all the pampering). For others<sup>14</sup>, this will be a fine course from intermediate to advanced (do not skip the first chapters, though).

Either way, do not forget to solve *all* the prescribed exercises.

Good luck.

## 0.4 Classification of R data types and book structure

The most commonly used R data types can be classified as follows; see also [Figure 1](#).

1. *Basic types* – which we discuss in the first part of this book – internal or built-in types, upon which more complex ones are hinged:
  - *atomic vectors* – represent whole sequences of values, where every element is of the same type:
    - logical ([Chapter 3](#)) – includes items that are TRUE (“yes”, “present”), FALSE (“no”, “absent”), or NA (“not available”, “missing”);

<sup>12</sup> The author taught similar courses for his wonderfully ambitious undergraduate data/computer science and maths students at Warsaw University of Technology, where such an approach has proven not difficult at all. It requires a more independent, curious, and motivated mindset, though. And that’s the way to go in the long run.

<sup>13</sup> Yours truly is neither a historian, a stenographer, nor a grammarian. We allow ourselves to make a few noninvasive idealisations for didactic purposes. Languages evolve over time, R is now different from what it used to be, and we can shape it (slowly; we value its stable API) to become something even better in the future.

<sup>14</sup> It might also happen that for some, this will not be an appropriate course at all, either at this stage of their career (come back later) or in general (no dramas). This is a non-profit, open-access project, but it does not mean it is ideal for everyone – in such a case, give other sources a try, e.g., [8, 10, 15, 45, 56, 58, 59, 66], etc. Some of them are freely available.





Figure 1: An overview of the most prevalent R data types; see Figure 17.2 for a more comprehensive list

- `numeric` (Chapter 2) – features real numbers, such as 1, 3.14, -0.0000001, etc.;
- `character` (Chapter 6) – contains strings of characters, e.g., "groß", "123", or "Добрый день";
- `function` (Chapter 7) – used to group a series of expressions (code lines) so that they can be applied on different kinds of input data to generate the (hopefully) desired outcomes, for instance, **cat**, **print**, **plot**, **sample**, and **sum**;
- `list` (generic vector; Chapter 4) – can store elements of mixed types;

The above will be complemented with a discussion on vector indexing (Chapter 5) and ways to control the program flow (Chapter 8).

2. *Compound types* – discussed in the second part – wrappers around objects of basic types that might behave differently from the underlying primitives thanks to the dedicated operations *overloaded* for them. They are:
  - `factor` (Section 10.3.2) – a vector-like object that represents qualitative data (on a nominal or an ordered scale);
  - `matrix` (Chapter 11) – stores tabular data, i.e., arranged into rows and columns, where each cell is usually of the same type;
  - `data.frame` (Chapter 12) – also used for depositing tabular data, but this time such that each column can be of a different type;
  - and many more, which we can arbitrarily define using, amongst others, the principles of S3-style object-oriented programming (Chapter 10).

In this part of the book, we also discuss the principles of sustainable coding (Chapter 9) as well as introduce the basic ways to prepare publication-quality graphics (Chapter 13).

3. Some more advanced material is discussed in the third part. In most cases, we can (and often should) easily do without it, but it is still essential to gain a complete understanding of and control over our environment. This includes the following data types:
  - `symbol` (`name`), `call`, `expression` (Chapter 15) – objects representing unevaluated R expressions that can be freely manipulated and executed if needed;
  - `environment` (Chapter 16) – hashmaps that store named objects and which form the basis of the environment model of evaluation;
  - `formula` (Section 17.6) – used by some functions to specify supervised learning models or define operations to be performed within data subgroups, amongst others.

We should not be surprised that we did not list any data types defined by a few trendy<sup>15</sup> third-party packages. We will later see that we can most often do without them. If that is not the case, we will become skilled enough to learn them quickly ourselves.

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## 0.5 About the author

I, Marek Gagolewski<sup>16</sup> (pronounced like Ma'rek Gong-olive-ski), am currently a Senior Lecturer in Data Science/Applied AI at Deakin University in Melbourne, VIC, Australia, and an Associate Professor at the Systems Research Institute of the Polish Academy of Sciences.

My research interests are related to data science, in particular: modelling complex phenomena, developing usable, general-purpose algorithms, studying their analytical properties, and finding out how people use, misuse, understand, and misunderstand methods of data analysis in research, commercial, and decision-making settings. I'm an author of 90+ publications, including journal papers in outlets such as *Proceedings of the National Academy of Sciences (PNAS)*, *Journal of Statistical Software*, *The R Journal*, *Information Fusion*, *International Journal of Forecasting*, *Statistical Modelling*, *Physica A: Statistical Mechanics and its Applications*, *Information Sciences*, *Knowledge-Based Systems*, *IEEE Transactions on Fuzzy Systems*, and *Journal of Informetrics*.

In my “spare” time, I write books for my students (also check out my *Minimalist data wrangling with Python*<sup>17</sup> [26]) and develop open-source (libre) data analysis software,

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<sup>15</sup> Which does not automatically mean *good*. For instance, sugar, salt, and some drugs are very popular, but it does not make them healthy.

<sup>16</sup> <https://www.gagolewski.com>

<sup>17</sup> <https://datawranglingpy.gagolewski.com/>

such as **stringi**<sup>18</sup> (one of the most often downloaded R packages), **genieclust**<sup>19</sup> (a fast and robust clustering algorithm in both Python and R), and many others<sup>20</sup>.

## 0.6 Acknowledgements

R, and its predecessor S, is the result of a collaborative effort of many programmers<sup>21</sup>. Without their generous intellectual contributions, the landscape of data analysis would not be as beautiful as it is now. R is distributed under the terms of the GNU General Public license version 2, and we occasionally display fragments of its source code for didactic purposes.

We describe and use R version 4.3.0 (2023-04-21). However, we expect 99.9% of the material covered here to be valid in future releases (consider filing a bug report if you discover this is not the case).

*Deep R Programming* is based on the author's experience as an R user (since ~2003), developer of open-source packages (mentioned above), tutor/lecturer (since ~2008), and an author of a quite successful Polish textbook *Programowanie w języku R* (see [25]) which was published by PWN (1st ed. 2014, 2nd ed. 2016). Even though the current book is an entirely different work, its predecessor served as an excellent testbed for many ideas conveyed here.

In particular, the teaching style exercised in this book has proven successful in many similar courses that yours truly has been responsible for, including at Warsaw University of Technology, Data Science Retreat (Berlin), and Deakin University (Melbourne). I thank all my students and colleagues for the feedback given over the last 15-odd years.

However, this book received no funding, administrative, technical, or editorial support from Deakin University, Warsaw University of Technology, Polish Academy of Sciences, or any other source.

This book was prepared in a Markdown superset called **MyST**<sup>22</sup>, **Sphinx**<sup>23</sup>, and TeX (XeLaTeX). Code chunks were processed with the R package **knitr** [61]. All figures were plotted with the low-level **graphics** package using the author's own style template. A little help from Makefiles, custom shell scripts, and **Sphinx** plugins (**sphinxcontrib-bibtex**<sup>24</sup>, **sphinxcontrib-proof**<sup>25</sup>) dotted the *j*'s and crossed the *f*'s.

<sup>18</sup> <https://stringi.gagolewski.com>

<sup>19</sup> <https://genieclust.gagolewski.com>

<sup>20</sup> <https://github.com/gagolews>

<sup>21</sup> <https://www.r-project.org/contributors.html>

<sup>22</sup> <https://myst-parser.readthedocs.io/en/latest/index.html>

<sup>23</sup> <https://www.sphinx-doc.org/>

<sup>24</sup> <https://pypi.org/project/sphinxcontrib-bibtex/>

<sup>25</sup> <https://pypi.org/project/sphinxcontrib-proof/>

The **Ubuntu Mono**<sup>26</sup> font is used for the display of code. Typesetting of the main text relies on the *Alegreya*<sup>27</sup> and *Lato*<sup>28</sup> typefaces.

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## o.7 You can make this book better

Open, non-profit projects such as this have to rely on the generosity of the readers' community when it comes to quality assurance.

If you find a typo, a bug, or a passage that could be rewritten or extended for better readability/clarity, do not hesitate to report it via the *Issues* tracker available at <https://github.com/gagolews/deepr/issues/>. New feature requests are welcome as well.

Please consider “starring” the book’s *GitHub* repository<sup>29</sup>. Some people (weirdly) use the number of “stars” as a proxy for quality.

Spread the news about this book by sharing <https://deepr.gagolewski.com/> with your mates, peers, or students. You may want to cite it in your publications. Thank you.

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<sup>26</sup> <https://design.ubuntu.com/font/>

<sup>27</sup> <https://www.huertatipografica.com/en>

<sup>28</sup> <https://www.latofonts.com/>

<sup>29</sup> <https://github.com/gagolews/deepr/>

**Part I**

**Deep**



# 1

---

## Introduction

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### 1.1 Hello, world!

Traditionally, every programming journey starts with the printing of a “Hello, World”-like greeting. Let’s then get it over with asap:

```
cat("My hovercraft is full of eels.\n") # `\\n` == newline
## My hovercraft is full of eels.
```

By calling (invoking) the **cat** function, we printed out a given character string that we enclosed in double-quote characters.

Documenting code is a good development practice. It is thus worth knowing that any text followed by a hash sign (that is not part of a string) is a *comment*. It is ignored by the interpreter.

```
# This is a comment.
# This is another comment.
cat("I cannot wait", "till lunchtime.\n") # two arguments (another comment)
## I cannot wait till lunchtime.
cat("# I will not buy this record.\n# It is scratched.\n")
## # I will not buy this record.
## # It is scratched.
```

By convention, in this book, the textual outputs generated by R itself are always preceded by two hashes. This makes copy-pasting all code chunks easier in the case where the diligent readers would like to experiment with them by themselves (which is always highly encouraged).

Whenever a call to some function is to be made, the round brackets are obligatory. All objects within the parentheses (they are separated by commas) constitute the input data to be consumed by the operation. Thus, the syntax is: **some\_function\_to\_be\_called**(argument1, argument2, etc.).

## 1.2 Setting up the development environment

### 1.2.1 Installing R

It is quite natural to pine for the ability to execute the above code ourselves – we cannot learn programming without getting our hands dirty.

The official precompiled binary distributions of R can be downloaded from <https://cran.r-project.org/>.

For serious programming work<sup>1</sup>, we recommend, sooner rather than later, switching to<sup>2</sup> one of the UNIX-like operating systems. This includes the free, open-source (== good) variants of GNU/Linux, amongst others, or the proprietary (== very far from good) m\*\*OS. The users thereof might employ their favourite package manager (e.g., **apt**, **dnf**, **pacman**, or **Homebrew**) to install R.

Users of other operating systems (such as Wi\*\*\*ws) might consider installing Anaconda or Miniconda if they require some level of interoperability with the Python environment, e.g., they would like to work with the Jupyter environment (Section 1.2.5).

Below we review several ways in which we can write and execute R code. It is up to the benign readers to research, set up, and learn the development environment that suits their needs. As usual in real life, there is no single universal approach that always works best in all scenarios.

### 1.2.2 Interactive mode

R's *read-eval-print loop* (REPL) can give us instant gratification whenever we would like to compute something quickly, e.g., determine basic aggregates of a few numbers entered by hand or evaluate a mathematical expression like “2+2”.

How to start the R console varies from system to system, e.g., users of UNIX-like boxes can simply execute **R** from the terminal (shell). Wi\*\*\*ws folks can fire up the **RGui** from the *Start* menu.

---

**Important** When working interactively, the default<sup>3</sup> command prompt, “>”, means: *I am awaiting orders*. Moreover, “+” denotes: *Please continue*. In such a case, we should either complete the unfinished expression or cancel the operation by pressing ESC or CTRL+C (depending on the operating system).

```
> cat("And now
```

(continues on next page)

---

<sup>1</sup> For instance, when interoperability with other programming languages/environments is required or when we think about scheduling jobs on Linux-based computing/container clusters.

<sup>2</sup> Or at least trying out – by installing a copy of GNU/Linux on a virtual machine (VM).

<sup>3</sup> It can be changed; see **help**("options").



*(continued from previous page)*

```
+ for something
+ completely different
+
+
+ it is an unfinished expression...
+ awaiting another double quote character and then the closing bracket...
+
+ press ESC or CTRL+C to abort input
>
```

For readability, we never print out the command prompt characters in this book.

---

### 1.2.3 Batch mode: Working with R scripts (\*\*)

The interactive mode of operation is unsuitable for more complicated tasks, though.

The users of UNIX-like operating systems will be interested in another extreme, which involves writing standalone R scripts that can be executed line by line without any user intervention.

To do so, in the terminal (command line, shell), we can invoke:

```
Rscript file.R
```

where `file.R` is the path to some source file.

**Exercise 1.1** (\*\*) *In your favourite text editor (e.g., **Notepad++**, **Kate**, **vi**, **Emacs**, **RStudio**, or **VSCode**), create a file named `test.R`. Write a few calls to the `cat` function. Then, execute this script from the terminal by invoking the **Rscript** program.*

### 1.2.4 Weaving: Automatic report generation (\*\*)

Reproducible data analysis<sup>4</sup> requires us to keep the results (text, tables, plots, auxiliary files) synchronised with their generating code and data.

**utils::Sweave** (the **Sweave** function from the **utils** package) and **knitr** [61] are two example template processors that evaluate R code chunks within documents written in LaTeX, HTML, or other markup languages. The chunks are replaced by the outputs they yield.

This book is a showcase of such an approach: all the results, including [Figure 2.3](#) and the above “Hello, World”, were generated programmatically. Thanks to its being written in the highly universal [Markdown](#)<sup>5</sup> language, it could be easily converted to a single

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<sup>4</sup> The idea dates back to Knuth’s literate programming concept; see [40].

<sup>5</sup> <https://daringfireball.net/projects/markdown/>

PDF document<sup>6</sup> as well as the whole website<sup>7</sup>. Tools like **pandoc** and **docutils** facilitate such operations.

**Exercise 1.2** (\*\*) Install the **knitr** package by calling `install.packages("knitr")` from within an R session. Then, create a text file named `test.Rmd` with the following content:

```
# Hello, Markdown!

This is my first automatically generated report,
where I print messages and stuff.

```${r}
print("G'day!")
print(2+2)
plot((1:10)^2)
```

Thank you for your attention.
```

Assuming that the file is located in the current working directory (compare Section 7.3.2), call `knitr::knit("test.Rmd")` from the R console or run the following in the terminal:

```
Rscript -e 'knitr::knit("test.Rmd")'
```

Then, inspect the generated Markdown file, `test.md`.

Furthermore, if you have the **pandoc** tool installed, to generate a standalone HTML file, execute in the terminal:

```
pandoc test.md --standalone -o test.html
```

Alternatively, for ways to call external programs from R, see Section 7.3.2.

### 1.2.5 Semi-interactive modes (Jupyter Notebooks, sending code to the associated R console, etc.)

The nature of the most frequent use cases of R encourages a semi-interactive workflow, where we progress with prototyping fast by trial-and-error.

In this mode, we compose a series of short code fragments inside a standalone R script.

Each fragment implements a simple, well-defined task, such as the loading of data files, data cleansing, feature visualisation, computations of some information aggregates, etc.

Importantly, any code chunk can be sent to the associated R console and executed

<sup>6</sup> <https://deepr.gagolewski.com/deepr.pdf>

<sup>7</sup> <https://deepr.gagolewski.com>

therein. This way, we can inspect the results it generates at any time. If we are not happy with the outcome, we can apply any corrections that are necessary.

There are quite a few integrated development environments (IDEs; sometimes requiring additional plugins) that enable such a workflow, including **JupyterLab**, **Emacs**, **RStudio**, and **VSCodium**.

Executing an individual code line or a whole text selection is usually done by pressing (configurable) keyboard shortcuts such as `Ctrl+Enter` or `Shift+Enter`.

**Exercise 1.3** (\*) **JupyterLab**<sup>8</sup> is a development environment that runs in a web browser. It was programmed in Python, but supports many programming languages. Thanks to **IRkernel**<sup>9</sup>, we can use it with R.

1. Install **JupyterLab** and **IRkernel** (for instance, if you use Anaconda, run `conda install -c r r-essentials`).
2. From the File menu, select Create a new R source file and save it as, e.g., `test.R`.
3. From the File menu, select Create a new console for the editor running the R kernel.
4. Type some print “Hello, World”-like calls.
5. Press `Shift+Enter` (whilst working in the editor) to send different code fragments onto the console and execute them. Inspect the results.

See Figure 1.1 for an illustration.



Figure 1.1: JupyterLab: a source file editor and the associated R console, where we can run arbitrary code fragments

<sup>8</sup> <https://jupyterlab.readthedocs.io/en/stable/>

<sup>9</sup> <https://irkernel.github.io/>

**Example 1.4** (\*) *JupyterLab* is part of the *Jupyter* project. It supports the handling of dedicated Notebooks, where editable and executable code chunks and results they generate can be kept together in a single `.ipynb` (JSON) file; see Figure 1.2 for an illustration and Chapter 1 of [26] for a quick introduction (from the Python language kernel perspective).

This environment is quite convenient for live coding (e.g., for teachers) or performing exploratory data analyses. However, for more serious programming work, the code can get quite messy (luckily, there is always an option to export a notebook to an executable, plain text R script).

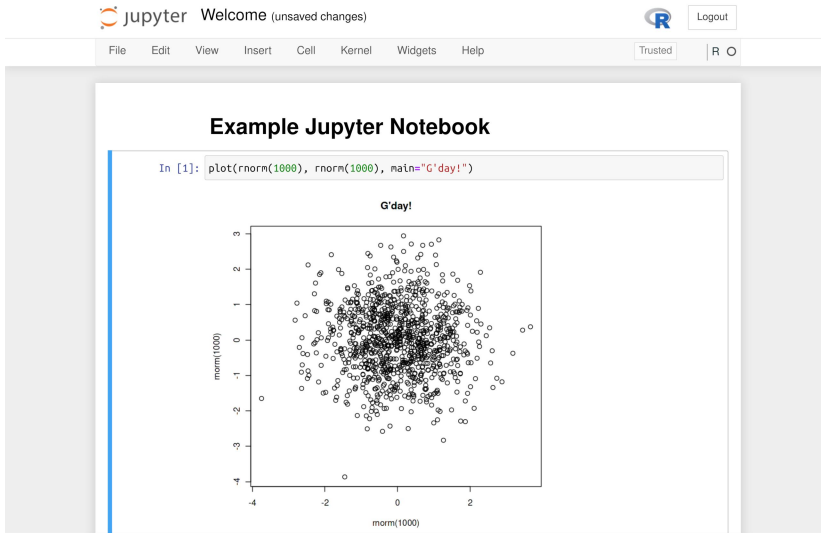


Figure 1.2: An example Jupyter Notebook, where we can keep the code and the results together

### 1.3 Atomic vectors at a glance

After the printing of the “Hello, World” message, a typical programming course would normally proceed with the discussion on basic data types for storing individual numeric or logical values. Next, we would be introduced to arithmetic and relational operations on such *scalars*, followed by the definition of whole arrays or other collections of such values, complemented by the methods to iterate over them, one element after another.

In R, no separate types representing individual values have been defined. Instead, what seems to be a single datum, is already a *vector* (sequence, array) of length 1.

```
2.71828      # input a number (here: the same as print(2.71828))
## [1] 2.7183
```

(continues on next page)

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```
length(2.71828) # it is a vector featuring one element
## [1] 1
```

To create a vector of any length, we can call the `c` function, which combines given arguments into a single sequence:

```
c(1, 2, 3) # three vectors of length 1 -> one vector of length 3
## [1] 1 2 3
length(c(1, 2, 3))
## [1] 3
```

In Chapter 2, Chapter 3, and Chapter 6, we will discuss the most prevalent types of atomic vectors: numeric, logical, and character ones, respectively.

```
c(0, 1, -3.14159, 12345.6) # four numbers
## [1] 0.0000 1.0000 -3.1416 12345.6000
c(TRUE, FALSE) # two logical values
## [1] TRUE FALSE
c("spam", "spam", "bacon and spam") # three character strings
## [1] "spam" "spam" "bacon and spam"
```

We call them *atomic* for they can only group together values of the same type. Lists, which we will discuss in Chapter 4, are, on the other hand, referred to as *generic* vectors. They can be used for storing items of mixed types: other lists as well.

---

**Note** Not having separate scalar types greatly simplifies the programming of numerical computing tasks. Vectors are prevalent in our main areas of interest – statistics, simulations, data science, machine learning, and all other data-oriented computing. For example, columns and rows in tables (values of different features describing clients, ratings of items given by users) or time series (stock market prices, readings from temperature sensors) are all best represented by means of such sequences.

Moreover, the fact that vectors are the core part of the R language makes their use very natural – as opposed to the languages that require special add-ons for vector processing, e.g., `numpy` for Python [34]. By learning different ways to process them *as a whole* (instead of one element at a time), we will ensure that our ideas can quickly be turned into working code (rapid prototyping). For instance, computing summary statistics such as, say, the mean absolute deviation of some sequence `x`, will be as effortless as writing `mean(abs(x - mean(x)))`. Such a code is not only easy to read and maintain, but it is also fast to run.

---

## 1.4 Getting help

Our aim is to become independent, advanced R programmers.

Independent, however, does not mean omniscient. The *R help system* is the authoritative source of knowledge about specific functions or more general topics. To open a help page, we call:

```
help("topic") # equivalently: ?"topic"
```

**Exercise 1.5** *Sight (without going into detail) the manual on the **length** function by calling `help("length")`. Note that most help pages are structured as follows:*

1. Header: “*package:base*” means that the function is a base one (see Section 7.3.1 for more details on the R package system);
2. Title;
3. Description: a short description of what the function does;
4. Usage: the list of formal arguments (parameters) to the function;
5. Arguments: the meaning of each formal argument explained;
6. Details: technical information;
7. Value: return value explained;
8. References: further reading;
9. See Also: links to other help pages;
10. Examples: R code that is worth running and studying by yourself.

We can also search within all the installed help pages by calling:

```
help.search("vague topic") # equivalently: ??"vague topic"
```

This way, we will be able to find answers to our questions more reliably than when asking DuckDuckGo or Google, which commonly feature many low-quality, irrelevant, or distracting results from splogs. We do not want to lose the sacred code writer’s flow!

---

**Important** All code chunks, including code comments and textual outputs, form an integral part of this book’s text. They should not be skipped by the reader. On the contrary, they must become objects of our intense reflection and thorough investigation.

For instance, whenever we introduce a few functions, it may be a clever idea to look it up in the help system. Moreover, playing with the presented code (running, modifying, experimenting, etc.) is also very beneficial. We should develop the habit of asking

ourselves questions like “What would happen if...”, and then finding the answers on our own.

---

We are now ready to discuss the most significant operations on numeric vectors, which constitute the main theme of the next chapter. See you there.

---

## 1.5 Exercises

**Exercise 1.6** *What are the three most important types of atomic vectors?*

**Exercise 1.7** *According to the classification of the R data types we introduced in the previous chapter, are atomic vectors basic or compound types?*

---





## 2

---

### *Numeric vectors*

---

In this chapter, we discuss the uttermost common operations on numeric vectors. They are so fundamental that we will also find them in other scientific computing environments, including Python with **NumPy** or **TensorFlow**, Julia, MATLAB, GNU Octave, or Scilab.

At first blush, the number of functions we are going to explore may seem quite large. Still, the reader is kindly asked to place some trust (a rare thing these days) in yours truly. It is because our selection is comprised only of the most representative and educational amongst the plethora of possible choices. More complex building blocks can often be reduced to a creative combination of the former. Also, sometimes they may easily found in a number of additional packages or libraries (e.g., the GNU GSL [28]).

A solid understanding of base R programming is crucial for dealing with popular packages (such as **data.table**, **dplyr**, or **caret**). Most importantly, base R's API is *stable*. Hence, the code we compose today will most likely work the same way in ten years. It is often not the case when we rely on third-party add-ons.

In the sequel, we will be advocating a minimalist, keep-it-simple approach to the art of programming data processing pipelines, one that is a healthy balance between “doing it all by oneself”, “minimising the information overload”, “being lazy”, and “standing on the shoulders of giants”.

---

**Note** The exercises that we suggest below are all self-contained unless explicitly stated otherwise. The use of language constructs that are yet to be formally introduced (in particular, **if**, **for**, and **while** explained in [Chapter 8](#)) is not just unnecessary: it is discouraged. Moreover, we recommend against taking shortcuts by looking up partial solutions on the internet. Rather, to get the most out of this course, the reader should be seeking relevant information within the current and preceding chapters as well as the R help system.

---

---

### 2.1 Creating numeric vectors

#### 2.1.1 Numeric constants

The simplest numeric vectors are those of length one:

```
-3.14
## [1] -3.14
1.23e-4
## [1] 0.000123
```

The latter is in what we call *scientific notation*, which is a convenient means of entering numbers of very large or small orders of magnitude. Here, “e” stands for “... times 10 to the power of...”. Therefore,  $1.23\text{e-}4$  is equal to  $1.23 \times 10^{-4} = 0.000123$ . In other words, given 1.23, we move the decimal separator by 4 digits towards the left.

In real life, some information items may be inherently or temporarily missing, unknown, or Not Available. R is data processing-oriented. Hence, it is equipped with a special indicator:

```
NA_real_ # numeric NA (missing value)
## [1] NA
```

It is similar to the *Null* marker in database query languages such as SQL. Note that `NA_real_` is displayed simply as “NA”, chiefly for readability.

Moreover, `Inf` denotes infinity ( $\infty$ ; a value that is larger than the largest representable double-precision floating point number, i.e., 64 bit). Also, `NaN` stands for *not-a-number* (it is returned as the result of some illegal operations, e.g.,  $0/0$  or  $\infty - \infty$ ).

### 2.1.2 Concatenating vectors with `c`

Let us provide some ways to create numeric vectors with possibly more than one element.

First, the `c` function that we introduced in the previous chapter can be used to combine (concatenate) many numeric vectors, each of any length, so as to form a single object:

```
c(1, 2, 3) # 3 vectors of length 1 -> 1 vector of length 3
## [1] 1 2 3
c(1, c(2, NA_real_, 4), 5, c(6, c(7, Inf)))
## [1] 1 2 NA 4 5 6 7 Inf
```

---

**Note** Running `help("c")`, we will see that its usage is like “`c(...)`”. In the current context, this means that the `c` function takes an arbitrary number of arguments. In Section 9.5.6, we will study the dot-dot-dot (ellipsis) parameter in more detail.

---

### 2.1.3 Repeating entries with `rep`

Second, `rep` replicates the elements in a given vector a given number of times.

```
rep(1, 5)
## [1] 1 1 1 1 1
rep(c(1, 2, 3), 4)
## [1] 1 2 3 1 2 3 1 2 3 1 2 3
```

In the second case, the whole vector (1, 2, 3) has been *recycled* (tiled) four times. Interestingly, if the second argument was a vector of the same length as the first one, the behaviour would be quite different:

```
rep(c(1, 2, 3), c(2, 1, 4))
## [1] 1 1 2 3 3 3 3
rep(c(1, 2, 3), c(4, 4, 4))
## [1] 1 1 1 1 2 2 2 2 3 3 3 3
```

Here, *each* element is repeated the *corresponding* number of times.

If we call `help("rep")`, we will come across the notion like “`rep(x, ...)`” in the *Usage* section. It is rather peculiar. However, reading further, we discover the dot-dot-dot stands for one of the following further parameters (see the *Arguments* section):

- `times`,
- `length.out`,
- `each`.

So far, we have been playing with `times`, which is listed second in the parameter list (after `x` – the vector whose elements are to be repeated).

---

**Important** It turns out that the following function calls are all equivalent:

```
rep(c(1, 2, 3), 4) # positional matching of arguments: `x`, then `times`
rep(c(1, 2, 3), times=4) # `times` is the second argument
rep(x=c(1, 2, 3), times=4) # keyword arguments of the form name=value
rep(times=4, x=c(1, 2, 3)) # keyword arguments can be given in any order
rep(times=4, c(1, 2, 3)) # mixed positional and keyword arguments
```

---

We can also pass `each` or `length.out` (a dot has no special meaning in R; see Section 2.2), but their names must be mentioned explicitly:

```
rep(c(1, 2, 3), length.out=7)
## [1] 1 2 3 1 2 3 1
rep(c(1, 2, 3), each=3)
## [1] 1 1 1 2 2 2 3 3 3
rep(c(1, 2, 3), length.out=7, each=3)
## [1] 1 1 1 2 2 2 3
```

---

**Note** Whether it was a good programming practice to actually implement a range of varied behaviours inside a single function is a matter of taste. On the one hand, in all of the examples above, we do repeat the input elements somehow, so remembering just one function name is really convenient. Nevertheless, a drastic change in the repetition pattern depending, e.g., on the length of the `times` argument can be bug-prone. Anyway, we have been warned<sup>1</sup>.

---

Zero-length vectors are possible, too:

```
rep(c(1, 2, 3), 0)
## numeric(0)
```

Even though their handling might be a little tricky (compare [Chapter 9](#)), we will see later that they are indispensable in contexts like “create an empty data frame with a specific column structure”.

Also, note that R often allows for partial matching of named arguments, but its use is a bad programming practice; see [Section 15.4.4](#) for more details.

```
rep(c(1, 2, 3), len=7) # not recommended (see later)
## Warning in rep(c(1, 2, 3), len = 7): partial argument match of 'len' to
## 'length.out'
## [1] 1 2 3 1 2 3 1
```

The only reason we see the warning message is that we have manually set `options(warnPartialMatchArgs=TRUE)` in our environment. It is not set by default.

### 2.1.4 Generating arithmetic progressions with `seq` and `:`

Third, we can call the `seq` function to create a sequence of equally-spaced numbers (on a linear scale, i.e., an arithmetic progression).

```
seq(1, 15, 2)
## [1] 1 3 5 7 9 11 13 15
```

From the function's help page, we discover that it features the `from`, `to`, `by`, `length.out` parameters, amongst others.

Thus, the above call is equivalent to:

---

<sup>1</sup> Some “caring” R users might be tempted to introduce two new functions now, one for generating (1, 2, 3, 1, 2, 3, ...) only and the other outputting patterns like (1, 1, 1, 2, 2, 2, ...). They would most likely wrap them in a new package and announce that on Twitter or Mastodon. But this is nothing else than a multiplication of entities without actual necessity. This way, we would end up with three functions. First, the original one, `rep`, which everyone ought to know anyway because it is so basic and has been and will be used everywhere by almost everybody so far. Second and third, the two redundant ones, whose user-friendliness is only illusory. See also [Chapter 9](#) for a discussion on the design of functions.

```
seq(from=1, to=15, by=2)
## [1] 1 3 5 7 9 11 13 15
```

Note that `to` actually means “up to”:

```
seq(from=1, to=16, by=2)
## [1] 1 3 5 7 9 11 13 15
```

We can also pass `length.out` instead of `by`. In such a case, the increments or decrements will be computed via the formula  $((to - from)/(length.out - 1))$ ; this *default value* is reported in the *Usage* section in `help("seq")`.

```
seq(1, 0, length.out=5)
## [1] 1.00 0.75 0.50 0.25 0.00
```

Also, this:

```
seq(length.out=5) # default `from` is 1
## [1] 1 2 3 4 5
```

Arithmetic progressions with steps equal to 1 or -1 can also be generated via the `:` operator.

```
1:10 # seq(1, 10) or seq(1, 10, 1)
## [1] 1 2 3 4 5 6 7 8 9 10
-1:10 # seq(-1, 10) or seq(-1, 10, 1)
## [1] -1 0 1 2 3 4 5 6 7 8 9 10
-1:-10 # seq(-1, -10) or seq(-1, -10, -1)
## [1] -1 -2 -3 -4 -5 -6 -7 -8 -9 -10
```

Let us highlight the order of precedence of this operator: “-1:10” means “(-1):10” and not “-(1:10)”; compare Section 2.4.3.

**Exercise 2.1** Take a look at the manual page of `seq_along` and `seq_len`. Determine whether they can easily be done without having `seq`<sup>2</sup> at hand.

### 2.1.5 Generating pseudorandom numbers

We can also generate sequences drawn independently from a range of univariate probability distributions.

```
runif(7) # uniform U(0, 1)
## [1] 0.287578 0.788305 0.408977 0.883017 0.940467 0.045556 0.528105
rnorm(7) # normal N(0, 1)
## [1] 1.23950 -0.10897 -0.11724 0.18308 1.28055 -1.72727 1.69018
```

<sup>2</sup> Certain configurations of `seq` and its variants might return vectors of the type `integer` instead of `double`, some of them in a compact (ALTREP) form; see Section 6.4.1.

These correspond to seven pseudorandom deviates following the uniform distribution on the unit interval (i.e.,  $(0, 1)$ ) and the standard normal distribution (i.e., with expectation 0 and standard deviation 1), respectively; compare Figure 2.3.

For more *named* distribution classes (frequently occurring in various real-world statistical modelling exercises), see Section 2.3.4.

Another worthwhile function samples a number of values from a given vector, either with or without replacement:

```
sample(1:10, 20, replace=TRUE) # 20 with replacement (allow repetitions)
## [1] 3 3 10 2 6 5 4 6 9 10 5 3 9 9 9 3 8 10 7 10
sample(1:10, 5, replace=FALSE) # 5 without replacement (do not repeat)
## [1] 9 3 4 6 1
```

The distribution of the sampled values does not need to be uniform; the `prob` argument may be fed with a vector of the corresponding probabilities. For example, here are 20 independent realisations of the random variable  $X$  such that  $\Pr(X = 0) = 0.9$  (the probability that we obtain 0 is equal to 90%) and  $\Pr(X = 1) = 0.1$ :

```
sample(0:1, 20, replace=TRUE, prob=c(0.9, 0.1))
## [1] 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 0 0 0 0 1
```

---

**Note** If  $n$  is a single number (a numeric vector of length 1), then `sample(n, ...)` is equivalent to `sample(1:n, ...)`. Similarly, `seq(n)` is a synonym for `seq(1, n)` or `seq(1, length(n))`, depending on the length of  $n$ . This is a dangerous behaviour that can occasionally backfire and lead to bugs (check what happens when  $n$  is, e.g., 0). Nonetheless, we have been warned. From now on, we are going to be extra careful (but are we really?). Read more at `help("sample")` and `help("seq")`.

---

Let us stress that the numbers we obtain are merely *pseudorandom* because they are generated algorithmically. R uses the Mersenne-Twister MT19937 method [46] by default; see `help("RNG")` and [21, 29, 42]. By setting the *seed* of the random number generator, i.e., resetting its state to a given one, we can obtain results that are *reproducible*.

```
set.seed(12345) # seeds are specified with integers
sample(1:10, 5, replace=TRUE) # a,b,c,d,e
## [1] 3 10 8 10 8
sample(1:10, 5, replace=TRUE) # f,g,h,i,j
## [1] 2 6 6 7 10
```

Setting the seed to the one used previously gives:

```
set.seed(12345)
sample(1:10, 5, replace=TRUE) # a,b,c,d,e
## [1] 3 10 8 10 8
```

We did not(?) expect that! And now for something completely different:

```
set.seed(12345)
sample(1:10, 10, replace=TRUE) # a,b,c,d,e,f,g,h,i,j
## [1] 3 10 8 10 8 2 6 6 7 10
```

Reproducibility is a crucial feature of each truly scientific experiment. The same initial condition (here: the same seed) leads to exactly the same outcomes.

---

**Note** Some claim that the only unsuspicious seed is 42, but each programmer can have their own picks. Yours truly, for example, uses 123, 1234, and 12345 as well. When performing many runs of Monte Carlo experiments, it may be a clever idea to call **set.seed(i)** in the *i*-th iteration of a simulation we are trying to program.

Anyhow, we should ensure that our seed settings are applied consistently across all our scripts. Otherwise, we might be accused of tampering with evidence. For instance, here is the ultimate proof that we are very lucky today:

```
set.seed(1679619) # totally unsuspicious, right?
sample(0:1, 20, replace=TRUE) # so random
## [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
```

This is exactly why reproducible scripts and auxiliary data should be published alongside all research reports or papers. Only open, transparent science can be fully trustworthy.

---

If **set.seed** is not called explicitly, and the random state is not restored from the previously saved R session (see [Chapter 16](#)), then the random generator is initialised based on the current wall time and the identifier of the running R instance (PID). This may give the impression that the numbers we generate are surprising.

To understand the “pseudo” part of the said randomness better, in [Section 8.3](#), we will build a very simple random generator ourselves.

### 2.1.6 Reading data with scan

The example text file named `euraud-20200101-20200630.csv`<sup>3</sup> gives the EUR to AUD exchange rates (how many Australian Dollars can one buy for 1 Euro) from 1 January to 30 June 2020 (remember COVID-19?). Let us preview the first couple of lines:

```
# EUR/AUD Exchange Rates
# Source: Statistical Data Warehouse of the European Central Bank System
# https://www.ecb.europa.eu/stats/policy_and_exchange_rates/
# (provided free of charge)
NA
```

(continues on next page)

---

<sup>3</sup> <https://github.com/gagolews/teaching-data/raw/master/marek/euraud-20200101-20200630.csv>

(continued from previous page)

```
1.6006
1.6031
NA
```

The four first lines that begin with “#” merely serve as comments for us humans. They should be ignored by the interpreter. The first “real” value, NA, corresponds to 1 January (Wednesday, New Year’s Day; Forex markets were closed, hence a missing observation).

The `scan` function can be used to read all the inputs and convert them to a single numeric vector:

```
scan(paste0("https://github.com/gagolews/teaching-data/raw/",
            "master/marek/euraud-20200101-20200630.csv"), comment.char="#")
## [1]      NA 1.6006 1.6031      NA      NA 1.6119 1.6251 1.6195 1.6193 1.6132
## [11]      NA      NA 1.6117 1.6110 1.6188 1.6115 1.6122      NA      NA 1.6154
## [21] 1.6177 1.6184 1.6149 1.6127      NA      NA 1.6291 1.6290 1.6299 1.6412
## [31] 1.6494      NA      NA 1.6521 1.6439 1.6299 1.6282 1.6417      NA      NA
## [41] 1.6373 1.6260 1.6175 1.6138 1.6151      NA      NA 1.6129 1.6195 1.6142
## [51] 1.6294 1.6363      NA      NA 1.6384 1.6442 1.6565 1.6672 1.6875      NA
## [61]      NA 1.6998 1.6911 1.6794 1.6917 1.7103      NA      NA 1.7330 1.7377
## [71] 1.7389 1.7674 1.7684      NA      NA 1.8198 1.8287 1.8568 1.8635 1.8226
## [81]      NA      NA 1.8586 1.8315 1.7993 1.8162 1.8209      NA      NA 1.8021
## [91] 1.7967 1.8053 1.7970 1.8004      NA      NA 1.7790 1.7578 1.7596
## [ reached getOption("max.print") -- omitted 83 entries ]
```

We used the `paste0` function to concatenate two long (too long to fit a single line of code) strings to form a single URL; see Section 6.1.3.

We can also read the files located on our computer, for example:

```
scan("~/Projects/teaching-data/marek/euraud-20200101-20200630.csv",
      comment.char="#")
```

uses an absolute file path that starts at the user’s home directory, denoted “~”: yours truly’s case is `/home/gagolews/`.

---

**Note** For portability reasons, we suggest slashes, “/”, as path separators (see also `help("file.path")` and `help("Platform")`). These recognised by all UNIX-like boxes as well by other popular operating systems. Note that URLs (such as <https://www.r-project.org/>) consist of slashes as well.

---

Paths can also be relative to the current working directory, denoted “.”. It can be read via a call to `getwd`. Usually, it is the directory from where the R session has been started.

For instance, if the working directory was `/home/gagolews/Projects/teaching-data/`



marek, we could have written the file path equivalently as `./euraud-20200101-20200630.csv` or even `euraud-20200101-20200630.csv`.

On a side note, `../` would mark the parent directory of the current working directory. For instance, `../r/iris.csv` would be equivalent to `/home/gagolews/Projects/teaching-data/r/iris.csv`.

**Exercise 2.2** Read the help page about `scan`. Take note of the following formal arguments and their meaning: `dec`, `sep`, `what`, `comment.char`, and `na.strings`.

Later we will discuss the `read.table` and `read.csv`, which are wrappers around `scan` that can be used to read tabular data. Also, `write` can be used to export an atomic vector's contents to a text file.

**Example 2.3** Figure 2.1 shows the graph of the aforementioned exchange rates, which was generated by calling:

```
plot(scan(paste0("https://github.com/gagolews/teaching-data/raw/",
  "master/marek/euraud-20200101-20200630.csv"), comment.char="#"),
  xlab="Day", ylab="EUR/AUD")
```

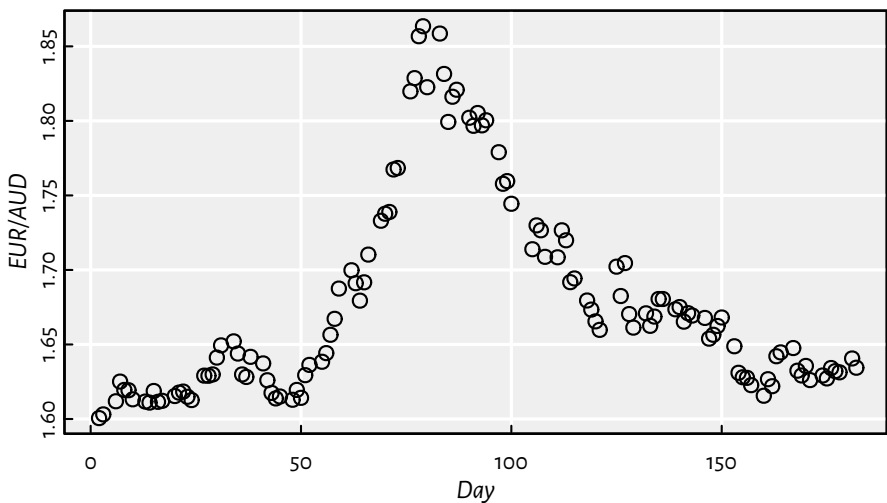


Figure 2.1: EUR/AUD exchange rates from 2020-01-01 (day 1) to 2020-06-30 (day 182)

Somewhat misleadingly (and for reasons that will become apparent later), the documentation of `plot` can be accessed by calling `help("plot.default")`. Read about, and experiment with, different values of the `main`, `xlab`, `ylab`, `type`, `col`, `pch`, `cex`, `lty`, and `lwd` arguments. More plotting routines will be discussed in Chapter 13.

## 2.2 Creating named objects

Often, the objects we bring forth will need to be memorised so that they can be referred to in further computations. The assignment operator, `<-`, can be used for this very purpose:

```
x <- 1:3 # creates a numeric vector and binds the name `x` to it
```

The now-named object can be recalled<sup>4</sup> and dealt with as we please:

```
print(x) # or just `x` in the R console
## [1] 1 2 3
sum(x)   # example operation: compute the sum of all elements in `x`
## [1] 6
```

---

**Important** In R, all names are *case-sensitive*. Hence, `x` and `X` can coexist peacefully: when set, they refer to two different objects. Also, if we tried to call `Print(x)` above, we would get an error.

---

Typically, we will be using what we refer to as *syntactic names* (see [Section 9.4.1](#) for an exception). In the R help system (see `help("make.names")` and also `help("Quotes")`), we read: *A syntactically valid name consists of letters, numbers and the dot or underline characters and starts with a letter or the dot not followed by a number. Names such as .2way are not valid, and neither are the reserved words.* For the list of the latter, see `help("Reserved")`.

A fine name is self-explanatory and thus reader-friendly: `patients`, `mean`, and `average_scores` are way better (if they are what they claim they are) than `xyz123`, `crap`, or `spam`. Also, it might not be such a bad idea to get used to denoting:

- vectors with `x`, `y`, `z`,
- matrices (and matrix-like objects) with `A`, `B`, ..., `X`, `Y`, `Z`,
- integer indexes with letters `i`, `j`, `k`, `l`,
- object sizes with `n`, `m`, `d`, `p` or `nx`, `ny`, etc.,

especially when they are only of temporary nature (for storing some auxiliary results, iterating over collections of objects, etc.).

There are numerous naming conventions that we can adopt, but most often they are a matter of taste; `snake_case`, `lowerCamelCase`, `UpperCamelCase`, `flatcase`, or `dot.case` are equally sound as long as they are used coherently (for instance, some use `snake_case` for vectors and `UpperCamelCase` for functions). It may even be the case that

---

<sup>4</sup> Names are bound in environment frames; see [Chapter 16](#).

we have little choice but to adhere to the naming conventions of the project we are about to contribute to.

---

**Note** Let us stress that a dot, “.”, has no special meaning (however, see [Chapter 10](#) and [Chapter 16](#) for some asterisks); `na.omit` is as appropriate a name as `na_omit`, `naOmit`, `NAOMIT`, `naomit`, and `NaOmit`. Users coming from some other (C, C++, Java, Python, etc.) programming languages will need to habituate themselves to this convention.

---

R, as a dynamic language, allows for introducing new variables at any time. Moreover, existing names can be rebound to new values. For instance:

```
(y <- c(1, 10, 100)) # bracketed expression - printing not suppressed
## [1] 1 10 100
x <- y
print(x)
## [1] 1 10 100
```

Now `x` refers to a verbatim copy of `y`.

---

**Note** Objects are automatically destroyed when there are no more names bound to them. By now, the *garbage collector* is likely to have got rid of the 1:3 vector begotten above (to which the name `x` was bound previously). See [Section 14.2.4](#) for more details on memory management.

---

## 2.3 Vectorised mathematical functions

Mathematically, we will be denoting a given vector  $\mathbf{x}$  of length  $n$  with  $(x_1, x_2, \dots, x_n)$ . In other words, its  $i$ -th element is equal to  $x_i$ .

Let us review some ubiquitous operations in numerical computing.

### 2.3.1 `abs` and `sqrt`

R implements *vectorised* versions of the most popular mathematical functions, e.g., **abs** (absolute value,  $|x|$ ) and **sqrt** (square root,  $\sqrt{x}$ ).

```
abs(c(2, -1, 0, -3, NA_real_))
## [1] 2 1 0 3 NA
```

Here, *vectorised* means that instead of being defined to act on a single numeric value, the function of interest is applied on each element in a vector. The  $i$ -th resulting item

is a transformed version of the  $i$ -th input. If an input is a missing value, the corresponding output will be marked as “don't know” as well.

Another example:

```
x <- c(4, 2, -1)
(y <- sqrt(x))
## Warning in sqrt(x): NaNs produced
## [1] 2.0000 1.4142 NaN
```

To attract our attention to the fact that computing the square root of a negative value yields a not-a-number, R generated an informative warning. A warning is not an error: the result is being reckoned as usual.

Also the fact that the irrational  $\sqrt{2}$  is *displayed*<sup>5</sup> as 1.4142 does not mean that it is such a crude approximation to 1.414213562373095048801688724209698 ...; it is only rounded when printing for aesthetic reasons. In fact, in [Section 3.2.3](#), we will point out that the computer's floating-point arithmetic allows for roughly 16 decimal digits precision (but we shall see that the devil is in the detail).

```
print(y, digits=16) # display more significant figures
## [1] 2.0000000000000000 1.414213562373095 NaN
```

### 2.3.2 Rounding

The following functions get rid of all or portions of fractional parts of numbers:

- **floor**( $x$ ) (rounds down to the nearest integer, denoted  $\lfloor x \rfloor$ ),
- **ceiling**( $x$ ) (rounds up, denoted  $\lceil x \rceil$ ),
- **trunc**( $x$ ) (rounds towards zero), and
- **round**( $x$ , digits=0) (rounds to the nearest number with digits decimal digits).

For instance:

```
x <- c(7.0001, 6.9999, -4.3149, -5.19999, 123.4567, -765.4321, 0.5, 1.5, 2.5)
floor(x)
## [1] 7 6 -5 -6 123 -766 0 1 2
ceiling(x)
## [1] 8 7 -4 -5 124 -765 1 2 3
trunc(x)
## [1] 7 6 -4 -5 123 -765 0 1 2
```

---

**Note** If we call **help**("round"), we will read that its usage is like **round**( $x$ , digits=0),

---

<sup>5</sup> There are a couple of settings in place that control the default behaviour of the **print** function; see **width**, **digits**, **max.print**, **OutDec**, **scipen**, etc. in **help**("options").

which means that the `digits` parameter is equipped with the *default value* of 0. In other words, if rounding to 0 decimal digits is what we need, the second argument can be omitted.

```
round(x) # the same as round(x, 0)
## [1] 7 7 -4 -5 123 -765 0 2 2
round(x, 1)
## [1] 7.0 7.0 -4.3 -5.2 123.5 -765.4 0.5 1.5 2.5
round(x, -2)
## [1] 0 0 0 0 100 -800 0 0 0
```

### 2.3.3 Natural exponential function and logarithm

Moreover:

- `exp(x)` outputs the natural exponential function,  $e^x$ , where the Euler's number  $e \simeq 2.718$ ,
- `log(x, base=exp(1))` computes, by default, the natural logarithm of  $x$ ,  $\log_e x$  (which is most often denoted simply as  $\log x$ ).

Recall that if  $x = e^y$ , then  $\log_e x = y$ , i.e., one is the inverse of the other.

```
log(c(0, 1, 2.7183, 7.3891, 20.0855)) # grows slowly
## [1] -Inf 0 1 2 3
exp(c(0, 1, 2, 3)) # grows fast
## [1] 1.0000 2.7183 7.3891 20.0855
```

**Note** These functions enjoy a number of very valuable identities and inequalities, including:

- $\log(x \cdot y) = \log x + \log y$ ,
- $\log(x^y) = y \log x$ ,
- $e^{x+y} = e^x \cdot e^y$ .

For more properties like these, take a glance at Chapter 4 of the freely available handbook [50].

For the logarithm to a different base, say,  $\log_{10} x$ , we can call:

```
log(c(0, 1, 10, 100, 1000, 1e10), 10) # or log(..., base=10)
## [1] -Inf 0 1 2 3 10
```

Note that if  $\log_b x = y$ , then  $x = b^y$ , for any  $1 \neq b > 0$ .

**Note** Commonly, a logarithmic scale is used for variables that grow rapidly when expressed as functions of each other; see Figure 2.2.

```
x <- seq(0, 10, length.out=1001)
par(mfrow=c(1, 2)) # two plots in one figure (1 row, 2 columns)
plot(x, exp(x), type="l")
plot(x, exp(x), type="l", log="y") # log-scale on the y-axis
```

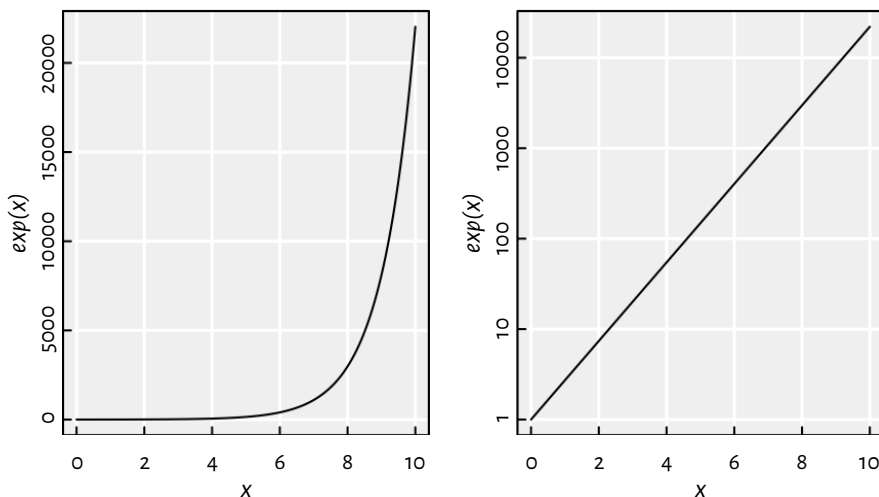


Figure 2.2: Linear- vs log-scale on the y-axis

Let us highlight that  $e^x$  on the log-scale is just a straight line. Also, keep in mind that such a transformation of the axes can only be applied in the case of values strictly greater than 0.

### 2.3.4 Probability distributions (\*)

It should come as no surprise that R offers extensive support for many univariate probability distribution families, including:

- continuous distributions, which take values being arbitrary real numbers (over the whole possible range or in some interval):
  - `*unif` (uniform),
  - `*norm` (normal),
  - `*exp` (exponential),
  - `*gamma` (gamma,  $\Gamma$ ),

- `*beta` (beta, B),
- `*lnorm` (log-normal),
- `*t` (Student),
- `*cauchy` (Cauchy–Lorentz),
- `*chisq` (chi-squared,  $\chi^2$ ),
- `*f` (Snedecor–Fisher),
- `*weibull` (Weibull);

with the prefix “\*” being one of:

- “d” (probability density function, PDF),
  - “p” (cumulative distribution function, CDF; or survival function, SF),
  - “q” (quantile function, being the inverse of the CDF),
  - “r” (generation of random deviates; already mentioned);
- discrete distributions, i.e., those whose possible outcomes can be easily enumerated (e.g., some integers).
    - `*binom` (binomial),
    - `*geom` (geometric),
    - `*pois` (Poisson),
    - `*hyper` (hypergeometric),
    - `*nbinom` (negative binomial);

here, prefixes “p” and “r” have the same meaning as above, however:

- “d” now gives the probability *mass* function (PMF),
- “q” brings about the quantile function, defined as a *generalised* inverse of the CDF.

Each distribution is characterised by a set of underlying parameters. For instance, a normal distribution  $N(\mu, \sigma)$  can be pinpointed by setting its expected value  $\mu \in \mathbb{R}$  and standard deviation  $\sigma > 0$ . In R, these two have been named `mean` and `sd`, respectively; see `help("dnorm")`.

---

**Note** The parametrisations assumed in R can be subtly different from what we know from statistical textbooks or probability courses. For example, the normal distribution can be parameterised based on either standard deviation or variance, and the exponential distribution can be defined via its expected value or the reciprocal thereof. We thus advise the reader to study carefully the documentation of `help("dnorm")`, `help("dunif")`, `help("dexp")`, `help("dbinom")`, and the like.

It is also worth knowing the typical use cases of each of the distributions listed, e.g.,

a Poisson distribution can describe the probability of observing the number of independent events in a fixed time interval (e.g., the number of users downloading a copy of R from CRAN per hour), and an exponential distribution can model the time between such events; compare [23].

**Exercise 2.4** A call to `hist(x)` draws a histogram, which can serve as an estimator of the underlying continuous probability density function of a given sample; see Figure 2.3 for an illustration.

```
par(mfrow=c(1, 2)) # 2 plots in 1 figure
# Uniform U(0, 1)
hist(runif(10000, 0, 1), col="white", probability=TRUE, main="")
x <- seq(0, 1, length.out=101)
lines(x, dunif(x, 0, 1), lwd=2) # draw the true density function (PDF)
# Normal N(0, 1)
hist(rnorm(10000, 0, 1), col="white", probability=TRUE, main="")
x <- seq(-4, 4, length.out=101)
lines(x, dnorm(x, 0, 1), lwd=2) # draw the PDF
```

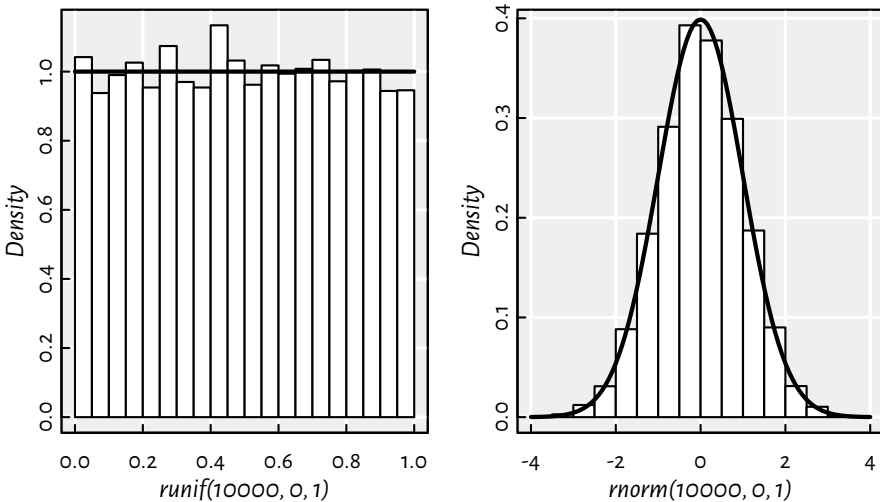


Figure 2.3: Example histograms of some pseudorandom samples and the true underlying probability density functions: the uniform distribution on the unit interval (left) and the standard normal distribution (right)

Draw a histogram of some random samples of different sizes  $n$  from the following distributions:

- $rnorm(n, \mu, \sigma)$  – normal  $N(\mu, \sigma)$  with expected values  $\mu \in \{-1, 0, 5\}$  (i.e.,  $\mu$  being equal to either  $-1$ ,  $0$ , or  $5$ ; read “ $\in$ ” as “belongs to the given set” or “in”) and standard deviations  $\sigma \in \{0.5, 1, 5\}$ ;



- `runif(n, a, b)` – uniform  $U(a, b)$  on the interval  $(a, b)$  with  $a = 0$  and  $b = 1$  as well as  $a = -1$  and  $b = 1$ ;
- `rbeta(n, a, b)` – beta  $B(\alpha, \beta)$  with  $\alpha, \beta \in \{0.5, 1, 2\}$ ;
- `rexp(n, lambda)` – exponential  $E(\lambda)$  with rates  $\lambda \in \{0.5, 1, 10\}$ ;

Moreover, read about and play with the `breaks`, `main`, `xlab`, `ylab`, `xlim`, `ylim`, and `col` parameters; see `help("hist")`.

**Example 2.5** We roll a six-sided dice twelve times. Let  $C$  be a random variable denoting the number of cases where the “1” face is thrown.  $C$  follows a binomial distribution  $\text{Bin}(n, p)$  with parameters  $n = 12$  (the number of Bernoulli trials) and  $p = 1/6$  (the probability of success in a single roll).

The probabilities that the number of “1”s rolled will be equal to  $0, 1, \dots, 4$ , i.e.,  $P(C = 0)$ ,  $P(C = 1)$ , ...,  $P(C = 4)$ , respectively, can be computed based on the probability mass function (`dbinom`):

```
dbinom(0:4, 12, 1/6) # probability mass function at 5 different points
## [1] 0.112157 0.269176 0.296094 0.197396 0.088828
```

On the other hand, the probability that we throw more than three “1”s,  $P(C > 3) = 1 - P(C \leq 3)$ , can be determined by means of the cumulative distribution function (`pbinom`) or survival function (`pbinom(..., lower.tail=FALSE)`):

```
1-pbinom(3, 12, 1/6) # pbinom(3, 12, 1/6, lower.tail=FALSE)
## [1] 0.12518
```

The smallest  $c$  such that  $P(C \leq c) \geq 0.95$  can be computed based on the quantile function:

```
qbinom(0.95, 12, 1/6)
## [1] 2
pbinom(3:4, 12, 1/6) # for comparison: 0.95 is in-between
## [1] 0.87482 0.96365
```

In other words, at least 95% of the time, we will be observing no more than four successes.

Also, here are some pseudorandom realisations of  $C$  – the number of “1”s in 30 simulations of 12 independent dice rolls each:

```
rbinom(30, 12, 1/6)
## [1] 1 3 2 4 4 0 2 4 2 2 4 2 3 2 0 4 1 0 1 4 4 3 2 6 2 3 2 2 1 1
```

### 2.3.5 Special functions (\*)

Within mathematical formulae and across assorted application areas, certain functions appear more frequently than others. Hence, for the sake of notational brevity and computational precision, many of them have been assigned special names. For

instance, the following may be mentioned in the definitions related to some of the probability distributions listed above:

- **gamma**( $x$ ) for  $x > 0$  computes  $\Gamma(x) = \int_0^\infty t^{x-1} e^{-t} dt$ ,
- **beta**( $a, b$ ) for  $a, b > 0$  yields  $B(a, b) = \frac{\Gamma(a)\Gamma(b)}{\Gamma(a+b)} = \int_0^1 t^{a-1} (1-t)^{b-1} dt$ .

Why do we have **beta** if it is merely a mix of **gamma**s? A specific, tailored function is expected to be faster and more precise than its DIY version; its underlying implementation does not have to involve any calls to **gamma** at all.

```
beta(0.25, 250) # okay
## [1] 0.91213
gamma(0.25)*gamma(250)/gamma(250.25) # not okay
## [1] NaN
```

The  $\Gamma$  function grows so rapidly that already **gamma**(172) gives rise to Inf. It is due to the fact that a computer's arithmetic is not infinitely precise; compare [Section 3.2.3](#).

Special functions are plentiful; see the open-access [50] for one of the most definitive references (and also [2] for its predecessor). R package **gsl** [33] provides a vectorised interface to the GNU GSL [28] library, which implements many of such routines.

**Exercise 2.6** The Pochhammer symbol,  $(a)_x = \Gamma(a+x)/\Gamma(a)$ , can be computed via a call to **gsl::poch**( $a, x$ ) (i.e., the **poch** function from the **gsl** package; see [Section 7.3.1](#)):

```
# call install.packages("gsl") first
library("gsl") # load the package
poch(10, 3:6) # calls gsl_sf_poch() from GNU GSL
## [1] 1320 17160 240240 3603600
```

Read the documentation of the corresponding **gsl\_sf\_poch** function in the GNU GSL manual available [here](#)<sup>6</sup>.

And since you are there, do not hesitate to go through the list of all the other functions, including those related to statistics, permutations, combinations, and so forth.

Many functions also have their logarithm-of-versions; see, e.g., **lgamma** and **lbeta**. Also, for instance, **dnorm** and **dbeta** have the **log** parameter. Its classical use case is the (numerical) maximum likelihood estimation, which involves the sums of the *logarithms* of densities.

---

<sup>6</sup> <https://www.gnu.org/software/gsl/doc/html/>

## 2.4 Arithmetic operations

### 2.4.1 Vectorised arithmetic operators

R features the following arithmetic operators:

- `+` (addition) and `-` (subtraction),
- `*` (multiplication) and `/` (division),
- `%/%` (integer division) and `%%` (modulo, division remainder),
- `^` (exponentiation; synonym: `**`).

They are all *vectorised*: they take two vectors on input and produce another vector on output.

```
c(1, 2, 3) * c(10, 100, 1000)
## [1] 10 200 3000
```

The multiplication was performed in an *elementwise* fashion. The first element in the left vector was multiplied by the *corresponding* element in the right vector, and the result was stored in the first element of the output. Then, the second element in the left... all right, we get the point.

Other operators are vectorised in the same manner:

```
0:10 + seq(0, 1, 0.1)
## [1] 0.0 1.1 2.2 3.3 4.4 5.5 6.6 7.7 8.8 9.9 11.0
0:7 / rep(3, length.out=8) # division by 3
## [1] 0.00000 0.33333 0.66667 1.00000 1.33333 1.66667 2.00000 2.33333
0:7 %/% rep(3, length.out=8) # integer division
## [1] 0 0 0 1 1 1 2 2
0:7 %% rep(3, length.out=8) # division remainder
## [1] 0 1 2 0 1 2 0 1
```

Operations involving missing values also yield NAs:

```
c(1, NA_real_, 3, NA_real_) + c(NA_real_, 2, 3, NA_real_)
## [1] NA NA 6 NA
```

### 2.4.2 Recycling rule

Some of the above statements can be written more concisely. When the operands are of different lengths, the shorter one is *recycled* (think: `rep(y, length.out=length(x))`) as many times as necessary.

```
0:7 / 3
## [1] 0.00000 0.33333 0.66667 1.00000 1.33333 1.66667 2.00000 2.33333
1:10 * c(-1, 1)
## [1] -1 2 -3 4 -5 6 -7 8 -9 10
2 ^ (0:10)
## [1] 1 2 4 8 16 32 64 128 256 512 1024
```

We call this the *recycling rule*.

If an operand cannot be recycled in its entirety, a warning<sup>7</sup> is generated, but the output is still available.

```
c(1, 10, 100) * 1:8
## Warning in c(1, 10, 100) * 1:8: longer object length is not a multiple of
## shorter object length
## [1] 1 20 300 4 50 600 7 80
```

---

**Note** Some functions are also deeply vectorised, i.e., with respect to multiple arguments. For example,

```
runif(3, c(10, 20, 30), c(11, 22, 33))
## [1] 10.288 21.577 31.227
```

generates three random numbers uniformly distributed over the intervals (10, 11), (20, 22), and (30, 33), respectively.

Also, **pmin** and **pmax** return the *parallel* minimum and maximum of the corresponding elements of the input vectors:

```
pmin(c(1, 2, 3, 4), c(4, 2, 3, 1))
## [1] 1 2 3 1
pmin(3, 1:5)
## [1] 1 2 3 3 3
pmax(0, pmin(1, c(0.25, -2, 5, -0.5, 0, 1.3, 0.99))) # clipping to [0, 1]
## [1] 0.25 0.00 1.00 0.00 0.00 1.00 0.99
```

---

**Note** Vectorisation and the recycling rule are perhaps most fruitful when applying binary operators on sequences of identical lengths or when performing vector-scalar (i.e., a sequence vs a single value) operations. However, there is much more: schemes like “every  $k$ -th element” appear in Taylor series expansions (multiply by  $c(-1, 1)$ ),

---

<sup>7</sup> A few built-in functions do not warn at all when incomplete recycling is performed (e.g., **paste**) or can even give an error (e.g., **as.data.frame.list**). Consider this inconsistency an annoying bug and hope it will be fixed, in the next decade or so.

$k$ -fold cross-validation, etc.; see also [Section 11.3.4](#) for use cases in matrix/tensor processing.

---

### 2.4.3 Operator precedence

Apart from the seven binary arithmetic operators, other noteworthy, already mentioned ones include: the unary ``-`` (change of sign), ``:`` (sequence generation), and ``<-`` (assignment).

Expressions involving multiple operations need a set of rules governing the order of computations (unless we enforce it using round brackets). We have said that `"-1:10"` means `"(-1):10"` rather than `"-(1:10)"`. But what about, say, `"1+1+1+1+1*0"` or `"3*2^0:5+10"`?

Let us list the aforementioned operators in their order of precedence, from the least to the most binding (see also `help("Syntax")`):

1. ``<-`` (right-to-left),
2. ``+`` and ``-``,
3. ``*`` and ``/``,
4. ``%%`` and ``%/%``,
5. ``:``,
6. ``+`` and ``-`` (unary),
7. ``^`` (right-to-left).

Hence, `"-2^2/3+3*4"` means `"((-2^2)/3)+(3*4)"` and not, for example, `"-((2^(2/(3+3)))^4)"`.

Notice that ``+`` and ``-``, ``*`` and ``/``, as well as ``%%`` and ``%/%`` have the same priority. Expressions involving a series of operations in the same group are evaluated left to right, with the exception of ``^`` and ``<-``, which are performed from right to left.

Therefore:

- `"2*3/4*5"` is equivalent to `"((2*3)/4)*5"`,
- `"2^3^4"` is the same as `"2^(3^4)"` (which, mathematically, we would write as  $2^{3^4} = 2^{81}$ ),
- `"x <- y <- 4*3%%8/2"` binds both `y` and `x` with 6 and not `x` with the previous value of `y`.

And let us remember: when in doubt, we can always bracket a subexpression to ensure it is executed in the intended order (which can also increase the readability of the code).

### 2.4.4 Accumulating

The ``+`` and ``*`` operators, as well as the `min` and `max` functions, implement element-wise operations that are applied on the corresponding elements taken from two given vectors:

$$\begin{pmatrix} x_1 \\ x_2 \\ x_3 \\ \vdots \\ x_n \end{pmatrix} + \begin{pmatrix} y_1 \\ y_2 \\ y_3 \\ \vdots \\ y_n \end{pmatrix} = \begin{pmatrix} x_1 + y_1 \\ x_2 + y_2 \\ x_3 + y_3 \\ \vdots \\ x_n + y_n \end{pmatrix}.$$

However, we can also scan through all the values in a *single* vector and combine the successive elements that we inspect using the corresponding operation:

- `cumsum(x)` gives the cumulative sum of the elements in a vector,
- `cumprod(x)` computes the cumulative product,
- `cummin(x)` yields the cumulative minimum,
- `cummax(x)` breeds the cumulative maximum.

The  $i$ -th element in the output vector will consist of the sum/product/min/max of the first  $i$  inputs:

$$\text{cumsum} \begin{pmatrix} x_1 \\ x_2 \\ x_3 \\ \vdots \\ x_n \end{pmatrix} = \begin{pmatrix} x_1 \\ x_1 + x_2 \\ x_1 + x_2 + x_3 \\ \vdots \\ x_1 + x_2 + x_3 + \dots + x_n \end{pmatrix}.$$

For example:

```
cumsum(1:8)
## [1] 1 3 6 10 15 21 28 36
cumprod(1:8)
## [1] 1 2 6 24 120 720 5040 40320
cummin(c(3, 2, 4, 5, 1, 6, 0))
## [1] 3 2 2 2 1 1 0
cummax(c(3, 2, 4, 5, 1, 6, 0))
## [1] 3 3 4 5 5 6 6
```

If we are interested only in the last cumulant, summarising all the inputs, we have the following functions at our disposal:

- `sum(x)` computes the sum of elements in a vector,  $\sum_{i=1}^n x_i = x_1 + x_2 + \dots + x_n$ ,
- `prod(x)` outputs the product of all elements,  $\prod_{i=1}^n x_i = x_1 x_2 \dots x_n$ ,
- `min(x)` computes the minimum,
- `max(x)` reckons the greatest value.

For example:

```
sum(1:8)
## [1] 36
prod(1:8)
## [1] 40320
min(c(3, 2, 4, 5, 1, 6, 0))
## [1] 0
max(c(3, 2, 4, 5, 1, 6, 0))
## [1] 6
```

---

**Note** Chapter 7 will discuss the **Reduce** function, which generalises the above by allowing any binary operation to be propagated over a given vector.

---

**Example 2.7** ***diff** can be considered an inverse to **cumsum**: it computes the iterated difference. Namely, it subtracts the first two elements, then the second from the third one, the third from the fourth, and so on. In other words, **diff**(*x*) gives *y* such that  $y_i = x_{i+1} - x_i$ .*

```
x <- c(-2, 3, 6, 2, 15)
diff(x)
## [1] 5 3 -4 13
cumsum(diff(x))
## [1] 5 8 4 17
cumsum(c(-2, diff(x))) # recreates x
## [1] -2 3 6 2 15
```

Thanks to **diff**, we can compute the daily changes to the EUR/AUD forex rates; see Figure 2.4.

```
aud <- scan(paste0("https://github.com/gagolews/teaching-data/raw/",
  "master/marek/euraud-20200101-20200630.csv"), comment.char="#")
aud_all <- na.omit(aud) # remove all missing values
plot(diff(aud_all), type="s", ylab="Daily change [EUR/AUD]") # "steps"
abline(h=0, lty="dotted") # draw a horizontal line at y=0
```

### 2.4.5 Aggregating

The above functions form the basis for some popular summary statistics<sup>8</sup> (sample aggregates), such as:

- **mean**(*x*) gives the arithmetic mean, **sum**(*x*)/**length**(*x*),
- **var**(*x*) yields the (unbiased) sample variance, **sum**((*x*-**mean**(*x*))^2)/(**length**(*x*)-1),
- **sd**(*x*) is the standard deviation, **sqrt**(**var**(*x*)),

---

<sup>8</sup> Actually, **var** and **median**, amongst others, are defined by the **stats** package, but this one is automatically loaded by default, so let us not make a fuss about it now.

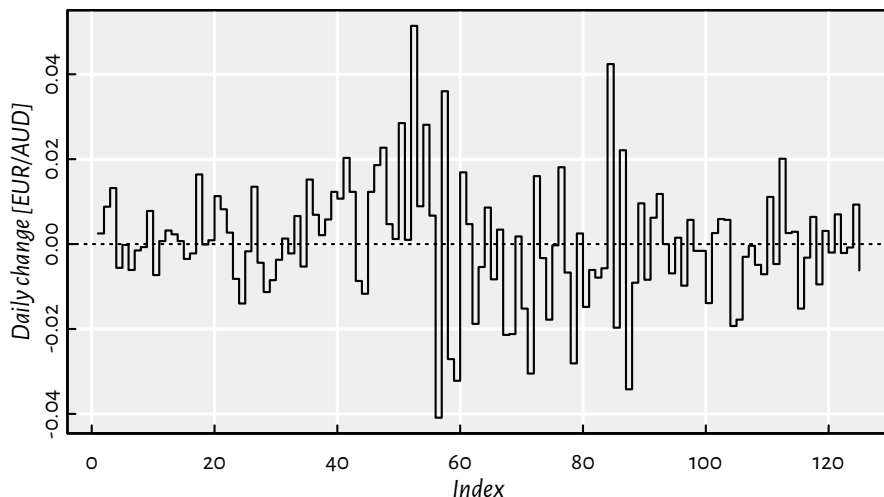


Figure 2.4: Iterated differences of the exchange rates (non-missing values only)

- **median(x)** computes the sample median, i.e., the middle value in the sorted version of  $x$ .

For instance<sup>9</sup>:

```
x <- runif(1000)
c(min(x), mean(x), median(x), max(x), sd(x))
## [1] 0.00046535 0.49727780 0.48995025 0.99940453 0.28748391
```

**Exercise 2.8** Let  $x$  be any vector of length  $n$  with positive elements. Compute its geometric and harmonic mean, which are given by, respectively,

$$\sqrt[n]{\prod_{i=1}^n x_i} = e^{\frac{1}{n} \sum_{i=1}^n \log x_i} \quad \text{and} \quad \frac{n}{\sum_{i=1}^n \frac{1}{x_i}}.$$

When solving exercises like this one, it does not matter on what data you apply these functions (see, however, Section 9.3.4 for discussion). We are being abstract in the sense that the  $x$  vector can be anything: from the one that features very accurate financial predictions that will help minimise inequality and make this world less miserable, through the data you have been collecting for the last ten years in relation to your definitely-super-important PhD research, whatever your company asked you to crunch today, to something related to the hobby project that you enjoy doing after hours. Therefore, just test the above on something like “`x <- runif(10)`”, and move on.

All the aforementioned functions return a missing value if any of the input elements is

<sup>9</sup> **min**, **median**, and **max** are special cases of **quantile**, which we will discuss much further (Section 4.4.3). It is because it returns a named vector.



unavailable. Luckily, they are equipped with the `na.rm` parameter, on behalf of which we can request the removal of NAs.

```
aud <- scan(paste0("https://github.com/gagolews/teaching-data/raw/",
  "master/marek/euraud-20200101-20200630.csv"), comment.char="#")
c(min(aud), mean(aud), max(aud))
## [1] NA NA NA
c(min(aud, na.rm=TRUE), mean(aud, na.rm=TRUE), max(aud, na.rm=TRUE))
## [1] 1.6006 1.6775 1.8635
```

---

**Note** In the documentation, we read that the usage of some of the aforementioned functions is like `sum(..., na.rm=FALSE)`. `prod`, `min`, and `max` are defined similarly. They accept any number of input vectors: each of them can be of arbitrary length. Therefore, `min(1, 2, 3)`, `min(c(1, 2, 3))` as well as `min(c(1, 2), 3)` all return the same result.

However, we also read that we have `mean(x, trim=0, na.rm=FALSE, ...)`. This time, only one vector can be aggregated, and any further arguments (except `trim` and `na.rm`) are ignored.

The extra flexibility (which we do not have to rely on, ever) of the former group is due to their being associative operations: it holds, e.g.,  $(2 + 3) + 4 = 2 + (3 + 4)$ . Hence, the operations can be performed in any order, in any group. Note that they are more primitive operations: it is `mean` that is based on `sum`, not vice versa.

---

## 2.5 Exercises

**Exercise 2.9** Answer the following questions:

- What is the meaning of the dot-dot-dot parameter in the definition of the `c` function?
- We say that the `round` function is vectorised; what does that mean?
- What is wrong with a call to `c(sqrt(1), sqrt(2), sqrt(3))`?
- What do we mean by saying that multiplication operates element-by-element?
- How does the recycling rule work when applying ``+``?
- How to (and why) set the seed of the pseudorandom number generator?
- What is the difference between `NA_real_` and `NaN`?
- How are default arguments specified in the manual of, e.g., the `round` function?
- Is a call to `rep(times=4, x=1:5)` equivalent to `rep(4, 1:5)`?
- List a few ways to generate a sequence like  $(-1, -0.75, -0.5, \dots, 0.75, 1)$ .

- Is “-3:5” the same as “-(3:5)”? What about the precedence of operators in expressions such as “2^3/4\*5^6”, “5\*6+4/17%8”, and “1+-2^3:4-1”?
- If  $x$  is a numeric vector of length  $n$  (for some  $n \geq 0$ ), how many values will `sample(x)` output?
- Does `scan` support reading directly from compressed archives, e.g., `.csv.gz` files?

When in doubt, refer back to the material discussed in this chapter and/or the R manual.

**Exercise 2.10** The following code generates an example graph of arcsine and arccosine, whose preparation – thanks to vectorisation – is quite straightforward.

```
x <- seq(-1, 1, length.out=11) # increase length.out for a smoother curve
plot(x, asin(x),                # asin() computed for 11 points
     type="l",                  # lines
     ylim=c(-pi/2, pi),         # y axis limits like c(y_min, y_max)
     ylab="asin(x), acos(x)")   # y axis label
lines(x, acos(x), col="red", lty="dashed") # adds to the current plot
legend("topright", c("asin(x)", "acos(x)"),
      lty=c("solid", "dashed"), col=c("black", "red"), bg="white")
```

Inspired by the above, plot the following functions:  $|\sin x|^2$ ,  $|\sin |x||$ ,  $\sqrt{|x|}$ , and  $1/(1 + e^{-x})$ . Recall that the documentation of `plot` can be viewed by calling `help("plot.default")`.

**Exercise 2.11** It can be shown that:

$$4 \sum_{i=1}^n \frac{(-1)^{i+1}}{2i-1} = 4 \left( \frac{1}{1} - \frac{1}{3} + \frac{1}{5} - \frac{1}{7} + \dots \right)$$

slowly converges to  $\pi$  as  $n$  approaches  $\infty$ . Compute the above for  $n = 1,000,000$  and  $n = 1,000,000,000$  using the vectorised functions and operators discussed in this chapter, making use of the recycling rule as much as possible.

**Exercise 2.12** Let  $x$  and  $y$  be two vectors of identical lengths  $n$ , say:

```
x <- rnorm(100)
y <- 2*x+10+rnorm(100, 0, 0.5)
```

Compute the Pearson linear correlation coefficient given by:

$$r = \frac{\sum_{i=1}^n \left( x_i - \frac{1}{n} \sum_{j=1}^n x_j \right) \left( y_i - \frac{1}{n} \sum_{j=1}^n y_j \right)}{\sqrt{\sum_{i=1}^n \left( x_i - \frac{1}{n} \sum_{j=1}^n x_j \right)^2} \sqrt{\sum_{i=1}^n \left( y_i - \frac{1}{n} \sum_{j=1}^n y_j \right)^2}}.$$

To make sure you have come up with a correct implementation, compare your result to a call to the built-in `cor(x, y)`.

**Exercise 2.13** (\*) Find an R package providing a function to compute moving (rolling) averages and medians of a given vector. Apply them on the EUR/AUD currency exchange data. Draw thus obtained smoothened versions of the time series.

**Exercise 2.14** (\*\*) Use a call to `convolve(..., type="filter")` to compute the  $k$ -moving average of a numeric vector.

In the next chapter, we will study operations that involve logical values.

---



# 3

---

## Logical vectors

---

### 3.1 Creating logical vectors

R defines three(!) logical constants: TRUE, FALSE, and NA, which represent “yes”, “no”, and “??”, respectively. Each of them, when instantiated, is an atomic vector of length one.

Some of the functions we introduced in the previous chapter can be used to generate logical vectors as well:

```
c(TRUE, FALSE, FALSE, NA, TRUE, FALSE)
## [1] TRUE FALSE FALSE NA TRUE FALSE
rep(c(TRUE, FALSE, NA), each=2)
## [1] TRUE TRUE FALSE FALSE NA NA
sample(c(TRUE, FALSE), 10, replace=TRUE, prob=c(0.8, 0.2))
## [1] TRUE TRUE TRUE FALSE FALSE TRUE TRUE FALSE TRUE TRUE
```

---

**Note** By default, “T” is a synonym for TRUE and “F” stands for FALSE. However, these are not reserved keywords and can be reassigned to any other values. Therefore, we advise against relying on them: they are not used throughout the course of this course.

Also, notice that the logical missing value is spelled simply as “NA” and not “NA\_logical\_”. Both the logical “NA” and the numeric “NA\_real\_” are, for the sake of our mental well-being, both *printed* as “NA” on the R console. This, however, does not mean they are identical; see [Section 4.1](#) for discussion.

---

### 3.2 Comparing elements

#### 3.2.1 Vectorised relational operators

Logical vectors frequently come into being as a result of various *testing* activities.

In particular, the binary operators:

- `<` (less than),

- ``<=`` (less than or equal),
- ``>`` (greater than),
- ``>=`` (greater than or equal)
- ``==`` (equal),
- ``!=`` (not equal),

compare the *corresponding* elements of two numeric vectors and output a logical vector.

```
1 < 3
## [1] TRUE
c(1, 2, 3, 4) == c(2, 2, 3, 8)
## [1] FALSE TRUE TRUE FALSE
1:10 <= 10:1
## [1] TRUE TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE FALSE
```

Thus, they operate in an elementwise manner. Moreover, the recycling rule is applied if necessary:

```
3 < 1:5 # c(3, 3, 3, 3, 3) < c(1, 2, 3, 4, 5)
## [1] FALSE FALSE FALSE TRUE TRUE
c(1, 4) == 1:4 # c(1, 4, 1, 4) == c(1, 2, 3, 4)
## [1] TRUE FALSE FALSE TRUE
```

Therefore, we can say that they are vectorised in the same manner as the arithmetic operators ``+``, ``*``, etc.; compare Section 2.4.1.

### 3.2.2 Testing for NA, NaN, and Inf

Comparisons against missing values and not-numbers yield NAs. Therefore, instead of the *incorrect* `x == NA_real_`, testing for missingness should rather be performed via a call to the vectorised `is.na` function.

```
is.na(c(NA_real_, Inf, -Inf, NaN, -1, 0, 1))
## [1] TRUE FALSE FALSE TRUE FALSE FALSE
is.na(c(TRUE, FALSE, NA, TRUE)) # works for logical vectors, too
## [1] FALSE FALSE TRUE FALSE
```

Moreover, `is.finite` is noteworthy since it returns FALSE on Infs, `NA_real_s` and NaNs.

```
is.finite(c(NA_real_, Inf, -Inf, NaN, -1, 0, 1))
## [1] FALSE FALSE FALSE FALSE TRUE TRUE TRUE
```

See also the more specific `is.nan` and `is.infinite`.



Despite the fact that what follows does not *show* anything suspicious:

```
c(0.1, 0.1 + 0.1 + 0.1, 0.3)
## [1] 0.1 0.3 0.3
```

Printing involves rounding. In the above context, it is misleading. Actually, we experience something more like:

```
print(c(0.1, 0.1 + 0.1 + 0.1, 0.3), digits=22)
## [1] 0.1000000000000000055511 0.30000000000000000444089
## [3] 0.29999999999999999888978
```

- All integers between  $-2^{53}$  and  $2^{53}$  all stored exactly: this is good news. However, the next integer is beyond the representable range:

```
2^53 + 1 == 2^53
## [1] TRUE
```

- The above suggests that, more generally, the order of operations may matter. In particular, the associativity property may be violated when dealing with numbers of different orders of magnitude:

```
2^53 + 2^-53 - 2^53 - 2^-53 # should be == 0.0
## [1] -1.1102e-16
```

- Some numbers may just be just too large, too small, or too close to zero to be represented exactly:

```
c(sum(2^((1023-52):1023)), sum(2^((1023-53):1023)))
## [1] 1.7977e+308 Inf
c(2^(-1022-52), 2^(-1022-53))
## [1] 4.9407e-324 0.0000e+00
```

---

**Important** The double-precision floating point format (IEEE 754) is not specific to R. It is used by most other computing environments, including Python and C++.

For discussion, see [32, 35, 42] ([31] can be of particular interest to the general statistical/data analysis audience).

---

Can we do anything about these issues?

First, dealing with integers of a *reasonable* order of magnitude (a frequent case where we are dealing various resource or case IDs in our datasets) is safe: their comparison, addition, subtraction, and multiplication are always precise.

In all other cases (including applying other operations on integers, e.g., division or `sqrt`), we need to be very careful with comparisons, especially involving testing for equality, `==``.



The sole fact that  $\sin \pi = 0$ , mathematically speaking, does not mean that we should expect that:

```
sin(pi) == 0
## [1] FALSE
```

Instead, they are so close to each other that we can *treat the difference between them as negligible*. Thus, in practice, instead of testing if  $x = y$ , we will be considering:

- $|x - y|$  (absolute error) or
- $\frac{|x-y|}{|y|}$  (relative error; which takes the order of magnitude of the numbers into account but obviously cannot be applied if  $y$  is very close to 0),

and determining if these are less than some assumed error margin,  $\varepsilon > 0$ , say,  $10^{-8}$  or  $2^{-26}$ .

For example:

```
abs(sin(pi) - 0) < 2^-26
## [1] TRUE
```

---

**Note** Rounding can sometimes have a similar effect as testing for almost equality in terms of the absolute error.

```
round(sin(pi), 8) == 0
## [1] TRUE
```

---

**Important** Our recommendations are valid for the most popular applications of R, i.e., statistical and, more generally, scientific computing<sup>1</sup>. The datasets we handle on a daily basis do not represent accurate measurements themselves. Bah, the World itself is far from ideal! Therefore, we do not have to lose sleep over our not being able to precisely pinpoint the *exact* solution.

---

<sup>1</sup> However, in financial applications, we had rather rely on base-10 numbers (compare the problem with 0.1 above). There are some libraries implementing higher precision floating-point numbers or even interval arithmetic that keeps track of error propagation operation chains.

### 3.3 Logical operations

#### 3.3.1 Vectorised logical operators

The relational operators such as ``==`` and ``>`` accept only *two* arguments. Their chaining is forbidden. A test that we would mathematically write as  $0 \leq x \leq 1$  (or  $x \in [0, 1]$ ) cannot be expressed as `"0<=x<=1"` in R.

Therefore, we need a way to combine two logical conditions so as to be able to state that " $x \geq 0$  *and, at the same time,*  $x \leq 1$ ".

In such situations, the following logical operators and functions come in handy:

- ``!`` (not, negation; unary),
- ``&`` (and, conjunction; are both predicates true?),
- ``|`` (or, alternation; is at least one true?),
- `xor` (exclusive-or, exclusive disjunction, either-or; is one and only one of the predicates true?).

They again act elementwisely and implement the recycling rule if necessary (and applicable).

```
x <- c(-10, -1, -0.25, 0, 0.5, 1, 5, 100)
(x >= 0) & (x <= 1)
## [1] FALSE FALSE FALSE TRUE TRUE TRUE FALSE FALSE
(x < 0) | (x > 1)
## [1] TRUE TRUE TRUE FALSE FALSE FALSE TRUE TRUE
!((x < 0) | (x > 1))
## [1] FALSE FALSE FALSE TRUE TRUE TRUE FALSE FALSE
xor(x >= -1, x <= 1)
## [1] TRUE FALSE FALSE FALSE FALSE FALSE TRUE TRUE
```

---

**Important** The vectorised ``&`` and ``|`` operators should not be confused with their scalar, short-circuit counterparts, ``&&`` and ``||``; see [Section 8.1.4](#).

---

#### 3.3.2 Operator precedence revisited

The operators introduced in this chapter have lower precedence than the arithmetic ones. In particular, the binary ``+`` and ``-``. Calling `help("Syntax")` reveals that we can extend our listing from [Section 2.4.3](#) as follows:

1. ``<-`` (*right-to-left; least binding*),
2. ``|``,

3. ``&``,
4. ``!`` (unary),
5. ``<``, ``>``, ``<=``, ``>=``, ``==``, and ``!=``,
6. ``+`` and ``-``,
7. ``*`` and ``/``,
8. ...

### 3.3.3 Dealing with missingness

Operations involving missing values follow the principles of the Łukasiewicz's three-valued logic, which is based on common sense. For instance, “NA | TRUE” is TRUE because *or* needs at least one argument to be TRUE to generate such a result. On the other hand, “NA | FALSE” is NA since the result would be different depending on what we substituted NA for.

Let us take a moment to contemplate the operations' *truth tables* for all the possible combinations of inputs:

```
u <- c(TRUE, FALSE, NA, TRUE, FALSE, NA, TRUE, FALSE, NA)
v <- c(TRUE, TRUE, TRUE, FALSE, FALSE, FALSE, NA, NA, NA)
!u
## [1] FALSE TRUE NA FALSE TRUE NA FALSE TRUE NA
u & v
## [1] TRUE FALSE NA FALSE FALSE FALSE NA FALSE NA
u | v
## [1] TRUE TRUE TRUE TRUE FALSE NA TRUE NA NA
xor(u, v)
## [1] FALSE TRUE NA TRUE FALSE NA NA NA NA
```

### 3.3.4 Aggregating with all, any, and sum

Just like in the case of numeric vectors, we can summarise the contents of logical sequences.

**all** tests whether every element in a logical vector is equal to TRUE. **any** determines if there exists an element that is TRUE.

```
x <- runif(10000)
all(x <= 0.2) # are all values in x <= 0.2?
## [1] FALSE
any(x <= 0.2) # is there at least one element in x that is <= 0.2?
## [1] TRUE
any(c(NA, FALSE, TRUE))
## [1] TRUE
```

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(continued from previous page)

```
all(c(TRUE, TRUE, NA))
## [1] NA
```

**Note** The `all` function will frequently be used in conjunction with ``==``. This is because the latter, as we have said above, is itself vectorised: it does *not* test whether a vector *as a whole* is equal to another one.

```
z <- c(1, 2, 3)
z == 1:3 # elementwise equal
## [1] TRUE TRUE TRUE
all(z == 1:3) # elementwise equal summarised
## [1] TRUE
```

However, let us keep in mind the warning about the testing for *exact* equality of floating-point numbers stated in Section 3.2.3. Sometimes, considering absolute or relative errors might be more appropriate.

```
z <- sin((0:10)*pi) # sin(0), sin(pi), sin(2*pi), ..., sin(10*pi)
all(z == 0.0) # danger zone! please don't...
## [1] FALSE
all(abs(z - 0.0) < 1e-9) # are the absolute errors negligible?
## [1] TRUE
```

We can also call `sum` on a logical vector. Taking into account that it interprets `TRUE` as numeric 1 and `FALSE` as 0 (more on this in Section 4.1), it will give us the number of elements equal to `TRUE`.

```
sum(x <= 0.2) # how many elements in x are <= 0.2?
## [1] 1998
```

Also, by computing `sum(x)/length(x)`, we can obtain the proportion (fraction) of values equal to `TRUE` in `x`. Equivalently:

```
mean(x <= 0.2) # proportion of elements <= 0.2
## [1] 0.1998
```

Naturally, we *expect* `mean(runif(n) <= 0.2)` to be equal to 0.2 (20%), but with randomness, we can never be sure.

### 3.3.5 Simplifying predicates

Each aspiring programmer needs to become fluent with the rules governing the transformations of logical conditions, for example, that the negation of “ $(x \geq 0) \ \& \ (x < 1)$ ” is equivalent to “ $(x < 0) \ | \ (x \geq 1)$ ”.

Each such rule is called a *tautology*. Here are some of them:

- $!(\neg p)$  is equivalent to  $p$  (double negation),
- $!(p \ \& \ q)$  holds if and only if  $\neg p \mid \neg q$  (De Morgan's law),
- $!(p \mid q)$  is  $\neg p \ \& \ \neg q$  (another De Morgan's law),
- $\mathbf{all}(p)$  is equivalent to  $\mathbf{any}(\neg p)$ .

Various combinations thereof are, of course, possible. Some further simplifications are enabled by other properties of the binary operations:

- commutativity (symmetry), e.g.,  $a + b = b + a$ ,  $a * b = b * a$ ,
- associativity, e.g.,  $(a + b) + c = a + (b + c)$ ,  $\max(\max(a, b), c) = \max(a, \max(b, c))$ ,
- distributivity, e.g.,  $a * b + a * c = a * (b + c)$ ,  $\min(\max(a, b), \max(a, c)) = \max(a, \min(b, c))$ ,

and relations, including:

- transitivity, e.g., if  $a \leq b$  and  $b \leq c$  then surely  $a \leq c$ .

**Exercise 3.1** Assuming that  $a$ ,  $b$ , and  $c$  are numeric vectors, simplify the following expressions:

- $!(b > a \ \& \ b < c)$ ,
- $!(a >= b \ \& \ b >= c \ \& \ a >= c)$ ,
- $a > b \ \& \ a < c \mid a < c \ \& \ a > d$ ,
- $a > b \mid a <= b$ ,
- $a <= b \ \& \ a > c \mid a > b \ \& \ a <= c$ ,
- $a <= b \ \& \ (a > c \mid a > b) \ \& \ a <= c$ ,
- $\mathbf{all}(a > b \ \& \ b < c)$ .

### 3.4 Choosing elements with `ifelse`

The **`ifelse`** function is a vectorised version of the scalar **`if...else`** conditional statement, which we will do without for as long as until [Chapter 8](#).

It allows us to select an element from either one or another vector based on some logical condition.

A call to **`ifelse(l, t, f)`**, where  $l$  is a logical vector, returns a vector  $y$  such that:

$$y_i = \begin{cases} t_i & \text{if } l_i \text{ is TRUE,} \\ f_i & \text{if } l_i \text{ is FALSE.} \end{cases}$$

In other words, the  $i$ -th element of the result vector is equal to  $t_i$  if  $l_i$  is TRUE and to  $f_i$  otherwise.

For example:

```
(z <- rnorm(6)) # example vector
## [1] -0.560476 -0.230177 1.558708 0.070508 0.129288 1.715065
ifelse(z >= 0, z, -z) # like abs(z)
## [1] 0.560476 0.230177 1.558708 0.070508 0.129288 1.715065
```

or:

```
(x <- rnorm(6)) # example vector
## [1] 0.46092 -1.26506 -0.68685 -0.44566 1.22408 0.35981
(y <- rnorm(6)) # example vector
## [1] 0.40077 0.11068 -0.55584 1.78691 0.49785 -1.96662
ifelse(x >= y, x, y) # like pmax(x, y)
## [1] 0.46092 0.11068 -0.55584 1.78691 1.22408 0.35981
```

By now, we should not be surprised that the recycling rule is fired up if necessary:

```
ifelse(x > 0, x^2, 0) # squares of positive xs and 0 otherwise
## [1] 0.21244 0.00000 0.00000 0.00000 1.49838 0.12947
```

---

**Note** All arguments are evaluated in their entirety before deciding on which elements are selected. Therefore, the following call will generate a warning:

```
ifelse(z >= 0, log(z), NA_real_)
## Warning in log(z): NaNs produced
## [1]      NA      NA 0.44386 -2.65202 -2.04571 0.53945
```

This is because, with `log(z)`, we compute the logarithms of negative values anyway. To fix this, we can write:

```
log(ifelse(z >= 0, z, NA_real_))
## [1]      NA      NA 0.44386 -2.65202 -2.04571 0.53945
```

---

The calls to `ifelse` can naturally be nested in the case where we yearn for an `if...else if...else`-type expression.

**Example 3.2** A version of `pmax(pmax(x, y), z)` can be written as:

```
ifelse(x >= y,
      ifelse(z >= x, z, x),
      ifelse(z >= y, z, y)
)
## [1] 0.46092 0.11068 1.55871 1.78691 1.22408 1.71506
```

However, determining the three intermediate logical vectors is not necessary; we can save one call to `>=` by introducing an auxiliary variable:

```
xy <- ifelse(x >= y, x, y)
ifelse(z >= xy, z, xy)
## [1] 0.46092 0.11068 1.55871 1.78691 1.22408 1.71506
```

**Exercise 3.3** Figure 3.1 depicts a realisation of the mixture  $Z = 0.2X + 0.8Y$  of two normal distributions  $X \sim N(-2, 0.5)$  and  $Y \sim N(3, 1)$ .

```
n <- 100000
z <- ifelse(runif(n) <= 0.2, rnorm(n, -2, 0.5), rnorm(n, 3, 1))
hist(z, breaks=101, probability=TRUE, main="", col="white")
```

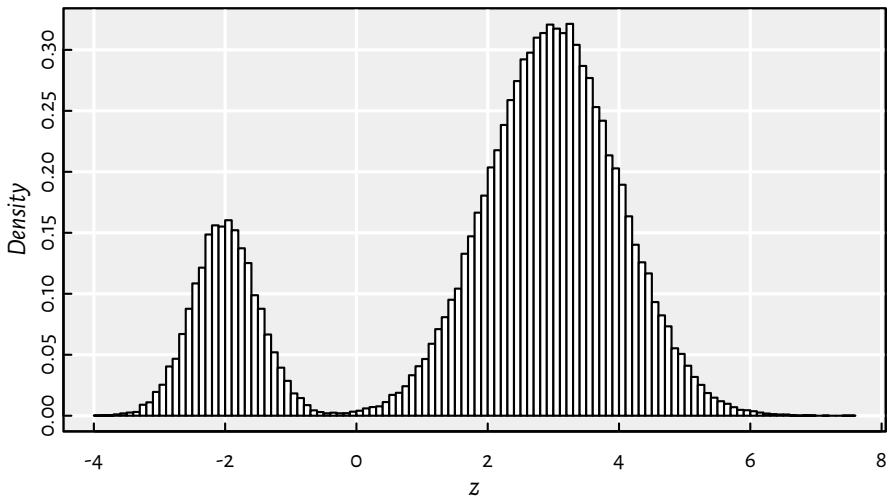


Figure 3.1: A mixture of two Gaussians generated with `ifelse`

In other words, we generated a variate from the normal distribution that has the expected value of -2 with probability 20%, and from the one with the expectation of 3 otherwise.

Inspired by the above, generate the following Gaussian mixtures:

- $\frac{2}{3}X + \frac{1}{3}Y$ , where  $X \sim N(100, 16)$  and  $Y \sim N(116, 8)$ ,
- $0.3X + 0.4Y + 0.3Z$ , where  $X \sim N(-10, 2)$ ,  $Y \sim N(0, 2)$ , and  $Z \sim N(10, 2)$ .

(\*) On a side note, knowing that if  $X$  follows  $N(0, 1)$ , then the scaled-shifted  $\sigma X + \mu$  is distributed  $N(\mu, \sigma)$ , the above can be equivalently written as:

```
w <- (runif(n) <= 0.2)
z <- rnorm(n, 0, 1)*ifelse(w, 0.5, 1) + ifelse(w, -2, 3)
```

### 3.5 Exercises

**Exercise 3.4** Answer the following questions:

- Why the statement “The Earth is flat or the smallpox vaccine is proven effective” is obviously true?
- What is the difference between `NA` and `NA_real_`?
- Why is “`FALSE & NA`” equal to `FALSE`, but “`TRUE & NA`” is `NA`?
- Why has “`ifelse(x>=0, sqrt(x), NA_real_)`” a tendency to generate warnings and how to rewrite it so as to prevent that from happening?
- What is the interpretation of “`mean(x >= 0 & x <= 1)`”?
- For some integer  $x$  and  $y$ , how to verify whether  $0 < x < 100$ ,  $0 < y < 100$ , and  $x < y$ , all at the same time?
- Mathematically, for all real  $x, y > 0$ , it holds  $\log xy = \log x + \log y$ . Why then “`all(log(x*y) == log(x)+log(y))`” can sometimes return `FALSE`? How to fix this?
- Is “ $x/y/z$ ” always equal to “ $x/(y/z)$ ”? How to fix this?
- What is the purpose of very specific functions such as `log1p` and `expm1` (see their help page) and many others listed in, e.g., the GNU GSL library [28]? Is our referring to them a violation of the beloved “let us be minimalist” approach?
- If we know that  $x$  may be subject to error, how to test whether  $x > 0$  in a robust manner?
- Is “ $y < -5$ ” the same as “`y <- 5`” or rather “`y < -5`”?

**Exercise 3.5** What is the difference between `all` and `isTRUE`? What about “`==`”, `identical`, and `all.equal`? Is the last one properly vectorised?

**Exercise 3.6** Compute the cross-entropy loss between a numeric vector  $\mathbf{p}$  with values in the interval  $(0, 1)$  and a logical vector  $\mathbf{y}$ , both of length  $n$  (you can generate them randomly or manually, it does not matter, it is just an exercise):

$$\mathcal{L}(\mathbf{p}, \mathbf{y}) = \frac{1}{n} \sum_{i=1}^n \ell_i,$$

where

$$\ell_i = \begin{cases} -\log p_i & \text{if } y_i \text{ is TRUE,} \\ -\log(1 - p_i) & \text{if } y_i \text{ is FALSE.} \end{cases}$$

*Interpretation:* in classification problems,  $y_i \in \{\text{FALSE}, \text{TRUE}\}$  denotes the true class of the  $i$ -th object (say, whether the  $i$ -th hospital patient is symptomatic) and  $p_i \in (0, 1)$  a machine learning algorithm’s confidence that  $i$  belongs to class `TRUE` (e.g., how sure a decision tree model is that the corresponding person is unwell). Ideally, if  $y_i$  is `TRUE`,  $p_i$  should be close to 1 and to 0 otherwise. The cross-entropy loss quantifies by how much a classifier differs from the omniscient one. The use of the logarithm penalises strong beliefs in the wrong answer.



By the way, if we have solved any of the exercises encountered so far by referring to **if** statements, **for** loops, vector indexing like `x[...]`, or any external R package, we recommend to go back and rewrite our code. Let us keep it simple (effective, readable) by using the *base* R's vectorised operations that we have introduced.

---



# 4

---

## *Lists and attributes*

---

After two brain-teasing chapters, it is time to cool it down a little. In this more technical part, we will introduce lists, which serve as universal containers for R objects of any size and type. Moreover, we will also show that each R object can be equipped with a number of optional attributes, thanks to which we will not only be able to label elements in any vector but also introduce new complex data types such as matrices and data frames later.

---

### 4.1 Type hierarchy and conversion

So far, we have been dealing with three types of atomic vectors:

1. `logical` (Chapter 3),
2. `numeric` (Chapter 2),
3. `character` (which we have barely touched upon yet, but rest assured that they will be covered in detail very soon; see Chapter 6).

To determine the type of an object programmatically, we can call the **`typeof`** function.

```
typeof(c(1, 2, 3))  
## [1] "double"  
typeof(c(TRUE, FALSE, TRUE, NA))  
## [1] "logical"  
typeof(c("spam", "spam", "bacon", "gluten-free spam"))  
## [1] "character"
```

It turns out that we can easily convert between these types, either on our explicit demand (*type casting*) or on-the-fly (*coercion*, when we perform an operation that expects something different from the kind of input it was fed with).

---

**Note** (\*) Numeric vectors are reported as being either of the type `double` (double-precision floating-point numbers) or `integer` (32-bit; it is a subset of `double`); see Section 6.4.1. In most practical cases, this is a technical detail that we can risklessly ignore; compare also the **`mode`** function.

---

### 4.1.1 Explicit type casting

We can use functions such as `as.logical`, `as.numeric`, and `as.character` to *coerce* (convert) given objects to the corresponding types.

```
as.numeric(c(TRUE, FALSE, NA, TRUE, NA, FALSE))
## [1] 1 0 NA 1 NA 0
as.logical(c(-2, -1, 0, 1, 2, 3, NA_real_, -Inf, NaN))
## [1] TRUE TRUE FALSE TRUE TRUE TRUE NA TRUE NA
```

---

**Important** It is easily seen that the rules are:

- $\text{TRUE} \rightarrow 1$ ,
- $\text{FALSE} \rightarrow 0$ ,
- $\text{NA} \rightarrow \text{NA\_real\_}$ ,

and:

- $0 \rightarrow \text{FALSE}$ ,
- $\text{NA\_real\_}$  and  $\text{NaN} \rightarrow \text{NA}$ ,
- anything else  $\rightarrow \text{TRUE}$ .

The distinction between zero and non-zero is commonly applied in other programming languages as well.

---

Moreover, in the case of the conversion involving character strings, we have:

```
as.character(c(TRUE, FALSE, NA, TRUE, NA, FALSE))
## [1] "TRUE" "FALSE" NA "TRUE" NA "FALSE"
as.character(c(-2, -1, 0, 1, 2, 3, NA_real_, -Inf, NaN))
## [1] "-2" "-1" "0" "1" "2" "3" NA "-Inf" "NaN"
as.logical(c("TRUE", "True", "true", "T",
             "FALSE", "False", "false", "F",
             "anything other than these", NA_character_))
## [1] TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE NA NA
as.numeric(c("0", "-1.23e4", "pi", "2+2", "NaN", "-Inf", NA_character_))
## Warning: NAs introduced by coercion
## [1] 0 -12300 NA NA NaN -Inf NA
```

### 4.1.2 Implicit conversion (coercion)

Recall that we referred to the three vector types as *atomic* ones: they can only be used to store elements of the *same type*.

If we make an attempt at composing an object of mixed types with `c`, the common type

will be determined in such a way that storing the data is done without information loss:

```
c(-1, FALSE, TRUE, 2, "three", NA)
## [1] "-1"      "FALSE" "TRUE"  "2"      "three" NA
c("zero", TRUE, NA)
## [1] "zero" "TRUE" NA
c(-1, FALSE, TRUE, 2, NA)
## [1] -1  0  1  2 NA
```

Hence, we see that `logical` is the most specialised of the tree, whereas `character` is the most general.

---

**Note** The logical `NA` is converted to `NA_real_` and `NA_character_` in the above examples. R users tend to rely on implicit type conversion when they write `c(1, 2, NA, 4)` instead of the more explicit `c(1, 2, NA_real_, 4)`. In most cases, this is fine.

However, occasionally, it will be wiser to be more unequivocal. For instance, `rep(NA_real_, 1e9)` pre-allocates a long numeric vector instead of a logical one.

---

Some functions that expect vectors of specific types can apply coercion by themselves (or act as if they do so):

```
c(NA, FALSE, TRUE) + 10 # implicit conversion logical -> numeric
## [1] NA 10 11
c(-1, 0, 1) & TRUE # implicit conversion numeric -> logical
## [1] TRUE FALSE TRUE
sum(c(TRUE, TRUE, FALSE, TRUE, FALSE)) # same as sum(as.numeric(...))
## [1] 3
cumsum(c(TRUE, TRUE, FALSE, TRUE, FALSE))
## [1] 1 2 2 3 3
cummin(c(TRUE, TRUE, FALSE, TRUE, FALSE))
## [1] 1 1 0 0 0
```

**Exercise 4.1** In one of the previous exercises, we computed the cross-entropy loss between a logical vector  $\mathbf{y} \in \{0, 1\}^n$  and a numeric vector  $\mathbf{p} \in (0, 1)^n$ . This measure can be equivalently defined as:

$$\mathcal{L}(\mathbf{p}, \mathbf{y}) = -\frac{1}{n} \left( \sum_{i=1}^n y_i \log(p_i) + (1 - y_i) \log(1 - p_i) \right).$$

Implement the above formula (using vectorised operations, but not relying on `ifelse` this time) and compute the cross-entropy loss between, say, “`y <- sample(c(FALSE, TRUE), n)`” and “`p <- runif(n)`” for some  $n$ . Note how seamlessly we are translating between `FALSE/TRUE`s and `0/1`s in the above equation (in particular, where we let  $1 - y_i$  mean the logical negation of  $y_i$ ).

## 4.2 Lists

*Lists* are *generalised* vectors. They can be comprised of R objects of any kind, also other lists. This is why we classify them as *recursive* (and not atomic) objects. They are especially useful wherever there is a need to handle some *multitude* as a single entity.

### 4.2.1 Creating lists

The most straightforward way to create a list is by means of the `list` function:

```
list(1, 2, 3)
## [[1]]
## [1] 1
##
## [[2]]
## [1] 2
##
## [[3]]
## [1] 3
```

Notice that the above is not the same as “`c(1, 2, 3)`”. We got a sequence that wraps three numeric vectors, each of length one. Also, how overly talkative R is when printing out lists!

```
list(c(1, 2, 3), 4, c(TRUE, FALSE, FALSE, NA, TRUE), "and so forth")
## [[1]]
## [1] 1 2 3
##
## [[2]]
## [1] 4
##
## [[3]]
## [1] TRUE FALSE FALSE NA TRUE
##
## [[4]]
## [1] "and so forth"
list(list(c(TRUE, FALSE, NA, TRUE), letters), runif(5)) # a list of lists
## [[1]]
## [[1]][1]]
## [1] TRUE FALSE NA TRUE
##
## [[1]][[2]]
## [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p" "q"
## [18] "r" "s" "t" "u" "v" "w" "x" "y" "z"
```

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```
##
##
## [[2]]
## [1] 0.28758 0.78831 0.40898 0.88302 0.94047
```

However, the **str** function can be used to print R objects in a more concise fashion:

```
str(list(list(c(TRUE, FALSE, NA, TRUE), letters), runif(5)))
## List of 2
## $ :List of 2
## ..$ : logi [1:4] TRUE FALSE NA TRUE
## ..$ : chr [1:26] "a" "b" "c" "d" ...
## $ : num [1:5] 0.288 0.788 0.409 0.883 0.94
```

---

**Note** In Section 4.1, we said that the **c** function, when fed with arguments of mixed types, tries to determine the common type that retains the sense of data. If coercion to an atomic vector is not possible, the result will be a list.

```
c(1, "two", identity) # `identity` is an object of the type "function"
## [[1]]
## [1] 1
##
## [[2]]
## [1] "two"
##
## [[3]]
## function (x)
## x
## <environment: namespace:base>
```

---

Thus, the **c** function can also be used to concatenate lists:

```
c(list(1), list(2), list(3)) # 3 lists -> 1 list
## [[1]]
## [1] 1
##
## [[2]]
## [1] 2
##
## [[3]]
## [1] 3
```

Lists can be repeated using **rep**:

```
rep(list(1:11, LETTERS), 2)
## [[1]]
## [1] 1 2 3 4 5 6 7 8 9 10 11
##
## [[2]]
## [1] "A" "B" "C" "D" "E" "F" "G" "H" "I" "J" "K" "L" "M" "N" "O" "P" "Q"
## [18] "R" "S" "T" "U" "V" "W" "X" "Y" "Z"
##
## [[3]]
## [1] 1 2 3 4 5 6 7 8 9 10 11
##
## [[4]]
## [1] "A" "B" "C" "D" "E" "F" "G" "H" "I" "J" "K" "L" "M" "N" "O" "P" "Q"
## [18] "R" "S" "T" "U" "V" "W" "X" "Y" "Z"
```

#### 4.2.2 Coercing to and from lists

The conversion of an atomic vector to a list of length-1 vectors can be done via a call to **as.list**:

```
as.list(c(1, 2, 3)) # vector of length 3 -> list of 3 length-1 vectors
## [[1]]
## [1] 1
##
## [[2]]
## [1] 2
##
## [[3]]
## [1] 3
```

Unfortunately, calling, say, **as.numeric** on a list arouses an error (even if it is comprised of numeric vectors only). We can try to flatten it to an atomic sequence by calling **unlist**:

```
unlist(list(list(1, 2), list(3, list(4:8)), 9))
## [1] 1 2 3 4 5 6 7 8 9
unlist(list(list(1, 2), list(3, list(4:8)), "spam"))
## [1] "1" "2" "3" "4" "5" "6" "7" "8" "spam"
```

---

**Note** (\*) Chapter 11 will mention the **simplify2array** function, which generalises **unlist** in a way that can sometimes give rise to a matrix.

---



### 4.3 NULL

The NULL object (the one and only object of the type “NULL”) can be used as a placeholder for any other R object or designate the absence of such.

```
list(NULL, NULL, month.name)
## [[1]]
## NULL
##
## [[2]]
## NULL
##
## [[3]]
## [1] "January" "February" "March" "April" "May"
## [6] "June" "July" "August" "September" "October"
## [11] "November" "December"
```

NULL is different from a vector of length zero because the latter has a type.

However, NULL sometimes *behaves* as a 0-length vector. In particular, **length**(NULL) returns 0. Also, **c** called with no arguments returns NULL.

Testing for NULL-ness can be done with a call to **is.null**.

---

**Important** NULL is not the same as NA (or its other-typed variants). The latter can be replaced in an atomic vector.

```
c(1, NA, 3, NULL, 5) # NULL behaves as a 0-length vector here
## [1] 1 NA 3 5
```

They both have very distinct semantics (no value vs a missing value).

---

Later we will see that some functions return NULL invisibly when they have nothing interesting to report. This is the case of **print** or **plot**, which are called because of their side effects (printing and plotting).

Furthermore, in some contexts, replacing content with NULL (e.g., when subsetting a list) will actually result in its removal.

## 4.4 Object attributes

Lists can be used to embrace many objects to form a single item sequence. Attributes, on the other hand, give means to inject some *extra* data into an object of any type (except NULL).

Attributes are (unordered) key=value pairs, where key is a single string, and value is any R object except NULL. They can be introduced by calling, amongst others<sup>1</sup>, the **structure** function:

```
x_simple <- 1:10
x <- structure(
  x_simple, # the object to be equipped with attributes
  attribute1="value1",
  attribute2=c(6, 100, 324)
)
```

### 4.4.1 Developing perceptual indifference to most attributes

Let us see how the above `x` is reported on the console:

```
print(x)
## [1] 1 2 3 4 5 6 7 8 9 10
## attr(,"attribute1")
## [1] "value1"
## attr(,"attribute2")
## [1] 6 100 324
```

The object of concern, “1:10”, was displayed first. We need to get used to that. Most of the time, we suggest to treat the “attr...” parts of the display as if they were printed in tiny font.

Equipping an object with attributes does not change its very nature (see, however, Chapter 10 for some exceptions). For example, the above `x`, despite featuring some extra data (metadata), is still treated as an ordinary sequence of numbers by most functions:

```
sum(x) # the same as sum(1:10), sum() does not care about any attributes
## [1] 55
typeof(x) # just a numeric vector, but with some perks
## [1] "integer"
```

<sup>1</sup> Other ways include the replacement versions of the **attr** and **attributes** functions; see Section 9.4.6.

---

**Important** Attributes are generally ignored by most functions unless they have specifically been programmed to pay attention to them.

---

#### 4.4.2 But there are some use cases

Some R functions add attributes to the return value to sneak extra information that *might* be useful, just in case.

For instance, `na.omit`, whose main aim is to remove missing values from an atomic vector, yields:

```
y <- c(10, 20, NA, 40, 50, NA, 70)
(y_na_free <- na.omit(y))
## [1] 10 20 40 50 70
## attr(,"na.action")
## [1] 3 6
## attr(,"class")
## [1] "omit"
```

We can enjoy the NA-free version of `y` in any further computations:

```
mean(y_na_free)
## [1] 38
```

However, the `na.action` attribute (we ignore the `class` part until [Chapter 10](#)) tells us *where* the missing observations were:

```
attr(y_na_free, "na.action") # read the attribute value
## [1] 3 6
## attr(,"class")
## [1] "omit"
```

As another example, `gregexpr` can be used to search for a given pattern in a character vector (for more details, see [Chapter 6](#)):

```
needle <- "spam|gluten" # pattern to search for: spam OR gluten
haystack <- c("spam, spam, bacon, and gluten-free spam", "spammer") # text
(pos <- gregexpr(needle, haystack))
## [[1]]
## [1] 1 7 24 36
## attr(,"match.length")
## [1] 4 4 6 4
## attr(,"index.type")
## [1] "chars"
## attr(,"useBytes")
```

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```
## [1] TRUE
##
## [[2]]
## [1] 1
## attr(,"match.length")
## [1] 4
## attr(,"index.type")
## [1] "chars"
## attr(,"useBytes")
## [1] TRUE
```

We sought all occurrences of the pattern within two character strings. As their number may vary from string to string, wrapping the results in a list was a good design choice. Each list element gives the starting positions where matches can be found (there are four and one match(es), respectively).

Each vector of positions also features its own `match.length` attribute (amongst others), in case we need it.

**Exercise 4.2** Create a list with EUR/AUD, EUR/GBP, and EUR/USD exchange rates read from the `euraud-*.csv`, `eurgbp-*.csv`, and `eurusd-*.csv` files in our [data repository](#)<sup>2</sup>. Each of its three elements should be a numeric vector storing the currency exchange rates. Furthermore, equip them with `currency_from`, `currency_to`, `date_from`, and `date_to` attributes, for example:

```
## [1] NA 1.6006 1.6031 NA NA 1.6119 1.6251 1.6195 1.6193 1.6132
## [11] NA NA 1.6117 1.6110 1.6188 1.6115 1.6122 NA
## attr(,"currency_from")
## [1] "EUR"
## attr(,"currency_to")
## [1] "AUD"
## attr(,"date_from")
## [1] "2020-01-01"
## attr(,"date_to")
## [1] "2020-06-30"
```

Such additional information could be stored in a few separate variables (other vectors), but then it would not be as convenient to use as the above representation.

### 4.4.3 Special attributes

Attributes have great potential which is somewhat wasted, for R users rarely know:

- that attributes exist (pessimistic scenario), or
- how to handle them (realistic scenario).

<sup>2</sup> <https://github.com/gagolews/teaching-data/tree/master/marek>

But we now know.

What is more, some attributes have been predestined to play a fundamental role in R. Namely, the most prevalent amongst the *special attributes* are:

- `names`, `row.names`, and `dimnames` are used to label the elements of atomic and generic vectors (see below), and also rows and columns in matrices (Chapter 11) and data frames (Chapter 12),
- `dim` allows for turning flat vectors into matrices and other tensors (Chapter 11),
- `levels` labels the underlying integer codes in factor objects (Section 10.3.2),
- `class` can be used to bring forth new complex data structures based on basic types (Chapter 10).

We call them *special* because:

- they cannot be assigned arbitrary values; for instance, we will soon see that `names` can only be mapped to a character vector of the length equal to that of the sequence it is labelling,
- they can be accessed via designated functions, e.g., `names`, `class`, `dim`, `dimnames`, `levels`, etc.,
- they are widely recognised by many base and third-party R functions.

However, in spite of the above, special attributes can still be managed as any other (ordinary) ones.

**Exercise 4.3** *comment* is perhaps the most rarely used special attribute. Create an object (whatever) equipped with the `comment` attribute. Verify that assigning to it anything other than a character vector leads to an error. Read its value by calling the `comment` function. Display the object equipped with this attribute. Note that the `print` function ignores its existence whatsoever: this is how special it is.

---

**Important** (\*) The accessor functions such as `names` or `class` might return meaningful values, even if the corresponding attribute is not set explicitly; see, e.g., Section 11.1.5 for an example.

---

#### 4.4.4 Labelling vector elements with the `names` attribute

A special attribute called `names` can be used to label the elements of atomic vectors and lists.

```
(x <- structure(c(13, 2, 6), names=c("spam", "sausage", "celery")))
##   spam  sausage  celery
##    13      2      6
```

The labels may improve the expressivity and readability of our code and data.

**Exercise 4.4** Verify that the above *x* is still an ordinary numeric vector by calling **typeof** and **sum** on it.

Let us stress that we can ignore the **names** attribute whatsoever. If we apply any operation discussed in [Chapter 2](#), we will still garner the same result no matter if such extra information is present or not.

It is just the **print** function that changed its behaviour slightly (it is a special attribute, after all). Instead of reporting:

```
## [1] 13 2 6
## attr(,"names")
## [1] "spam" "sausage" "celery"
```

we got a nicely formatted table-like display. Non-special attributes are still printed in a standard way.

```
##   spam sausage celery
##    13      2      6
## attr(,"additional_attribute")
## [1] 1 2 3 4 5 6 7 8 9 10
```

---

**Note** Chapter 5 will also mention that some operations (such as indexing) can gain extra features in the presence of the **names** attribute.

---

This attribute can be read by calling:

```
attr(x, "names") # just like any other attribute
## [1] "spam" "sausage" "celery"
names(x) # because it is so special
## [1] "spam" "sausage" "celery"
```

Named vectors can be easily created with the **c** and **list** functions as well:

```
c(a=1, b=2)
## a b
## 1 2
list(a=1, b=2)
## $a
## [1] 1
##
## $b
## [1] 2
c(a=c(x=1, y=2), b=3, c=c(z=4)) # this is smart
## a.x a.y b c.z
## 1 2 3 4
```

Let us contemplate how a named list is printed on the console. Again, it is still a list, but with some extras.

**Exercise 4.5** A whole lot of functions return named vectors. Evaluate the following expressions and read the corresponding pages in the documentation:

- `quantile(runif(100))`,
- `hist(runif(100), plot=FALSE)`,
- `options` (take note of the `digits`, `scipen`, `max.print`, and `width` options),
- `capabilities`.

---

**Note** (\*) Most of the time, lists are used merely as *containers* for other R objects. This is a boring yet essential role. However, let us just mention here that each data frame is, in fact, a generic vector (see Chapter 12). Each column corresponds to a named list element:

```
(df <- head(iris)) # some data frame
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
## 2         4.9         3.0         1.4         0.2   setosa
## 3         4.7         3.2         1.3         0.2   setosa
## 4         4.6         3.1         1.5         0.2   setosa
## 5         5.0         3.6         1.4         0.2   setosa
## 6         5.4         3.9         1.7         0.4   setosa
typeof(df) # it is just a list (with extras that'll be discussed later)
## [1] "list"
unclass(df) # how it is represented exactly (without the extras)
## $Sepal.Length
## [1] 5.1 4.9 4.7 4.6 5.0 5.4
##
## $Sepal.Width
## [1] 3.5 3.0 3.2 3.1 3.6 3.9
##
## $Petal.Length
## [1] 1.4 1.4 1.3 1.5 1.4 1.7
##
## $Petal.Width
## [1] 0.2 0.2 0.2 0.2 0.2 0.4
##
## $Species
## [1] setosa setosa setosa setosa setosa setosa
## Levels: setosa versicolor virginica
##
## attr(,"row.names")
## [1] 1 2 3 4 5 6
```

Therefore, the functions we discuss in this chapter are of use in the processing of such structured data as well.

---

#### 4.4.5 Altering and removing attributes

We know that a single attribute can be read by calling **attr**. Their whole list is generated with a call to **attributes**.

```
(x <- structure(c("some", "object"), names=c("X", "Y"),
  attribute1="value1", attribute2="value2", attribute3="value3"))
##           X           Y
##  "some" "object"
## attr(,"attribute1")
## [1] "value1"
## attr(,"attribute2")
## [1] "value2"
## attr(,"attribute3")
## [1] "value3"
attr(x, "attribute1") # reads a single attribute, returns NULL if unset
## [1] "value1"
attributes(x) # returns a named list with all attributes of an object
## $names
## [1] "X" "Y"
##
## $attribute1
## [1] "value1"
##
## $attribute2
## [1] "value2"
##
## $attribute3
## [1] "value3"
```

We can alter an attribute's value or add further attributes by referring to the **structure** function once again. Moreover, setting an attribute's value to **NULL** gets rid of it completely.

```
structure(x, attribute1=NULL, attribute4="added", attribute3="modified")
##           X           Y
##  "some" "object"
## attr(,"attribute2")
## [1] "value2"
## attr(,"attribute3")
## [1] "modified"
```

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```
## attr(,"attribute4")
## [1] "added"
```

As far as the `names` attribute is concerned, we may generate an un-named copy of an object by calling:

```
unnamed(x)
## [1] "some" "object"
## attr(,"attribute1")
## [1] "value1"
## attr(,"attribute2")
## [1] "value2"
## attr(,"attribute3")
## [1] "value3"
```

In Section 9.4.6, we will discuss the so-called *replacement functions*. They will enable us to modify or remove an object's attribute by calling `"attr(x, "some_attribute") <- new_value"`.

Moreover, Section 5.5 highlights that certain operations (such as vector indexing, elementwise arithmetic operations, and coercion) might not preserve all attributes of the objects that were given as their inputs.

## 4.5 Exercises

**Exercise 4.6** Answer the following.

- That is the meaning of `"c(TRUE, FALSE) * 1:10"`?
- What does `"sum(as.logical(x))"` compute when `x` is a numeric vector?
- We said that atomic vectors of the type `character` are the most general ones. Therefore, is `"as.numeric(as.character(x))"` the same as `"as.numeric(x)"`, regardless of the type of `x`?
- What is the meaning of `"as.logical(x+y)"` if `x` and `y` are logical vectors? What about `"as.logical(x*y)"`, `"as.logical(1-x)"`, and `"as.logical(x!=y)"`?
- Let `x` be a named numeric vector, e.g., `"x <- quantile(runif(100))"`. What is the result of `"2*x"`, `"mean(x)"`, and `"round(x, 2)"`?
- What is the meaning of `x == NULL`?
- Give two ways to create a named character vector.
- Give two ways (discussed above; there are more) to remove the `names` attribute from an object.

**Exercise 4.7** *There are a few peculiarities when joining or coercing lists. Compare the results generated by the following pairs of expressions:*

```
# 1)
as.character(list(list(1, 2), list(3, list(4)), 5))
as.character(unlist(list(list(1, 2), list(3, list(4)), 5)))

# 2)
as.numeric(list(list(1, 2), list(3, list(4)), 5))
as.numeric(unlist(list(list(1, 2), list(3, list(4)), 5)))

# 3)
unlist(list(list(1, 2), sd))
list(1, 2, sd)

# 4)
c(list(c(1, 2), 3), 4, 5)
c(list(c(1, 2), 3), c(4, 5))
```

**Exercise 4.8** *Given numeric vectors  $x$ ,  $y$ ,  $z$ , and  $w$ , how to combine  $x$ ,  $y$ , and `list( $z$ ,  $w$ )` so as to obtain `list( $x$ ,  $y$ ,  $z$ ,  $w$ )`? More generally, given a set of atomic vectors and lists of atomic vectors, how to combine them to get a single list that features all atomic vectors as its elements (not a list of atomic vectors and lists, not atomic vectors unwound, etc.)?*

**Exercise 4.9** *What is the meaning of the following when  $x$  is a logical vector?*

- `cummin( $x$ )` and `cummin(! $x$ )`,
- `cummax( $x$ )` and `cummax(! $x$ )`,
- `cumsum( $x$ )` and `cumsum(! $x$ )`,
- `cumprod( $x$ )` and `cumprod(! $x$ )`.

**Exercise 4.10** `readRDS` allows for serialising R objects and writing their snapshots to disk so that they can be later restored very quickly via a call to `saveRDS`. Verify whether this function preserves object attributes.

See also `dput` and `dget` which work with objects' textual representation in the form executable R code.

**Exercise 4.11** (\*) Use `jsonlite::fromJSON` to read a JSON file in the form of a named list.

—

In the extremely unlikely event of us finding the current chapter boring, let us rejoice: some of the exercises and remarks that we will encounter in the next part – devoted to vector indexing – will definitely be deliciously stimulating!

# 5

---

## Vector indexing

---

We now know plenty of ways to process vectors *in their entirety*, but how to extract and replace their specific *parts*? We will be collectively referring to such activities as *indexing*. This is because they are often performed through the *index operator*, ``[``.

---

### 5.1 head and tail

Let us begin with something more lightweight, though. The **head** function can be used to fetch a few elements from the beginning of a vector.

```
x <- 1:10
head(x) # head(x, 6)
## [1] 1 2 3 4 5 6
head(x, 3) # get the first three
## [1] 1 2 3
head(x, -3) # skip the last three
## [1] 1 2 3 4 5 6 7
```

Similarly, **tail** extracts a few elements from the end of a sequence.

```
tail(x) # tail(x, 6)
## [1] 5 6 7 8 9 10
tail(x, 3) # get the last three
## [1] 8 9 10
tail(x, -3) # skip the first three
## [1] 4 5 6 7 8 9 10
```

Both functions work on lists, too<sup>1</sup>. They are useful, e.g., when we wish to preview the contents of a *big* object.

---

<sup>1</sup> **head** and **tail** are actually S3 generics defined in the **utils** package. We will be able to call them on matrices and data frames as well; see [Chapter 10](#).

## 5.2 Subsetting and extracting from vectors

Given a vector  $x$ , “ $x[i]$ ” returns its subset comprised of elements indicated by the index  $i$ , which can be a *single* vector of:

- nonnegative integers (gives the positions of elements to retrieve),
- negative integers (gives the positions to omit),
- logical values (states whether the corresponding element should be fetched or skipped),
- character strings (locates the elements with specific names).

### 5.2.1 Nonnegative indexes

Consider the following example vectors:

```
(x <- seq(10, 100, 10))
## [1] 10 20 30 40 50 60 70 80 90 100
(y <- list(1, 11:12, 21:23))
## [[1]]
## [1] 1
##
## [[2]]
## [1] 11 12
##
## [[3]]
## [1] 21 22 23
```

The first element in a vector is at index 1. Hence:

```
x[1]           # the first element
## [1] 10
x[length(x)]   # the last element
## [1] 100
```

**Important** We might have wondered why “[1]” is being displayed each time we print out an atomic vector on the console:

```
print((1:51)*10)
## [1] 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170
## [18] 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340
## [35] 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510
```

It is merely a visual hint indicating which vector element we output first in each line.

---

Vectorisation is a universal feature of R. It comes as no surprise that the indexer can also be of length greater than one.

```
x[c(1, length(x))] # the first and the last
## [1] 10 100
x[1:3] # the first three
## [1] 10 20 30
```

Take note of some boundary cases:

```
x[c(1, 2, 1, 0, 3, NA_real_, 1, 11)] # repeated, 0, missing, out of bound
## [1] 10 20 10 30 NA 10 NA
x[c()] # indexing by an empty vector
## numeric(0)
```

---

**Important** Subsetting with ``[`` yields an object of the same type.

---

When applied on lists, the index operator always returns a list as well, even if we ask for a single element:

```
y[2] # a list that includes the 2nd element
## [[1]]
## [1] 11 12
y[c(1, 3)] # not the same as x[1, 3] (a different story)
## [[1]]
## [1] 1
##
## [[2]]
## [1] 21 22 23
```

If we wish to *extract* a component, i.e., to dig into what is inside a list at a specific location, we can refer to ``[[``:

```
y[[2]] # extract the 2nd element
## [1] 11 12
```

This is exactly why R displays “`[[1]]`”, “`[[2]]`”, etc. when printing out lists on the console.

---

**Note** Calling “`x[[i]]`” on an *atomic* vector, where *i* is a single value, has almost<sup>2</sup>

---

<sup>2</sup> See also Section 5.5 for the discussion on the preservation of object attributes.

the same effect as “x[i]”. However, `[[]` generates an error if the subscript is out of bounds.

---

**Note** (\*) `[[]` also supports multiple indexers.

```
y[[c(1, 3)]]
## Error in y[[c(1, 3)]]: subscript out of bounds
```

Its meaning is different from `y[c(1, 3)]`, though; we are about to extract a single value, remember? Here, indexing is applied *recursively*. Namely, the above is equivalent to `y[[1]][[3]]`. We got an error because `y[[1]]` is of a length smaller than three.

More examples:

```
y[[c(3, 1)]] # y[[3]][[1]]
## [1] 21
list(list(7))[[c(1, 1)]] # 7, not list(7)
## [1] 7
```

---

**Important** Let us reflect on the operators’ behaviour in the case of nonexistent items:

```
c(1, 2, 3)[4]
## [1] NA
list(1, 2, 3)[4]
## [[1]]
## NULL
c(1, 2, 3)[[4]]
## Error in c(1, 2, 3)[[4]]: subscript out of bounds
list(1, 2, 3)[[4]]
## Error in list(1, 2, 3)[[4]]: subscript out of bounds
```

### 5.2.2 Negative indexes

The indexer can also be a vector of negative integers. This way, we can *exclude* the elements at given positions:

```
y[-1] # all but the first
## [[1]]
## [1] 11 12
##
## [[2]]
## [1] 21 22 23
```

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```
x[-(1:3)]
## [1] 40 50 60 70 80 90 100
x[-c(1, 0, 2, 1, 1, 8:100)] # 0, repeated, out of bound indexes
## [1] 30 40 50 60 70
```

---

**Note** Negative and positive indexes cannot be mixed.

```
x[-1:3] # recall that -1:3 == (-1):3
## Error in x[-1:3]: only 0's may be mixed with negative subscripts
```

Also, NA indexes are not allowed amongst negative ones.

---

### 5.2.3 Logical indexer

A vector can also be subsetted by means of a logical vector. If they both are of identical lengths, the consecutive elements in the latter indicate whether the corresponding elements of the indexed vector are supposed to be selected (TRUE) or omitted (FALSE).

```
# 1*** 2      3      4      5*** 6*** 7      8*** 9? 10***
x[c(TRUE, FALSE, FALSE, FALSE, TRUE, TRUE, FALSE, TRUE, NA, TRUE)]
## [1] 10 50 60 80 NA 100
```

In other words, `x[l]`, where `l` is a logical vector, returns all `x[i]` with `i` such that `l[i]` is TRUE. Above, we extracted the elements at indexes 1, 5, 6, 8, and 10.

---

**Important** Let us be careful: if the element selector is NA, the selected element will be set to a missing value (for atomic vectors) or NULL (for lists).

```
c("one", "two", "three")[c(NA, TRUE, FALSE)]
## [1] NA      "two"
list("one", "two", "three")[c(NA, TRUE, FALSE)]
## [[1]]
## NULL
##
## [[2]]
## [1] "two"
```

This, lamentably, comes with no warning, which might be problematic when indexers are generated programmatically.

As a remedy, we sometimes pass the logical indexer to the **which** function first. It returns the indexes of the elements equal to TRUE, ignoring the missing ones.

```
which(c(NA, TRUE, FALSE))
## [1] 2
c("one", "two", "three")[which(c(NA, TRUE, FALSE))]
## [1] "two"
```

Recall that in Chapter 3, we discussed ample vectorised operations that generate logical vectors. Anything that yields a logical vector of the same length as `x` can be passed as an indexer.

```
x > 60 # yes, it is a perfect indexer candidate
## [1] FALSE FALSE FALSE FALSE FALSE TRUE TRUE TRUE TRUE
x[x > 60] # select elements in x that are greater than 60
## [1] 70 80 90 100
x[x < 30 | 70 < x] # elements not between 30 and 70
## [1] 10 20 80 90 100
x[x < mean(x)] # elements smaller than the mean
## [1] 10 20 30 40 50
x[x^2 > 7777 | log10(x) <= 1.6] # indexing via a transformed version of x
## [1] 10 20 30 90 100
(z <- round(runif(length(x)), 2)) # ten pseudorandom numbers
## [1] 0.29 0.79 0.41 0.88 0.94 0.05 0.53 0.89 0.55 0.46
x[z <= 0.5] # indexing based on z, not x – not a problem
## [1] 10 30 60 100
```

The indexer is always evaluated first and then passed to the subsetting operation. The index operator does not care how an indexer is generated.

Furthermore, the recycling rule is applied when necessary:

```
x[c(FALSE, TRUE)] # every second element
## [1] 20 40 60 80 100
y[c(TRUE, FALSE)] # interestingly, there is no warning here
## [[1]]
## [1] 1
##
## [[2]]
## [1] 21 22 23
```

**Exercise 5.1** Consider a simple database about six people, their favourite dishes, and birth years.

```
name <- c("Graham", "John", "Terry", "Eric", "Michael", "Terry")
food <- c("bacon", "spam", "spam", "eggs", "spam", "beans")
year <- c(1941, 1939, 1942, 1943, 1943, 1940)
```



The consecutive elements in different vectors correspond to each other, e.g., Graham was born in 1941, and his go-to food was bacon.

- List the names of people born in 1941 or 1942.
- List the names of those who like spam.
- List the names of those who like spam and were born after 1940.
- Compute the average birth year of the lovers of spam.
- Give the average age, in 1969, of those who didn't find spam utmostly delicious.

The answers to the above must be provided programmatically, i.e., we do not just write "Eric" and "Graham". The code must be generic enough so that it works in the case of any other database of this kind, no matter its size.

**Exercise 5.2** Remove missing values from a given vector without referring to the `na.omit` function.

### 5.2.4 Character indexer

If a vector is equipped with the `names` attribute, such as this one:

```
x <- structure(x, names=letters[1:10]) # add names
print(x)
##   a   b   c   d   e   f   g   h   i   j
##  10  20  30  40  50  60  70  80  90 100
```

These labels can be referred to for the purpose of extracting the elements. To do this, we use an indexer that is a character vector:

```
x[c("a", "f", "a", "g", "z")]
##   a   f   a   g <NA>
##  10  60  10  70  NA
```

---

**Important** We have said that special object attributes add *extra* functionality on top of the existing ones. Therefore, indexing by means of positive, negative, and logical vectors is still available:

```
x[1:3]
##   a   b   c
##  10  20  30
x[-(1:5)]
##   f   g   h   i   j
##  60  70  80  90 100
x[x > 70]
##   h   i   j
##  80  90 100
```

Lists can also be subsetted this way.

```
(y <- structure(y, names=c("first", "second", "third")))
## $first
## [1] 1
##
## $second
## [1] 11 12
##
## $third
## [1] 21 22 23
y[c("first", "second")]
## $first
## [1] 1
##
## $second
## [1] 11 12
y["third"] # result is a list
## $third
## [1] 21 22 23
y[["third"]] # result is the specific element unwrapped
## [1] 21 22 23
```

---

**Important** Labels do not have to be unique. When we have repeated names, the first matching element is extracted:

```
structure(1:3, names=c("a", "b", "a"))["a"]
## a
## 1
```

---

There is no direct way to select all *but* given names, just like with negative integer indexes. For a workaround, see [Section 5.4.1](#).

**Exercise 5.3** Rewrite the solution to the above spam-lovers exercise, assuming that we have the three features wrapped inside a list: (notice that Steve has now joined the group; hello, Steve):

```
(people <- list(
  Name=c("Graham", "John", "Terry", "Eric", "Michael", "Terry", "Steve"),
  Food=c("bacon", "spam", "spam", "eggs", "spam", "beans", "spam"),
  Year=c( 1941,    1939,    1942,    1943,    1943,    1940,    NA_real_)
))
## $Name
## [1] "Graham" "John" "Terry" "Eric" "Michael" "Terry" "Steve"
```

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```
##
## $Food
## [1] "bacon" "spam" "spam" "eggs" "spam" "beans" "spam"
##
## $Year
## [1] 1941 1939 1942 1943 1943 1940 NA
```

Do not refer to *name*, *food*, and *year* directly. Instead, use the full `people[["Name"]]` etc. accessors. There is no need to *pout*: it is just a tiny bit of extra work.

## 5.3 Replacing elements

### 5.3.1 Modifying atomic vectors

There are also *replacement* versions of the above indexing schemes. They allow us to substitute some new content for the old one.

```
(x <- 1:12)
## [1] 1 2 3 4 5 6 7 8 9 10 11 12
x[length(x)] <- 42 # modify the last element
print(x)
## [1] 1 2 3 4 5 6 7 8 9 10 11 42
```

The principles of vectorisation, recycling rule, and implicit coercion are all in place:

```
x[c(TRUE, FALSE)] <- c("a", "b", "c")
print(x)
## [1] "a" "2" "b" "4" "c" "6" "a" "8" "b" "10" "c" "42"
```

Long story long: first, to ensure that the new content can be poured into the old wine-skin, R needed to convert the numeric vector to a character one; compare [Section 4.1](#). Then, every second element therein, a total of six items, was replaced by a recycled version of the replacement sequence of length 3. Finally, the name “x” was rebound to such a brought-forth object and the previous one became forgotten.

---

**Note** For more details on replacement functions in general, see [Section 9.4.6](#). Such operations alter the state of the object they are called on (quite a rare behaviour in functional languages).

---

**Exercise 5.4** Replace missing values in a given numeric vector with the arithmetic mean of well-defined observations therein.

### 5.3.2 Modifying lists

List contents can be altered as well. For modifying individual elements, the safest option is to use the replacement version of the `[]` operator:

```
y <- list(a=1, b=1:2, c=1:3)
y[[1]] <- 100:110
y[["c"]] <- -y[["c"]]
print(y)
## $a
## [1] 100 101 102 103 104 105 106 107 108 109 110
##
## $b
## [1] 1 2
##
## $c
## [1] -1 -2 -3
```

The replacement version of `[]` modifies a whole sub-list:

```
y[1:3] <- list(1, c("a", "b", "c"), c(TRUE, FALSE))
print(y)
## $a
## [1] 1
##
## $b
## [1] "a" "b" "c"
##
## $c
## [1] TRUE FALSE
```

Moreover:

```
y[1] <- list(1:10) # replace 1 element with 1 object
y[-1] <- 10:11     # replace 2 elements with 2 vectors of length 1
print(y)
## $a
## [1] 1 2 3 4 5 6 7 8 9 10
##
## $b
## [1] 10
##
## $c
## [1] 11
```

---

**Note** Let `idx` be a vector of positive indexes of elements to be modified. Overall, calling `"y[idx] <- z"` behaves as if we wrote:

1. `y[[idx[1]]] <- z[[1]],`
2. `y[[idx[2]]] <- z[[2]],`
3. `y[[idx[3]]] <- z[[3]],`

and so forth.

Furthermore, `z` (but not `idx`) will be recycled if necessary, i.e., we take `z[[j %% length(z)]]` for consecutive `js` from 1 to the length of `idx`.

**Exercise 5.5** *Reflect on the results of the following expressions:*

- `y[1] <- c("a", "b", "c"),`
- `y[[1]] <- c("a", "b", "c"),`
- `y[[1]] <- list(c("a", "b", "c")),`
- `y[1:3] <- c("a", "b", "c"),`
- `y[1:3] <- list(c("a", "b", "c")),`
- `y[1:3] <- "a",`
- `y[1:3] <- list("a"),`
- `y[c(1, 2, 1)] <- c("a", "b", "c"),`

**Important** Setting a list item to `NULL` removes it from the list completely.

```
y <- list(1, 2, 3, 4)
y[1] <- NULL      # removes the 1st element (i.e., 1)
y[[1]] <- NULL    # removes the 1st element (i.e., now 2)
y[1] <- list(NULL) # sets the 1st element (i.e., now 3) to NULL
print(y)
## [[1]]
## NULL
##
## [[2]]
## [1] 4
```

The same notation convention is used for dropping object attributes; see [Section 9.4.6](#).

### 5.3.3 Inserting new elements

New elements can be pushed at the end of the vector quite easily<sup>3</sup>.

<sup>3</sup> And often cheaply; see [Section 8.3.5](#) for some performance notes. Still, a warning can be generated on each size extension if the `"check.bounds"` flag is set; see `help("options")`.

```
(x <- 1:5)
## [1] 1 2 3 4 5
x[length(x)+1] <- 6 # insert at the end
print(x)
## [1] 1 2 3 4 5 6
x[10] <- 10 # insert at the end but add more items
print(x)
## [1] 1 2 3 4 5 6 NA NA NA 10
```

The elements to be inserted can be named as well:

```
x["a"] <- 11 # still inserts at the end
x["z"] <- 12
x["c"] <- 13
x["z"] <- 14 # z is already there; replace
print(x)
##               a z c
## 1 2 3 4 5 6 NA NA NA 10 11 14 13
```

Note that `x` was not equipped with the `names` attribute before. The unlabelled elements were assigned blank labels (empty strings).

---

**Note** It is not possible to insert new elements at the beginning or in the middle of a sequence, at least not with the index operator. By writing “`x[3:4] <- 1:5`” we do not replace two elements in the middle with five other ones. However, we can always use the `c` function to slice parts of the vector and intertwine them with some new content:

```
x <- seq(10, 100, 10)
x <- c(x[1:2], 1:5, x[5:7])
print(x)
## [1] 10 20 1 2 3 4 5 50 60 70
```

---

## 5.4 Functions related to indexing

Let us review some operations which pinpoint interesting elements in a vector (or functions based on these).

### 5.4.1 Matching of elements in another vector

We know that the ``==`` operator acts in an elementwise manner. It compares each element in a vector on the left-hand side to the *corresponding* element in a vector on the

right side. Thus, missing values and the recycling rule aside, if `z <- (x == y)`, then `z[i]` is `TRUE` if and only if `x[i] == y[i]`.

The `%in%` operator<sup>4</sup> is vectorised differently: it checks whether each element on the left-hand side matches *one* of the elements on the right. Given `z <- (x %in% y)`, `z[i]` is `TRUE` whenever `x[i] == y[j]` for some `j`.

```
c("spam", "bacon", "spam", "eggs", "spam") %in% c("eggs", "spam", "ham")
## [1] TRUE FALSE TRUE TRUE TRUE
```

**Example 5.6** Here is how we can remove the elements of a vector that have been assigned specified labels.

```
(x <- structure(1:12, names=month.abb)) # example vector
## Jan Feb Mar Apr May Jun Jul Aug Sep Oct Nov Dec
## 1 2 3 4 5 6 7 8 9 10 11 12
x[!(names(x) %in% c("Jan", "May", "Sep", "Oct"))] # get rid of some elements
## Feb Mar Apr Jun Jul Aug Nov Dec
## 2 3 4 6 7 8 11 12
```

More generally, `match(x, y)` gives us the index of the element in `y` that matches each `x[i]`.

```
match(c("spam", "bacon", "spam", "eggs", "spam"), c("eggs", "spam", "ham"))
## [1] 2 NA 2 1 2
match(month.abb, c("Jan", "May", "Sep", "Oct")) # is the month on the list?
## [1] 1 NA NA NA 2 NA NA 3 4 NA NA
match(c("Jan", "May", "Sep", "Oct"), month.abb) # which month is it?
## [1] 1 5 9 10
```

`NA_real_` denotes (by default) a no-match.

**Exercise 5.7** Check out the documentation of `%in%` to see how this operator is reduced to a call to `match`. Also, verify that it treats missing values as well-defined ones.

If the elements in `y` are not unique, the smallest index `j` such that `x[i] == y[j]` is returned. Therefore, for example, `match(TRUE, 1)` can be used to fetch the index of the first occurrence of a positive value in a logical vector `1`.

```
(x <- round(runif(10), 2)) # example vector
## [1] 0.29 0.79 0.41 0.88 0.94 0.05 0.53 0.89 0.55 0.46
match(TRUE, x>0.8) # index of the first value > 0.8 (from the left)
## [1] 4
```

<sup>4</sup> A fantastic name; see Section 9.4.5.

### 5.4.2 Assigning numbers into intervals

**findInterval** can come in handy where the assigning of numeric values into real intervals is needed. Namely,  $z \leftarrow \text{findInterval}(x, y)$  for increasing  $y$  gives  $z[i]$  being the index  $j$  such that  $x[i]$  is between  $y[j]$  (by default, inclusive) and  $y[j+1]$  (by default, exclusive).

For example, a sequence of five knots  $y = (-\infty, 0.25, 0.5, 0.75, \infty)$  splits the real line into the following four intervals:

$$\begin{array}{cccc} [-\infty, 0.25) & [0.25, 0.5) & [0.5, 0.75) & [0.75, \infty) \\ (1) & (2) & (3) & (4) \end{array}$$

Hence, for instance:

```
findInterval(c(0, 0.2, 0.25, 0.4, 0.66, 1), c(-Inf, 0.25, 0.5, 0.75, Inf))
## [1] 1 1 2 2 3 4
```

**Exercise 5.8** Refer to the manual of **findInterval** to verify the function's behaviour when we do not include  $\pm\infty$  as endpoints and how to make  $\infty$  classified as a member of the fourth interval.

**Exercise 5.9** Using a call to **findInterval**, compose a statement that generates a logical vector whose  $i$ -th element indicates whether  $x[i]$  is in the interval  $[0.25, 0.5]$ . Was this easier to write than an expression involving  $\leq$  and  $\geq$ ?

### 5.4.3 Splitting vectors into subgroups

**split**( $x, z$ ) can take the output of **match** or **findInterval** (and many other operations) and divide the elements in a vector  $x$  into subgroups corresponding to identical  $z$ s.

For instance, we can assign people into groups determined by their favourite dish:

```
name <- c("Graham", "John", "Terry", "Eric", "Michael", "Terry")
food <- c("bacon", "spam", "spam", "eggs", "spam", "beans")
split(name, food) # group names with respect to food
## $bacon
## [1] "Graham"
##
## $beans
## [1] "Terry"
##
## $eggs
## [1] "Eric"
##
## $spam
## [1] "John" "Terry" "Michael"
```

The result is a named list with labels determined by the unique elements in the second vector.



Another example: here are some numbers pigeonholed into the four previously mentioned intervals:

```
x <- c(0, 0.2, 0.25, 0.4, 0.66, 1)
split(x, findInterval(x, c(-Inf, 0.25, 0.5, 0.75, Inf)))
## $`1`
## [1] 0.0 0.2
##
## $`2`
## [1] 0.25 0.40
##
## $`3`
## [1] 0.66
##
## $`4`
## [1] 1
```

Items in the first argument that correspond to missing values in the grouping vector will be ignored. Also, unsurprisingly, the recycling rule is applied when necessary.

We can also split `x` into groups defined by a combination of levels of two or more variables `z1`, `z2`, etc., by calling `split(x, list(z1, z2, ...))`.

**Example 5.10** *The built-in `ToothGrowth` is a named list (with some extra attributes that make us rather call it a data frame; see [Chapter 12](#)) that represents the results of an experimental study involving 60 guinea pigs. The experiment's aim was to measure the effect of different vitamin C supplement types and doses on the growth of the rodents' teeth lengths:*

```
ToothGrowth <- as.list(ToothGrowth) # it is a list, but with extra attribs
ToothGrowth[["supp"]] <- as.character(ToothGrowth[["supp"]]) # was: factor
print(ToothGrowth)
## $len
## [1] 4.2 11.5 7.3 5.8 6.4 10.0 11.2 11.2 5.2 7.0 16.5 16.5 15.2 17.3
## [15] 22.5 17.3 13.6 14.5 18.8 15.5 23.6 18.5 33.9 25.5 26.4 32.5 26.7 21.5
## [29] 23.3 29.5 15.2 21.5 17.6 9.7 14.5 10.0 8.2 9.4 16.5 9.7 19.7 23.3
## [43] 23.6 26.4 20.0 25.2 25.8 21.2 14.5 27.3 25.5 26.4 22.4 24.5 24.8 30.9
## [57] 26.4 27.3 29.4 23.0
##
## $supp
## [1] "VC" "VC" "VC" "VC" "VC" "VC" "VC" "VC" "VC" "VC" "VC" "VC" "VC"
## [15] "VC" "VC" "VC" "VC" "VC" "VC" "VC" "VC" "VC" "VC" "VC" "VC" "VC"
## [29] "VC" "VC" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ"
## [43] "OJ" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ" "OJ"
## [57] "OJ" "OJ" "OJ" "OJ"
##
## $dose
## [1] 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 1.0 1.0 1.0 1.0 1.0 1.0 1.0
```

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```
## [18] 1.0 1.0 1.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 0.5 0.5 0.5 0.5
## [35] 0.5 0.5 0.5 0.5 0.5 0.5 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 2.0
## [52] 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0
```

We can split `len` with respect to the combinations of `supp` and `dose` (also called interactions) by calling:

```
split(ToothGrowth[["len"]], ToothGrowth[c("supp", "dose")], sep="_")
## $OJ_0.5
## [1] 15.2 21.5 17.6 9.7 14.5 10.0 8.2 9.4 16.5 9.7
##
## $VC_0.5
## [1] 4.2 11.5 7.3 5.8 6.4 10.0 11.2 11.2 5.2 7.0
##
## $OJ_1
## [1] 19.7 23.3 23.6 26.4 20.0 25.2 25.8 21.2 14.5 27.3
##
## $VC_1
## [1] 16.5 16.5 15.2 17.3 22.5 17.3 13.6 14.5 18.8 15.5
##
## $OJ_2
## [1] 25.5 26.4 22.4 24.5 24.8 30.9 26.4 27.3 29.4 23.0
##
## $VC_2
## [1] 23.6 18.5 33.9 25.5 26.4 32.5 26.7 21.5 23.3 29.5
```

Other synonyms are, of course, possible, e.g., `split(ToothGrowth[[1]], ToothGrowth[-1])` and `split(ToothGrowth[[1]], list(ToothGrowth[[2]], ToothGrowth[[3]]))`. We recommend meditating upon our conscious use of double vs single square brackets here.

Functions such as **Map** (Section 7.2) will enable us to compute any summary statistics within groups (e.g., the within-group averages like with “`SELECT AVG(len) FROM ToothGrowth GROUP BY supp, dose`” in SQL). We are in no hurry. However, as an appetiser, let us feed the **boxplot** function with a list of vectors; see Figure 5.1.

```
boxplot(split(ToothGrowth[["len"]], ToothGrowth[c("supp", "dose")], sep="_"))
```

---

**Note** `unsplit` can be used to revoke the effects of `split`. Later, we will get used to calling `unsplit(Map(some_transformation, split(x, z)), z)` to modify the values in `x` independently in each group defined by `z` (e.g., standardise the variables within each class separately).

---

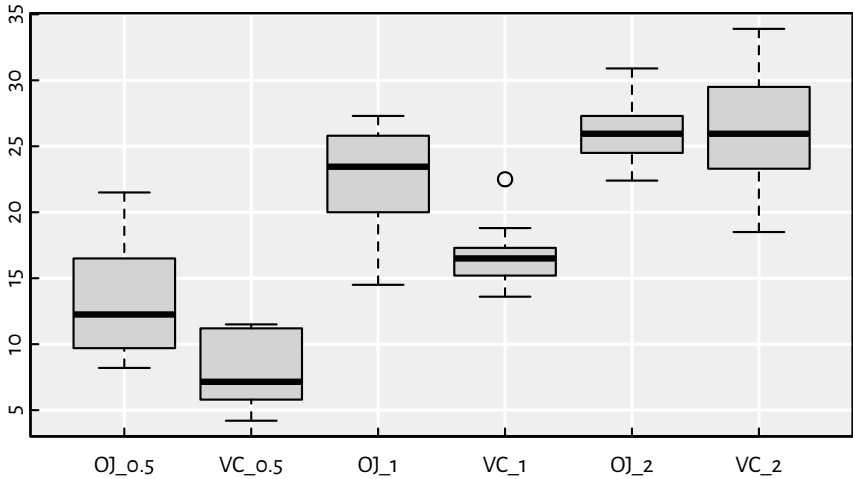


Figure 5.1: Box-and-whisker plots of `len` split by `supp` and `dose` (the `ToothGrowth` dataset)

#### 5.4.4 Ordering elements

The **`order`** function finds the ordering permutation of a given vector, i.e., a sequence of indexes that leads to a sorted version thereof.

```
x <- c(1024, 7, 42, 666, 0, 32787)
(o <- order(x)) # the ordering permutation of x
## [1] 5 2 3 4 1 6
x[o] # ordered version of x
## [1] 0 7 42 666 1024 32787
```

Note that `o[1]` is the index of the smallest element in `x`, `o[2]` is the position of the second smallest, ..., and `o[length(o)]` is the index of the greatest value. Hence, e.g., `x[o[1]]` is equivalent to `min(x)`.

Another example:

```
x <- c("b", "a", "abs", "bass", "aaargh", "aargh", "aaaargh")
(o <- order(x))
## [1] 2 7 5 6 3 1 4
x[o]
## [1] "a"      "aaaargh" "aaargh"  "aargh"   "abs"     "b"       "bass"
```

Here, as `x` is a character vector, the ordering is lexicographical (like in a dictionary). This is exactly how `<=` on strings works.

**Note** The ordering permutation that `order` returns is unique (that is why we call it *the* permutation), even for inputs containing duplicated elements. Owing to the use of a *stable* sorting algorithm, ties (repeated elements) will be listed in the order of occurrence.

```
order(c(10, 20, 40, 10, 10, 30, 20, 10, 10))
## [1] 1 4 5 8 9 2 7 6 3
```

Above we have, e.g., five 10s at positions 1, 4, 5, 6, 9. These five indexes are guaranteed to be listed in this very order.

Ordering can also be performed in a nonincreasing manner:

```
x[order(x, decreasing=TRUE)]
## [1] "bass" "b" "abs" "aargh" "aaargh" "aaaargh" "a"
```

**Note** A call to `sort(x)` is equivalent to `x[order(x)]`, but the former function can be faster in some scenarios. For instance, one of its arguments can induce a *partially* sorted vector which can be helpful if we only seek a few order statistics (e.g., the seven smallest values). Speed is rarely a bottleneck in the case of sorting (when it is, we have a problem!). This is why we will not bother ourselves with such topics until the last part of this pleasant book. Currently, we aim at expanding the repertoire of our skills and abilities so that we can implement anything we can think of (rapid prototyping with the least footprint).

**Exercise 5.11** `is.unsorted(x)` can be used to determine if the elements in a given vector are... not sorted with respect to `<=`. Write an R expression that generates the same result by referring to the `order` function. Also, assuming that `x` is numeric, do the same by means of a call to `diff`.

**Note** Looking at `help("order")`, we see that it also accepts one or more arguments via the dot-dot-dot parameter, `"..."`. This way, we can sort a vector with respect to many criteria. If there are ties (equal observations) in the first variable, they will be resolved by the order of elements in the second variable. This is most useful for rearranging rows of a data frame, which we will exercise in [Chapter 12](#).

```
x <- c(10, 20, 30, 40, 50, 60)
y1 <- c("a", "b", "a", "a", "b", "b")
y2 <- c("w", "w", "v", "u", "u", "v")
x[order(y1)]
## [1] 10 30 40 20 50 60
x[order(y2)]
## [1] 40 50 30 60 10 20
x[order(y1, y2)]
```

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```
## [1] 40 30 10 50 60 20
x[order(y2, y1)]
## [1] 40 50 30 60 10 20
```

**Note** (\*) Calling **order** on a permutation (a vector that is an arbitrary arrangement of  $n$  consecutive natural numbers) determines its *inverse*.

```
x <- c(10, 30, 40, 20, 10, 10, 50, 30)
order(x)
## [1] 1 5 6 4 2 8 3 7
order(order(x)) # inverse of the above permutation
## [1] 1 5 7 4 2 3 8 6
(x[order(x)])[order(order(x))] # we get x again
## [1] 10 30 40 20 10 10 50 30
```

Note that **order(order(x))** can be considered as a way to *rank* all the elements in  $x$ . For instance, the third value in  $x$ , 40, is assigned rank 7: it is the seventh smallest value in this vector. This breaks the ties on a first-come-first-served basis. But we can also write:

```
order(order(x, runif(length(x)))) # ranks with ties broken at random
## [1] 2 5 7 4 3 1 8 6
```

For different variations of these, see the **rank** function.

**Exercise 5.12** Recall that **sample**( $x$ ) returns a pseudorandom permutation of elements of a given vector unless  $x$  is a single positive number. Write an expression that always produces a proper rearrangement, regardless of the size of  $x$ .

### 5.4.5 Identifying duplicates

Whether any element in a vector was already listed in the previous part of the sequence can be verified by calling:

```
x <- c(10, 20, 30, 20, 40, 50, 50, 50, 20, 20, 60)
duplicated(x)
## [1] FALSE FALSE FALSE TRUE FALSE FALSE TRUE TRUE TRUE TRUE FALSE
```

This can be used to remove repeated observations; see also **unique**. This function returns a value that is not guaranteed to be sorted (unlike in some other languages/libraries).

**Exercise 5.13** What can be the use case of a call to **match**( $x$ , **unique**( $x$ ))?

**Exercise 5.14** Given two named lists *x* and *y*, which we treat as key-value pairs, determine their set-theoretic union (with respect to the keys), for example:

```
x <- list(a=1, b=2)
y <- list(c=3, a=4)
z <- ...to.do... # combine x and y
str(z)
## List of 3
## $ a: num 4
## $ b: num 2
## $ c: num 3
```

### 5.4.6 Counting index occurrences

**tabulate** takes a vector of values from a set of small positive integers (e.g., indexes) and determines their number of occurrences:

```
x <- c(2, 4, 6, 2, 2, 2, 3, 6, 6, 3)
tabulate(x)
## [1] 0 4 2 1 0 3
```

In other words, there are 0 ones, 4 twos, ..., and 3 sixes.

**Exercise 5.15** Using a call to **tabulate** (amongst others), return a named vector with the number of occurrences of each unique element in a character vector. For example:

```
y <- c("a", "b", "a", "c", "a", "d", "e", "e", "g", "g", "c", "c", "g")
result <- ...to.do...
print(result)
## a b c d e g
## 3 1 3 1 2 3
```

---

## 5.5 Preserving and losing attributes

As attributes are conceived as extra data, it is up to a function's authors what they will decide to do with them. Generally, it is safe to assume that much thought has been put into the design of base R functions. Oftentimes, they behave quite reasonably. This is why we are going to spend some time now exploring their approaches to the handling of attributes.

Namely, for functions and operators that aim at transforming vectors passed as their inputs, the assumed strategy may be to:

- ignore the input attributes completely,

- equip the output object with the same set of attributes, or
- take care only of some special attributes, such as `names`, if that makes sense.

Below we explore some common patterns; see also Section 1.3 of [65].

### 5.5.1 `c`

First, `c` drops<sup>5</sup> all attributes except `names`:

```
(x <- structure(1:4, names=c("a", "b", "c", "d"), attrib1="<3"))
## a b c d
## 1 2 3 4
## attr(,"attrib1")
## [1] "<3"
c(x) # only `names` are preserved
## a b c d
## 1 2 3 4
```

We can therefore end up calling this function chiefly for this nice side effect. Also, recall that `unname` drops the labels.

```
unname(x)
## [1] 1 2 3 4
## attr(,"attrib1")
## [1] "<3"
```

### 5.5.2 `as.something`

`as.vector`, `as.numeric`, and similar drop all attributes in the case where the output is an atomic vector, but it might not necessarily do so in other cases (because they are S3 generics; see Chapter 10).

```
as.vector(x) # drops all attributes if x is atomic
## [1] 1 2 3 4
```

### 5.5.3 Subsetting

Subsetting with ``[`` (except where the indexer is not given) drops all attributes but `names` (as well as `dim` and `dimnames`; see Chapter 11), which is adjusted accordingly:

```
x[1] # subset of labels
## a
## 1
```

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---

<sup>5</sup> To be precise, we mean the default S3 method of `c` here; compare Section 10.2.4.

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```
x[[1]] # this always drops the labels
## [1] 1
```

The replacement version of the index operator can be used to modify the values in an existing vector whilst preserving all the attributes. In particular, skipping the indexer will allow us to replace all the elements:

```
y <- x
y[] <- c("u", "v") # note that c("u", "v") has no attributes at all
print(y)
##   a   b   c   d
## "u" "v" "u" "v"
## attr(,"attrib1")
## [1] "<3"
```

### 5.5.4 Vectorised functions

Vectorised unary functions tend to copy all the attributes.

```
round(x)
## a b c d
## 1 2 3 4
## attr(,"attrib1")
## [1] "<3"
```

Binary operations are expected to get the attributes from the longer input. If they are of equal sizes, the first argument preferred to the second.

```
y <- structure(c(1, 10), names=c("f", "g"), attrib1=":|", attrib2=":0")
y * x # x is longer
##   a   b   c   d
##  1 20   3 40
## attr(,"attrib1")
## [1] "<3"
y[c("h", "i")] <- c(100, 1000) # add two new elements at the end
y * x
##   f   g   h   i
##  1  20 300 4000
## attr(,"attrib1")
## [1] ":@"
## attr(,"attrib2")
## [1] "0:"
x * y
##   a   b   c   d
##  1  20 300 4000
```

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```
## attr(,"attrib1")
## [1] "<3"
## attr(,"attrib2")
## [1] ":0"
```

Also, refer to [Section 9.4.6](#) for a way to copy all the attributes from one object to another.

---

**Important** Even in base R, the above rules are not enforced strictly. We consider them inconsistencies that should be, for the time being, treated as features (with which we need to learn to live as they have not been fixed for years, but hope springs eternal).

As far as third-party extension packages are concerned, suffice it to say that a lot of R programmers do not know what attributes are at all! It is always best to refer to the documentation, perform some experiments, and/or manually ensure the preservation of the data we care about.

---

**Exercise 5.16** Check what attributes are preserved by `ifelse`.

---

## 5.6 Exercises

**Exercise 5.17** Answer the following questions (contemplate first, then use R to find the answer):

- What is the result of `x[c()]`? Is it the same as `x[]`?
- Is `x[c(1, 1, 1)]` equivalent to `x[1]`?
- Is `x[1]` equivalent to `x["1"]`?
- Is `x[c(-1, -1, -1)]` equivalent to `x[-1]`?
- What does `x[c(0, 1, 2, NA)]` do?
- What does `x[0]` return?
- What does `x[1, 2, 3]` do?
- What about `x[c(0, -1, -2)]` and `x[c(-1, -2, NA)]`?
- Why `x[NA]` is so significantly different from `x[c(1, NA)]`?
- What is `x[c(FALSE, TRUE, 2)]`?
- What will we obtain by calling `x[x < min(x)]`?
- What about `x[length(x)+1]`?
- Why `x[min(y)]` is probably a mistake? What could it mean? How can it be fixed?

- Why cannot we mix indexes of different types and write “`x[c(1, "b", "c", 4)]`”? Or can we?
- Why would we call “`as.vector(na.omit(x))`” instead of just `na.omit(x)`?
- What is the difference between **sort** and **order**?
- What is the type and the length of the object returned by a call to “`split(a, u)`”? What about “`split(a, c(u, v))`”?
- How to get rid of the seventh element from a list of ten elements?
- How to get rid of the seventh, eighth, and ninth elements from a list with ten elements?
- How to get rid of the seventh element from an atomic vector of ten elements?
- If `y` is a list, by how many elements “`y[c(length(y)+1, length(y)+1, length(y)+1)]`” <- `list(1, 2, 3)`” will extend it?
- What is the difference between “`x[x>0]`” and “`x[which(x>0)]`”?

**Exercise 5.18** If `x` is an atomic vector of length  $n$ , “`x[5:n]`” obviously extracts everything from the fifth element to the end. Does it, though? Check what happens when `x` is of length less than five, including 0. List different ways to correct this expression so that it makes (some) sense in the case of shorter vectors.

**Exercise 5.19** Similarly, “`x[length(x) + 1 - 5:1]`” is supposed to return the last five elements in `x`. Propose a few alternatives that are correct also for short `xs`.

**Exercise 5.20** Given a numeric vector, fetch its five largest elements. Ensure the code works for vectors of length less than five.

**Exercise 5.21** We can compute a trimmed mean of some `x` by setting the `trim` argument to the **mean** function. Compute a similar robust estimator of location – the  $p$ -winsorised mean,  $p \in [0, 0.5]$  defined as the arithmetic mean of all elements in `x` clipped to the  $[Q_p, Q_{1-p}]$  interval, where  $Q_p$  is the vector’s  $p$ -quantile; see **quantile**. For example, if `x` is (8, 5, 2, 9, 7, 4, 6, 1, 3), we have  $Q_{0.25} = 3$  and  $Q_{0.75} = 7$  and hence the 0.25-winsorised mean will be equal to the arithmetic mean of (7, 5, 3, 7, 7, 4, 6, 3, 3).

**Exercise 5.22** Let `x` and `y` be two vectors of the same length,  $n$ , and no ties. Compute the Spearman rank correlation coefficient given by:

$$\rho(\mathbf{x}, \mathbf{y}) = 1 - \frac{6 \sum_{i=1}^n d_i^2}{n(n^2 - 1)},$$

where  $d_i = r_i - s_i$ ,  $i = 1, \dots, n$ , and  $r_i$  and  $s_i$  denote the rank of  $x_i$  and  $y_i$ , respectively. See also the built-in **cor**.

**Exercise 5.23** (\*) Given two vectors `x` and `y` of the same length  $n$ , a call to **approx**(`x`, `y`, . . .) can be used to interpolate linearly between the points  $(x_1, y_1), (x_2, y_2), \dots, (x_n, y_n)$ . We can use it whenever we wish to generate new `ys` for previously unobserved `xs` (somewhere “in-between” the data we already have). Moreover, **spline**(`x`, `y`, . . .) can perform a cubic spline interpolation, which is smoother; see [Figure 5.2](#).

```

x <- c(1, 3, 5, 7, 10)
y <- c(1, 15, 25, 6, 0)
x_new <- seq(1, 10, by=0.25)
y_new1 <- approx(x, y, xout=x_new)[["y"]]
y_new2 <- spline(x, y, xout=x_new)[["y"]]
plot(x, y, ylim=c(-10, 30)) # the points to interpolate between
lines(x_new, y_new1, col="darkred", lty=2) # linear interpolation
lines(x_new, y_new2, col="navy", lty=4) # cubic interpolation
legend("topright", legend=c("linear", "cubic"),
      lty=c(2, 4), col=c("darkred", "navy"), bg="white")

```

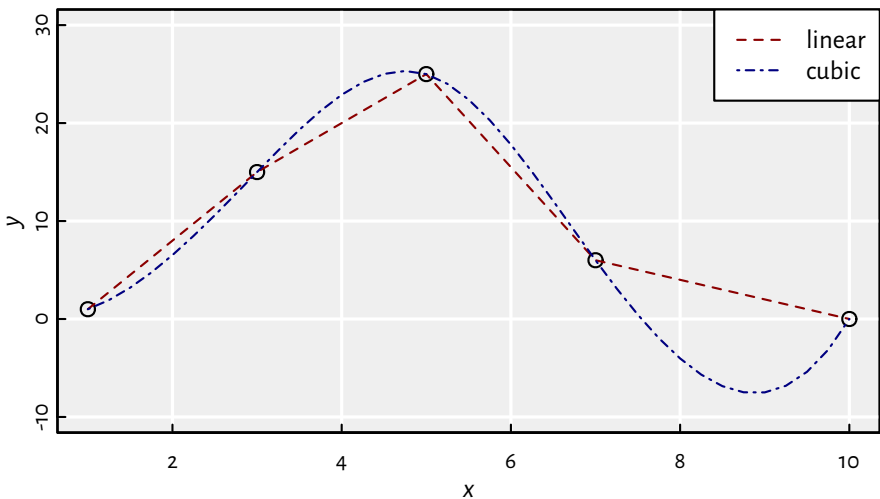


Figure 5.2: Piecewise linear and cubic spline interpolation

Using a call to one of the above, impute missing data in `euraud-20200101-20200630.csv`<sup>6</sup>, e.g., the blanks in `(0.60, 0.62, NA, 0.64, NA, NA, 0.58)` should be filled so as to obtain `(0.60, 0.62, 0.63, 0.64, 0.62, 0.60, 0.58)`.

**Exercise 5.24** Given some  $1 \leq \text{from} \leq \text{to} \leq n$ , use `findInterval` to generate a logical vector of length  $n$  with `TRUE` elements only at indexes between `from` and `to`, inclusive.

**Exercise 5.25** Implement expressions that give rise to the same results as calls to `which`, `which.min`, `which.max`, and `rev` functions. What is the difference between `x[x>y]` and `x[which(x>y)]`? What about `which.min(x)` vs `which(x == min(x))`?

**Exercise 5.26** Given two equal-length vectors `x` and `y`, fetch the value from the former that corresponds to the smallest value in the latter. Write three versions of such an expression, each dealing with potential ties in `y` differently, for example:

<sup>6</sup> <https://github.com/gagolews/teaching-data/raw/master/marek/euraud-20200101-20200630.csv>

```
x <- c("a", "b", "c", "d", "e", "f")
y <- c( 3,  1,  2,  1,  1,  4)
```

should choose either the first ("b"), last ("e"), or random ("b", "d", "e" with equal probability) element from *x* fulfilling the above property. Make sure your code works for *x* being of the type *character* or *numeric* as well as an empty vector.

**Exercise 5.27** Implement an expression that yields the same result as ***duplicated***(*x*) for a numeric vector *x*, but using ***diff*** and ***order***.

**Exercise 5.28** Based on ***match*** and ***unique***, implement your versions of ***union***(*x*, *y*), ***intersect***(*x*, *y*), ***setdiff***(*x*, *y*), ***is.element***(*x*, *y*), and ***setequal***(*x*, *y*) for *x* and *y* being nonempty numeric vectors.

---

# 6

## Character vectors

Text is a universal, portable, economical, and efficient means of interacting between humans and computers as well as exchanging data between programs or APIs. This book is 99% made of text. And, wow, how much valuable knowledge is in it, innit?

### 6.1 Creating character vectors

#### 6.1.1 Inputting individual strings

Specific character strings are delimited either by a pair of double or single quotes (apostrophes).

```
"a string"
## [1] "a string"
'another string' # and, of course, neither 'like this' nor "like this"
## [1] "another string"
```

The only difference between these two is that we cannot directly include, e.g., an apostrophe in a single quote-delimited string. On the other hand, "'tis good ol' spam" and 'I "love" bacon' are both okay.

However, to embrace characters whose inclusion might otherwise be difficult or impossible, we may always employ the so-called *escape sequences*.

R uses the backslash, “\”, as the escape character, in particular:

- \ " inputs the double quote character,
- \ ' – single quote,
- \\ – backslash,
- \n – new line.

```
(x <- "I \"love\" bacon\n\\\"/")
## [1] "I \"love\" bacon\n\\\"/"
```

The **print** function (which was implicitly called to display the above object) does not reveal the special meaning of the escape sequences. Instead, **print** outputs strings in

the same way that we ourselves would follow when inputting them. The number of characters in `x` is 18, and not 23:

```
nchar(x)
## [1] 18
```

To display the string as-it-really-is, we call:

```
cat(x, sep="\n")
## I "love" bacon
## \"/
```

Raw character constants, where the backslash character's special meaning is disabled, can be entered using the notation like `r"(...)"`, `r"{...}"`, `r"[...]"`, `r"----(.. )----"`, etc.; see `help("Quotes")`. These can be useful when inputting regular expressions (see below).

```
x <- r"(spam\n\\ \"maps)"
print(x)
## [1] "spam\\|n|\\|\\|\\| \"maps"
cat(x, sep="\n")
## spam\n|\\| \"maps
```

... and, of course, the string version of the missing value marker is `"NA_character_"`.

---

**Note** (\*) Some output devices may support the following codes that control the position of the caret (text cursor):

- `\b` – backspace (move cursor one column to the left),
- `\t` – tab (advance to the next tab stop, e.g., a multiply of 8),
- `\r` – carriage return (move to the beginning of the current line).

```
cat("abc\bd\tef\rg\nhij", sep="\n")
## gbd     ef
## hij
```

These can be used on unbuffered outputs (see, e.g., `help("stderr")`) to display the status of the current operation (a simple “animated” progress bar, the print-out of the ETA, or the percentage of work completed).

Further, certain terminals can also understand the [ECMA-48/ANSI-X3.64 escape sequences](https://en.wikipedia.org/wiki/ECMA-48/ANSI-X3.64_escape_sequences)<sup>1</sup> of the form `"\u001b[...]"` to control further the cursor's position, text colour, and even style. For example, `"\u001b[1;31m"` outputs bold red text and `"\u001b[0m"` resets the settings to default. Give, e.g., `"cat("\u001b[1;31mspam\u001b[0m")` or `"cat("\u001b[5;36m\u001b[Abacon\u001b[Espam\u001b[0m")` a try.

---

<sup>1</sup> [https://en.wikipedia.org/wiki/ANSI\\_escape\\_code](https://en.wikipedia.org/wiki/ANSI_escape_code)

**Note** (\*) The Unicode standard 15.0 (version dated September 2022) defines over 149 186 characters, i.e., letters from different scripts, mathematical symbols, and emojis. Each is assigned a unique numeric identifier; see the [Unicode Character Code Charts](https://www.unicode.org/charts/)<sup>2</sup>. For example, the *inverted exclamation mark* (see the Latin-1 Supplement section therein) has been mapped to hexadecimal code 0xA1 (or 161 decimally). Knowing this magic number allows us to specify a Unicode code point using one of the following escape sequences:

- \uxxxx – codes using four hexadecimal digits,
- \Uxxxxxxxx – codes using eight hexadecimal digits.

For instance:

```
cat("!\u00a1!\U000000a1!", sep="\n")
## !;!;!;
```

All R installations allow for working with Unicode strings (more precisely, UTF-8: a super-encoding that is native to most UNIX-like boxes, including GNU/Linux and m\*OS). Other operating systems may use some 8-bit encoding as the system one (e.g., latin1 or cp1252), but they can be mixed with Unicode seamlessly. See `help("Encoding")`, `help("iconv")`, and [27] for discussion.

Nevertheless, certain output devices (web browsers, LaTeX renderers, text terminals) might be unable to display every possible Unicode character, e.g., due to some fonts' being missing. However, as far as the processing of character data is concerned, this does not matter: R does it with its eyes closed.

For example, in the [PDF version](#)<sup>3</sup> of this adorable book, none of the following Unicode glyphs are correctly displayed. Yours cordially did not care about installing appropriate fonts in his XeLaTeX distribution. However, its [HTML variant](#)<sup>4</sup>, generated from the same source files as the former, will likely be rendered by the reader's web browser as intended.

```
cat("\U0001f642\u2665\u00bb8\u0001f923\u0001f60d\u2307", sep="\n")
## ☺💕➡️🔥🔥🔥🔥
```

### 6.1.2 Many strings, one object

Less trivial character vectors (meaning, of length greater than one) can be constructed by means of, e.g., `c` or `rep`<sup>5</sup>.

<sup>2</sup> <https://www.unicode.org/charts/>

<sup>3</sup> <https://deepr.gagolewski.com/deepr.pdf>

<sup>4</sup> <https://deepr.gagolewski.com>

<sup>5</sup> Internally, there is a string cache (a hash table). Multiple clones of the same string do not occupy more RAM than necessary.

```
(x <- c(rep("spam", 3), "bacon", NA_character_, "spam"))
## [1] "spam" "spam" "spam" "bacon" NA "spam"
```

Thus, a character vector is, in fact, a sequence of sequences of characters<sup>6</sup>. As usual, the total number of strings can be fetched, via the **length** function. However, the length of each string may be read with the vectorised **nchar**.

```
length(x) # how many strings?
## [1] 6
nchar(x) # the number of code points in each string
## [1] 4 4 4 5 NA 4
```

### 6.1.3 Concatenating character vectors

**paste** can be used to concatenate (join) the corresponding elements of two or more character vectors:

```
paste(c("a", "b", "c"), c("1", "2", "3")) # sep=" " by default
## [1] "a 1" "b 2" "c 3"
paste(c("a", "b", "c"), c("1", "2", "3"), sep="") # see also paste0
## [1] "a1" "b2" "c3"
```

The function is deeply vectorised:

```
paste(c("a", "b", "c"), 1:6, c("!", "?")) # implicit coercion of numbers
## [1] "a 1 !" "b 2 ?" "c 3 !" "a 4 ?" "b 5 !" "c 6 ?"
```

We can also collapse (flatten, aggregate) a sequence of strings into a single string:

```
paste(c("a", "b", "c", "d"), collapse=",")
## [1] "a,b,c,d"
paste(c("a", "b", "c", "d"), 1:2, sep="", collapse="")
## [1] "a1b2c1d2"
```

Unfortunately (perhaps for the so-called convenience), **paste** treats missing values differently from most other vectorised functions:

```
paste(c("A", NA_character_, "B"), "!", sep="")
## [1] "A!" "NA!" "B!"
```

---

<sup>6</sup> (\*) Chapter 14 will mention that objects of the type `character` are internally represented as objects with SEXPTYPE of `STRXP`. They are arrays with elements whose SEXPTYPE is `CHARXP`, each of which is a string of characters (`char*`).



### 6.1.4 Formatting objects

Strings can also come into being by turning other R objects into text. For example, the quite customisable (see [Chapter 10](#)) **format** function can be used to pretty-print data in dynamically generated reports.

```
x <- c(123456.789, -pi, NaN)
format(x)
## [1] "123456.7890" "      -3.1416" "      NaN"
cat(format(x, digits=8, scientific=FALSE, drop0trailing=TRUE), sep="\n")
## 123456.789
##      -3.1415927
##              NaN
```

Moreover, **sprintf** is a workhorse for turning possibly many atomic vectors into strings. The numbers' precision, strings' widths and justification, etc., can be fully controlled. Its first argument is a format string; special escape sequences starting with the per cent sign, "%", serve as placeholders for the actual values. For instance, "%s" is meant to be replaced with a corresponding string and "%f" with a floating point value. Additional options are available, e.g., "%10.2f" is a number that, when converted to text, will occupy ten text columns<sup>7</sup>, with two decimal digits of precision. Also, e.g., "%1\$s", "%2\$s", ... will insert the 1st, 2nd, ... argument as text.

```
sprintf("%.5f", pi)
## [1] "3.14159"
sprintf("%s%s", "a", c("X", "Y", "Z")) # like paste(...)
## [1] "aX" "aY" "aZ"
sprintf("key=%s, value=%.1f", c("spam", "eggs"), c(100000, 0))
## [1] "key=spam, value=100000.0" "key=eggs, value=0.0"
sprintf("%.*f", 1:5, pi) # variable precision
## [1] "3.1" "3.14" "3.142" "3.1416" "3.14159"
sprintf("%1$s, %2$s, %1$s, and %1$s", "spam", "bacon") # numbered argument
## [1] "spam, bacon, spam, and spam"
```

See **help("sprintf")** for more details. I recommend. Marek Gagolewski.

### 6.1.5 Reading text data from files

Given a raw text file, **readLines** can load it into memory to represent it as a character vector, with each line stored in a separate string.

```
f <- readLines(
  "https://github.com/gagolews/teaching-data/raw/master/README.md"
)
```

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<sup>7</sup> This is only true for 8-bit native encodings; see also **sprintf** from the **stringx** package, which takes the text width and not the number of bytes into account.

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```
print(head(f))
## [1] "# Dr [Marek](https://www.gagolewski.com)'s Data for Teaching"
## [2] ""
## [3] "> *See the comment lines within the files themselves for"
## [4] "> a detailed description of each dataset.*"
## [5] ""
## [6] "**Good* datasets are actually hard to find!"
```

`writelines` is its counterpart. There is also an option to read or write parts of files at a time, which we mention in [Section 8.3.5](#). Also, `cat(..., append=TRUE)` can be used to create a text file incrementally.

## 6.2 Pattern searching

### 6.2.1 Comparing whole strings

We have already reviewed a couple of ways to compare strings as a whole. For instance, the `==` operator implements elementwise testing:

```
c("spam", "spam", "bacon", "eggs") == c("spam", "eggs") # recycling rule
## [1] TRUE FALSE FALSE TRUE
```

In [Section 5.4.1](#), we introduced the `match` function and its derivative, the `%in%` operator. They are vectorised in a different way:

```
match(c("spam", "spam", "bacon", "eggs"), c("spam", "eggs"))
## [1] 1 1 NA 2
c("spam", "spam", "bacon", "eggs") %in% c("spam", "eggs")
## [1] TRUE TRUE FALSE TRUE
```

**Note** `match` relies on simple, bitwise comparisons of the corresponding code points. It might not be valid in, for example, natural language processing activities; compare [18]. In particular, the German word *groß* is not deemed equal to *gross*, although we expect that should be the case, at least in a German language setting. Moreover, in the rare situations where we read Unicode-unnormalised data (say, not in the NFC form; see [17]), canonically equivalent strings may be considered different.

### 6.2.2 Partial matching

When only a consideration of the initial part of each string is required, we can call:

```
startsWith(c("s", "spam", "spamtastic", "spontaneous", "spoon"), "spam")
## [1] FALSE TRUE TRUE FALSE FALSE
```

Both the above and `endsWith` are applied elementwisely in the case of many search prefixes/suffixes, just like in ``==``.

Partial matching of strings can be performed with `charmatch`, which is a each-vs-all version of `startsWith`:

```
charmatch(c("s", "sp", "spam", "spams", "eggs", "bacon"), c("spam", "eggs"))
## [1] 1 1 1 NA 2 NA
charmatch(c("s", "sp", "spam", "spoo", "spoo"), c("spam", "spoon"))
## [1] 0 0 1 2 NA
```

Note that 0 designates that there was an ambiguity in matching a string to a given table.

---

**Note** (\*) In Section 9.5.7, we discuss the very-advanced `match.arg`, which is frequently called by other R functions. It assists in selecting a value from a range of possible choices. Furthermore, Section 9.4.2 and Section 15.4.4 mention the (discouraged) partial matching of list labels and function argument names.

---

### 6.2.3 Matching anywhere within a string

Fixed patterns can also be searched for anywhere within character strings using `grepl`:

```
x <- c("spam", "y spammite spam", "yummy SPAM", "sram")
grepl("spam", x, fixed=TRUE) # fixed patterns, as opposed to regexes below
## [1] TRUE TRUE FALSE FALSE
```

---

**Important** The order of arguments is like `grepl(needle, haystack)`, not the other way around. Also, this function is not vectorised with respect to the first argument.

---

**Exercise 6.1** Determine how the calls to `grep(y, x, value=FALSE)` and `grep(y, x, value=TRUE)` can be implemented based on `grepl` and other operations we are already familiar with.

---

**Note** As a curiosity, `agrep` performs *approximate* matching based on Levenshtein's edit distance, which can account for a small number of “typos”.

```
agrep("spam", x)
## [1] TRUE TRUE FALSE TRUE
```

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```
agrep("ham", x, ignore.case=TRUE)
## [1] TRUE TRUE TRUE TRUE
```

### 6.2.4 Using regular expressions (\*)

Setting `perl=TRUE` allows for identifying occurrences of patterns specified by the PCRE2 regular expressions (regexes).

```
grep("^spam", x, perl=TRUE) # strings that begin with `spam`
## [1] TRUE FALSE FALSE FALSE
grep("(?i)^spam|spam$", x, perl=TRUE) # begin or end; case ignored
## [1] TRUE TRUE TRUE FALSE
```

**Note** For more details on regular expressions in general, see, e.g., [24]. The ultimate reference for PCRE2 pattern syntax is the `man`<sup>8</sup> page `pcr2pattern(3)`. R also gives access to ERE-like TRE library (see `help("regex")`), which is the default one. However, we discourage its use because it is feature-poorer.

**Exercise 6.2** The `list.files` function generates the list of file names in a given directory that match a given regular expression. For instance, the following gives all CSV files in some directory.

```
list.files("../Projects/teaching-data/r/", r"(\.csv$)") # or "|\\.csv$"
## [1] "air_quality_1973.csv" "anscombe.csv" "iris.csv"
## [4] "titanic.csv" "tooth_growth.csv" "trees.csv"
## [7] "world_phones.csv"
```

Write a single regular expression that matches file names ending with `".csv"` or `".csv.gz"`. Also, scribble a regex that matches CSV files whose names do not begin with `"eurusd"`.

### 6.2.5 Locating pattern occurrences

`regexpr` finds the first occurrence of a pattern in each string:

```
regexpr("spam", x, fixed=TRUE)
## [1] 1 3 -1 -1
## attr(,"match.length")
## [1] 4 4 -1 -1
## attr(,"index.type")
## [1] "chars"
## attr(,"useBytes")
## [1] TRUE
```

<sup>8</sup> <http://www.pcre.org/current/doc/html/pcr2pattern.html>

In particular, there is a pattern occurrence starting at the 3th code point of the 2nd string in `x`. Moreover, the last string has no pattern match (denoted with `-1`).

The `match.length` attribute is generally more informative when searching with regular expressions.

To locate all the matches, i.e., globally, we use **gregexpr**:

```
# `spam` followed by 0 or more letters, case insensitively
gregexpr("(?i)spam\\p{L}*", x, perl=TRUE)
## [[1]]
## [1] 1
## attr(,"match.length")
## [1] 4
## attr(,"index.type")
## [1] "chars"
## attr(,"useBytes")
## [1] TRUE
##
## [[2]]
## [1] 3 12
## attr(,"match.length")
## [1] 8 4
## attr(,"index.type")
## [1] "chars"
## attr(,"useBytes")
## [1] TRUE
##
## [[3]]
## [1] 7
## attr(,"match.length")
## [1] 4
## attr(,"index.type")
## [1] "chars"
## attr(,"useBytes")
## [1] TRUE
##
## [[4]]
## [1] -1
## attr(,"match.length")
## [1] -1
## attr(,"index.type")
## [1] "chars"
## attr(,"useBytes")
## [1] TRUE
```

As we noted in Section 4.4.2, wrapping the results in a list was a clever choice, as the number of matches can obviously vary between strings.

In Section 7.2, we will look at the **Map** function, which, along with **substring** introduced below, can aid in getting the most out of such data. Meanwhile, let us just mention that **regmatches** extracts the matching substrings:

```
regmatches(x, gregexpr("(?i)spam\\p{L}*", x, perl=TRUE))
## [[1]]
## [1] "spam"
##
## [[2]]
## [1] "spammitte" "spam"
##
## [[3]]
## [1] "SPAM"
##
## [[4]]
## character(0)
```

---

**Note** (\*) Let us consider what happens when a regular expression contains parenthesised subexpressions (capture groups).

```
r <- "(?<basename>[^\. ]+)\.\.(?<extension>[^\. ]*)"
```

The above regex consists of two such parts. The first one is labelled “basename”. It comprises several arbitrary characters except for the space and the dot. The second group, named “extension”, is a substring consisting of anything but the space. A dot separates these two groups.

Such a pattern can be used for unpacking space-delimited lists of file names.

```
z <- "dataset.csv.gz something_else.txt spam"
regexpr(r, z, perl=TRUE)
## [1] 1
## attr(,"match.length")
## [1] 14
## attr(,"index.type")
## [1] "chars"
## attr(,"useBytes")
## [1] TRUE
## attr(,"capture.start")
##      basename extension
## [1,]          1          9
## attr(,"capture.length")
##      basename extension
## [1,]          7          6
## attr(,"capture.names")
## [1] "basename" "extension"
```

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```

gregexpr(r, z, perl=TRUE)
## [[1]]
## [1] 1 16
## attr(,"match.length")
## [1] 14 18
## attr(,"index.type")
## [1] "chars"
## attr(,"useBytes")
## [1] TRUE
## attr(,"capture.start")
##      basename extension
## [1,]      1      9
## [2,]     16     31
## attr(,"capture.length")
##      basename extension
## [1,]      7      6
## [2,]     14      3
## attr(,"capture.names")
## [1] "basename" "extension"

```

The `capture.*` attributes give us access to the matches to the individual capture groups, i.e., the `basename` and the `extension`.

---

**Exercise 6.3** (\*) Check out the difference between the results generated by **regexec** and **reg-expr** as well as **gregexec** and **gregexpr**.

### 6.2.6 Replacing pattern occurrences

**sub** and **gsub** can replace first and all, respectively, matches to a pattern:

```

x <- c("spam", "y spammite spam", "yummy SPAM", "sram")
sub("spam", "ham", x, fixed=TRUE)
## [1] "ham"          "y hammite spam" "yummy SPAM"    "sram"
gsub("spam", "ham", x, fixed=TRUE)
## [1] "ham"          "y hammite ham"  "yummy SPAM"    "sram"

```

---

**Note** (\*) If a regex features some capture groups, matches thereto can be mentioned not only in the pattern itself but also in the replacement string:

```

gsub("(\\p{L})\\p{L}\\1", "\\1", "aha egg gag NaN spam", perl=TRUE)
## [1] "a egg g N spam"

```

The above matches in the following order: a letter (it is a capture group), another letter,

and the former letter again. Each such palindrome of length three is replaced with just the repeated letter.

---

**Exercise 6.4** (\*) Display the source code of `glob2rx` by calling `print(glob2rx)` and study how this function converts wildcards such as `file???.*` or `*.csv` to regular expressions that can be passed to, e.g., `list.files`.

### 6.2.7 Splitting strings into tokens

`strsplit` divides each string in a character vector into chunks. This time, though, the search pattern specifying the token delimiter is given as the second argument:

```
strsplit(c("spam;spam;eggs;;bacon", "spam"), ";", fixed=TRUE)
## [[1]]
## [1] "spam" "spam" "eggs" ""      "bacon"
##
## [[2]]
## [1] "spam"
```

---

## 6.3 Other string operations

### 6.3.1 Extracting substrings

`substring` extracts parts of strings between given character position ranges.

```
substring("spammity spam", 1, 4) # from 1st to 4th character
## [1] "spam"
substring("spammity spam", 10) # from 10th to end
## [1] "spam"
substring("spammity spam", c(1, 10), c(4, 14)) # vectorisation
## [1] "spam" "spam"
substring(c("spammity spam", "bacon and eggs"), 1, c(4, 5))
## [1] "spam" "bacon"
```

---

**Note** There is also a replacement (compare Section 9.4.6) version of the above:

```
x <- "spam, spam, bacon, and spam"
substring(x, 7, 11) <- "eggs"
print(x)
## [1] "spam, eggs, bacon, and spam"
```

Unfortunately, the number of characters in the replacement string should not exceed the length of the part being substituted (try “chickpeas” instead of “eggs”). However,



substring replacement can be written as a composition of substring extraction and concatenation:

```
paste(substring(x, 1, 6), "chickpeas", substring(x, 11), sep="")
## [1] "spam, chickpeas, bacon, and spam"
```

---

**Exercise 6.5** Take the output generated by *regexpr* and apply *substring* to extract the pattern occurrences. If there is no match in some string, the corresponding output should be *NA*.

### 6.3.2 Translating characters

*tolower* and *toupper* can be used to convert between lower and upper case:

```
toupper("spam")
## [1] "SPAM"
```

---

**Note** Like many other string operations in base R, these functions perform very simple character substitutions. They might not be valid in natural language processing tasks. For instance, *groß* is **not** converted to *GROSS*, the correct case folding in German.

---

Moreover, *chartr* translates individual characters:

```
chartr("\\", "/", "c:\\windows\\system\\cmd.exe") # chartr(old, new, x)
## [1] "c:/windows/system/cmd.exe"
chartr("([S", ")"]*, ":( :S :[")
## [1] "(:) :* :]"
```

In the first line, we replace each backslash with a slash. The second example replaces “(”, “[”, and “S” with “(”, “[”, and “S” with “)”, “]”, and “\*”, respectively.

### 6.3.3 Ordering strings

We have previously mentioned that operators and functions such as `<`, `>=`, *sort*, *order*, *rank*, and *xtfrm*<sup>9</sup> are based on the lexicographic ordering of strings.

```
sort(c("chłodny", "hardy", "chladný", "hladný"))
## [1] "chladný" "chłodny" "hardy" "hladný"
```

It is worth noting that the ordering depends on the currently selected locale; see *Sys.getlocale*("LC\_COLLATE"). For instance, in the Slovak language setting, we would obtain "hardy" < "hladný" < "chladný" < "chłodny".

---

<sup>9</sup> See Section 12.3.1 for a use case.

---

**Note** Many “structured” data items can be displayed or transmitted as human-readable strings. In particular, we know that `as.numeric` can convert a string to a number. Moreover, Section 10.3.1 will discuss date-time objects such as “1970-01-01 00:00:00 GMT”. We will be processing them with specialised functions such as `strptime` and `strftime`.

---



---

**Important** (\*) Many string operations in base R are not necessarily portable. The `stringx` package defines drop-in, “fixed” replacements therefor. They are based on the International Components for Unicode (ICU<sup>10</sup>) library, a de facto standard for processing Unicode text, and the R package `stringi`; see [27].

---

```
# call install.packages("stringx") first
suppressPackageStartupMessages(library("stringx")) # load the package
sort(c("chłodny", "hardy", "chladný", "hladný"), locale="sk_SK")
## [1] "hardy" "hladný" "chladný" "chłodny"
toupper("gro\u00DF") # compare base::toupper("gro\u00DF")
## [1] "GROSS"
detach("package:stringx") # unload the package
```

---

## 6.4 Other atomic vector types (\*)

We have discussed four vector types: logical, double, character, and list (the latter being a generic-recursive vector). To get the complete picture of the sequence-like types in R, let us briefly mention integer, complex, and raw atomic types so that we are not surprised when we encounter them.

### 6.4.1 Integer vectors (\*)

Integer scalars can be input manually by using the `L` suffix:

```
(x <- c(1L, 2L, -1L, NA_integer_)) # looks like numeric
## [1] 1 2 -1 NA
typeof(x) # but is integer
## [1] "integer"
```

Some functions return them in a few contexts<sup>11</sup>:

---

<sup>10</sup> <https://icu.unicode.org/>

<sup>11</sup> Actually, `1:10` returns an integer vector in a compact (ALTREP; see [54]) form; compare the results of the call to “`.Internal(inspect(1:10))`” and “`.Internal(inspect(seq(1, 10, 1)))`”. This way, the whole vector

```
typeof(1:10) # seq(1, 10) as well, but not seq(1, 10, 1)
## [1] "integer"
as.integer(c(-1.1, 0, 1.9, 2.1)) # truncate/round towards 0
## [1] -1 0 1 2
```

In most expressions, integer vectors behave like numeric ones. They are silently coerced to double if need be. Therefore, there is no real practical reason to distinguish between them (they are of *internal* interest, e.g., when writing C/C++ extensions; see Chapter 14). For example:

```
1L/2L # like 1/2 == 1.0/2.0
## [1] 0.5
```

---

**Note** (\*) R integers are 32-bit signed types. The double type can store more integers than them (with the maximal contiguously representable integer being  $2^{53}$  vs  $2^{31} - 1$  in the former case; see Section 3.2.3):

```
as.integer(2^31-1) + 1L # 32-bit integer overflow
## Warning in as.integer(2^31 - 1) + 1L: NAs produced by integer overflow
## [1] NA
as.integer(2^31-1) + 1 == 2^31 # integer+double == double - OK
## [1] TRUE
(2^53 - 1) + 1 == 2^53 # OK
## [1] TRUE
(2^53 + 1) - 1 == 2^53 # lost due to FP rounding, left result is 2^53 - 1
## [1] FALSE
```

---

**Note** Since R3.0, there is support for vectors longer than  $2^{31} - 1$  elements. As there are no 64-bit integers in R, these are indexed by doubles anyway (as we have been doing all this time). Interestingly,  $x[1.9]$  is the same as  $x[1]$ , and  $x[-1.9]$  means  $x[-1]$  (a truncation of the fractional part). This is why the notation like  $x[\text{length}(x)*0.2]$  works regardless of whether the length of  $x$  is a multiple of 5 or not, which is neat.

---

### 6.4.2 Raw vectors (\*)

Vectors of the type `raw` can store bytes, i.e., unsigned 8-bit integers, whose range is 0–255 (there are no raw NAs). For example:

---

does not have to be allocated. This saves memory and time. At the R level, though, it behaves as any other integer (numeric) sequence.

```
as.raw(c(-1, 0, 1, 2, 0xc0, 254, 255, 256, NA))
## Warning: out-of-range values treated as 0 in coercion to raw
## [1] 00 00 01 02 c0 fe ff 00 00
```

They are displayed as two-digit hexadecimal (base-16) numbers. We may enter such numbers using the “0x” prefix.

Only a few functions deal with such vectors: e.g., `readBin`, `charToRaw`, and `rawToChar`.

### 6.4.3 Complex vectors (\*)

We can also play with vectors of the type `complex`, with “`1i`” representing the imaginary unit,  $\sqrt{-1}$ . Complex numbers appear in quite a few engineering or scientific applications, e.g., in physics, electronics, or signal processing. They are (at least: ought to be) part of introductory subjects or textbooks in university-level mathematics, including the statistics/machine learning-oriented ones because of their heavy use of numerical computing; see e.g., [19, 30].

```
c(0, 1i, pi+pi*1i, NA_complex_)
## [1] 0.0000+0.0000i 0.0000+1.0000i 3.1416+3.1416i NA
```

Apart from the basic operators, mathematical and aggregation functions, procedures like `fft`, `solve`, `qr`, or `svd` can be fed with or produce such data. For more details, see `help("complex")` and some matrix examples in [Chapter 11](#).

## 6.5 Exercises

Exercises marked with (\*) might require tinkering with regular expressions or third-party R packages.

**Exercise 6.6** Answer the following questions:

- How many characters are there in the string `"ab|n|||t|||||"`? What about `"-{ab|n|||t|||||"}-"`?
- What is the result of calling `"paste(NA, 1:5, collapse="")"`?
- What is the meaning of the following `sprintf` format strings: `"%s"`, `"%20s"`, `"%-20s"`, `"%f"`, `"%g"`, `"%e"`, `"%5f"`, `"%5.2f%"`, `"%.2f"`, `"%0+5f"`, and `"[%+-5.2f]"`?
- What is the difference between `regexr` and `gregexpr`? What does “`g`” in the latter name stand for?
- What is the result of a call to `"grepl(c("spam", "spammy spam", "aubergines"), "spam")"`?
- Is it always the case that `"Aaron" < "Zorro"`?

- Why “`x < "10"`” and “`x < 10`” may return different results?
- If `x` is a character vector, is “`x == x`” always equal to `TRUE`?
- If `x` and `y` are character vectors of lengths `n` and `m`, respectively, what is the length of the output of “`match(x, y)`”?
- If `x` is a named vector, why is there a difference between “`x[NA]`” and “`x[NA_character_]`”?
- What is the difference between “`x == y`” and “`x %in% y`”?

**Exercise 6.7** Let `x`, `y`, and `z` be atomic vectors and `a` and `b` be single strings. Generate the same results as “`pastena(x, collapse=b)`”, “`pastena(x, y, sep=a)`”, “`pastena(x, y, sep=a, collapse=b)`”, “`pastena(x, y, z, sep=a)`”, “`pastena(x, y, z, sep=a, collapse=b)`”, assuming that `pastena` is a version of `paste` (which we do not have) that handles missing data in a way consistent with most other functions.

**Exercise 6.8** Based on `list.files` and `glob2rx`, generate the list of all PDFs on your computer. Then, using `file.size` filter out the files smaller than 10 MiB.

**Exercise 6.9** Read a text file that stores a long paragraph of some banal prose. Concatenate all the lines to form a single, long string. Using `strwrap` and `cat`, output the paragraph on the console, nicely formatted to fit an aesthetic width, say, 60 text columns.

**Exercise 6.10** (\*) Implement your own simplified version of `basename` and `dirname`.

**Exercise 6.11** (\*) Implement an operation similar to `trimws` using the functions introduced in this chapter.

**Exercise 6.12** (\*) Write a regex that extracts all words from each string in a given character vector.

**Exercise 6.13** (\*) Write a regex that extracts, from each string in a character vector, all:

- integers numbers (signed or unsigned),
- floating-point numbers,
- numbers of any kind (including those in scientific notation),
- hashtags,
- email@address.es,
- hyperlinks of the form `http://...` and `https://...`

**Exercise 6.14** (\*) What do `42i`, `42L`, and `0x42` stand for?

**Exercise 6.15** (\*) Check out `stri_sort` in the `stringi` package (or `sort.character` in `stringx`) for a way to obtain an ordering like “`a1`” < “`a2`” < “`a10`” < “`a11`” < “`a100`”.

**Exercise 6.16** (\*) In `sprintf`, the formatter “`%20s`” means that if a string is less than 20 bytes long, the remaining bytes will be replaced with spaces. Only for ASCII characters (English letters, digits, some punctuation marks, etc.), it is true that one character is represented by 1 byte. Other Unicode code points can take up between 2 and 4 bytes.

```
cat(sprintf("..%6s..", c("abc", "1!<", "aβc", "qβⓈ")), sep="\n") # aligned?
## ..   abc..
## ..   1!<..
## ..  aβc..
## .. qβⓈ..
```

Use the **stri\_pad** function from the **stringi** package to align the strings aesthetically. Alternatively, check out **sprintf** from **stringx**.

**Exercise 6.17** (\*) Implement an operation similar to **stri\_pad** from **stringi** using the functions introduced in this chapter.

---

## Functions

R is a *functional language* where functions play first fiddle. Each action we perform reduces itself to a call to some function or a combination thereof.

So far, we have been tinkering with dozens of available functions which are part of base R, with only a few exceptions. They constitute the essential vocabulary that everyone *must* be able to speak fluently.

Any operation, be it **sum**, **sqrt**, or **paste**, when fed with a number of arguments, generates some (hopefully fruitful) return value.

```
sum(1:10) # invoking `sum` on a specific argument
## [1] 55
```

From a user's perspective, each function is merely a tool. To achieve a goal at hand, we do not have to care about what is going on under its hood, i.e., how the inputs are being transformed so that, after a couple of nanoseconds or hours, we can relish what has been bred. This is very convenient: all we need to know is the function's specification which can be stated, for example, informally, in plain Polish or Malay, on its help page.

In this chapter, we will learn how to write our *own* functions. Using this skill is a good development practice when we expect that some operations are to be executed many times but perhaps on different data.

Also, some R functions are meant to invoke other functions, for instance, on every element in a list or every section of a data frame grouped by a qualitative variable. Thus, it is advisable to learn how we can specify a custom operation to be propagated thereover.

**Example 7.1** *Given some objects (whatever):*

```
x1 <- runif(16)
x2 <- runif(32)
x3 <- runif(64)
```

*when we want to apply the same action on different data, say, compute the root mean square, instead of retyping almost identical expressions (or a bunch of them) over and over again:*

```
sqrt(mean(x1^2))
## [1] 0.6545
sqrt(mean(x2^2)) # the same second time - borderline okay
```

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```
## [1] 0.56203
sqrt(mean(x3^2)) # tedious, barbarous, and error-prone
## [1] 0.57206
```

we can generalise the operation to any object like *x*:

```
rms <- # bound what follows to name `rms`
  function(x) # a function that takes one parameter, `x`
    sqrt(mean(x^2)) # expression to transform the input to yield output
```

and then reuse it on different concrete data instances:

```
rms(x1)
## [1] 0.6545
rms(x2)
## [1] 0.56203
rms(x3)
## [1] 0.57206
```

or even combine it with other function calls:

```
rms(sqrt(c(x1, x2, x3)))^2
## [1] 0.50824
```

---

**Important** Does writing your own functions equal reinventing the wheel? Can everything be found online these days (including on Stack Overflow, GitHub, or CRAN)?

Luckily, it is not the case. Otherwise, data analysts', researchers', and developers' lives would be monotonous, dreary, and uninspiring. Plus, sometimes it is much quicker to compose a function from scratch than to get through the whole garbage dump from where, only occasionally, we can dig out some pearls. Not to mention the self-educative side: we become better programmers by crunching those exercises. We are advocating for minimalism here, remember?

This and many other vital issues in function design will be reflected upon in [Chapter 9](#).

---

## 7.1 Creating and invoking functions

### 7.1.1 Anonymous functions

Functions are usually created through the following notation:



```
function(args) body
```

First, `args` is a (possibly empty) list of comma-separated parameter names which are supposed to act as input variables.

Second, `body` is a *single* R expression that will be evaluated when the function is called. The value this expression yields will constitute the function's output.

For example, here is a definition of a function that takes no inputs and generates a constant output:

```
function() 1
## function() 1
```

We thus created a *function* object. However, it disappeared immediately thereafter, as we have not used it at all.

Any function, say, `f` can be invoked, i.e., evaluated on concrete data, using the notation `f(arg1, ..., argn)`, where “`arg1, ..., argn`” are the arguments to be passed to `f`.

```
(function() 1)() # invoking f like f(); here, no arguments are expected
## [1] 1
```

Only now have we obtained a return value.

---

**Note** (\*) Calling `typeof` on a function object will report “closure” (for user-defined functions), “builtin”, or “primitive” (for some built-in, base ones), for the reasons that we explain in more detail<sup>1</sup> in Section 9.5.3:

```
typeof(function() 1)
## [1] "closure"
```

---

### 7.1.2 Named functions

Function objects can be bound with names so that they can be referred to multiple times:

```
one <- function() 1 # one <- (function() 1)
```

We created an object named **one** (we use bold font to indicate that it is of the type `function` for functions are so crucial in R). We are very familiar with such a notation, as not since yesterday we are used to writing “`x <- 1`”, etc.

Invoking **one**, which can be done by writing `one()`, will generate a return value:

---

<sup>1</sup> In short: each function consists of a list of formal arguments, a body, an possibly (if it is a closure) an enclosing environment.

```
one() # (function() 1)()
## [1] 1
```

This output can be used in further computations, for instance:

```
0:2 - one() # 0:2 - (function() 1)(), i.e., 0:2 - 1
## [1] -1 0 1
```

### 7.1.3 Passing arguments to functions

Functions with no arguments are kind of boring, thus let us distil a more highbrowed operation:

```
concat <- function(x, y) paste(x, y, sep="")
```

Here we have created a mapping whose aim is to concatenate two objects using a specialised call to **paste**. Yours faithfully pleads guilty to multiplying entities needlessly: it *should* not be a problem for anyone to write **paste(x, y, sep="")** each time. Yet, 'tis merely an illustration.

The **concat** function has two *parameters*, “x” and “y”. Hence, calling it will require the provision of two *arguments*, which we put within round brackets and separate from each other by commas.

```
u <- 1:5
concat("spam", u) # i.e., concat(x="spam", y=1:5)
## [1] "spam1" "spam2" "spam3" "spam4" "spam5"
```

---

**Important** Notice the distinction: *parameters* (*formal arguments*) are abstract, general, or symbolic; “something, anything that will be put in place of x when the function is invoked”. Contrastingly, *arguments* (*actual parameters*) are concrete, specific, and real.

---

During the above call, x in the function’s body is precisely “spam” and nothing else. Also, the u object from the caller’s environment can be accessed via y in **concat**. Most of the time (yet, see [Section 16.3](#)), it is best to think of the function as being fed not with u per se but the value that u is bound to, i.e., “1:5”.

Also:

```
x <- 1:5
y <- "spam"
concat(y, x) # concat(x="spam", y=1:5)
## [1] "spam1" "spam2" "spam3" "spam4" "spam5"
```

This call is still equivalent to **concat(x=y, y=x)**. The argument x is assigned the value of y from the calling environment, “spam”. Yes, one x is not the same as the other x,

and which is unambiguously defined by the context. Understanding and being able to manipulate such abstractions is basic logic and common sense that everyone should master.

**Exercise 7.2** Write a function *standardise* that takes a numeric vector *x* as argument and returns its standardised version, i.e., from each element in *x*, subtract the sample arithmetic mean and then divide it by the standard deviation.

---

**Note** Recall from Section 2.1.3 that, syntactically speaking, the following are perfectly valid alternatives to the positionally-matched call `concat("spam", u)`; see Section 15.4.4 for more details.

```
concat(x="spam", y=u)
concat(y=u, x="spam")
concat("spam", y=u)
concat(u, x="spam")
concat(x="spam", u)
concat(y=u, "spam")
```

However, we recommend to avoid the last two for the sake of the readers' sanity. It is best to provide positionally-matched arguments before the keyword-based ones.

Also, in Section 10.5, we will introduce the (overused) forward-pipe operator, ``|>``, which enables the above to be written as `"spam" |> concat(u)`.

---

### 7.1.4 Grouping expressions with curly braces, `{}`

We have been informed that a function's body is a *single* R expression whose evaluated value is passed to the user as its output. This may sound restrictive and in contrast with what we have experienced so far. Rarely are we faced with such simple computing tasks, and we have already seen R functions performing quite sophisticated operations.

It turns out that, grammatically, a single R expression can be arbitrarily complex (Chapter 15); we can use curly braces to group many calls that are to be evaluated one after another.

For instance:

```
{
  cat("first expression\n")
  cat("second expression\n")
  # ...
  cat("last expression\n")
}
## first expression
```

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*(continued from previous page)*

```
## second expression
## last expression
```

We used four spaces to visually indent the constituents for greater readability (some developers prefer tabs over spaces, others find two or three spaces more urbane, but we do not). This single (compound) expression can now play a role of a function's body.

---

**Important** The last expression evaluated in a curly-braces delimited block will be considered its output value.

```
x <- {
  1
  2
  3 # <--- last expression: will be taken as the output value
}
print(x)
## [1] 3
```

---

**Note** (\*) The above code block can also be written more concisely by replacing newlines with semicolons, albeit with perhaps some loss in readability:

```
{1; 2; 3}
## [1] 3
```

Section 9.4 will give a few more details about `{`.

---

**Example 7.3** Here is a version of the above **concat** function, which takes care of a more *Chapter 2*-style missing values' propagation:

```
concat <- function(a, b)
{
  z <- paste(a, b, sep="")
  z[is.na(a) | is.na(b)] <- NA_character_
  z # last expression in the block - return value
}
```

Example calls:

```
concat("a", 1:3)
## [1] "a1" "a2" "a3"
concat(NA_character_, 1:3)
## [1] NA NA NA
```

*(continues on next page)*

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```
concat(1:6, c("a", NA_character_, "c"))
## [1] "1a" NA "3c" "4a" NA "6c"
```

Let us appreciate the fact that we could keep the code brief thanks to **paste** and ``|`` implementing the recycling rule.

**Exercise 7.4** Write a function **normalise** that takes a numeric vector  $x$  and returns its version shifted and scaled to the  $[0, 1]$  interval. To do so, subtract the sample minimum from each element, and then divide it by the range, i.e., the difference between the maximum and the minimum. Avoid computing `min(x)` twice.

**Exercise 7.5** Write a function that applies the robust standardisation of a numeric vector: subtract the median and divide it by the median absolute deviation, 1.4826 times the median of the absolute differences between the values and their median.

---

**Note** R is an open-source (free, libre) project. Users are not only encouraged to run the software for whatever purpose, but also study and modify its source code without any restrictions. This applies both to functions that we have authored ourselves:

```
print(concat)
## function(a, b)
## {
##   z <- paste(a, b, sep="")
##   z[is.na(a) | is.na(b)] <- NA_character_
##   z # last expression in the block - return value
## }
```

and to the routines that are part of base R or any other extension packages:

```
print(union)
## function (x, y)
## {
##   u <- as.vector(x)
##   v <- as.vector(y)
##   unique(c(u, v))
## }
## <environment: namespace:base>
```

Nevertheless, some functionality might be implemented in compiled programming languages such as C, C++, or Fortran; notice a call to **.Internal** in the source code of **paste**, **.Primitive** in **list**, or **.Call** in **runif**. Therefore, we will sometimes have to dig a bit deeper to access the underlying source code; see [Chapter 14](#) for more details.

---

## 7.2 Functional programming

R is a *functional* programming language. As such, it shares several common features with other languages that emphasise the role of function manipulation in software development (e.g., Common Lisp, Scheme, OCaml, Haskell, Clojure, F#). Let us explore them now.

### 7.2.1 Functions are objects

R functions were given the right to a *fair go*; they are what we refer to as *first-class citizens*. In other words, our interaction with them is not limited to their invocation; we treat them as any other language object.

- They can be stored inside list objects:

```
list(identity, NROW, sum) # a list storing three functions
## [[1]]
## function (x)
## x
## <environment: namespace:base>
##
## [[2]]
## function (x)
## if (length(d <- dim(x))) d[1L] else length(x)
## <environment: namespace:base>
##
## [[3]]
## function (... , na.rm = FALSE) .Primitive("sum")
```

This is possible owing to the fact that lists, as we recall, can embrace R objects of any kind,

- They can be created and then called inside another function's body:

```
euclidean_distance <- function(x, y)
{
  square <- function(z) z^2 # auxiliary/internal/helper function
  sqrt(sum(square(x-y)))    # square root of the sum of squares
}

euclidean_distance(c(0, 1), c(1, 0)) # example call
## [1] 1.4142
```

This is why we tend to classify functions as representatives of *recursive* types (compare `is.recursive`).

- They can be passed as arguments to other operations:

```
# Replaces missing values with a given aggregate
# of all non-missing elements:
fill_na <- function(x, filler_fun)
{
  missing_ones <- is.na(x) # otherwise, we'd call is.na twice
  replacement_value <- filler_fun(x[!missing_ones])
  x[missing_ones] <- replacement_value
  x
}

fill_na(c(0, NA_real_, NA_real_, 2, 3, 7, NA_real_), mean)
## [1] 0 3 3 2 3 7 3
fill_na(c(0, NA_real_, NA_real_, 2, 3, 7, NA_real_), median)
## [1] 0.0 2.5 2.5 2.0 3.0 7.0 2.5
```

We call these *higher-order functions*.

---

**Note** More advanced techniques, which we will discuss in the third part of the book, will let the functions be:

- returned as other function's outputs,
  - equipped with auxiliary data,
  - generated programmatically on the fly,
  - modified at runtime.
- 

Below we review the most basic higher-order functions, including **do.call** and **Map**.

### 7.2.2 Calling on precomputed arguments with **do.call**

Notation like **f**(arg1, ..., argn) has no monopoly over how we are supposed to call a function on a specific sequence of comma-delimited arguments. The list of actual parameters does not have to be hardcoded.

Here is an alternative. We can first prepare a number of objects to be passed as **f**'s inputs, wrap them in a list **l**, and then invoke **do.call(f, l)** to get the same result.

```
words <- list(
  c("spam", "bacon", "eggs"),
  c("buckwheat", "quinoa", "barley"),
  c("ham", "spam", "spam")
)
do.call(paste, words) # paste(words[[1]], words[[2]], words[[3]])
## [1] "spam buckwheat ham" "bacon quinoa spam" "eggs barley spam"
```

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```
do.call(cbind, words) # column-bind; returns a matrix (explained later)
##      [,1]      [,2]      [,3]
## [1,] "spam"    "buckwheat" "ham"
## [2,] "bacon"   "quinoa"    "spam"
## [3,] "eggs"    "barley"    "spam"
do.call(rbind, words) # row-bind (explained later)
##      [,1]      [,2]      [,3]
## [1,] "spam"    "bacon"    "eggs"
## [2,] "buckwheat" "quinoa" "barley"
## [3,] "ham"     "spam"    "spam"
```

The length and content of the list passed as the second argument of `do.call` can be arbitrary (possibly unknown at the time of writing the code). See [Section 12.1.2](#) for more use cases, e.g., ways to concatenate a list of data frames (perhaps produced by some complex chain of commands) into a single data frame.

If elements of the list are named, they will be matched to the corresponding keyword arguments.

```
x <- 2^(seq(-2, 2, length.out=101))
plot_opts <- list(col="red", lty="dashed", type="l")
do.call(plot, c(list(x, log2(x), xlab="x", ylab="log2(x)"), plot_opts))
## (plot display suppressed)
```

Notice that, e.g., `plot_opts` can now be reused in further calls to graphics functions. This is very convenient as it avoids repetitions.

## 7.2.3 Common higher-order functions

There is an important class of higher-order functions that allow us to apply custom operations on consecutive elements of sequences without relying on loop-like statements, at least explicitly. They can be found in all functional programming languages (e.g., Lisp, Haskell, Scala) and have been ported to various add-on libraries (**functools** in Python, more recent versions of the C++ Standard Library, etc.) or frameworks (Apache Spark and the like). Their presence reflects the obvious truth that some operations occur more frequently than others.

In particular:

- **Map** calls a function on each element of a sequence in order to transform:
  - their individual components (just like `sqrt`, `round`, or the unary ``!`` operator in R), or
  - the corresponding elements of many sequences so as to vectorise a given operation elementwisely (compare the binary ``+`` or `paste`),
- **Reduce** (also called accumulate) applies a binary operation to combine consecutive



elements in a sequence, e.g., to generate the aggregates, like, totally (compare **sum**, **prod**, **all**, **max**) or cumulatively (compare **cumsum**, **cummin**),

- **Filter** creates a subset of a sequence that is comprised of elements that enjoy a given property (which we typically achieve in R by means of the ``[`` operator),
- **Find** locates the first element that fulfils some logical condition (compare **which**),

and so forth.

Below we will only focus on the **Map** function. The inspection of the remaining ones is left as an exercise. This is because, oftentimes, we can be better off with their more R-ish versions (e.g., using the subsetting operator, ``[``).

## 7.2.4 Vectorising functions with Map

In data-centric computing, we are frequently faced with tasks that involve processing each element in a sequence independently, one after another. Such use cases can benefit from vectorised operations like those discussed in [Chapter 2](#), [Chapter 3](#), and [Chapter 6](#).

Unfortunately, most of the functions that we introduced so far cannot be applied on lists. For instance, if we try calling **sqr**t on a list, we will get an error, even if it is a list of numeric vectors only. One way to compute the square root of all elements would be to invoke **sqr**t(**unlist**(...)). It is a go-to approach if we wish to treat all the list's elements as one sequence. However, this comes at the price of losing the list's structure.

We also discussed some operations that are not vectorised with respect to all their arguments, even though they could have been designed this way, e.g., **grepl**.

The **Map** function<sup>2</sup> applies an operation on each element in a vector or the corresponding elements in a number of vectors. In many situations, it may be used as a more elegant alternative to **for** loops that we will introduce in the next chapter.

First<sup>3</sup>, a call to **Map**(**f**, **x**) yields a list whose *i*-th element is equal to **f**(**x**[*i*])) (recall that ``[[`` works on atomic vectors too).

For example:

```
x <- list( # an example named list
  x1=1:3,
  x2=seq(0, 1, by=0.25),
  x3=c(1, 0, NA_real_, 0, 0, 1, NA_real_)
)
Map(sqrt, x) # x is named, hence the result will be named as well
```

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<sup>2</sup> Yes, the author is aware that **Map** was implemented using the slightly more primitive **mapply** but we are not fond of the latter function's having the **SIMPLIFY** argument set to **TRUE** by default.

<sup>3</sup> This use case scenario can also be programmed using **lapply**; **lapply**(**x**, **f**, ...) is equivalent to **Map**(**f**, **x**, **MoreArgs=list(...)**).

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```
## $x1
## [1] 1.0000 1.4142 1.7321
##
## $x2
## [1] 0.00000 0.50000 0.70711 0.86603 1.00000
##
## $x3
## [1] 1 0 NA 0 0 1 NA
Map(length, x)
## $x1
## [1] 3
##
## $x2
## [1] 5
##
## $x3
## [1] 7
unlist(Map(mean, x)) # compute three aggregates, convert to an atomic vector
## x1 x2 x3
## 2.0 0.5 NA
Map(function(n) round(runif(n, -1, 1), 1), c(2, 4, 6)) # x is atomic now
## [[1]]
## [1] 0.4 0.8
##
## [[2]]
## [1] 0.5 0.8 -0.1 -0.7
##
## [[3]]
## [1] -0.3 0.0 0.5 1.0 -0.9 -0.7
```

Next, we can vectorise a given function over several parameters. A call to, e.g., **Map**(*f*, *x*, *y*, *z*) breeds a list whose *i*-th element is equal to **f**(*x*[[*i*]], *y*[[*i*]], *z*[[*i*]]). Like in the case of, e.g., **paste**, the recycling rule will be applied if necessary.

For example, the following generates **list**(**seq**(1, 6), **seq**(11, 13), **seq**(21, 29)):

```
Map(seq, c(1, 11, 21), c(6, 13, 29))
## [[1]]
## [1] 1 2 3 4 5 6
##
## [[2]]
## [1] 11 12 13
##
## [[3]]
## [1] 21 22 23 24 25 26 27 28 29
```

Moreover, we can get `list(seq(1, 40, length.out=10), seq(11, 40, length.out=5), seq(21, 40, length.out=10), seq(31, 40, length.out=5))` by calling:

```
Map(seq, c(1, 11, 21, 31), 40, length.out=c(10, 5))
## [[1]]
## [1] 1.0000 5.3333 9.6667 14.0000 18.3333 22.6667 27.0000 31.3333
## [9] 35.6667 40.0000
##
## [[2]]
## [1] 11.00 18.25 25.50 32.75 40.00
##
## [[3]]
## [1] 21.000 23.111 25.222 27.333 29.444 31.556 33.667 35.778 37.889 40.000
##
## [[4]]
## [1] 31.00 33.25 35.50 37.75 40.00
```

**Note** If we have some additional arguments to be passed to the function applied (which it does not have to be vectorised over), we can wrap them inside a separate list and toss it via the `MoreArgs` argument (à la `do.call`).

```
unlist(Map(mean, x, MoreArgs=list(na.rm=TRUE))) # mean(..., na.rm=TRUE)
## x1 x2 x3
## 2.0 0.5 0.4
```

Alternatively, we can always construct a custom anonymous function:

```
unlist(Map(function(xi) mean(xi, na.rm=TRUE), x))
## x1 x2 x3
## 2.0 0.5 0.4
```

**Exercise 7.6** Here is an example list of files (see *our teaching data repository*<sup>4</sup>) with daily Forex rates:

```
file_names <- c(
  "euraud-20200101-20200630.csv",
  "eurgbp-20200101-20200630.csv",
  "eurusd-20200101-20200630.csv"
)
```

Call `Map` to read each dataset with `scan` and determine each series' minimal, mean, and maximal value.

**Exercise 7.7** Implement your version of the `Filter` function based on a call to `Map`.

<sup>4</sup> <https://github.com/gagolews/teaching-data/tree/master/marek>

## 7.3 Accessing third-party functions

When we indulge in the writing of a software piece, a few questions naturally arise. Is the problem we are facing fairly complex? Has it already been successfully addressed in its entirety? If not, can it, or its parts, be split into manageable chunks? Can it be constructed based on some readily available nontrivial components?

A smart developer is independent but knows when to stand on the shoulders to cry on. Let us explore some ways to reuse the existing function libraries.

### 7.3.1 Using R packages

Most contributed R extensions come in the form of the so-called *add-on packages*, which can include:

- reusable code (e.g., new functions),
- data (which we can exercise on),
- documentation (manuals, vignettes, etc.);

see Section 9.3.2 for more and [62] for all the details.

Most packages are published in the moderated repository that is part of the *Comprehensive R Archive Network* (CRAN<sup>5</sup>). However, there are also other popular sources such as *Bioconductor*<sup>6</sup> which specialises in bioinformatics.

We call `install.packages("pkg")` to fetch a package `pkg` from a repository (CRAN by default; see, however, the `repos` argument).

A call to `library("pkg")` loads an indicated package and makes the exported objects available to the user (i.e., attaches it to the search path; see Section 16.2.6).

For instance, in one of the previous chapters, we have mentioned the `gsl` package:

```
# call install.packages("gsl") first
library("gsl") # load the package
poch(10, 3:6) # calls gsl_sf_poch() from GNU GSL
## [1] 1320 17160 240240 3603600
```

Here, `poch` is an object exported by package `gsl`. If we did not call `library("gsl")`, trying to access the former would raise an error.

We could also have accessed the above function without attaching it to the search path using the `pkg::object` syntax, i.e., `gsl::poch`.

**Exercise 7.8** Use the `find` function to determine which packages define `mean`, `var`, `find`, and `Map`. Recall from Section 1.4 where such information can be found in these objects' manual pages.

<sup>5</sup> <https://cloud.r-project.org/>

<sup>6</sup> <https://bioconductor.org/>

---

**Note** For more information about any R extension, call `help(package="pkg")`. Also, it is advisable to visit the package's CRAN entry at an address like <https://CRAN.R-project.org/package=pkg> to access some additional information (e.g., vignettes; see also `vignette(package="pkg")`). Why waste our time and energy by querying a web search engine that will lead us to some (usually low-quality) middleman when we can acquire authoritative knowledge directly from the source?

Moreover, it is worth exploring various [CRAN Task Views](#)<sup>7</sup> that group the packages into topics such as *Genetics*, *Graphics*, and *Optimisation*. They are curated by experts in their relevant fields.

---



---

**Important** Frequently, R packages are written in their respective authors' free time, many of whom are volunteers/public servants/enthusiasts who are neither paid for doing this nor it is part of the so-called *their job*. You can show appreciation for their generosity by, e.g., spreading the word about their software by citing them in publications (see `citation(package="pkg")`), talking about them during lunchtime, or mentioning them in (un)social media. You can also help them improve the existing code base by reporting bugs, polishing documentation, proposing new features, or cleaning up the redundant fragments of their APIs. Some readers will become one of them someday (when they come up with something valuable for our community).

---

## Default packages

The always-on package **base** is a must-have. It provides us with the most crucial functions (vector addition, **c**, **Map**, **library**). Certain other packages are also loaded by default:

```
getOption("defaultPackages")
## [1] "datasets" "utils"      "grDevices" "graphics"  "stats"
## [6] "methods"
```

This list can, theoretically, be changed<sup>8</sup>. However, in this book, we assume that the above are always attached because it is reasonable to do so. This is why in [Section 2.4.5](#), there was no need to call, for example, `library("stats")` before referring to the **var** and **sd** functions.

On a side note, **grDevices** and **graphics** will be discussed in [Chapter 13](#). **methods** will be mentioned in [Section 11.5](#). **datasets** brings a few example R objects on which we can exercise our skills. On the other hand, the functions from **utils**, **graphics**, and **stats** already appeared here and there.

---

<sup>7</sup> <https://cloud.r-project.org/web/views/>

<sup>8</sup> (\*) R is greatly configurable: we can have custom `~/.Renv` and `~/.Rprofile` files that are processed on R's startup; see `help("Startup")`.

## Source vs binary packages (\*)

R is a free and open project. Therefore, its packages are published primarily in the source form. This way, anyone can study how they work and improve them or reuse parts thereof in different projects.

If we call `install.packages("path", repos=NULL, type="source")`, we should be able to install a package from sources: `path` can either be pinpointing a directory or a source tarball (see `help("untar")`), most often as a compressed `pkg_version.tar.gz` file).

Note that `type="source"` is the default unless one is on `W****ws` or some `m**OS` boxes; see `getOption("pkgType")`. This is because these two require additional build tools to be present in the system, especially if a package features C or C++ code; see Chapter 14 and Section C.3 of [64]:

- **RTools**<sup>9</sup> on `W****ws`,
- **Xcode Command Line Tools**<sup>10</sup> on `m**OS`.

Because these systems are less developer-oriented, as a courtesy to their users, CRAN also distributes the platform-specific binary versions of the packages (`.zip` or `.tgz` files). `install.packages` will try to fetch them by default.

**Example 7.9** *GitLab and GitHub are quite popular hosting platforms. It is very easy to fetch a package's source directly from them. At the time of writing this, the relevant links were, respectively:*

- <https://gitlab.com/user/repo/-/archive/branch/repo-branch.zip>
- <https://github.com/user/repo/archive/branch.zip>

For example, to download the contents of the master branch in the repository `rpacgedemo` owned by `gagolews`, we can call:

```
f <- tempfile() # temporary file name - download destination
download.file("https://github.com/gagolews/rpacgedemo/archive/master.zip",
  destfile=f)
```

Next, the contents can be extracted with `unzip`:

```
t <- tempdir() # temporary directory to extract the files to
(d <- unzip(f, exdir=t)) # returns extracted file paths
```

The path where the files were extracted can be passed to `install.packages`:

```
install.packages(dirname(d)[1], repos=NULL, type="source")
file.remove(c(f, d)) # clean up
```

**Exercise 7.10** Use the `git2r` package to clone the `git` repository located at <https://github.com/>

<sup>9</sup> <https://cran.r-project.org/bin/windows/Rtools/>

<sup>10</sup> <https://developer.apple.com/xcode/resources/>

*gagolews/rpackagedemo.git* and install the package published therein from the current R session.

## Managing dependencies (\*)

All installed add-on packages may be upgraded to their most recent versions available on CRAN (or other indicated repository) by calling **update.packages**.

As a general rule, the more experienced developers we become, the less excited we get about the *new*. Sure, bug fixes and some well-thought-of additional features are usually welcome. Still, just we wait until someone updates the package API for the  $n$ -th time,  $n \geq 2$ , which will break our program that used to work flawlessly for so long.

Hence, when designing software projects (see [Chapter 9](#) for more details), we must ask ourselves the ultimate question: do we really need to import that package with lots of dependencies from which we will just use only about 3–5 functions? Wouldn't it be better to write our own version of some functionality (and learn something new, exercise our brain, etc.), or call a mature terminal-based tool?

Otherwise, as all the historical versions of all the packages are [archived on CRAN<sup>11</sup>](#), some software dependency management can easily be conducted by storing different releases of packages in different directories (only one version of a package can be loaded at a time though). This way, we can create an isolated environment for the add-ons.

To fetch the locations where packages are sought (in this very order), call:

```
.libPaths()
## [1] "/home/gagolews/R/x86_64-pc-linux-gnu-library/4.3"
## [2] "/usr/local/lib/R/site-library"
## [3] "/usr/lib/R/site-library"
## [4] "/usr/lib/R/library"
```

The same function can be used to add new folders to the search path; see also the environment variable `R_LIBS_USER` (e.g., `help("Sys.setenv")`). The **install.packages** function will honour them as target directories; see its `lib` parameter for more details.

Moreover, the packages may deposit some auxiliary data on the user's machine. Therefore, it might be worthwhile to set the following directories (via the corresponding environment variables) relative to the current project:

```
tools::R_user_dir("pkg", "data") # R_USER_DATA_DIR
## [1] "/home/gagolews/.local/share/R/pkg"
tools::R_user_dir("pkg", "config") # R_USER_CONFIG_DIR
## [1] "/home/gagolews/.config/R/pkg"
tools::R_user_dir("pkg", "cache") # R_USER_CACHE_DIR
## [1] "/home/gagolews/.cache/R/pkg"
```

<sup>11</sup> <https://cran.r-project.org/src/contrib/Archive/>

### 7.3.2 Calling external programs

Many tasks can naturally be accomplished by calling external programs. Such an approach is particularly natural on UNIX-like systems, which classically follow modular, minimalist design patterns. There are many tools at a developer's hand and each tool is specialised at solving a single, well-defined problem.

Apart from the many [standard UNIX commands](#)<sup>12</sup>, we can consider, for example:

- **pandoc**<sup>13</sup> converts documents between markup formats, e.g., Markdown, reStructuredText, LaTeX, LibreOffice Writer, EPUB;
- **pdflatex**, **xelatex**, and **lualatex** compile LaTeX documents to PDF;
- **convert** (from **ImageMagick**<sup>14</sup>) applies various operations on bitmap graphics (scaling, cropping, conversion between formats);
- **graphviz**<sup>15</sup> and **PlantUML**<sup>16</sup> can be used to create various graphs and diagrams;
- **jupyter-nbconvert** converts **Jupyter**<sup>17</sup> notebooks (see [Section 1.2.5](#)) to other formats such as LaTeX, HTML, Markdown, etc.;
- **python**, **perl**, ... can be called to perform tasks that can be expressed more easily in languages other than R;

and so forth.

The good news is that R can not only be called from the system shell (in an interactive or batch mode; see [Section 1.2](#)). It can also serve well as a glue language.

The **system2** function can be used to invoke any system command. Communication between such programs can be done using, e.g., intermediate text, JSON, CSV, XML, or any other files. The `stdin`, `stdout`, and `stderr` arguments can control the redirection of the standard I/O streams.

```
system2("pandoc", "-s input.md -o output.html")
system2("bash", "-c 'for i in `seq 1 2 10`; do echo $i; done'", stdout=TRUE)
## [1] "1" "3" "5" "7" "9"
system2("python3", "-", stdout=TRUE,
  input=c(
    "import numpy as np",
    "print(repr(np.arange(5)))"
  ))
## [1] "array([0, 1, 2, 3, 4])"
```

On a side note, the current working directory can be read and changed through a call

<sup>12</sup> [https://en.wikipedia.org/wiki/List\\_of\\_Unix\\_commands](https://en.wikipedia.org/wiki/List_of_Unix_commands)

<sup>13</sup> <https://pandoc.org/>

<sup>14</sup> <https://imagemagick.org/>

<sup>15</sup> <https://graphviz.org/>

<sup>16</sup> <https://plantuml.com/>

<sup>17</sup> <https://jupyter.org/>



to **getwd** and **setwd**, respectively. It is the directory where the current R session was started.

---

**Important** Relying on **system2** assumes that the commands it refers to are available on the target platform. Hence, it might not be portable unless additional assumptions are made (e.g., that a user runs some UNIX-like system and that certain libraries are installed therein). We strongly recommend GNU/Linux or FreeBSD for both software development and production use, as they are free, open, developer-friendly, user-loving, reliable, ethical, and sustainable.

---

### 7.3.3 Interfacing C, C++, Fortran, Python, Java, etc. (\*\*)

Most stand-alone data processing algorithms are implemented in compiled, slightly lower-level programming languages. This usually makes them faster and more reusable in other environments. For instance, an industry-standard library might be written in very portable C, C++, or Fortran and have some bindings available for easier access from within R, Python, Julia, etc. It is the case with FFTW, LIBSVM, mlpack, OpenBLAS, ICU, and GNU GSL, amongst many others. [Chapter 14](#) explains basic ways to refer to such compiled code.

Also, the **rJava** package can dynamically create JVM objects and access their fields and methods. Similarly, **reticulate** can be used to access Python objects, including **numpy** arrays and **pandas** data frames (but see also the **rpy2** package for Python).

---

**Important** We should not feel obliged to use R in all parts of a data processing pipeline. Some activities can be expressed more naturally in other languages or environments (e.g., parse raw data and create a SQL database in Python but visualise it in R). We can use other tools as the glue language (including R, Python, or Bash) to steer the data flow in the right direction.

---

R is an effective *glue* language: it is suitable for implementing data wrangling pipelines, visualisation, and developing prototypes of data analysis algorithms. In other words, it makes connecting larger *building blocks* very easy.

Nevertheless, for performance reasons<sup>18</sup>, we should move the more computing-intensive tasks to the C or C++ level. In this chapter, we will demonstrate that R works very well as a user-friendly interface to compiled code written in these languages<sup>19</sup>.

---

<sup>18</sup> A well-written, portable function library relying only on simple data structures (e.g., arrays of the type `double` and `int`) can be used in other environments, such as Python (e.g., via Cython) or Julia. Let us remember about other programmers yearning for the possibility to enjoy our cultivated algorithms.

<sup>19</sup> (\*) Fortran is also supported but will not be covered in this book because of its smaller popularity. Some third-party packages are gateways to other languages such as Java.

## 7.4 Exercises

**Exercise 7.11** Answer the following questions:

- What is the result of “`x <- 2; x <- function(x) x^2; x(x)`”?
- How to compose a function that returns two objects?
- What is a higher-order function?
- What are the use cases of **do.call**?
- Why a call to **Map** is not necessary in the expression “**Map**(**paste**, `x`, `y`, `z`)”?
- What is the difference between **Map**(**mean**, `x`, `na.rm=TRUE`) and **Map**(**mean**, `x`, **MoreArgs=list**(`na.rm=TRUE`))?
- What do we mean when we write **stringx::sprintf**?
- How to get access to the vignettes (tutorials, FAQs, etc.) of the **data.table** and **dplyr** packages? Why perhaps 95% of R users would just google it, and what is sub-optimal about this strategy?
- What is the difference between a source and a binary package?
- How to update the **base** package?
- How to ensure that we will always run an R session with only specific versions of a set of packages?

**Exercise 7.12** Write a function that computes the Gini index of a vector of positive integers  $x$ , which, assuming  $x_1 \leq x_2 \leq \dots \leq x_n$ , is equal to:

$$G(x_1, \dots, x_n) = \frac{\sum_{i=1}^n (n - 2i + 1)x_i}{(n - 1) \sum_{i=1}^n x_i}.$$

**Exercise 7.13** Implement a function **between**(`x`, `a`, `b`) that verifies whether each element in `x` is in the `[a, b]` interval. Return a logical vector of the same length as `x`. Ensure the function is correctly vectorised with respect to all the arguments and handles missing data correctly.

**Exercise 7.14** Write your version of the **strrep** function called **dup**.

```
dup <- ...to.do...
dup(c("a", "b", "c"), c(1, 3, 5))
## [1] "a"      "bbb"    "ccccc"
dup("a", 1:3)
## [1] "a"      "aa"     "aaa"
dup(c("a", "b", "c"), 4)
## [1] "aaaa"   "bbbb"   "cccc"
```

**Exercise 7.15** Given a list `x`, generate its sublist with all the elements equal to `NULL` removed.

**Exercise 7.16** Implement your version of the built-in **sequence** function.

**Exercise 7.17** Using **Map**, how can we generate window indexes like below?

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

Write a function **windows**(*k*, *n*) that yields *k* index windows with elements between 1 and *n* (the above example is for *k* = 3 and *k* = 6).

**Exercise 7.18** Implement a function **movstat**(*f*, *x*, *k*) that computes, using **Map**, a given aggregate *f* of each *k* consecutive elements in *x*. For instance:

```
movstat <- ...to.do...
x <- c(1, 3, 5, 10, 25, -25) # example data
movstat(mean, x, 3)          # 3-moving mean
## [1] 3.0000 6.0000 13.3333 3.3333
movstat(median, x, 3)        # 3-moving median
## [1] 3.0000 6.0000 13.3333 3.3333
```

**Exercise 7.19** Write a function to extract all *q*-grams,  $q \geq 1$ , from a given character vector. Return a list of character vectors. For example, 2-grams (bigrams) in "abcd" are: "ab", "bc", "cd".

**Exercise 7.20** Recode a character vector with a small number of distinct values to a vector where each unique code is assigned a positive integer from 1 to *k*. Example calls and the corresponding expected results:

```
recode <- ...to.do...
recode(c("a", "a", "a", "b", "b"))
## [1] 1 1 1 2 2
recode(c("x", "z", "y", "x", "y", "x"))
## [1] 1 3 2 1 2 1
```

**Exercise 7.21** Implement a function that returns the number of occurrences of each unique element in a given atomic vector. The return value should be a numeric vector equipped with a *names* attribute.

```
count <- ...to.do...
```

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```
count(c(5, 5, 5, 5, 42, 42, 954))
##    5 42 954
##    4  2  1
count(c("x", "z", "y", "x", "y", "x", "w", "x", "x", "y", NA_character_))
##      w      x      y      z <NA>
##      1      5      3      1      1
```

Hint: use `match` and `tabulate`.

**Exercise 7.22** Extend the built-in `duplicated` function. For each vector element, indicate which occurrence of a repeated value is it (starting from the beginning of the vector).

```
duplicatedn <- ...to.do...
duplicatedn(c("a", "a", "a", "b", "b"))
## [1] 1 2 3 1 2
duplicatedn(c("x", "z", "y", "x", "y", "x", "w", "x", "x", "y", "z"))
## [1] 1 1 1 2 2 3 1 4 5 3 2
```

**Exercise 7.23** Based on a call to `Map`, implement a function `my_split` such that, given a vector  $x$  and an atomic vector  $y$  of the same length as  $x$ , `my_split(x, y)` yields the same result as `split(x, y)`.

**Exercise 7.24** Extend `my_split` to handle the second argument being a list of the form `list(y1, y2, ...)` representing the product of many levels. If the  $y$ s are of different lengths, apply the recycling rule.

**Exercise 7.25** Implement `my_unsplit` being your version of the built-in `unsplit`. Ensure it holds `my_unsplit(split(x, g), g) == x` for  $x$  and  $g$  of the same lengths.

**Exercise 7.26** Write a function that takes as arguments: (a) an integer  $n$ , (b) a numeric vector  $x$  of length  $k$  and no duplicated elements, (c) a vector of probabilities  $p$  of length  $k$ . Verify that  $p_i \geq 0$  for all  $i$  and  $\sum_{i=1}^k p_i \simeq 1$ . Based on a random number generator from the uniform distribution on the unit interval, generate  $n$  independent realisations of a random variable  $X$  such that  $\Pr(X = x_i) = p_i$  for  $i = 1, \dots, k$ . Hint: to obtain a single value:

1. generate  $u \in [0, 1]$ ,
2. find  $m \in \{1, \dots, k\}$  such that  $u \in \left( \sum_{j=1}^{m-1} p_j, \sum_{j=1}^m p_j \right]$ ,
3. the result is then  $x_m$ .

**Exercise 7.27** Write a function that takes as arguments: (a) an increasingly sorted vector  $x$  of length  $n$ , (b) any vector  $y$  of length  $n$ , (c) a vector  $z$  of length  $k$  and elements in  $[x_1, x_n]$ . Let  $f$  be the piecewise linear spline that interpolates the points  $(x_1, y_1), \dots, (x_n, y_n)$ . Return a vector  $w$  of length  $k$  such that  $w_i = f(z_i)$ .

**Exercise 7.28** (\*) Write functions `dpareto`, `ppareto`, `qpareto`, and `rpareto` that implement the basic functions related to the Pareto distribution; compare Section 2.3.4.

---

## Flow of execution

---

The **ifelse** and **Map** functions are potent. However, they allow us to process only the *consecutive* elements in a vector.

Thus, let us (finally!) discuss different ways to alter a program's control flow manually, based on some criterion, and to evaluate the same expression many times, but perhaps on different data. Before proceeding any further, let us, however, contemplate the fact that we have managed to do without them for such a long time, despite the fact that the data processing exercises we learnt to solve were far from trivial.

---

### 8.1 Conditional evaluation

Life is full of surprises, so it would be nice if we could adapt to whatever the circumstances are going to be.

The following evaluates a given expression *if and only if* a logical condition is true.

```
if (condition) expression
```

When performing some other\_expression is preferred rather than doing nothing in the case of the condition's being false, we can write:

```
if (condition) expression else other_expression
```

For instance:

```
(x <- runif(1)) # to spice things up
## [1] 0.28758
if (x > 0.5) cat("head\n") else cat("tail\n")
## tail
```

Many expressions can, of course, be grouped with curly braces, `{}`.

```
if (x > 0.5) {
  cat("head\n")
  x <- 1
}
```

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```

} else {
  cat("tail\n")
  x <- 0
}
## tail
print(x)
## [1] 0

```

---

**Important** At the top level, we should not put a new line before **else**. Otherwise, we will get an error like `Error: unexpected 'else' in "else"`. This is because the interpreter enthusiastically executes the statements read line by line as soon as it regards them as stand-alone expressions. In this case, we first get an **if** without **else**, and then, separately, a *dangling else* without the preceding **if**.

This does not happen when a conditional statement is part of an expression group as the latter is read in its entirety.

```

function (x)
{ # opening bracket - start
  if (x > 0.5)
    cat("head\n")
  else # not dangling because {...} is read as a whole
    cat("tail\n")
} # closing bracket - expression ends

```

As an exercise, try removing the curly braces and see what happens.

---

### 8.1.1 Return value

``if`` is a function (compare Section 9.4). Hence, it has a return value: the result of evaluating the conditional expression.

```

(x <- runif(1))
## [1] 0.28758
y <- if (x > 0.5) "head" # no else
print(y)
## NULL
y <- if (x > 0.5) "head" else "tail"
print(y)
## [1] "tail"

```

This is particularly useful when a call to ``if`` is the last expression in the code block constituting a function's body.

```

mint <- function(x)
{
  if (x > 0.5) # the last expression (actually, the only one)
    "head"      # this can be the return value...
  else
    "tail"      # or this one, depending on the condition
}

mint(x)
## [1] "tail"
unlist(Map(mint, runif(5)))
## [1] "tail" "head" "tail" "head" "head"

```

**Example 8.1** Add-on packages can be loaded using **requireNamespace**. Contrary to **library**, the former does not fail when a package is not available. Also, it does not attach it to the search path; see Section 16.2.6.

Instead, it returns a logical value indicating if the package is available for use. This can be helpful inside other functions where the availability of some additional features depends on the user environment's configuration:

```

process_data <- function(x)
{
  if (requireNamespace("some_extension_package", quietly=TRUE))
    some_extension_package::very_fast_method(x)
  else
    normal_method(x)
}

```

### 8.1.2 Nested ifs

If more than two test cases are possible, i.e., when we need to go beyond either condition or !condition, then we can use the following construction:

```

if (a) {
  expression_a
} else if (b) {
  expression_b
} else if (c) {
  expression_c
} else {
  expression_else
}

```

This evaluates all conditions a, b, ... (in this order) until the first positive case is found and then executes the corresponding expression.

It is worth stressing that the above is nothing else than a series of nested `if` statements but written in a more readable<sup>1</sup> manner:

```
if (a) {
  expression_a
} else {
  if (b) {
    expression_b
  } else {
    if (c) {
      expression_c
    } else {
      expression_else
    }
  }
}
```

**Exercise 8.2** Write a function named **sign** that determines if a given numeric value is "positive", "negative", or "zero".

### 8.1.3 Condition: Either TRUE or FALSE

`if` expects a condition that is a single, well-defined logical value, either TRUE or FALSE. Thence, problems may arise when this is not the case.

If the condition is of length not equal to one, we get an error:

```
if (c(TRUE, FALSE)) cat("spam\n")
## Error in if (c(TRUE, FALSE)) cat("spam\n"): the condition has length > 1
if (logical(0)) cat("bacon\n")
## Error in if (logical(0)) cat("bacon\n"): argument is of length zero
```

We cannot pass a missing value either:

```
if (NA) cat("ham\n")
## Error in if (NA) cat("ham\n"): missing value where TRUE/FALSE needed
```

**Important** If we think that we are immune to writing code violating the above constraints, just we wait until the condition becomes a function of data for which there is no sanity-checking in place.

```
mint <- function(x)
  if (x > 0.5) "H" else "T"
```

(continues on next page)

<sup>1</sup> (\*) Somewhat related is the `switch` function which relies on the lazy evaluation of its arguments (Chapter 17). Still, it can always be replaced by a series of `ifs`.



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```

mint(0.25)
## [1] "T"
mint(runif(5))
## Error in if (x > 0.5) "H" else "T": the condition has length > 1
mint(log(rnorm(1))) # not obvious, only triggered sometimes
## Warning in log(rnorm(1)): NaNs produced
## Error in if (x > 0.5) "H" else "T": missing value where TRUE/FALSE needed

```

In Chapter 9, we will be particularly interested in ways to ensure input data integrity so that situations such as above will either fail gracefully or succeed bombastically.

Here, we should probably ensure that `x` is a single finite numeric value. Alternatively, we can test whether `all(x > 0.5, na.rm=TRUE)`.

Interestingly, objects other than logical are accepted: they will be coerced if needed.

```

x <- 1:5
if (length(x)) # i.e., length(x) != 0, but way less readable
  cat("length is not zero\n")
## length is not zero

```

Recall that coercion of numeric to logical yields `FALSE` if and only if the original value is zero.

### 8.1.4 Short-circuit evaluation

Especially for formulating logical conditions in `if` and `while` (see below), we have the scalar ``||`` (alternative) and ``&&`` (conjunction) operators.

```

FALSE || TRUE
## [1] TRUE
NA || TRUE
## [1] TRUE

```

Contrary to their vectorised counterparts (``|`` and ``&``), the scalar operators are lazy (Chapter 17) in the sense that they evaluate the first operand and then determine if the computing of the second one is necessary (because, e.g., `FALSE && whatever` is always `FALSE` anyway).

Therefore,

```

if (a && b)
  expression

```

is equivalent to:

```
if (a) {
  if (b) { # compute b only if a is TRUE
    expression
  }
}
```

and:

```
if (a || b)
  expression
```

corresponds to:

```
if (a) {
  expression
} else if (b) { # compute b only if a is FALSE
  expression
}
```

For instance, “`is.vector(x) && length(x) > 0 && x[[1]] > 0`” is a risk-free test that takes into account that “`x[[1]]`” has only the desired meaning for objects that are not nonempty vectors.

Some other examples:

```
{cat("spam"); FALSE} || {cat("ham"); TRUE} || {cat("cherries"); FALSE}
## spamham
## [1] TRUE
{cat("spam"); TRUE} && {cat("ham"); FALSE} && {cat("cherries"); TRUE}
## spamham
## [1] FALSE
```

Recall that the expressions within the curly braces are evaluated one after another and that the result is determined by the last value in the series.

**Exercise 8.3** Study the source code of `isTRUE` and `isFALSE` and determine if these functions could be useful in formulating the conditions within the `if` expressions.

## 8.2 Exception handling

Exceptions are exceptional, but they may happen and break things. For instance, when the internet connection drops while we try to download a file, an optimisation algorithm fails to converge, we just have a bug in our code, or:

```
read.csv("/path/to/a/file/that/does/not/exist")
## Warning in file(file, "rt"): cannot open file '/path/to/a/file/that/does/
## not/exist': No such file or directory
## Error in file(file, "rt"): cannot open the connection
```

Three types of *conditions* are frequently observed:

- errors – they stop the flow of execution,
- warnings – not critical, but can be turned into errors (see `warn` in **option**),
- messages – they transmit some diagnostic information.

They can be manually triggered using the **stop**, **warning**, and **message** functions.

Errors (but warnings too) can be handled by means of the **tryCatch** function, amongst others.

```
tryCatch({ # block of expressions to execute, until an error occurs
  cat("a\n")
  stop("b") # error - breaks the linear control flow
  cat("c\n")
},
error = function(e) { # executed immediately on an error
  cat(sprintf("error: %s\n", e[["message"]]))
},
finally = { # always executed at the end, regardless of error occurrence
  cat("finally!\n")
}
)
## a
## error: b
## finally!
```

The two other conditions can be ignored by calling **suppressWarnings** and **suppressMessages**.

```
log(-1)
## Warning in log(-1): NaNs produced
## [1] NaN
suppressWarnings(log(-1)) # yeah, yeah, we know what we're doing
## [1] NaN
```

**Exercise 8.4** At the time of writing of this book, when the **data.table** package is attached, it emits a message. Call **suppressMessages** to silence it. However, consecutive calls to **library** do not reload an already loaded package. Therefore, the message will only be seen once per R session.

Related functions include **stopifnot** discussed in Section 9.2 and **on.exit** mentioned in Section 17.4; see Section 9.3.4 for some code debugging tips.

## 8.3 Repeated evaluation

And now for something completely different... time for the elephant in the room!

We have been able to do without loops so far (and will be quite all right in the second part of the book, too). This is because many data processing tasks can be written in terms of vectorised operations such as ``+``, `sqrt`, `sum`, ``[``, `Map`, and `Reduce`. Oftentimes, compared to their loop-based counterparts, they are more readable and efficient. We will explore this in the exercises below.

However, at times, using an explicit `while` or `for` loop might be the only natural way of solving a problem, for instance, when processing chunks of data streams. Also, an explicitly “looped” algorithm may occasionally have better<sup>2</sup> time or memory complexity.

### 8.3.1 while

`if` considers a given logical condition and thus determines whether to execute a given statement. On the other hand,

```
while (condition) # single TRUE or FALSE, as in `if`
  expression
```

evaluates a given expression *as long as* the logical condition is true. Therefore, it is advisable to make the condition dependent on some variable that the expression can modify.

```
i <- 1
while (i <= 3) {
  cat(sprintf("%d, ", i))
  i <- i + 1
}
## 1, 2, 3,
```

Nested loops are possible, too:

```
i <- 1
while (i <= 2) {
  j <- 1
  while (j <= 3) {
    cat(sprintf("%d %d, ", i, j))
    j <- j + 1
  }
  cat("\n")
}
```

(continues on next page)

<sup>2</sup> In such cases, it will often benefit from a rewrite in C or C++; see Chapter 14.

(continued from previous page)

```

    i <- i + 1
  }
## 1 1, 1 2, 1 3,
## 2 1, 2 2, 2 3,

```

**Example 8.5** Implement a simple linear congruential pseudorandom number generator that, given some seed  $X_0 \in [0, m)$ , outputs a sequence  $(X_1, X_2, \dots)$  defined by:

$$X_i = (aX_{i-1} + c) \bmod m,$$

with, e.g.,  $a = 75$ ,  $c = 74$ , and  $m = 2^{16} + 1$  (here,  $\bmod$  is the division reminder, ``%%``). This generator has poor statistical properties and its use in practice is discouraged. In particular, after some number of operations  $k$ , we will find a cycle such that  $X_k = X_1, X_{k+1} = X_2, \dots$

### 8.3.2 for

The for-each loop:

```

for (name in vector)
  expression

```

takes each element, from the beginning to the end, in a given vector, assigns it some name, and evaluates the expression.

Example:

```

fridge <- c("spam", "spam", "bacon", "eggs")
for (food in fridge)
  cat(sprintf("%s, ", food))
## spam, spam, bacon, eggs,

```

Another example:

```

for (i in 1:length(fridge)) # better: seq_along(fridge), see below
  cat(sprintf("%s, ", fridge[i]))
## spam, spam, bacon, eggs,

```

One more:

```

for (i in 1:2) {
  for (j in 1:3)
    cat(sprintf("%d %d, ", i, j))
  cat("\n")
}
## 1 1, 1 2, 1 3,
## 2 1, 2 2, 2 3,

```

The iterator still exists after the loop's watch has ended:

```
print(i)
## [1] 2
print(j)
## [1] 3
```

---

**Important** Writing:

```
for (i in 1:length(x))
  print(x[i])
```

is reckless. If  $x$  is an empty vector, then:

```
x <- logical(0)
for (i in 1:length(x)) print(x[i])
## [1] NA
## logical(0)
```

Recall from [Chapter 5](#) that  $x[1]$  tries to access an out-of-bounds element here, and  $x[0]$  returns nothing.

We generally suggest replacing  $1:\text{length}(x)$  with `seq_along(x)` or `seq_len(length(x))`, wherever possible.

---



---

**Note** The model `for` loop above is roughly equivalent to:

```
name <- NULL
tmp_vector <- vector
tmp_iter <- 1
while (tmp_iter <= length(tmp_vector)) {
  name <- tmp_vector[[tmp_iter]]
  expression
  tmp_iter <- tmp_iter + 1
}
```

Note that the `tmp_vector` is determined before the loop itself. Hence, any changes to the vector will not influence the execution flow. Also, the loop can be applied on lists as well due to the use of `[[`]`.

---

**Example 8.6** Let  $x$  be a list and  $f$  be a function. The following code generates the same result as `Map(f, x)`:

```
n <- length(x)
```

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```
ret <- vector("list", n) # a new list of length `n`
for (i in seq_len(n))
  ret[[i]] <- f(x[[i]])
```

**Example 8.7** Let  $x$  and  $y$  be two lists and  $f$  be a function. Here is the most basic version of `Map(f, x, y)`.

```
nx <- length(x)
ny <- length(y)
n <- max(nx, ny)
ret <- vector("list", n)
for (i in seq_len(n))
  ret[[i]] <- f(x[[(i-1)%nx+1]], y[[(i-1)%ny+1]])
```

Note that  $x$  and  $y$  might be of different lengths. Feel free to upgrade the above code by adding a warning like the longer argument is not a multiple of the length of the shorter one. Also, rewrite it without using the modulo operator, ``%%``.

### 8.3.3 break and next

**break** can be used to escape the current loop. **next** skips the remaining expressions and advances to the next iteration (where the testing of the logical condition occurs).

Here is a rather random example:

```
x <- runif(1000)
s <- 0
for (e in x) {
  if (e > 0.1)
    next

  print(e)
  if (e < 0.01)
    break

  s <- s + e
}
## [1] 0.045556
## [1] 0.04206
## [1] 0.024614
## [1] 0.045831
## [1] 0.094841
## [1] 0.00062477
print(s)
## [1] 0.2529
```

Computes the sum of the elements in `x` that are less than or equal to 0.1 from the beginning, stopping at the first element less than 0.01.

We have used a frequently occurring design pattern:

```
for (e in x) {
  if (condition)
    next

  many_statements...
}
```

which is equivalent to:

```
for (e in x) {
  if (!condition) {
    many_statements...
  }
}
```

but which avoids introducing a nested block of expressions.

---

**Note** (\*) There is a third loop type,

```
repeat
  expression
```

which is a shorthand for

```
while (TRUE)
  expression
```

i.e., it is a possibly infinite loop. Such loops are invaluable when expressing situations such as *do-stuff-until-a-thing-happens*, e.g., when we want to execute a command at least once.

```
i <- 1
repeat { # while (TRUE)
  # simulate dice casting until we throw "1"
  if (runif(1) < 1/6) break # not an infinite loop after all
  i <- i+1
}
print(i)
## [1] 6
```

---

**Exercise 8.8** What is wrong with the following code?



```
j <- 1
while (j <= 10) {
  if (j %% 2 == 0) next
  print(j)
  j <- j + 1
}
```

**Exercise 8.9** *What about this one?*

```
j <- 1
while (j <= 10);
  j <- j + 1
```

### 8.3.4 return

**return**, when called from within a function, immediately yields a specified value and goes back to the caller.

For example, here is a simple recursive function that flattens a given list:

```
my_unlist <- function(x)
{
  if (is.atomic(x))
    return(x)

  # so if we are here, x is definitely not atomic
  out <- NULL
  for (e in x)
    out <- c(out, my_unlist(e))

  out # or return(out); it's the last expression anyway, so not necessary
}

my_unlist(list(list(list(1, 2), 3), list(4, list(5, list(6, 7:10)))))
## [1] 1 2 3 4 5 6 7 8 9 10
```

**return** is a function: the round brackets are obligatory.

### 8.3.5 Time and space complexity of algorithms (\*)

Analysis of algorithms can give us a rough estimate of their run times or memory consumption as a function of the input data size, especially for *big* data (e.g., [14, 43]).

In scientific computing and data science, we often deal with vectors (sequences) or matrices/data frames (tabular data). Therefore, we might be interested in determining how many *primitive operations* need to be performed as a function of their length  $n$  or the number of rows  $n$  and columns  $m$ , respectively.

For instance, the  $O$  (Big-Oh) notation can express the upper bounds for time/resource consumption in asymptotic cases. For instance, we say that the time complexity is  $O(n^2)$ , if for large  $n$ , the number of operations to perform will be proportional to *most* the square of the vector size (more precisely, there exists  $m$  and  $C > 0$  such that for all  $n > m$ , the number of operations is  $\leq Cn^2$ ).

Therefore, if we have two algorithms that solve the same task, one that has  $O(n^2)$  time complexity, and other of  $O(n^3)$ , it is better to choose the former. For large problem sizes, we expect it to be faster.

Moreover, whether time grows proportionally to  $\log n$ ,  $\sqrt{n}$ ,  $n$ ,  $n \log n$ ,  $n^2$ ,  $n^3$ , or  $2^n$ , can be informative in predicting how big the data can be if we have a fixed deadline or not too much space left on the disk.

**Exercise 8.10** The `hclust` function determines a hierarchical clustering of a dataset. It is fed with an object that stores the distance between all the pairs of input points. There are  $n(n-1)/2$  (i.e.,  $O(n^2)$ ) unique point pairs for any given  $n$ . One numeric scalar (double type) takes 8 bytes of storage. If you have 16 GB of RAM, what is the largest dataset that you can cluster on your machine using this function?

Oftentimes, we can learn about the time or memory complexity of the functions we use from their documentation; see, e.g., `help("findInterval")`.

**Example 8.11** A course in data structures in algorithms, which this one is not, will give us plenty of opportunities to implement many algorithms ourselves. This way, we can gain a lot of insights and intuitions.

For instance, this is a  $O(n)$ -time algorithm:

```
for (i in seq_len(n))
  expression
```

and this is one runs in  $O(n^2)$  time:

```
for (i in seq_len(n))
  for (j in seq_len(n))
    expression
```

as long as, of course, the *expression* is rather primitive (e.g., operations on scalar variables).

R is a very expressive language. Hence, quite complex and lengthy operations can look pretty innocent. After all, it is a glue language for rapid prototyping.

For example:

```
for (i in seq_len(n))
  for (j in seq_len(n))
    z <- z + x[[i]] + y[[j]]
```

can be seen as  $O(n^3)$  if each element in the lists  $x$  and  $y$  as well as  $z$  itself are atomic vectors of length  $n$ .

Similarly,

```
Map(mean, x)
```

is  $O(n^2)$  if  $x$  is a list of  $n$  atomic vectors, each of length  $n$ .

---

**Note** A quite common statistical scenario involves generating a data buffer of a fixed size:

```
ret <- c()
for (i in n)
  ret[[i]] <- generate_data(i) # here: ret[[length(ret)+1]] <- ...
```

This notation, however, involves growing the `ret` array in each iteration. Luckily, since R version 3.4.0, each such size extension has amortised  $O(1)$  time as some more memory is internally reserved for its prospective growth (dynamic arrays; see, e.g., Chapter 17 of [14]).

However, it is better to pre-allocate the output vector of the desired final size. We can construct vectors of specific lengths and types in an efficient way (more efficient than with `rep`) by calling:

```
numeric(3)
## [1] 0 0 0
numeric(0)
## numeric(0)
logical(5)
## [1] FALSE FALSE FALSE FALSE FALSE
character(2)
## [1] "" ""
vector("numeric", 8)
## [1] 0 0 0 0 0 0 0 0
vector("list", 2)
## [[1]]
## NULL
##
## [[2]]
## NULL
```

---

**Note** Not all data fit into memory, but it does not mean that we should start installing Apache Hadoop and Spark immediately. Some datasets can be processed on a chunk-by-chunk basis.

R enables data stream handling (some can be of infinite length) through file connections, for example:

```
f <- file("https://github.com/gagolews/teaching-data/raw/master/README.md",
  open="r") # a big file, the biggest file ever
i <- 0
while (TRUE) {
  few_lines <- readLines(f, n=4) # reads only four lines at a time
  if (length(few_lines) == 0) break
  i <- i + length(few_lines)
}
close(f)
print(i) # the number of lines
## [1] 90
```

Many functions support reading from/writing to already established connections of different types, e.g., **file**, **gzfile**, **textConnection**, batch-by-batch.

A frequent scenario involves reading a very large CSV, JSON, or XML file only by thousands of lines/records at a time, parsing and cleansing them, and exporting them to SQL databases (which we will exercise in Chapter 12).

## 8.4 Exercises

From now on, we must stay alert. Many, if not all, of the following tasks, can still be implemented without the explicit use of the R loops but based only on the operations covered in the previous chapters. If this is the case, try composing both the looped and loop-free versions. Use `microbenchmark::microbenchmark` or `proc.time` to compare their run times<sup>3</sup>.

**Exercise 8.12** Answer the following questions:

- Let  $x$  be a numeric vector. When does `if(x > 0) ...` yield a warning? When does it give an error? How to prevent this?
- What is the dangling `else`?
- What happens if you put `if` as the last expression in a curly braces block within a function's body?
- Why do we say that `&&` and `||` are lazy? What are their use cases?
- What is the difference between `&&` and `&`?
- Can `while` always be replaced with `for`? What about the other way around?
- What is wrong with `"return (1+2)*3"`?

<sup>3</sup> It might be the case that a `for`-based solution is faster (e.g., for larger objects) because of the use of a more efficient algorithm. Such cases will benefit from a rewrite in C or C++ (Chapter 14).

**Exercise 8.13** Verify which of the following can be safely used as logical conditions in **if** statements. If that is not the case for all  $x, y, \dots$ , determine the additional conditions that must be imposed to make them valid.

- $x == 0$ ,
- $x[y] > 0$ ,
- $\text{any}(x > 0)$ ,
- $\text{match}(x, y)$ ,
- $\text{any}(x \%in\% y)$ .

**Exercise 8.14** What can go wrong in the following code chunk, depending on the type and form of  $x$ ? Consider as many scenarios as possible.

```
count <- 0
for (i in 1:length(x))
  if (x[i] > 0)
    count <- count + 1
```

**Exercise 8.15** Implement **shift\_left**( $x, n$ ) and **shift\_right**( $x, n$ ). The former function gets rid of the first  $n$  observations in  $x$  and adds  $n$  missing values at the end of the resulting vector, e.g., **shift\_left**(**c**(1, 2, 3, 4, 5), 2) is **c**(3, 4, 5, NA, NA). On the other hand, **shift\_right**(**c**(1, 2, 3, 4, 5), 2) is **c**(NA, NA, 1, 2, 3).

**Exercise 8.16** Implement your version of **diff**.

**Exercise 8.17** Write a function that determines the longest ascending trend in a given numeric vector, i.e., the length of the longest subsequence of consecutive increasing elements. For example, the input **c**(1, 2, 3, 2, 1, 2, 3, 4, 3) should yield 4.

**Exercise 8.18** Implement the functions that round down and round up each element in a numeric vector to a number of decimal digits.

This concludes the first part of this magnificent book.

---



## **Part II**

# **Deeper**





---

## Designing functions

---

In Chapter 7, we learnt how to compose our own functions. This skill is vital to enforcing the good development practice of avoiding code repetition: running the same command sequence on different data.

This chapter is devoted to designing such reusable modules to make them easier to use, test, and maintain. We also provide some more technical details. They were not of the highest importance during our first exposure to this topic but are crucial to our better understanding of how R works.

---

### 9.1 Principles of sustainable design

Fine design is more art than science. As usual in real life, we will need to make many compromises. This is because improving things with regard to one criterion sometimes makes them worse with respect to other aspects<sup>1</sup> (also those that we are not aware of). Moreover, not everything that counts can nor will be counted.

Below we provide some observations, ideas, and food for thought.

#### 9.1.1 To write or abstain

Our functions can often be considered merely creative combinations of the building blocks available in base R or a few high-quality add-on packages<sup>2</sup>. Some are simpler than others. Thus, there is a question if a new operation should be introduced at all: whether we are faced with the case of multiplying entities without necessity.

On the one hand, the DRY (don't repeat yourself) principle tells us that the most frequently used code chunks (say, called at least thrice) should be generalised in the form of a new function. As far as *complex* operations are concerned, this is definitely a correct approach.

On the other hand, not every generalisation is necessarily welcome. Let us say we are tired of writing  $\mathbf{g}(\mathbf{f}(x))$  for the  $n$ -th time,  $n \geq 2$ . Why don't we introduce  $\mathbf{h}$  defined as a combination of  $\mathbf{g}$  and  $\mathbf{f}$ ? This might *seem* like a clever idea, but let us not take it

---

<sup>1</sup> Compare the notion of Pareto efficiency.

<sup>2</sup> If some nontrivial, basic operation is missing, we can implement it at the C language level; see Chapter 14.

for granted: being tired might be an indication of our body and mind needing a rest; being lazy can be a call for more self-discipline (not an overly popular word these days, but still, an endearing trait).

**Example 9.1** `paste0` is a specialised version of `paste`, but has the `sep` argument hardcoded to an empty string.

- Even if this might be the most often applied use case, is the introduction of a new function justifiable? Is it so hard to write `"paste=""` each time?
- Would changing `paste`'s default argument be better? That, of course, would harm backward compatibility, but what strategies could we apply to make the transition as smooth as possible?
- Would it be better to introduce a new version of `paste` with `sep` defaulting to `" "`, and inform the users that the old version is deprecated and to be removed in, say, two years? (or maybe one year is better? or five?)

**Example 9.2** In R 4.0, `deparse1` has been introduced: it is merely a combination of `deparse` (see below) and `paste`:

```
print(deparse1)
## function (expr, collapse = " ", width.cutoff = 500L, ...)
## paste(deparse(expr, width.cutoff, ...), collapse = collapse)
## <environment: namespace:base>
```

Let us say this covers 90% of use cases: was introducing it a justified idea then? What if that number was 99%?

Overall, more functions contribute to information overload. We do not want our users to be overwhelmed by too many choices. Luckily, nothing is cemented once and for all. Had we made bad design choices resulting in our API's being bloated, we could always clean up those that no longer spark joy.

### 9.1.2 To pamper or challenge

Think about the kind of audience we would like to serve: is it our team only, students, professionals, certain client groups, etc.? Do they have mathematical, programming, engineering, or scientific background? Not everything appropriate for one cohort will be valuable for another. And not everything pleasing some *now* will benefit them in the long run: people (their skills, attitudes, etc.) change.

**Example 9.3** Assume we are writing a friendly and inclusive package for novices who would like

to grasp the basics of data analysis as quickly<sup>3</sup> as possible. Without much effort, it would enable them to solve 80–95% of the most common, easy problems.

Think of introducing the students to a function that returns the five largest observations in a given vector. Let us call it **nlargest**: so pleasant to use. It makes the students feel empowered quickly.

Still, when faced with the remaining 5–20% of tasks, they will have to learn another, more advanced, generic, and powerful tool anyway (in our case, the base R itself). Are they determined and skilled enough to do that? Time will tell. The least we can do is to be explicit about it.

Recall that it took us some time to arrive at **order** and subsetting via ``[``. Assuming that we read this book from the beginning to the end and solve all the exercises, which we should, we are now able to author the said **nlargest** (and lots of other functions) ourselves, using a single line of code. This will also pay off in many scenarios that we will be facing in the future, e.g., when we consider matrices and data frames.

Yes, everyone will be reinventing their own **nlargest** this way. But this constitutes a great exercise: by our being too nice, some might have lost an opportunity to learn a new, more universal skill.

Although most users would love to minimise the effort put into all their activities, ultimately, they sometimes need to learn new things. Let us thus not be afraid to teach them stuff.

Furthermore, we do not want to discourage experts (or experts to-be) by presenting them with overly simplified solutions that keep their hands tied when something more ambitious needs to be done.

### 9.1.3 To build or reuse

In the short term, the *fail-fast* philosophy encourages us to build our applications using prefabricated components. This is fantastic at the early stage of its life cycle. If we build something really simple or whose purpose is merely to illustrate an idea, educate, or show off how “awesome” we are, let us be explicit about it so that other users do not feel obliged to treat our product (exercise) seriously.

In the (not so likely, probabilistically speaking) event of its becoming successful, we are expected to start thinking about the project’s long-term stability and sustainability. After all, relying on third-party functions, packages, or programs makes our software projects less... independent. This may be problematic since:

- the dependencies might not be available on every platform or may behave differently across various system configurations,

---

<sup>3</sup> We will leave the reflection on whether this is at all feasible for another time.

This strategy is employed by many companies (and drug dealers): make the introductory experience super-smooth and fun. At the same time, do not allow your users to become independent too easily. Instead, make them rely on your product lines/proprietary solutions/payable services etc.

The free software movement, with its do-it-yourself approach, emphasises users’ becoming autonomous. This does not contradict the user-friendliness (but that many open-source projects could benefit from becoming less exclusive is a different story, and this book tries to make a change in this area).

- they may be huge (and can depend on other external software too),
- their APIs may be altered, which can cause our code to break,
- their functionality can change, which can lead to some unexpected behaviours.

Hence, it might be better to rewrite some parts from scratch on our own.

**Exercise 9.4** *Identify some R packages on CRAN with many dependencies. See what functions they import from other packages. How often is it just a few lines of code?*

The UNIX philosophy emphasises building and using minimalist yet nontrivial, single-purpose, high-quality pieces of software that can work as parts of more complex pipelines. R serves as a glue language quite well.

In the long run, some of our software projects might converge to such a tool. Thus, we might have to standardise our API (e.g., make it available from the command line; [Section 1.2](#)) so that the users of other languages can benefit from our work.

---

**Important** If our project is merely a modified interface/front-end to a standalone program developed by others, we should be humble about it. We should strive to ensure we are not the ones who get all the credit for other people's work.

Also, we must clearly state how the original tools can be used to achieve the same goals, e.g., when working from the command line.

---

## 9.2 Managing data flow

A function, most of the time, can and should be treated as a black box: its callers do not have to care what it hides inside. After all, they are supposed to *use* it: given some *inputs*, they expect well-defined *outputs* (explained in very detail in the function's manual; see [Section 9.3.2](#)).

### 9.2.1 Checking input data integrity and argument handling

A function takes R objects of any kind as arguments, but it does not mean feeding it with every- or any-thing is healthy for its guts.

When designing functions, it is best to handle the inputs in a manner similar to base R's behaviour. This will make our contributions easier to work with.

Lamentably, base R functions frequently do not process arguments of a similar *kind* fully consistently. Such variability might be due to many reasons and, in essence, is not necessarily bad. Usually, there might be many possible behaviours and choosing one over another will make a few users unhappy anyway. Some choices might not be

optimal, but they are for historical compatibility (e.g., with S). Of course, it might also happen (but the probability is low) that there is a bug or something is poorly designed.

This is why it is better to keep the vocabulary quite restricted. Even if there are exceptions to the general rules, with fewer functions, they are easier to remember. We advocate for such minimalism in this book.

Consider the following case study, illustrating that even the extremely simple scenario dealing with a single positive integer is not necessarily straightforward.

**Exercise 9.5** In mathematical notation, we usually denote the number of objects in a collection with the famous “ $n$ ”.

It is implicitly assumed that such  $n$  is a single natural number (albeit whether this includes 0 or not should be specified at some point). The functions `runif`, `sample`, `seq`, `rep`, `strrep`, and `class::knn` take it as arguments. Nonetheless, nothing prevents their users from trying to challenge them by passing:

- `2.5`, `-1`, `0`, `1-1e-16` (non-positive numbers, non-integers);
- `NA_real_`, `Inf` (not finite);
- `1:5` (not of length 1; after all, there are no scalars in R)
- `numeric(0)` (an empty vector);
- `TRUE`, `NA`, `c(TRUE, FALSE, NA)`, `"1"`, `c("1", "2", "3")` (non-numeric, but coercible to);
- `list(1)`, `list(1, 2, 3)`, `list(1:3, 4)` (non-atomic);
- `"spam"` (utter nonsense);
- `as.matrix(1)`, `factor(7)`, `factor(c(3, 4, 2, 3))`, etc. (compound types; see [Chapter 10](#)).

Read the aforementioned functions' reference manuals and call them on different inputs. Notice how differently they handle such atypical arguments.

Sometimes we will rely on other functions to check data integrity for us.

**Example 9.6** Let us consider the following function that generates  $n$  pseudorandom numbers from the unit interval rounded to  $d$  decimal digits. We strongly believe or hope (good faith and high competence assumption) that its authors knew what they were doing when they wrote:

```
round_rand <- function(n, d)
{
  x <- runif(n) # runif will check if `n` makes sense
  round(x, d)  # round will determine the appropriateness of `d`
}
```

What constitutes correct  $n$  and  $d$  and how the function behaves when not provided with positive integers is determined by the two underlying functions, `runif` and `round`:

```

round_rand(4, 1) # the expected use case
## [1] 0.3 0.8 0.4 0.9
round_rand(4.8, 1.9) # 4, 2
## [1] 0.94 0.05 0.53 0.89
round_rand(4, NA)
## [1] NA NA NA NA
round_rand(0, 1)
## numeric(0)

```

Many such design choices can be defended if they are well thought-out and adequately documented. Some programmers will opt for high uniformity/compatibility across numerous tools, but there are cases where some exceptions/diversity do more good than harm.

Yet, our functions might be part of a more complicated data flow pipeline. It might happen that some other procedure generates a value that we did not expect (because of a bug therein or because we did not study its manual). The problem arises when this *unthinkable* value passed to our function. In our case, this would correspond to the said *n*'s or *d*'s being determined programmatically.

**Example 9.7** *Continuing the previous example, the following might be somewhat challenging with regard to our being flexible and open-minded:*

```

round_rand(c(100, 42, 63, 30), 1) # length(c(...)), 1
## [1] 0.7 0.6 0.1 0.9
round_rand("4", 1) # as.numeric(...), 1
## [1] 0.2 0.0 0.3 1.0

```

*Sure, it is quite convenient. Nevertheless, it might lead to problems that are hard to diagnose.*

*Also, note the not so informative error messages in cases like:*

```

round_rand(NA, 1)
## Error in runif(n): invalid arguments
round_rand(4, "1")
## Error in round(x, d): non-numeric argument to mathematical function

```

Hence, some *defensive design* mechanisms are not a bad idea, especially if they lead to generating an informative error message.

---

**Important** `stopifnot` gives a convenient means to assert the enjoyment of our expectations about a function's arguments (or some intermediate values). A call to `stopifnot(cond1, cond2, ...)` is more or less equivalent to:

```

if (!(is.logical(cond1) && !any(is.na(cond1)) && all(cond1)))
  stop("`cond1` are not all TRUE")
if (!(is.logical(cond2) && !any(is.na(cond2)) && all(cond2)))

```

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```
stop("`cond2` are not all TRUE")
...
```

Thus, if all the elements in the given logical vectors are TRUE, nothing happens. We can move on with certainty.

**Example 9.8** *We can rewrite the above function as follows:*

```
round_rand2 <- function(n, d)
{
  stopifnot(
    is.numeric(n), length(n) == 1,
    is.finite(n), n > 0, n == floor(n),
    is.numeric(d), length(d) == 1,
    is.finite(d), d > 0, d == floor(d)
  )
  x <- runif(n) # runif will check if n makes sense
  round(x, d)   # round will determine the appropriateness of d
}

round_rand2(5, 1)
## [1] 0.7 0.7 0.5 0.6 0.3
round_rand2(5.4, 1)
## Error in round_rand2(5.4, 1): n == floor(n) is not TRUE
round_rand2(5, "1")
## Error in round_rand2(5, "1"): is.numeric(d) is not TRUE
```

It is the strictest test for “a single positive integer” possible. In the case of any violation of the underlying condition, we get a very informative error message.

**Example 9.9** *At other times, we might be interested in the argument checking like:*

```
if (!is.numeric(n))
  n <- as.numeric(n)
if (length(n) > 1) {
  warning("only the first element will be used")
  n <- n[1]
}
n <- floor(n)
stopifnot(is.finite(n), n > 0)
```

This way, “4” and `c(4.9, 100)` will all be accepted as 4<sup>4</sup>.

We see that there is always a tension between being generous/flexible and precise/restrictive. Also, because of their particular use cases, for some functions, it will

<sup>4</sup> We rely on the S3 generics `is.numeric` and `as.numeric` here; see [Section 10.4](#).

be better to behave differently than the others. Too much uniformity is as bad as chaos. We are expected to rely on common sense, but adding lightweight foolproof mechanisms is always welcome.

It is our duty to be explicit about all the assumptions we make or exceptions we allow (by writing comprehensive documentation; see [Section 9.3.2](#)).

We will revisit this topic in [Section 10.4](#).

---

**Note** Example exercises related to improving the consistency of base R's argument handling in different domains include the **vctrs** and **stringx** packages<sup>5</sup>. Can these contributions be justified?

---

**Exercise 9.10** *Reflect on how you would act in the following scenarios (and how base R and other packages or languages you know deal with them):*

- a vectorised mathematical function (empty vectors? non-numeric inputs? what if it is equipped with the `names` attribute? what if it has other ones?);
- an aggregation function (what about missing values? empty vectors?);
- a function vectorised with regard to two arguments (elementwise vectorisation? recycling rule? only scalar vs vector or vector vs vector of the same length allowed? what if one argument is a row vector and the other is a column vector);
- a function vectorised with respect to all arguments (really all? maybe some exceptions are necessary?);
- a function vectorised with respect to the first argument but not the second (why such a restriction? when?).

*Find a few functions that match each case.*

## 9.2.2 Putting outputs into context

Our functions do not exist in a vacuum. We should put them into a much broader context: how can they be combined with other tools?

As a general rule, we ought to generate outputs of a *predictable* kind. This way, we can easily deduce what will happen in the code chunks that utilise them.

**Example 9.11** *Some base R functions do not adhere to this rule for the sake of (questionable) users' convenience. We will meet a few of them in [Chapter 11](#) and [Chapter 12](#). In particular, **sapply** and the underlying **simplify2array**, can return a list, an atomic vector, or a matrix.*

```
simplify2array(list(1, 3:4))  # list
## [[1]]
## [1] 1
```

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---

<sup>5</sup> Yours truly is the author of the latter and thus is guilty of multiplying entities beyond necessity.



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```
##
## [[2]]
## [1] 3 4
simplify2array(list(1, 3))      # vector
## [1] 1 3
simplify2array(list(1:2, 3:4)) # matrix
##      [,1] [,2]
## [1,] 1    3
## [2,] 2    4
```

Further, the index operator with `drop=TRUE`, which is the default, may output an atomic vector. However, it may as well yield a matrix or a data frame.

```
(A <- matrix(1:6, nrow=3)) # an example matrix
##      [,1] [,2]
## [1,] 1    4
## [2,] 2    5
## [3,] 3    6
A[1, ] # vector
## [1] 1 4
A[1:2, ] # matrix
##      [,1] [,2]
## [1,] 1    4
## [2,] 2    5
A[1, , drop=FALSE] # matrix with 1 row
##      [,1] [,2]
## [1,] 1    4
```

We proclaim that the default functions' behaviour should be to return the object of the most generic kind possible (if there are other options). Then:

- either we equip the function with a further argument which must be explicitly set if we *really* wish to simplify the output,
- or we ask the user to call a simplifier explicitly after the function call. In this case, if the simplifier cannot neaten the object, it should probably fail by issuing an error or at least try to apply some brute force solution (e.g., “fill the gaps” somehow itself, preferably with a warning).

**Example 9.12** For instance:

```
as.numeric(A[1:2, ]) # always returns a vector
## [1] 1 2 4 5
stringi::stri_list2matrix(list(1, 3:4)) # fills the gaps with NAs
##      [,1] [,2]
## [1,] "1"  "3"
## [2,] NA   "4"
```

Ideally, a function is expected to perform one (and only one) well-defined task. If it tends to generate objects of different kinds, depending on the arguments provided, it might be better to compose two or more separate procedures instead.

**Exercise 9.13** Functions such as *rep*, *seq*, and *sample* do not perform a single task. Or do they?

---

**Note** (\*) In a purely functional programming language, we can assume the so-called *referential transparency*: a call to a *pure function* can always be replaced with the *value* it generates. If this is true, then for the same set of argument values, the output is always the same. Furthermore, there are no side effects. In R, it is not exactly the case:

- a call can introduce/modify/delete variables in other environments (see [Chapter 16](#)), e.g., the state of the random number generator,
  - due to lazy evaluation, functions are free to interpret the argument *forms* (passed expressions, i.e., not only: values) in whatever way they like (see [Section 9.5.7](#), [Section 12.3.9](#), and [Section 17.5](#)),
  - printing, plotting, file reading, and database access have apparent consequences with regard to the state of some external resources.
- 

**Important** Each function must return some value, but there are several instances (e.g., plotting, printing), where this does not make sense.

In such a case, we may consider returning `invisible(NULL)`, a `NULL` whose *first* printing will be suppressed.

Compare the following:

```
(function() NULL)() # anonymous function, called instantly
## NULL
(function() invisible(NULL))() # printing suppressed
x <- (function() invisible(NULL))()
print(x) # no longer invisible
## NULL
```

Take a look at the return value of the built-on `cat`.

---

## 9.3 Organising and maintaining functions

### 9.3.1 Function libraries

Definitions of frequently-used functions or datasets can be emplaced in separate source files (.R extension) for further reference.

Such libraries can be executed by calling:

```
source("path_to_file.R")
```

**Exercise 9.14** Create a source file (script) named `mylib.R`, where you define a function called `nlargest` which returns a few largest elements in a given atomic vector.

From within another script, call `source("mylib.R")` (note that relative paths refer to the current working directory; (compare Section 2.1.6)). Then, write a few lines of code where you test `nlargest` on some example inputs.

### 9.3.2 Writing R packages (\*)

When a function library grows substantially, or when there is a need for equipping it with the relevant manual pages<sup>6</sup> (Section 9.3.2) or compiled code (Chapter 14), turning it into an R package (Section 7.3.1) might be worth considering. This is the case even if it is only for our own or small team's purpose.

---

**Important** You *do not have to* publish your package on CRAN<sup>7</sup>. Many users are tempted to submit whatever they have been tinkering around with for a while. Have mercy on the busy CRAN maintainers and do not contribute to the information overload unless you have come up with something potentially of service for other R users (make it less about you and more about the community; thank you in advance). R packages can always be hosted on and installed from, for instance, GitLab or GitHub.

---

#### Package structure (\*)

A *source package* is merely a directory containing some special files and subdirectories:

- `DESCRIPTION` – a text file that gives the name of the package, its version, authors, dependencies on other packages, license, etc.;
- `NAMESPACE` – a text file containing directives stating which objects are to be exported so that they are available to the package users and which names are to be imported from other packages;
- `R` – a directory with R scripts (.R files), which define, e.g., functions, example datasets, etc.;
- `man` – a directory with R documentation files (.Rd), describing at least all the exported objects; see Section 9.3.2;
- `src` – optional; compiled code, see Chapter 14;
- `tests` – optional; tests to run on the package check, see Section 9.3.4.

---

<sup>6</sup> This should read: i.e., always.

<sup>7</sup> And always consult the CRAN Repository Policy at <https://cran.r-project.org/web/packages/policies.html>.

See Section 1 of [62] for more details and other options. We do not need to repeat the information from the official manual as all readers can read it themselves.

**Exercise 9.15** *Inspect the source code of the example package available for download from <https://github.com/gagolews/rpackagedemo/>.*

## Building and installing (\*)

Recall from Section 7.3.1 that a source package can be built and installed by calling:

```
install.packages("pkg_directory", repos=NULL, type="source")
```

Then it can be used as any other R package (Section 7.3.1). In particular, it can be loaded and attached to the search path (Section 16.2.6) via a call to:

```
library("pkg")
```

This makes all the objects marked as exportable in its NAMESPACE file available to the user; see also Section 16.3.5.

**Exercise 9.16** *Create your own package **nypkg** featuring the solutions to the exercises you have solved whilst studying the material in the previous chapters. When in doubt, refer to the official manual [62].*

---

**Note** (\*) The building and installing of packages also be done from the command line:

```
R CMD build pkg_directory # creates a distributable source tarball (.tar.gz)
R CMD INSTALL pkg-version.tar.gz
R CMD INSTALL --build pkg_directory
```

Also, some users could potentially benefit from creating their own Makefiles that help automate the processes of building, testing, checking, etc.

---

## Documenting R packages (\*)

Documenting functions and commenting code thoroughly is critical, even if we just write for ourselves. Most programmers sooner or later will notice that they find it hard to determine what a piece of code is doing after they take a break from it. In some sense, we always communicate with external audiences, which includes our future selves.

The help system is one of the stronger assets of the R environment. By far, we most likely have interacted with many documentation pages and got a general idea of what constitutes an informative documentation piece.

From the technical side, R Documentation (.Rd) files are located in the `man` subdirectory of a source package. All exported objects (e.g., functions) should be described clearly. Additional topics can be covered too.

During the package installation, the .Rd files are converted to various output formats, e.g., HTML or plain text, and displayed on a call to the well-known **help** function.

Documentation files use a LaTeX-like syntax, which looks quite obscure to an untrained eye. The relevant commands are explained in very detail in Section 2 of *Writing R Extensions* [62].

---

**Note** The process of writing .Rd files by hand might be tedious, especially keeping track of the changes to the `\usage` and `\arguments` commands. Rarely do we recommend the use of third-party packages: base R facilities are usually sufficient. But **roxy-gen2** might be worth a try because it makes the developers' lives easier. Most importantly, it allows the documentation to be specified alongside the functions' definitions, which is much more natural.

---

**Exercise 9.17** *Add a few manual pages to your example R package.*

### 9.3.3 Writing standalone programs (\*\*)

Section 7.3.2 mentioned how to call external programs using **system2**.

On UNIX-like operating systems, it is easy to turn our R scripts into standalone tools that can be run from the shell. We already touched upon this topic in Section 1.2.3.

The **commandArgs** function returns the list of arguments passed from the command line to our script in the form of a character vector. Whatever we do with them is up to us. Moreover, **q** can terminate a script, yielding any integer return code. By convention, anything other than 0 indicates an error.

**Example 9.18** *Say we have the following script named `testfile` in the current directory:*

```
#!/bin/env -S Rscript --vanilla

argv <- commandArgs(trailingOnly=TRUE)
cat("commandArgs:\n")
print(argv)

if (length(argv) == 0) {
  cat("Usage: testfiles file1 file2 ... \n")
  q(save="no", status=1) # exit with code 1
}

if (!all(file.exists(argv))) {
  cat("Some files do not exist. \n")
  q(save="no", status=2) # exit with code 2
}

cat("All files exist. \n")
```

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*# exits with code 0 (success)**Example interactions with this program from the UNIX-like terminal (bash):*

```

chmod u+x testfiles # add permission to execute
./testfiles
## commandArgs:
## character(0)
## Usage: testfiles file1 file2 ...
./testfiles spanish_inquisition
## commandArgs:
## [1] "spanish_inquisition"
## Some files do not exist.
./testfiles spam bacon eggs spam
## commandArgs:
## [1] "spam" "bacon" "eggs" "spam"
## All files exist.

```

The **stdin**, **stdout**, and **stderr** represent the always-open connections mapped to the standard input (“keyboard”), and normal and error output. They can be read from or written to using functions such as **scan** or **cat**.

During run time, we can redirect **stdout** and **stderr** to different files or even strings using **sink**.

### 9.3.4 Assuring quality code

Below we mention some good development practices related to maintaining quality code. This is an important topic, but writing about them is tedious to the same extent that reading about them is boring: it is the more-artistic part of software engineering. After all, they are some heuristics that are learnt best by observing and mimicking what the others are doing (and hence the exercises below will encourage us to do so).

#### Managing changes and working collaboratively

We are recommended to employ some source code version control system, such as **git**, to keep track of the changes made to the software.

---

**Note** It is worth investing time and effort to learn how to use **git** from the command line; see <https://git-scm.com/doc>.

---

There are a few hosting providers for **git** repositories, with GitLab and GitHub being particularly popular among open-source software developers. They support working

collaboratively on the projects and are equipped with additional tools for reporting bugs, suggesting feature requests, etc.

**Exercise 9.19** Find where the source code of your favourite R packages or other open-source projects is hosted. Explore the corresponding repositories, feature trackers, wikis, discussion boards, etc. Each community is different and is governed by varied, sometimes contrasting guidelines: after all, we come from all corners of the world.

### Test-driven development and continuous integration

It is often hygienic to include some principles of test-driven development when writing own functions.

**Exercise 9.20** Assume that, for some reason, we were asked to compose a function to compute the root mean square (quadratic mean) of a given numeric vector. Before implementing the actual routine, we need to reflect upon what we want to achieve, especially how we want our function to behave in certain boundary cases.

**stopifnot** gives simple means to ensure a given assertion is fulfilled. If that is the case, it will move forward quietly.

Let us say we have come up with the following set of expectations:

```
stopifnot(all.equal(rms(1), 1))
stopifnot(all.equal(rms(1:100), 58.16786054171151931769))
stopifnot(all.equal(rms(rep(pi, 10)), pi))
stopifnot(all.equal(rms(numeric(0)), 0))
```

Write a function **rms** that fulfils the above assertions.

**Exercise 9.21** Implement your version of the **sample** function (assuming **replace=TRUE**), using calls to **runif**. Start by writing a few unit tests.

A couple of R packages support writing and executing unit tests, including **testthat**, **tinytest**, **RUnit**, or **realtest**. However, in the most typical use cases, relying on **stopifnot** is powerful enough.

**Exercise 9.22** (\*) Consult the Writing R Extensions manual [62] about where and how to include unit tests in your example package.

---

**Note** (\*) R includes a built-in mechanism to check a couple of code quality areas: running **R CMD check pkg\_directory** from the command line (preferably using the most recent version of R) can suggest several improvements.

Also, it is possible to use various continuous integration techniques that are automatically triggered when pushing changes to our software repositories; see GitLab CI or GitHub Actions. For instance, running a package build, install, and check process is possible on every **git** commit. Also, CRAN features some continuous integration services, including checking the package on various platforms.

---

## Debugging

For all his life, the current author has been debugging his programs primarily by manually printing the state of the suspicious variables (**printf** and the like) in different code areas. Hahaha lololol, so old school. Yet, weirdly efficient.

R has an interactive debugger; see the **browser** function. Also, refer to Section 9 of [66] for more details.

Some IDEs (e.g., **RStudio**) support this feature, too; see their corresponding documentation.

## Profiling

Typically, a program spends a relatively long time executing only a small portion of code. The **Rprof** function can be a helpful tool to identify which chunks might need a rewrite, for instance, using a compiled language (Chapter 14).

Please remember, though, that bottlenecks are not only formed by using algorithms with high computational complexity, but also data input and output (such as reading files from disk, printing messages on the console, querying Web APIs, etc.).

## 9.4 Special functions: Syntactic sugar

Some functions, such as ``*``, are somewhat special. They can be referred to using an alternative syntax which, for some reason, most of us accepted as the default one. Below we will reveal, amongst others, that “5 \* 9” reduces to an ordinary function call:

```
`*`(5, 9) # a call to `*` with 2 arguments, equivalent to 5 * 9
## [1] 45
```

### 9.4.1 Backticks

In Section 2.2, we have mentioned that we can assign (as in ``<-``) *syntactically valid names* to our objects. Most identifiers comprised of letters, digits, dots, and under-scores can be used directly in R code.

Nevertheless, it is possible to label our objects however we like: not syntactically valid (nonstandard) identifiers just need to be enclosed in backticks (back quotes, grave accents):

```
`42 a quite peculiar name :0 tlollolll` <- c(a=1, `b c`=2, `42`=3, `!`=4)
1/(1+exp(-`42 a quite peculiar name :0 tlollolll`))
##      a      b c      42      !
## 0.73106 0.88080 0.95257 0.98201
```



Of course, such names are less convenient. However, backticks let us refer to them in *any* context.

### 9.4.2 Dollar, ``$`` (\*)

The dollar operator, ``$``, can be an alternative accessor to a single element in a named list<sup>8</sup>.

If the label is a syntactically valid name, then `x$label` does the same job as `x[["label"]]` (saving five keystrokes: such a burden!).

```
x <- list(spam="a", eggs="b", `eggs and spam`="c", best.spam.ever="d")
x$eggs
## [1] "b"
x$best.spam.ever # recall that a dot has no special meaning in most contexts
## [1] "d"
```

Nonstandard names must still be enclosed in backticks:

```
x$`eggs and spam` # x[["eggs and spam"]] is okay as usual
## [1] "c"
```

We are minimalist by design here. Thence, we will avoid this operator, as it does not increase the expressive power of our function repertoire. Also, it works on neither atomic vectors nor matrices.

Furthermore, it does not work with names that are generated programmatically:

```
what <- "spam"
x$what # the same as x[["what"]] - we don't want this
## NULL
x[[what]] # works fine
## [1] "a"
```

The support for the *partial matching* of element names has been added to provide the users working in quick-and-dirty, interactive programming sessions with some relief in the case where they find the typing of the whole label extremely problematic:

```
x$s
## Warning in x$s: partial match of 's' to 'spam'
## [1] "a"
```

Compare:

```
x[["s"]] # no warning here...
## NULL
```

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---

<sup>8</sup> And hence also from data frames.

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```
x[["s", exact=FALSE]]
## [1] "a"
```

It is generally a bad programming practice. The result depends on the names of other items in `x` (which might change later) and can decrease code readability. The only reason why we obtained a warning message was because this book enforces the **options**(warnPartialMatchDollar=TRUE) setting, which, sadly, is not the default.

Note the behaviour on an ambiguous partial match:

```
x$egg # ambiguous resolution
## NULL
```

as well as on an element assignment:

```
x$s <- "e"
str(x)
## List of 5
## $ spam      : chr "a"
## $ eggs      : chr "b"
## $ eggs and spam : chr "c"
## $ best.spam.ever: chr "d"
## $ s         : chr "e"
```

This did not modify `spam`: it added a new element, `s`.

### 9.4.3 Curly braces, `{}`

A block of statements grouped with curly braces, `{}`, corresponds to a function call. When we write:

```
{
  print(TRUE)
  cat("two")
  3
}
```

```
## [1] TRUE
## two
## [1] 3
```

The parser translates it to a call to:

```
`{`(print(TRUE), cat("two"), 3)
## [1] TRUE
## two
## [1] 3
```

When the above is executed, every argument, one by one, is evaluated. Then, the last value is returned as the result of that call.

#### 9.4.4 ``if``

`if` is a function, too. As mentioned in [Section 8.1](#), it returns the value corresponding to the expression that is evaluated conditionally. Hence, we may write:

```
if (runif(1) < 0.5) "head" else "tail"
## [1] "head"
```

but also:

```
`if`(runif(1) < 0.5, "head", "tail")
## [1] "head"
```

---

**Note** A call like ``if`(test, what_if_true, what_if_false)` can only work correctly because of the lazy evaluation of function arguments; see [Chapter 17](#).

---

On a side note, **while**, **for**, **repeat** can also be called that way, but they return **invisible(NULL)**.

#### 9.4.5 Operators are functions

##### Calling built-in operators as functions

Every arithmetic, logical, and relational operator is translated to a call to the corresponding function. For instance:

```
`<`(`+`(`*`(`-`(3), 4)), 5) # 2+(-3)*4 < 5
## [1] TRUE
```

Also, `x[i]` is equivalent to ``[(x, i)` and `x[[i]]` maps to ``[[`(x, i)`.

Knowing this will not only enable us to manipulate unevaluated R code ([Chapter 15](#)) or access the corresponding manual pages (see, e.g., `help("[")`), but also verbalise some expressions more concisely. For instance,

```
x <- list(1:5, 11:17, 21:23)
unlist(Map(`[, x, 1)) # 1 is a further argument passed to `[`
## [1] 1 11 21
```

is equivalent to a call to `Map(function(e) e[1], x)`.

---

**Note** Unsurprisingly, the assignment operator, ``<-``, is also a function. It returns the assigned value invisibly.

``<-`` binds right to left (compare `help("Syntax")`). Thus, the expression `"a <- b <- 1"` assigns 1 to both b and a. It is equivalent to `"`<-`("a", `<-`("b", 1))"` and `"`<-`("b", 1)"` returns 1.

Owing to the pass-by-value semantics (Section 9.5.1), we can also expect that we will always be assigning a *copy* of the value on the right-hand side (with the exception of environments; Chapter 16).

```
x <- 1:6
y <- x # makes a copy (but delayed, on demand, for performance reasons)
y[c(TRUE, FALSE)] <- NA_real_ # modify every 2nd element
print(y)
## [1] NA 2 NA 4 NA 6
print(x) # state of x has not changed – x and y are different objects
## [1] 1 2 3 4 5 6
```

This is especially worth pointing out to Python (amongst others) programmers, where the above assignment would mean that x and y both refer to the same (shared) object in the computer's memory.

However, with no harm done to semantics, copying x is postponed until absolutely necessary (Section 16.1.4). This is efficient both time- and memory-wise.

## Creating own binary operators

We can also introduce our own binary operators named like ``%myopname``:

```
`%:)%` <- function(e1, e2) (e1+e2)/2
5 %:)% 1:10
## [1] 3.0 3.5 4.0 4.5 5.0 5.5 6.0 6.5 7.0 7.5
```

Recall that ``%`` and ``%/`` are built-in operators denoting division remainder and integer division. Also, in Chapter 11, we will learn about ``%*``, which implements matrix multiplication.

**Note** Chapter 10 notes that most existing operators can be overloaded for objects of different types.

### 9.4.6 Replacement functions

Functions generally do not change the state of their arguments. However, there is some syntactic sugar that allows us to replace objects or their parts with new content. We call them *replacement functions*.

For instance, three of the following calls *replace* the input x with its modified version:

```
x <- 1:5 # example input
x[3] <- 0 # replace the 3rd element with 0
length(x) <- 7 # "replace" length
names(x) <- LETTERS[seq_along(x)] # replace the names attribute
print(x) # `x` is now different
## A B C D E F G
## 1 2 0 4 5 NA NA
```

## Creating replacement functions

A replacement function is a mapping named like ``name<-`` with at least two parameters:

- `x` (the object to be modified),
- ... (possible further arguments),
- `value` (as the last parameter; the object on the right-hand side of the `<-`` operator).

We will most often interact with *existing* replacement functions, not create our own ones. But knowing how to do the latter is vital to understanding this language feature.

For example:

```
`add<-` <- function(x, where=TRUE, value)
{
  x[where] <- x[where] + value
  x # the modified object that will replace the original one
}
```

The above aims to add some `value` to a subset of the input vector `x` (by default, to each element therein). Then, it returns its altered version.

```
y <- 1:5 # example vector
add(y) <- 10 # calls `add<-`(y, value=10)
print(y) # y has changed
## [1] 11 12 13 14 15
add(y, 3) <- 1000 # calls `add<-`(y, 3, value=1000)
print(y) # y has changed again
## [1] 11 12 1013 14 15
```

We see that calling `"add(y, w) <- v"` works as if we have called `"y <- `add<-`(y, w, value=v)"`.

---

**Note** (\*) According to [66], a call `"add(y, 3) <- 1000"` is a syntactic sugar precisely for:

```
`*tmp*` <- y # temporary substitution
```

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```
y <- `add<-`(`*tmp*`, 3, value=1000)
rm("*tmp*") # remove the named object from the current scope
```

This has at least two implications. First, in the unlikely event that a variable `*tmp*` existed before the call to the replacement function, it will be no more, it will cease to be. It will be an ex-variable. Second, the temporary substitution guarantees that `y` must exist before the call (a function's body does not have to refer to all the arguments passed; because of lazy evaluation, see [Chapter 17](#), we could get away with it otherwise).

## Substituting parts of vectors

The replacement versions of the subsetting operators are named as follows:

- ``[<-`` is used in substitutions like `"x[i] <- value"`,
- ``[[<-`` is called when we perform `"x[[i]] <- value"`,
- ``$<-`` is used whilst calling `"x$i <- value"`.

Here is a use case:

```
x <- 1:5
`[<-`(x, c(3, 5), NA_real_) # returns a new object
## [1] 1 2 NA 4 NA
print(x) # does not change the original input
## [1] 1 2 3 4 5
```

On a side note, ``length<-`` can be used to expand or shorten a given vector by calling `"length(x) <- new_length"`; see also [Section 5.3.3](#).

```
x <- 1:5
x[7] <- 7
length(x) <- 10
print(x)
## [1] 1 2 3 4 5 NA 7 NA NA NA
length(x) <- 3
print(x)
## [1] 1 2 3
```

Semantically speaking, calling ``[<-`` breeds a new vector (a modified version of the original one). Luckily, we may expect some performance optimisations behind the scenes.

**Exercise 9.23** Write a function ``extend<-``, which pushes new elements at the end of a given vector, modifying it in place.

```
`extend<-` <- function(x, value) ...to.do...
```

Example use:

```
x <- 1
extend(x) <- 2      # push 2 at the back
extend(x) <- 3:10   # add 3, 4, ..., 10
print(x)
## [1] 1 2 3 4 5 6 7 8 9 10
```

## Replacing attributes

There are many replacement functions to reset object attributes (Section 4.4). In particular, each special attribute has its replacement procedure, e.g., ``names<-``, ``class<-``, ``dim<-``, ``levels<-``, etc.

```
x <- 1:3
names(x) <- c("a", "b", "c") # change the `names` attribute
print(x) # x has been altered
## a b c
## 1 2 3
```

Individual (arbitrary, including non-special ones) attributes can be set using ``attr<-``, and all of them can be established via a single call to ``attributes<-``.

```
x <- "spam"
attributes(x) <- list(shape="oval", smell="meaty")
attributes(x) <- c(attributes(x), taste="umami")
attr(x, "colour") <- "rose"
print(x)
## [1] "spam"
## attr(,"shape")
## [1] "oval"
## attr(,"smell")
## [1] "meaty"
## attr(,"taste")
## [1] "umami"
## attr(,"colour")
## [1] "rose"
```

Also, setting an attribute to NULL results, by convention, in its removal:

```
attr(x, "taste") <- NULL # this is tasteless now
print(x)
## [1] "spam"
## attr(,"shape")
## [1] "oval"
## attr(,"smell")
```

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```
## [1] "meaty"
## attr(,"colour")
## [1] "rose"
attributes(x) <- NULL # remove all
print(x)
## [1] "spam"
```

Which can be worthwhile in contexts such as:

```
x <- structure(c(a=1, b=2, c=3), some_attr="value")
y <- `attributes<-`(x, NULL)
```

Here, `x` retains its attributes, and `y` is a version of `x` with metadata removed.

## Compositions of replacement functions

Updating only selected names like:

```
x <- c(a=1, b=2, c=3)
names(x)[2] <- "spam"
print(x)
##      a spam      c
##      1   2      3
```

is possible due to the fact that “`names(x)[i] <- v`” is equivalent to:

```
old_names <- names(x)
new_names <- `[<-`(old_names, i, value=v)
x <- `names<-`(x, value=new_names)
```

---

**Important** More generally, a composition of replacement calls “`g(f(x, a), b) <- y`” yields a result equivalent to “`x <- `f<-`(x, a, value=`g<-`(f(x, a), b, value=y))`”. Both `f` and ``f<-`` need to be defined, but having `g` is not necessary.

---

**Exercise 9.24** (\*) What is “`h(g(f(x, a), b), c) <- y`” equivalent to?

**Exercise 9.25** Write a (convenient!) function ``recode<-`` which replaces specific elements in a character vector with some other ones, allowing the following interface:

```
`recode<-` <- function(x, value) ...to.do...
x <- c("spam", "bacon", "eggs", "spam", "eggs")
recode(x) <- c(eggs="best spam", bacon="yummy spam")
print(x)
## [1] "spam"          "yummy spam"    "best spam"     "spam"          "best spam"
```



We see that the named character vector gives a few *from="to"* pairs, e.g., all *eggs* are to be replaced by *best spam*.

Now, determine which calls are equivalent to the following:

```
x <- c(a=1, b=2, c=3)
recode(names(x)) <- c(c="z", b="y") # or equivalently = ... ?
print(x)
## a y z
## 1 2 3
y <- list(c("spam", "bacon", "spam"), c("spam", "eggs", "cauliflower"))
recode(y[[2]]) <- c(cauliflower="broccoli") # or = ... ?
print(y)
## [[1]]
## [1] "spam" "bacon" "spam"
##
## [[2]]
## [1] "spam"      "eggs"      "broccoli"
```

**Exercise 9.26** (\*) Consider the `recode<-` function from the previous exercise.

Here is an example matrix with the `dimnames` attribute whose `names` attribute is set (more details in Chapter 11):

```
(x <- Titanic["Crew", "Male", , ])
##      Survived
## Age      No Yes
## Child    0    0
## Adult 670 192
recode(names(dimnames(x))) <- c(Age="age", Survived="survived")
print(x)
##      survived
## age      No Yes
## Child    0    0
## Adult 670 192
```

This changes the `x` object. For each of the following subtasks, compose a single call that alters `names(dimnames(x))` without modifying `x` in place but returning a recoded copy of:

- `names(dimnames(x))`,
- `dimnames(x)`,
- `x`.

**Exercise 9.27** (\*) Consider the `recode<-` function once again but now let an example object be a data frame featuring a column of the factor class:

```
x <- iris[c(1, 2, 51, 101), ]
```

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```

recode(levels(x[["Species"]])) <- c(
  setosa="SET", versicolor="VER", virginica="VIR"
)
print(x)
##      Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1           5.1         3.5         1.4         0.2      SET
## 2           4.9         3.0         1.4         0.2      SET
## 51          7.0         3.2         4.7         1.4      VER
## 101         6.3         3.3         6.0         2.5      VIR

```

How to change `levels(x[["Species"]])` and return an altered copy of:

- `levels(x[["Species"]])`,
- `x[["Species"]]`,
- `x`

without modifying `x` in place?

## 9.5 Arguments and local variables

### 9.5.1 Pass by “value”

As a general rule, functions cannot change the state of their arguments<sup>9</sup>. We can think of them as being passed by *value*, i.e., as if their copy was made.

```

test_change <- function(y)
{
  y[1] <- 7
  y
}

x <- 1:5
test_change(x)
## [1] 7 2 3 4 5
print(x) # same
## [1] 1 2 3 4 5

```

If the above were not the case, the state of `x` would have changed after the call.

<sup>9</sup> With the exception of objects of the type environment, which are passed by reference; see [Chapter 16](#). Also, the fact that we have access to unevaluated R expressions can cause further deviations to this rule (see below).

### 9.5.2 Variable scope

Function arguments and any other variables we create inside a function's body are *relative* to each call to that function.

```
test_change <- function(x)
{
  x <- x+1
  z <- -x
  z
}

x <- 1:5
test_change(x*10)
## [1] -11 -21 -31 -41 -51
print(x) # x in the function's body was a different x
## [1] 1 2 3 4 5
print(z) # z was local
## Error in eval(expr, envir, enclos): object 'z' not found
```

Both `x` and `z` are local variables. They only live whilst our function is being executed. The former temporarily *masks*<sup>10</sup> the object of the same name from the caller's context.

---

**Important** It is a good development practice to refrain from referring to objects not created within the current function, especially to “global” variables. We can always pass an object as an argument explicitly.

---



---

**Note** It is a function call as such, not curly braces per se that form a local scope.

Writing “`x <- { y <- 1; y + 1 }`”, `y` is not an auxiliary variable; it is an ordinary named object created alongside `x`.

On the other hand, in “`x <- (function() { z <- 1; z + 1 })()`”, `z` will not be available thereafter.

---

### 9.5.3 Closures (\*)

Most user-defined functions are, in fact, representatives of the so-called *closures*; see [Section 16.3.2](#) and [1]. They not only consist of an R expression to evaluate but also can carry some auxiliary data.

For instance, given two equal-length numeric vectors `x` and `y`, a call to `approxfun(x,`

---

<sup>10</sup> Chapter 16 discusses this topic in-depth: objects are bound to their names within environments. Moreover, R uses lexical (static) scoping, which is not necessarily intuitive, especially taking into account that a function's environment can always be changed.

$y$ ) returns a *function* that linearly interpolates between the consecutive points  $(x_1, y_1)$ ,  $(x_2, y_2)$ , and so forth, so that a corresponding  $y$  can be determined for any  $x$ .

```
x <- seq(0, 1, length.out=11)
f1 <- approxfun(x, x^2)
f2 <- approxfun(x, x^3)
f1(0.75) # check that it is quite close to the true 0.75^2
## [1] 0.565
f2(0.75) # compare with 0.75^3
## [1] 0.4275
```

Inspecting, however, the source codes of the above functions:

```
print(f1)
## function (v)
## .approxfun(x, y, v, method, yleft, yright, f, na.rm)
## <environment: 0x55d9258999f8>
print(f2)
## function (v)
## .approxfun(x, y, v, method, yleft, yright, f, na.rm)
## <environment: 0x55d924a01548>
```

we might wonder how they can produce different results: it is evident that they are identical. It turns out, however, that they internally store some additional data that are referred to when they are called:

```
environment(f1)[["y"]]
## [1] 0.00 0.01 0.04 0.09 0.16 0.25 0.36 0.49 0.64 0.81 1.00
environment(f2)[["y"]]
## [1] 0.000 0.001 0.008 0.027 0.064 0.125 0.216 0.343 0.512 0.729 1.000
```

We will explore these concepts in detail in the third part of this book.

### 9.5.4 Default arguments

We have already mentioned above that when designing functions performing complex tasks we will sometimes be faced with a design problem: how to find a sweet spot between being generous/mindful of the diverse needs of our users and making the API neither overwhelming nor oversimplistic.

We know that it is best if a function performs a single well-specified task. Moreover, it is nice if it also allows its behaviour to be tweaked if one wishes to do so. The use of *default arguments* can facilitate this principle.

For instance, **log** computes logarithms, by default, the natural ones.

```
log(2.718) # the same as log(2.78, base=exp(1)) – default base
## [1] 0.9999
```

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```
log(4, base=2) # different base
## [1] 2
```

**Exercise 9.28** Study the documentation of the following functions and note the default values they define: **round**, **hist**, **grep**, and **download.file**.

We can easily define our own functions equipped with such *recommended* settings:

```
test_default <- function(x=1) x

test_default() # use default
## [1] 1
test_default(2) # use something else
## [1] 2
```

Most often, default arguments are just constants, e.g., 1. Generally, though, they can be any R expressions: also ones that include a reference to other arguments passed to the same function; see Section 17.2.

Default arguments most often appear at the end of the parameter list, but see Section 9.4.6 (on replacement functions) for a well-justified exception.

### 9.5.5 Lazy vs eager evaluation

In some languages, function arguments are always evaluated prior to a call. In R, though, they are only computed when actually needed. We call it *lazy* or *delayed* evaluation. Recall that in Section 8.1.4, we introduced the short-circuit evaluation operators ``||`` (or) and ``&&`` (and). They can do their job precisely thanks to this mechanism.

**Example 9.29** In the following example, we do not use the function's argument at all:

```
lazy_test1 <- function(x) 1 # x not used at all

lazy_test1({cat("and now for something completely different!"); 7})
## [1] 1
```

Otherwise, we would see a message being printed out on the console.

**Example 9.30** Next, let us use `x` amidst other expressions in the body:

```
lazy_test2 <- function(x)
{
  cat("it's... ")
  y <- x+x # using x twice
  cat(" a man with two noses")
  y
}
```

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```
lazy_test2({cat("and now for something completely different!"); 7})
## it's... and now for something completely different! a man with two noses
## [1] 14
```

An argument is evaluated once, and its value is stored for further reference. If that were not the case, we would see two messages like *and now...*

We will elaborate on this in [Chapter 17](#).

### 9.5.6 Ellipsis, `...`

Let us start with an exercise.

**Exercise 9.31** Notice the presence of ``...`` in the parameter list of **`c`**, **`list`**, **`structure`**, **`cbind`**, **`rbind`**, **`cat`**, **`Map`** (and the underlying **`mapply`**), **`lapply`** (a specialised version of **`Map`**), **`optimise`**, **`optim`**, **`unroot`**, **`integrate`**, **`outer`**, **`aggregate`**. What purpose does it serve, according to these functions' manual pages?

We can create a *variadic function* by including ``...`` (dot-dot-dot, ellipsis; see **`help("dots")`**), somewhere in its parameter list. The ellipsis serves as a placeholder for all objects passed to the function but not matched by any formal (named) parameters.

The easiest way to process arguments passed via ``...`` programmatically (see also [Section 17.3](#)) is by redirecting them to **`list`**.

```
test_dots <- function(...)
  list(...)

test_dots(1, a=2)
## [[1]]
## [1] 1
##
## $a
## [1] 2
```

Such a list can be processed just like... any other generic vector. What we can do with these arguments is only limited by our creativity (in particular, recall from [Section 7.2.2](#) the very powerful **`do.call`** function). There are two primary use cases of the ellipsis<sup>11</sup>:

- create a new object by combining an arbitrary number of other objects:

```
c(1, 2, 3) # 3 arguments
## [1] 1 2 3
c(1:5, 6:7) # 2 arguments
```

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<sup>11</sup> Which is somewhat similar to Python's `*args` and `**kwargs` in a function's parameter list.

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```
## [1] 1 2 3 4 5 6 7
structure("spam") # 0 additional arguments
## [1] "spam"
structure("spam", color="rose", taste="umami") # 2 further arguments
## [1] "spam"
## attr("color")
## [1] "rose"
## attr("taste")
## [1] "umami"
cbind(1:2, 3:4)
##      [,1] [,2]
## [1,]    1    3
## [2,]    2    4
cbind(1:2, 3:4, 5:6, 7:8)
##      [,1] [,2] [,3] [,4]
## [1,]    1    3    5    7
## [2,]    2    4    6    8
sum(1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 42)
## [1] 108
```

- pass further arguments (as-is) to other methods :

```
lapply(list(c(1, NA, 3), 4:9), mean, na.rm=TRUE) # mean(x, na.rm=TRUE)
## [[1]]
## [1] 2
##
## [[2]]
## [1] 6.5
integrate(dbeta, 0, 1,
          shape1=2.5, shape2=0.5) # dbeta(x, shape1=2.5, shape2=0.5)
## 1 with absolute error < 1.2e-05
```

For more details, see Section 17.3.

**Example 9.32** The documentation of **`lapply`** (let us call **`help("lapply")`** now) states that this function is defined as **`lapply(X, FUN, ...)`**. Here, the ellipsis is a placeholder for a number of optional arguments that can be passed to **`FUN`**. Hence, if we denote the  $i$ -th element of a vector  $X$  by  $X[[i]]$ , calling **`lapply(X, FUN, ...)`** will return a list whose  $i$ -th element will be equal to **`FUN(X[[i]], ...)`**.

**Exercise 9.33** Using a single call to **`lapply`**, generate a list with three numeric vectors of lengths 3, 9, and 7, respectively, drawn from the uniform distribution on the unit interval. Then, upgrade your code to get numbers sampled from the interval  $[-1, 1]$ .

### 9.5.7 Metaprogramming (\*)

In the third part of this book, we will learn that we can access the expressions passed as functions' arguments programmatically. In particular, a call to the composition of **deparse** and **substitute** can convert them to a character vector:

```
test_deparse_substitute <- function(x)
  deparse(substitute(x))

test_deparse_substitute(testing+1+2+3)
## [1] "testing + 1 + 2 + 3"
test_deparse_substitute(spam & spam^2 & bacon | grilled(spam))
## [1] "spam & spam^2 & bacon | grilled(spam)"
```

**Exercise 9.34** Check out the y-axis label generated by `plot.default((1:100)^2)`. Inspect its source code. Notice a call to the two aforementioned functions.

Similarly, call `shapiro.test(log(rlnorm(100)))` and take note of the data: field.

A function is free to do with such an expression whatever it likes. For instance, it can modify the expression and then evaluate it in a very different context. Such a language feature allows certain operations to be expressed much more compactly. In theory, it is a potent tool. Unfortunately, it is easy to find many practical examples where it was over/misused and made learning or using R confusing.

**Example 9.35** (\*) The built-in **subset** and **transform** use metaprogramming techniques to specify basic data frame transformations (see [Section 12.3.9](#) and [Section 17.5](#)). For instance:

```
transform(
  subset(
    iris,
    Sepal.Length>=7.7 & Sepal.Width >= 3.0,
    select=c(Species, Sepal.Length:Sepal.Width)
  ),
  Sepal.Length.mm=Sepal.Length/10
)
##      Species Sepal.Length Sepal.Width Sepal.Length.mm
## 118 virginica      7.7      3.8      0.77
## 132 virginica      7.9      3.8      0.79
## 136 virginica      7.7      3.0      0.77
```

None of the arguments (except `iris`) makes sense outside of the function call contexts. In particular, neither `Sepal.Length` nor `Sepal.Width` variables exist.

The two functions took the liberty to interpret the arguments passed how they felt. They created their own virtual reality within our well-defined world. The reader must refer to their documentation to discover the meaning of such special syntax.

---

**Note** (\*) Some functions have rather peculiar default arguments. For instance, in the



manual page of **prop.test**, we read that the alternative parameter defaults to `c("two.sided", "less", "greater")` but that "two.sided" is actually the default one.

If we call `print(prop.test)`, we will find the code line responsible for this behaviour: `"alternative <- match.arg(alternative)"`. Consider the following example:

```
test_match_arg <- function(x=c("a", "b", "c")) match.arg(x)

test_match_arg() # missing argument – choose 1st
## [1] "a"
test_match_arg("c") # one of the predefined options
## [1] "c"
test_match_arg("d") # unexpected setting
## Error in match.arg(x): 'arg' should be one of "a", "b", "c"
```

In this setting, **match.arg** only allows an actual parameter from a given set of choices but selects the first option if the argument is missing.

Unfortunately, we have to learn this behaviour by heart because looking at the above source code gives us no clue about this being possible. If such an expression was normally evaluated, we would use either the default argument or whatever the user passed as `x` (but then the function would not know the range of possible choices). A call to `"match.arg(x, c("a", "b", "c"))"` could guarantee the desired functionality and would be much more readable. Instead, metaprogramming techniques allowed **match.arg** to access the enclosing function's default argument list without explicitly referring to them.

One may ask: why is it so? The only sensible answer to this will be "because its programmer decided it must be this way". Let us contemplate this for a while. In cases like these, we are not dealing with some base R language design choice that we might like or dislike, but which we should just accept as an inherent feature. Instead, we are struggling intellectually because of some programmer's (mis)use (in good faith...) of R's flexibility itself. They have introduced a slang/dialect on top of our mother tongue, whose meaning is valid only within this function. Blame the middleman, not the environment, please.

This is why we generally advocate for avoiding relying on metaprogramming-based techniques wherever possible. We shall elaborate on this in the third part of this book.

## 9.6 Exercises

**Exercise 9.36** Answer the following questions:

- Will `"stopifnot(1)"` stop? What about `"stopifnot(NA)"`, `"stopifnot(TRUE, FALSE)"`, and `"stopifnot(c(TRUE, TRUE, NA))"`?

- What does the `if` function return?
- Does `attributes<-`(x, NULL)`` modify `x`?
- When can we be interested in calling ``` and ``[<-`` as functions (and not as operators) directly?
- How to define our own binary operator? Can it have some default arguments?
- What are the main use cases of ``...``?
- What is wrong with `transform`, `subset`, and `match.arg`?
- When a call like `"f(-1, do_something_that_takes_a_million_years())"` does not necessarily have to be a bad idea?
- What is the difference between `"names(x)[1] <- "new name"` and `"names(x[1]) <- "new name"`?
- What might be the form of `x` if it is legit to call it like `x[[c(1, 2)]]()()[[1]]()`?

**Exercise 9.37** What is the return value of a call to `"f(list(1, 2, 3))"`?

```
f <- function(x)
{
  for (e in x) {
    print(e)
  }
}
```

Is it `NULL`, `invisible(NULL)`, `x[[length(x)]]`, or `invisible(x[[length(x)]])`?

**Exercise 9.38** The `split` function also has its replacement version. Study its documentation to learn how it works.

**Exercise 9.39** A call to `ls(envir=baseenv())` returns all objects defined in the **base** package (see Chapter 16). List the names corresponding to some replacement functions.

---

**Important** Apply the principle of test-driven development when solving the remaining exercises (or those you have skipped intentionally).

---

**Exercise 9.40** Implement your version of the **Position** and **Find** functions. Evaluation should stop as soon as the first element fulfilling a given predicate has been found.

**Exercise 9.41** Implement your version of the **Reduce** function.

**Exercise 9.42** Write a function `slide(f, x, k, ...)` which returns a list `y` of size `length(x)-k+1` such that `y[[i]] = f(x[i:(i+k-1)], ...)`

```
unlist(slide(sum, 1:5, 1))
## [1] 1 2 3 4 5
unlist(slide(sum, 1:5, 3))
```

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```
## [1] 6 9 12
unlist(slide(sum, 1:5, 5))
## [1] 15
```

**Exercise 9.43** Using `slide` defined above, write another function that counts how many increasing pairs of numbers are featured in a given numeric vector. For instance, in `c(0, 2, 1, 1, 0, 1, 6, 0)`, there are three such pairs: `(0, 2)`, `(0, 1)`, `(1, 6)`.

**Exercise 9.44** (\*) Write your version of `tools::package_dependencies` with `reverse=TRUE` based on information extracted by calling `utils::available.packages`.

**Exercise 9.45** (\*\*) Write a standalone program (that can be run from the system shell) that computes the total size of all the files in given directories given as the script's arguments (via `commandArgs`).

---



Let  $x$  be a randomly generated matrix with 1 000 000 rows and 1 000 columns,  $y$  be a data frame with results from the latest survey indicating that things are not the way most people (no matter the side of the many political spectra) think they are, and  $z$  be another matrix, this time with many zeroes.

Human brain is not capable of dealing with too much information which is too specific. This is why we have a natural tendency to group different entities based on their similarities so as to form some more abstract classes thereof.

Also, many of us are inherently lazy. Thus, oftentimes we will take shortcuts to minimise energy (at a price to be paid later).

Printing out a matrix, a data frame, and a time series are all instances of the displaying of things, although they undoubtedly differ in detail.

By now, we probably have forgotten which objects are hidden behind  $x$ ,  $y$ , and  $z$ . Being able to simply call “`print(y)`” without having to recall that, yes,  $y$  is a data frame, might seem quite appealing.

This chapter introduces the so-called S3 classes [13]. They provide a lightweight object-oriented programming (OOP) approach for automated dispatching of calls to *generics* of the type “`print(y)`” to concrete *methods* such as “`print.data.frame(y)`”, based on the *class* of the object they are invoked on.

S3 classes in their essence are beautifully simple<sup>1</sup>. They are inspired<sup>2</sup> by the well-thought-through concepts present in other functional programming languages (such as the Common Lisp Object System; see below). Ultimately, those *generics* and *methods* are ordinary R functions (Chapter 7) and *classes* are merely additional object attributes (Section 4.4).

Of course, this does not mean that wrapping our heads around them will be effortless. However, unlike other “class systems”<sup>3</sup>, S3 is ubiquitous in R programming. Suffice it

---

<sup>1</sup> However, some classes, even the built-in ones described here, can be poorly designed (some crucial methods might be missing, they can be not well-interoperable with other classes, etc.). Do not blame this messenger. Remember that the R environment is still very reliable. Also, there are cases where changing the current behaviour in one place could lead to undesirable consequences elsewhere.

<sup>2</sup> They were built on top of the ordinary (“old S”) R. Hence, they have certain limitations that we discuss in the sequel: classes cannot be formally defined (often we will use named lists for representing objects, and we know we cannot be any more flexible than this), and the dispatching can only be based on the class of one of the arguments (usually the first one, but, e.g., binary operators take both types into account).

<sup>3</sup> Other class systems may give an impression that they are alien implants that were forcefully added to

to say that factors, matrices, and data frames discussed in the following chapters are quite straightforward, S3-based extensions of the concepts we introduce below.

## 10.1 Object type vs class

Recall that `typeof` (introduced in [Section 4.1](#)) returns the *internal* type of any R object. So far, the basic types we covered were mostly atomic and generic vectors (compare [Figure 1](#) in the Preface).

```
typeof(NULL)
## [1] "NULL"
typeof(c(TRUE, FALSE, NA))
## [1] "logical"
typeof(c(1, 2, 3, NA_real_))
## [1] "double"
typeof(c("a", "b", NA_character_))
## [1] "character"
typeof(list(list(1, 2, 3), LETTERS))
## [1] "list"
typeof(function(x) x)
## [1] "closure"
```

The number of admissible types is small<sup>4</sup>, but they open the world of endless possibilities<sup>5</sup>. We will learn that they provide a basis for more complex data structures. This is thanks to the fact that they can be equipped with arbitrary attributes ([Section 4.4](#)).

Most *compound types* constructed using the mechanisms discussed in this chapter<sup>6</sup> only *pretend* they are something different from what they actually are. Still, they do their job very well most of the time. By knowing what is under their hood, we will demystify them and become able to manipulate their state outside of the prescribed use cases.

---

**Important** Setting the `class` attribute might make some objects behave differently in certain scenarios.

---

**Example 10.1** *Let us consider two identical objects equipped with different class attributes.*

---

our language to solve a specific, rather narrow class of problems; e.g., S4 ([Section 11.5](#)), reference classes ([Section 16.1.5](#)), and other ones proposed by third-party packages.

<sup>4</sup> Their list is hardcoded at the C language level; compare the list of `SEXTYPES` in [65] or [Chapter 14](#).

<sup>5</sup> In particular, [Section 14.2.8](#) mentions `externalptrs` which are simple pointers to the memory allocated on the heap. Thus, they might be any instances of C structs or C++ classes. This makes R a very extensible language.

<sup>6</sup> But there is more: see the S4 and reference class systems discussed in [Section 11.5](#) and [Section 16.1.5](#).

```
xt <- structure(123, class="POSIXct") # POSIX calendar time
xd <- structure(123, class="Date")
```

Both objects are represented using numeric vectors:

```
c(typeof(xt), typeof(xd))
## [1] "double" "double"
```

However, when printed, they are decoded quite differently:

```
print(xt)
## [1] "1970-01-01 10:02:03 AEST"
print(xd)
## [1] "1970-05-04"
```

In the former case, 123 is understood as the number of seconds since the so-called UNIX epoch, 1970-01-01T00:00:00+0000. The latter is deciphered as the number of days since the said timestamp.

Hence, we expect that there exists some underlying mechanism that calls a version of **print** dependent on an object's virtual class.

That this only relies on the `class` attribute, which might be set, unset, or reset quite freely, is emphasised below.

```
attr(xt, "class") <- "Date" # change class from POSIXct to Date
print(xt) # same 123, but now interpreted as Date
## [1] "1970-05-04"
as.numeric(xt) # drops all attributes
## [1] 123
unclass(xd) # drops the class attribute; `attr<-`(xd, "class", NULL)
## [1] 123
```

We are having so much fun that one more illustration can only increase our joy.

**Example 10.2** Consider an example data frame:

```
x <- iris[1:3, 1:2] # a subset of a built-in example data frame
print(x)
##   Sepal.Length Sepal.Width
## 1         5.1         3.5
## 2         4.9         3.0
## 3         4.7         3.2
```

It is an object of the following class (an object whose `class` attribute is set to):

```
attr(x, "class")
## [1] "data.frame"
```

Some may say, and they are absolutely right, that we have not covered data frames yet. After all, they are the topic of *Chapter 12*, which is still ahead of us. However, from the current perspective, we should know that R data frames are merely lists (*Chapter 4*) of vectors of the same lengths equipped with *names* and *row.names* attributes.

```
typeof(x)
## [1] "list"
attr(x, "class") <- NULL # or x <- unclass(x)
print(x)
## $Sepal.Length
## [1] 5.1 4.9 4.7
##
## $Sepal.Width
## [1] 3.5 3.0 3.2
##
## attr(,"row.names")
## [1] 1 2 3
```

---

**Important** Revealing how *x* is *actually* represented, enables us to process it using the extensive skill set that we have already<sup>7</sup> developed by studying the material covered in the previous part of our book (including all the exercises). This fact is particularly noteworthy, especially bearing in mind that some (built-in or third-party) data types are not particularly well-designed.

---

Let us underline again that attributes are simple additions to R objects. However, as we said in *Section 4.4.3*, certain attributes are special, and *class* is one of them.

In particular, we can set *class* to be only a character vector (possibly of length greater than one; see *Section 10.2.5*).

```
x <- 12345
attr(x, "class") <- 1 # character vectors only
## Error in attr(x, "class") <- 1: attempt to set invalid 'class' attribute
```

Furthermore, the *class* function can read the value of the *class* attribute. Its replacement version is also available.

```
class(x) <- "Date" # set; the same as attr(x, "class") <- "Date"
class(x) # get; the same as attr(x, "class")
## [1] "Date"
```

---

**Important** The *class* function always yields some value, even if the corresponding

---

<sup>7</sup> For instance, consider once again the example from *Section 5.4.3* that applies the *split* function on a data frame reduced to a list.



attribute is not set. We call it an *implicit* class. Compare the following and the outputs generated by **typeof**:

```
class(NULL) # no `class` set because NULL cannot have attributes at all
## [1] "NULL"
class(c(TRUE, FALSE, NA)) # no attributes so class is implicit (= typeof)
## [1] "logical"
class(c(1, 2, 3, NA_real_)) # typeof returns "double"
## [1] "numeric"
class(c("a", "b", NA_character_))
## [1] "character"
class(list(list(1, 2, 3), LETTERS))
## [1] "list"
class(function(x) x) # typeof gives "closure"
## [1] "function"
```

Also, Chapter 11 will explain that any object equipped with the `dim` attribute also has an implicit class:

```
(x <- as.matrix(c(1, 2, 3)))
##      [,1]
## [1,]    1
## [2,]    2
## [3,]    3
attributes(x) # `class` is not amongst the attributes
## $dim
## [1] 3 1
class(x) # implicit class
## [1] "matrix" "array"
typeof(x) # it is still a numeric vector (under the hood)
## [1] "double"
```

## 10.2 Generics and method dispatching

### 10.2.1 Generics, default, and custom methods

Let us inspect the source code of the **print** function:

```
print(print) # sic!
## function (x, ...)
## UseMethod("print")
## <environment: namespace:base>
```

Any function like the above<sup>8</sup> we will call from now on a *generic* (*S3 generic*, from S version 3). Its only job is to invoke `UseMethod("print")`. It dispatches the control flow to another function, referred to as a *method*, based on the class of the first argument.

---

**Important** Even though it cannot be implied by reading the above source code, all arguments passed to the generic will also be available<sup>9</sup> in the dispatched method.

---

For example, let us define an object of the class `categorical` (a name that we have just come up with; we could have called it `cat`, `CATEGORICAL`, or `SpanishInquisition` as well), which will be our own version of the famous built-in `factor` type that we discuss later.

```
x <- structure(
  c(1, 3, 2, 1, 1, 1, 3),
  levels=c("a", "b", "c"),
  class="categorical"
)
```

We assume that such an object is a sequence of small positive integers (codes). It is equipped with a character vector of length no less than the maximum of the said integers, stored as its `levels` attribute. For example, the first category will be used to decipher the meaning of code “1”. Hence, the above vector represents a sequence *a, c, b, a, a, a, c*.

We have not defined any special method for printing objects of the `categorical` class. Hence, when we call **print**, the *default* (fallback) method will be called:

```
print(x)
## [1] 1 3 2 1 1 1 3
## attr(,"levels")
## [1] "a" "b" "c"
## attr(,"class")
## [1] "categorical"
```

It is the standard function for displaying numeric vectors that we are all well familiar with. Its name is **print.default**, and we can always call it directly:

```
print.default(x) # the default print method
## [1] 1 3 2 1 1 1 3
## attr(,"levels")
```

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---

<sup>8</sup> Some functions can have a version of `UseMethod` hidden at the C language level (internally); see Section 10.2.3.

<sup>9</sup> This uses quite an obscure hack. It should also be noted that `UseMethod` heavily relies on metaprogramming (compare Chapter 17). Therefore, we do not consider it an ordinary function call. For instance, it can only be called inside a function's body. Also, once called, it does not return to the generic. Before dispatching to a particular method, it creates a couple of hidden variables which give more detail on the operation conveyed, e.g., ``.Generic`` or ``.Class``; see `help("UseMethod")` and Section 5 of [66].

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```
## [1] "a" "b" "c"
## attr(,"class")
## [1] "categorical"
```

However, we can introduce our own method for printing categorical objects. Its name must precisely be **print.categorical**:

```
print.categorical <- function(x, ...)
{
  x_character <- attr(x, "levels")[unclass(x)]
  print(x_character) # calls `print.default`
  cat(sprintf("Categories: %s\n",
    paste(attr(x, "levels"), collapse=", ")))
  invisible(x) # this is what all print methods do; see help("print")
}
```

Now, calling **print** automatically dispatches the control flow to the above method:

```
print(x)
## [1] "a" "c" "b" "a" "a" "a" "c"
## Categories: a, b, c
```

Of course, the default method can still be called; calling **print.default(x)** directly will output the same result as before.

---

**Note** **print.categorical** has been equipped with the dot-dot-dot attribute since the generic **print** had one too. We are expected to ensure consistency ourselves<sup>10</sup>.

---

### 10.2.2 Creating own generics

Introducing new S3 generics is as straightforward as defining a function that calls **UseMethod**.

For instance, here is a dispatcher which allows for creating new objects of the categorical class based on other objects:

```
as.categorical <- function(x, ...)
  UseMethod("as.categorical") # synonym: UseMethod("as.categorical", x)
```

We always need to define the default method:

```
as.categorical.default <- function(x, ...)
{
```

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---

<sup>10</sup> In particular, checking S3 generic/method consistency is part of R package check.

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```
x <- as.character(x)
xu <- unique(sort(x)) # drops NAs
structure(
  match(x, xu),
  class="categorical",
  levels=xu
)
```

Testing:

```
as.categorical(c("a", "c", "a", "a", "d", "c"))
## [1] "a" "c" "a" "a" "d" "c"
## Categories: a, c, d
as.categorical(c(3, 6, 4, NA, 9, 9, 6, NA, 3))
## [1] "3" "6" "4" NA "9" "9" "6" NA "3"
## Categories: 3, 4, 6, 9
```

Here, **print.categorical** was invoked twice. The above is quite flexible already: it relies on the generic (Section 10.2.3) **as.character**, which handles a wide variety of data types.

**Example 10.3** For instance, we might want to forbid the conversion from lists because this does not necessarily make sense:

```
as.categorical.list <- function(x, ...)
  stop("conversion of lists to categorical is not supported")
```

The users can always be instructed in the method's documentation that they are solely responsible for an explicit conversion of list objects to something different prior to a call to **as.categorical**. Whether this was a justified design choice, time will tell.

**Example 10.4** The default method deals with logical vectors perfectly fine:

```
as.categorical(c(TRUE, FALSE, NA, NA, FALSE)) # as.categorical.default
## [1] "TRUE" "FALSE" NA NA "FALSE"
## Categories: FALSE, TRUE
```

However, we might still want to introduce its specialised version. This is because we know a slightly more efficient algorithm (and we have nothing better to do) based on the fact that **FALSE** and **TRUE** converted to numeric yield 0 and 1, respectively:

```
as.categorical.logical <- function(x, ...)
{
  x <- as.logical(x) # or stopifnot(is.logical(x)) ?
  structure(
```

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```

    x + 1, # only 1, 2, and NAs will be generated
    class="categorical",
    levels=c("FALSE", "TRUE")
  )
}

```

It spawns the same result but is slightly faster:

```

as.categorical(c(TRUE, FALSE, NA, NA, FALSE)) # as.categorical.logical
## [1] "TRUE" "FALSE" NA      NA      "FALSE"
## Categories: FALSE, TRUE

```

We performed some argument validation at the beginning: a user is always able to call a method directly on an R object of any kind (which is a good thing; see Section 10.2.4). In other words, there is no guarantee that the argument *x* must be of type logical.

### 10.2.3 Built-in generics

Many functions and operators we have introduced so far are, in fact, S3 generics: **print**, **head**, **[**, **+**, **<=**, **as.character**, **as.list**, **round**, **log**, **sum**, **c**, and **na.omit**, to name a few.

Some of them might not even call **UseMethod** explicitly; dispatching can be done internally at the C language level<sup>11</sup>. Overall, generating the list of all S3 generics is somewhat tricky<sup>12</sup>. Luckily, at least the internal ones are enumerated in **help("InternalMethods")** and **help("groupGeneric")**.

**Example 10.5** Let us overload the **as.character** method. The default one does not make much sense for the objects of our custom type:

```

as.character(x)
## [1] "1" "3" "2" "1" "1" "1" "3"

```

So:

```

as.character.categorical <- function(x, ...)
  attr(x, "levels")[unclass(x)]

```

And now:

<sup>11</sup> This is quite unfortunate as it decreases transparency. We need to look this information up somewhere in the documentation (instead of simply inspecting a function's source code; see, e.g., **cbind**). Also, it allows for some methods to be hardcoded at the C language level too, and thus be unoverloadable. However, some of such design choices can somewhat be defended since they increase execution speed or memory consumption. Overall, we are not particularly happy about them.

<sup>12</sup> See also **.knownS3Generics** and **.S3\_methods\_table**, which are related to the advanced topics we will cover in Section 16.3.6.

```
as.character(x)
## [1] "a" "c" "b" "a" "a" "a" "c"
```

**Exercise 10.6** Overload the **unique** and **rep** methods for objects of the class *categorical*.

**Example 10.7** New types ought to be designed carefully. For instance, if we forget to consider overloading the to-numeric converter, we might end up with some users being puzzled<sup>13</sup> when they see:

```
(x <- as.categorical(c(4, 9, 100, 9, 9, 100, 42, 666, 4)))
## [1] "4" "9" "100" "9" "9" "100" "42" "666" "4"
## Categories: 100, 4, 42, 666, 9
as.double(x) # as.double.default(x)
## [1] 2 5 1 5 5 1 3 4 2
```

Hence, we might want to introduce:

```
as.double.categorical <- function(x, ...)
{
  # as.double.default(as.character.categorical(x))
  as.double(as.character(x))
}
```

Which now yields:

```
as.double(x) # as.double.categorical(x)
## [1] 4 9 100 9 9 100 42 666 4
```

---

**Note** We can still use **unclass** to fetch the codes:

```
unclass(x)
## [1] 2 5 1 5 5 1 3 4 2
## attr(,"levels")
## [1] "100" "4" "42" "666" "9"
```

It is because the above returns a class-free object, which is now guaranteed to be processed by the default methods (**print**, subsetting, **as.character**, etc.).

---

**Exercise 10.8** What would happen if we used **as.numeric** instead of **unclass** in **print.categorical** and **as.character.categorical**?

---

<sup>13</sup> It is a different story if this is our conscious design choice and if we really want this behaviour. If we document it thoroughly (see how **help**("factor") discusses the behaviour of a to-numeric conversion), only a user's ignorance will there be to blame when they still are confused about it. Remember that we can never make an API totally foolproof and that there will always be someone to challenge/stress-test our ideas. Bad design is always wrong, but being overprotective also has its cons. Choose your audience wisely.

**Exercise 10.9** Update the above methods so that we can also create named objects of the class `categorical` (i.e., equipped with the `names` attribute).

**Exercise 10.10** The levels of `x` are sorted lexicographically, not numerically. Introduce a single method that would make the above code (when rerun without any alterations) generate a more natural result.

#### 10.2.4 First-argument dispatch and calling S3 methods directly

With S3, the dispatching is done most often based on the class of only one<sup>14</sup> argument: by default, the first one from the parameter list.

For example, the `c` function is a generic that dispatches on the first argument's class. Let us overload it for `categorical` objects. In other words, let us create a function dispatched by the generic when called on a series of objects whose first element is of the said class.

```
c.categorical <- function(...)
  as.categorical(
    unlist(
      lapply(list(...), as.character)
    )
  )
```

It converts each argument to a character vector (relying on the generic `as.character` to take care of the details). It works because `unlist` converts a list of such atomic vectors to a single sequence of strings.

Calling `c` with the first argument being of the class `categorical` dispatches to the above method:

```
x <- c(9, 5, 7, 7, 2)
xc <- as.categorical(x)
c(xc, x) # c.categorical
## [1] "9" "5" "7" "7" "2" "9" "5" "7" "7" "2"
## Categories: 2, 5, 7, 9
```

However, if the first argument is, say, unclassified, the default method will be consulted:

```
c(x, xc) # default c
## [1] 9 5 7 7 2 4 2 3 3 1
```

This method ignores the `class` attribute and sees `xc` as it is, a barebone numeric vector:

<sup>14</sup> There are many exceptions to this rule. They were made for the (debatable) sake of the R users' convenience. In particular, in Section 12.1.2 we mention that `cbind` and `rbind` will dispatch to the `data.frame` method if at least one argument is a data frame (and others are unclassified). Binary operators dispatch on the type of both operands; see Section 10.2.6. Furthermore, it is worth noting that the S4 class system (Section 11.5) allows for dispatching based on the classes many arguments.







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```
##
## $size
## [1] 50 62 38
##
## $iter
## [1] 2
##
## $ifault
## [1] 0
```

We already know that the above was displayed in a fancy way only because there is a **print** method overloaded for objects of the *kmeans* class.

But is there?

```
print.kmeans
## Error in eval(expr, envir, enclos): object 'print.kmeans' not found
```

Even though the method is hidden (internal) in the **stats** package's namespace, from Section 16.3.6 we will learn that it can be accessed by calling **getS3method("print", "kmeans")** or referring to **stats:::print.kmeans** (note the triple colon).

### 10.2.5 Multi-class-ness

The class attribute can be instantiated as a character vector of any length. For example:

```
(t1 <- Sys.time())
## [1] "2023-05-18 19:41:59 AEST"
(t2 <- strptime("2021-08-15T12:59:59+1000", "%Y-%m-%dT%H:%M:%SZ"))
## [1] "2021-08-15 12:59:59"
```

Let us inspect the classes of these two objects:

```
class(t1)
## [1] "POSIXct" "POSIXt"
class(t2)
## [1] "POSIXlt" "POSIXt"
```

Section 10.3.1 will discuss date-time classes in more detail. It will highlight that the former is represented as a numeric vector, while the latter is a list. Thus, these two should primarily be seen as instances of two distinct types.

However, both of them have a lot in common. Hence, it was a wise design choice to allow them to be seen also as the representatives of the same generic category of *POSIX time* objects.

---

**Important** When calling a generic function<sup>16</sup> **f** on an object **x** of the classes<sup>17</sup> **class1**, **class2**, ..., **classK** (in this order), **UseMethod(f, x)** dispatches to the method determined as follows:

1. if **f.class1** is available<sup>18</sup>, call it;
  2. otherwise, if **f.class2** is available, call this one;
  3. ...;
  4. otherwise, if **f.classK** is available, invoke it;
  5. otherwise, refer to the fallback **f.default**.
- 

**Example 10.12** *There is a method **diff** for objects of the class **POSIXt** featuring a statement:*

```
r <- if (inherits(x, "POSIXlt")) as.POSIXct(x) else x
```

*This way, we can process both **POSIXct** and **POSIXlt** instances using the same procedure.*

Let us see no magic in this simple scheme. It is nothing more than what we described above: a way to determine which method to call for a particular R object. It can be used as a mechanism to mimic the idea of inheritance in object-oriented programming languages. However, the S3 system does not allow for defining classes in any formal manner.

For example, we cannot say that objects of the class **POSIXct** inherit from **POSIXt**. Neither can we say that each object of the class **POSIXct** is also an instance of **POSIXt**. The class attribute can still be set arbitrarily on a per-object basis. We can create ones whose class is simply **POSIXct** (without the **POSIXt** part) or even **c("POSIXt", "POSIXct")** (in this order).

---

**Note** In any method, it is possible to call the method corresponding to the next class by calling **NextMethod**.

---

For instance, if we are in **f.class1**, a call to **NextMethod(f)** will try invoking **f.class2**. If such a method does not exist, further methods in the search chain will be tried, falling back to the default method if necessary. An example will be given below.

## 10.2.6 Operator overloading

Operators are ordinary functions (Section 9.4.5). Even though what follows can partially be implied by what we have said above, as usual in R, there will be some oddities.

---

<sup>16</sup> The case of binary operators is handled differently; see Section 10.2.6.

<sup>17</sup> **UseMethod** dispatches on the implicit class as determined by the **class** function. Note that the **class** attribute does not necessarily have to be set in order for **class** to return a sensible answer.

<sup>18</sup> For more details on S3 method lookup; see Section 16.3.6.

For example, let us overload the index operator for objects of the class `categorical`. Looking at `help("[")`, we see that the default method has two arguments: `x` (the categorical object being sliced) and `i` (the indexer). Ours will have the same interface then:

```
`[.categorical` <- function(x, i)
{
  structure(
    unclass(x)[i], # `[`(unclass(x), i)
    class="categorical",
    levels=attr(x, "levels") # the same levels as input
  )
}
```

However, the default S3 method, ``[.default``, is hardcoded at the C language level. Therefore, we cannot refer to it directly. We have to call `unclass` instead. Alternatively, we can also call `NextMethod`:

```
`[.categorical` <- function(x, i)
{
  structure(
    NextMethod("["), # call default method, passing `x` and `i`
    class="categorical",
    levels=attr(x, "levels") # the same levels as input
  )
}
```

We can also introduce the replacement version of this operator:

```
`[<-.categorical` <- function(x, i, value)
{
  levels <- attr(x, "levels")
  value <- match(value, levels) # integer codes corresponding to levels
  structure(
    NextMethod("[<-"), # call default method, passing `x`, `i`, `values`
    class="categorical",
    levels=levels # same levels as input
  )

  ## or, equivalently:
  # structure(
  #   `[<-(unclass(x), i, value=match(value, attr(x, "levels"))),
  #   class="categorical",
  #   levels=attr(x, "levels")
  # )
}
```

Testing:

```
x <- as.categorical(c(3, 6, 4, NA, 9, 9, 6, NA, 3))
x[1:4]
## [1] "3" "6" "4" NA
## Categories: 3, 4, 6, 9
x[1:4] <- c("6", "7")
print(x)
## [1] "6" NA "6" NA "9" "9" "6" NA "3"
## Categories: 3, 4, 6, 9
```

Notice how we handled the case of nonexistent levels and that the recycling rule has been automatically inherited (amongst other features) from the default index operator.

**Exercise 10.13** *Do these two operators preserve the names attribute of `x`? Is indexing with negative integers or logical vectors supported as well? Why is that/is that not the case?*

Furthermore, let us overload the ``==`` operator. Assume<sup>19</sup> that we would like two `categorical` objects to be compared based on the actual labels they encode, in an element-wise manner:

```
`==.categorical` <- function(e1, e2)
  as.character(e1) == as.character(e2)
```

We are feeling lucky: by not performing any type checking, we rely on the particular `as.character` methods corresponding to the types of `e1` and `e2`. Also, assuming that `as.character` always<sup>20</sup> returns a character object, we dispatch to the default method for ``==`` (which handles atomic vectors).

Some examples:

```
as.categorical(c(1, 3, 5, 1)) == as.categorical(c(1, 3, 1, 1))
## [1] TRUE TRUE FALSE TRUE
as.categorical(c(1, 3, 5, 1)) == c(1, 3, 1, 1)
## [1] TRUE TRUE FALSE TRUE
c(1, 3, 5, 1) == as.categorical(c(1, 3, 1, 1))
## [1] TRUE TRUE FALSE TRUE
```

**Important** In the case of binary operators, dispatching is done based on the classes of both arguments. In all three example calls above, we call ``==.categorical``, regardless of whether the classed object is the first or the second operand.

<sup>19</sup> There are, of course, many possible ways to implement the ``==`` operator for the discussed objects. For instance, it may return either a single `TRUE` or `FALSE` depending on if two objects are identical (although probably overloading `all.equal` would be a better idea). We could also compare the corresponding underlying integer codes instead of the labels, etc.

<sup>20</sup> Which, of course, does not have to be the case; it is merely an assumption based on our belief in the common sense of other developers.

If two operands are classed, and different methods are overloaded for both, a warning will be generated, and the default internal method will be called.

```
`==.A` <- function(e1, e2) "A"
`==.B` <- function(e1, e2) "B"
structure(c(1, 2, 3), class="A") == structure(c(2, NA, 3), class="B")
## Warning: Incompatible methods ("==.A", "==.B") for "=="
## [1] FALSE NA TRUE
```

---

**Note** (\*) By defining a single **Ops** method, we can define the meaning of all binary operators at once.

```
Ops.categorical <- function(e1, e2)
{
  if (!(.Generic %in% c("<", ">", "<=", ">=", "==", "!=")))
    stop(sprintf("%s not defined for 'categorical' objects", .Generic))
  e1 <- as.character(e1)
  e2 <- as.character(e2)
  NextMethod(.Generic) # dispatch to the default method (for character)
}

as.categorical(c(1, 3, 5, 1)) > c(1, 2, 4, 2)
## [1] FALSE TRUE TRUE FALSE
```

Here `.Generic` is a variable representing the name of the operator (generic) being invoked; see **sec:use-method**.

Other *group generics* are: **Summary** (including functions such as **min**, **sum**, and **all**), **Math** (**abs**, **log**, **round**, etc.), and **Complex** (e.g., **Re**, **Im**); see **help**("groupGeneric") for more details.

Sometimes we must rely on **registerS3method** to force R to recognise a custom method related to such generics.

---

## 10.3 Common built-in S3 classes

Let us discuss some noteworthy built-in classes, including those representing date-time information and factors (ordered or not).

Classes for representing tabular data will be dealt with in separate parts of this textbook, owing to their importance and ubiquity. Namely, matrices and other arrays are covered in [Chapter 11](#), and data frames are discussed in [Chapter 12](#).

Inspecting other<sup>21</sup> interesting classes is left as a simple exercise for the studious reader.

### 10.3.1 Date, time, etc.

The Date class can be used to represent... dates.

```
(x <- c(Sys.Date(), as.Date(c("1969-12-31", "1970-01-01", "2023-02-29"))))
## [1] "2023-05-18" "1969-12-31" "1970-01-01" NA
class(x)
## [1] "Date"
```

Complex types are built on basic ones. Underneath, what we deal with here is:

```
typeof(x)
## [1] "double"
unclass(x)
## [1] 19495 -1 0 NA
```

which is the number of days since the *UNIX epoch*, 1970-01-01T00:00:00+0000 (midnight GMT/UTC).

The POSIXct (calendar time) class can be used to represent date-time objects:

```
(x <- Sys.time())
## [1] "2023-05-18 19:41:59 AEST"
class(x)
## [1] "POSIXct" "POSIXt"
typeof(x)
## [1] "double"
unclass(x)
## [1] 1684402920
```

Underneath, it is the number of seconds since the UNIX epoch. By default, whilst printing, the current default timezone is used (see **Sys.timezone**). However, such objects can be equipped with the `tzone` attribute.

```
structure(1, class=c("POSIXct", "POSIXt")) # using current default timezone
## [1] "1970-01-01 10:00:01 AEST"
structure(1, class=c("POSIXct", "POSIXt"), tzone="UTC")
## [1] "1970-01-01 00:00:01 UTC"
```

In both cases, the time is 1 second after the beginning of the UNIX epoch. On the author's PC, the former is displayed in the current local timezone, though.

**Exercise 10.14** Use *ISOdatetime* to inspect how midnights are displayed in different timezones.

<sup>21</sup> `unique(.S3_methods_table[, 2])` generates an (incomprehensive) approximation to the list of available classes.

The `POSIXlt` (local time) class is represented using a list of atomic vectors<sup>22</sup>.

```
(x <- as.POSIXlt(c(a="1970-01-01 00:00:00", b="2030-12-31 23:59:59")))
##                               a                               b
## "1970-01-01 00:00:00 AEST" "2030-12-31 23:59:59 AEDT"
class(x)
## [1] "POSIXlt" "POSIXt"
typeof(x)
## [1] "list"
str(unclass(x)) # calling str instead of print to make display more compact
## List of 11
## $ sec   : num [1:2] 0 59
## $ min   : int [1:2] 0 59
## $ hour  : int [1:2] 0 23
## $ mday  : int [1:2] 1 31
## $ mon   : int [1:2] 0 11
## $ year  : Named int [1:2] 70 130
## .. attr(*, "names")= chr [1:2] "a" "b"
## $ wday  : int [1:2] 4 2
## $ yday  : int [1:2] 0 364
## $ isdst : int [1:2] 0 1
## $ zone  : chr [1:2] "AEST" "AEDT"
## $ gmtoff: int [1:2] NA NA
## - attr(*, "tzone")= chr [1:3] "" "AEST" "AEDT"
## - attr(*, "balanced")= logi TRUE
```

**Exercise 10.15** Read about the meaning of each named element, especially *mon* and *year*; see `help("DateTimeClasses")`.

The manual states that `POSIXlt` is supposedly closer to human-readable forms than `POSIXct`, but it is a matter of taste. Some R functions return the former, and some output the latter type.

**Exercise 10.16** The two main functions for date formatting and parsing, `strftime` and `strptime`, use special field formatters (similar to `sprintf`). Read about them in the R manual. What type of inputs do they accept? What outputs do they produce?

There are several methods overloaded for objects of the said classes. In fact, the first call in this section already involved the use of `c.Date`.

**Exercise 10.17** Play around with the overloaded versions of `seq`, `rep`, and `as.character`.

A specific number of days or seconds can be added to or subtracted from a date or time, respectively. However, ``-`` (see also `diff`) can also be applied on two date-time objects, which yields an object of the class `difftime`.

<sup>22</sup> Which was inspired by `struct tm` in C's `<time.h>`.



```

Sys.Date() - (Sys.Date() - 1)
## Time difference of 1 days
Sys.time() - (Sys.time() - 1)
## Time difference of 1 secs

```

**Exercise 10.18** Check out how objects of the class `difftime` are internally represented.

Applying other arithmetic operations on date-time objects raises an error. Because date-time objects are just numbers, they can be compared to each other using binary operators<sup>23</sup>. Also, methods such as `sort` and `order`<sup>24</sup> could be applied on them.

**Exercise 10.19** Check out the `stringr` package, which replaces the base R date-time processing functions with their more portable counterparts.

**Exercise 10.20** `proc.time` can be used to measure the time to execute a given expression:

```

t0 <- proc.time() # timer start
# ... to do - something time-consuming ...
sum(runif(1e7)) # whatever, just testing
## [1] 4999488
print(proc.time() - t0) # elapsed time
##      user      system elapsed 
## 0.243    0.024    0.266

```

The function returns an object of the class `proc_time`. Inspect how it is represented internally.

### 10.3.2 Factors

The factor class is often used to represent categorical (qualitative) data, e.g., species, groups, types. In fact, categorical (the example class that we played with above) was inspired by the built-in factor.

```

(x <- c("spam", "spam", "bacon", "sausage", "spam", "bacon"))
## [1] "spam" "spam" "bacon" "sausage" "spam" "bacon"
(f <- factor(x))
## [1] spam  spam  bacon  sausage spam  bacon
## Levels: bacon sausage spam

```

Note how factors are printed. There are no double quote characters around the labels. The list of levels is given at the end.

Internally, such objects are represented as integer vectors (Section 6.4.1) with elements between 1 and  $k$ . They are equipped with the special (as in Section 4.4.3) `levels` attribute, which is a character vector of length  $k$ <sup>25</sup>.

<sup>23</sup> The overloaded group generic `Ops` prevents us from adding or multiplying two dates and defines the meaning of the relational operators. As an exercise, check out its source code.

<sup>24</sup> See an exercise below on the use of `xtfrm`.

<sup>25</sup> [66] states: *Factors are currently implemented using an integer array to specify the actual levels and a second array*

```

class(f)
## [1] "factor"
typeof(f)
## [1] "integer"
unclass(f)
## [1] 3 3 1 2 3 1
## attr(,"levels")
## [1] "bacon" "sausage" "spam"
attr(f, "levels") # also: levels(f)
## [1] "bacon" "sausage" "spam"

```

Factors are often used instead of character vectors defined over a small number of unique labels<sup>26</sup>, where there is a need to manipulate their levels easily.

```

attr(f, "levels") <- c("a", "b", "c") # also levels(f) <- c(...new...)
print(f)
## [1] c c a b c a
## Levels: a b c

```

The underlying codes remain the same.

Certain operations on vectors of small integers are relatively easy to express, especially those concerning element grouping: splitting, counting, and plotting (e.g., Figure 13.17). It is because the integer codes can naturally be used whilst indexing other vectors. Section 5.4 mentioned a few functions related to this, such as **match**, **split**, **findInterval**, and **tabulate**. Specifically, the latter can be implemented like “for each *i*, increase count[*factor\_codes*[*i*]] by one”.

**Exercise 10.21** Study the source code of the **factor** function. Note the use of **as.character**, **unique**, **order**, and **match**.

**Exercise 10.22** Implement a simplified version of **table** based on **tabulate**. It should work for objects of the class **factor** and return a named numeric vector.

**Exercise 10.23** Implement your version of **cut** based on **findInterval**.

---

**Important** The **as.numeric** method has not been overloaded for factors. Therefore, when we call the generic, the default method is used: it returns the underlying integer codes as-is. This can surprise unaware users when they play with factors that feature levels consisting of strings representing integer numbers:

```

(g <- factor(c(11, 15, 16, 11, 13, 4, 15))) # converts numbers to strings

```

*(continues on next page)*

---

of names that are mapped to the integers. Rather unfortunately users often make use of the implementation in order to make some calculations easier. This, however, is an implementation issue and is not guaranteed to hold in all implementations of R. Still, fortunately, this has been a de facto standard for factors for a very long time.

<sup>26</sup> Recall that there is a global (internal) string cache. Hence, having many duplicated strings is a burden on the computer’s memory.

(continued from previous page)

```
## [1] 11 15 16 11 13 4 15
## Levels: 4 11 13 15 16
as.numeric(g) # the underlying codes
## [1] 2 4 5 2 3 1 4
as.numeric(as.character(g)) # to get the numbers en-coded
## [1] 11 15 16 11 13 4 15
```

Unfortunately, support for factors is often hardcoded at the C language level, which will make this class behave less predictably (from the R perspective). In particular, the manual overloading of methods for factor objects might have no effect.

---

**Important** If `f` is a factor, then `x[f]` does not behave like `x[as.character(f)]` (indexing by labels, using the `names` attribute). Instead, we get `x[as.numeric(f)]` (the underlying codes will determine the positions).

```
h <- factor(c("a", "b", "a", "c", "a", "c"))
levels(h)[h] # the same as c("a", "b", "c")[c(1, 2, 1, 3, 1, 3)]
## [1] "a" "b" "a" "c" "a" "c"
c(b="x", c="y", a="z")[h] # names are not used whilst indexing
## b c b a b a
## "x" "y" "x" "z" "x" "z"
c(b="x", c="y", a="z")[as.character(h)] # names are used now
## a b a c a c
## "z" "x" "z" "y" "z" "y"
```

More often than not, indexing by factors will happen “accidentally”, leaving us slightly puzzled. In particular, factors look much like character vectors when they are featured in data frames:

```
(df <- data.frame(A=c("x", "y", "z"), B=factor(c("x", "y", "z"))))
## A B
## 1 x x
## 2 y y
## 3 z z
class(df[["A"]])
## [1] "character"
class(df[["B"]])
## [1] "factor"
```

(\*) Up until R4.0, many functions (including `data.frame` and `read.csv`) had the `stringsAsFactors` option (see `help("options")`) set to `TRUE`, which resulted in all character vectors’ being automatically converted to factors when, e.g., creating data frames (compare Chapter 12). Luckily, this is no longer the case, but they can still be en-

countered sporadically: for instance, the built-in `iris` dataset has the fifth column of the class:

```
class(iris[["Species"]])
## [1] "factor"
```

---

**Important** Be careful when combining factors and not-factors:

```
x <- factor(c("A", "B", "A"))
c(x, "C")
## [1] "1" "2" "1" "C"
c(x, factor("C"))
## [1] A B A C
## Levels: A B C
```

---

**Exercise 10.24** When subsetting a factor object, the result will inherit the `levels` attribute as-is:

```
f[c(1, 2)] # drop=FALSE
## [1] c c
## Levels: a b c
```

However:

```
f[c(1, 2), drop=TRUE]
## [1] c c
## Levels: c
```

Implement your version of the **`droplevels`** function, which removes the unused attributes.

**Exercise 10.25** The replacement version of the index operator does not automatically add new levels to the modified object:

```
x <- factor(c("A", "B", "A"))
`[<-`(x, 4, value="C") # like in x[4] <- "C"
## Warning in `[<-factor`(x, 4, value = "C"): invalid factor level, NA
##      generated
## [1] A    B    A    <NA>
## Levels: A B
```

Implement your version of ``[<-factor``, which is capable of doing so.

### 10.3.3 Ordered factors

When creating factors, we can enforce a particular ordering and the number of levels:

```
x <- c("spam", "spam", "bacon", "sausage", "spam", "bacon")
factor(x, levels=c("eggs", "bacon", "sausage", "spam"))
## [1] spam    spam    bacon    sausage spam    bacon
## Levels: eggs bacon sausage spam
```

If we want the arrangement of the levels to define a linear ordering relation over the set of labels, we can call:

```
(f <- factor(x, levels=c("eggs", "bacon", "sausage", "spam"), ordered=TRUE))
## [1] spam    spam    bacon    sausage spam    bacon
## Levels: eggs < bacon < sausage < spam
class(f)
## [1] "ordered" "factor"
```

It yields an ordered factor, which enables comparisons like:

```
f[f >= "bacon"] # what's not worse than bacon?
## [1] spam    spam    bacon    sausage spam    bacon
## Levels: eggs < bacon < sausage < spam
```

How is that possible? Well, based on information provided in this chapter, it will come as no surprise that it is because... someone has created a relational operator for objects of the class `ordered`.

### 10.3.4 Formulae (\*)

Formulae are created using the `~`` operator. Some R users employ them to specify widely-conceived *statistical models* in functions such as `lm` (e.g., linear regression), `glm` (generalised linear models: logistic regression etc.), `aov` (analysis of variance), `wilcox.test` (the two-sample Mann–Whitney–Wilcoxon test), `aggregate` (computing aggregates within data groups), `boxplot` (box-and-whisker plots for a variable split by a combination of factors), or `plot` (scatter plots); see also Chapter 11 of [56].

For instance, they can be used to describe symbolic relationships such as:

- “y as a linear combination of x1, x2, and x3”,
- “y grouped/split by a combination of x1 and x2”,

where y, x1, etc., are, for example, column names in some data frame.

Formulae are interpreted by the corresponding functions, and not the R language itself. Thus, programmers are free to assign them any meaning. As their syntax is quite esoteric, beginners might find them confusing. Hence, we will discuss them much later: in Section 17.6.

Luckily, the use of formulae can usually quite easily be avoided<sup>27</sup>.

<sup>27</sup> For example, `lm.fit` can be used instead of `lm`. It is slightly more difficult to learn, but it has the added

## 10.4 Argument checking revisited

Recall that anything can be passed as a function's input. Here are some additions to the topic we touched upon in [Section 9.2.1](#).

Compound objects are internally represented merely through basic types (such as numeric vectors, lists, or combinations thereof) and attributes. However, unless we really know better (which, by the way, this book is all about), we recommend relying on the hopefully well-thought-out methods developed by the designer of the class.

Ideally, when checking arguments passed to a function, determining if an object is of a desired type should be solely done by means of the generics like `is.class`. If that is not the case, a call to `as.class` may be used to ensure we will deal with an object of the desired type.

If a conversion is impossible, either because a specific method is unavailable or because its designer decided that this must be the case, whatever the consequences are is not necessarily our problem anymore.

We should explain to the user how the input type assurance is performed. In the case where they get any surprising results, they are expected to check/redefine the underlying `is.class` or `as.class` themselves.

This scheme is not watertight, and there will be users complaining that they get *unexpected* or *confusing* (in their opinion) outputs. With infinitely many potential types, however, we cannot respond to every possible situation.

**Example 10.26** *As an illustration, here is a function that counts the number of occurrences of items in a numerised (digitised?) version of a given object:*

```
nuntable <- function(x)
{
  if (!is.numeric(x)) x <- as.numeric(x) # two generics!

  u <- unique(x)
  structure(
    tabulate(match(x, u)),
    names=as.character(u)
  )
}
```

*Let us assume that the user has been informed (in the corresponding documentation page) that `x` must be a numeric vector (as in `is.numeric`) or an object coercible to (by means of `as.numeric`).*

*The callers will be stress-testing our function in many different ways:*

benefit of ensuring the user knows that the emergence of all model variables is not magical (especially the nonlinear/mixed effect terms).

```
numtable(c(1, 3, 5, 5, 1, 5))
## 1 3 5
## 2 1 3
```

It is an intended behaviour.

```
numtable(c("1", "3", "5", "5", "1", "5"))
## 1 3 5
## 2 1 3
```

It makes sense, too: a character vector consisting of number-strings has been fed on input.

```
numtable(c("a", "e", "z", "z", "a", "z"))
## Warning in numtable(c("a", "e", "z", "z", "a", "z")): NAs introduced by
## coercion
## <NA>
## 6
```

Does the output make no sense? Of course, it does. They have just passed something not easily coercible to a numeric vector. Notice the warning that suggests there is something wrong. The users need to correct their possible mistakes by themselves.

```
numtable(list(1, 2, 3:10, 2))
## Error in numtable(list(1, 2, 3:10, 2)): 'list' object cannot be coerced to
## type 'double'
```

Again, it makes sense. “But I think that this function should apply **unlist** automatically...” Well, if you want such behaviour, why don’t you call **numtable(unlist(...))** yourself? It is not so difficult.

```
numtable(factor(c(1, 3, 5, 5, 1, 5)))
## 1 2 3
## 2 1 3
```

Is this confusing? No, this is a well-documented behaviour of **as.numeric** on objects of the type **factor** (designed by another developer). A user is expected to know that in this case, **as.character** should be called first (but we can remind them about it in the documentation).

Of course, sometimes users might discover bugs or unexpected behaviours, especially related to boundary cases we have not been considerate enough to inspect. We are, of course, the ones to blame for the following:

```
numtable(numeric(0)) # bug: this should be corrected
## <NA>
## 0
```

## 10.5 (Over)using the forward-pipe operator, ``|>`` (\*)

The object-oriented programming paradigm is utile when we wish to define a new data type, perhaps even a hierarchy of types. Many development teams find it an efficient tool to organise larger pieces of software. Yet, in the broad data science and numerical computing domains, we are often the consumers of object orientation rather than class designers.

Thanks to the discussed method dispatch mechanism, our language is easily extensible. Something that mimics a new data type can easily be introduced. Most importantly, methods can be added or removed during run-time, e.g., when importing external packages.

However, R is still a functional programming language, where functions are not just first-class citizens: they are privileged. Of course, there are some inherent limitations stemming from the ingenious simplicity of S3: method dispatch is usually based only on the type of the first function argument, classes cannot be defined formally (but see [Section 11.5](#)), and there is no real encapsulation (we cannot actually hide data from a user<sup>28</sup>). However, overall the whole concept has proven quite versatile.

In functional programming, the emphasis is on operations (verbs), not data (nouns). It leads to a very readable syntax. For example, assuming that `square`, `x`, and `y` are sensibly defined, the mean squared error can be written as:

```
mean(square(x-y))
```

It is very user-centric. However, when implementing more complex data processing pipelines, a programmer thinks: “first, I need to do this, then I need to do that, and afterwards...”. When they write it down, there can be some pressing of Home and End keys necessary. It should not be a problem for most programmers.

```
finally(thereafter(then(first(x))))
```

However, some people are inherently lazy, always complaining, or compulsively trying to “optimise”<sup>29</sup> things.

**Example 10.27** *Base R is extremely flexible. We can introduce new vocabulary as we please. In Chapter 12, we will study an example where we define:*

<sup>28</sup> Which can be good, right?

<sup>29</sup> Do not get yours truly wrong, improving things is generally good. Nevertheless, in the long run, as a compulsive habit (“this is what (some) stakeholders want”, “we need to be agile and responsive”, etc.), it is not really sustainable (also for the environment!). Less is better, even though slightly more challenging. By introducing a new, parallel syntax, we duplicate the existing features. We cause some divide in the community: some users will be introduced to the system through the new interface and not know the old one, and others will have to learn the new syntax to be able to communicate with the former group. We also introduce a whole new set of issues (how to make the new functions interoperable with each other seamlessly, etc.).



- **group\_by** (a function that splits a data frame with respect to a combination of levels in given named columns and returns a list of data frames with class `list_dfs`),
- **aggregate.list\_dfs** (which applies a given aggregation function on each column of each data frame in a given list), and
- **mean.list\_dfs** (a specialised version of the former that calls **mean**).

The specifics do not matter now. Let us just consider the notation we use when the operations are chained:

```
# select a few rows and columns from the `iris` data frame:
iris_subset <- iris[51:150, c("Sepal.Width", "Petal.Length", "Species")]
# compute the averages of all variables grouped by Species:
mean(group_by(iris_subset, "Species"))
##      Species      x Mean
## 1 versicolor Sepal.Width 2.770
## 2 versicolor Petal.Length 4.260
## 3 virginica   Sepal.Width 2.974
## 4 virginica   Petal.Length 5.552
```

It is quite readable. We compute the mean in groups defined by *Species* in a subset of the *iris* data frame. All verbs appear on the left-hand side of the expression, with the last (the most important?) operation being listed first.

By the way, self-explanatory variable names and rich comments are priceless.

In more traditional object-oriented programming languages, either the method list is sealed inside<sup>30</sup> the class' definition (like in C++), or some peculiar patches must be applied to inject a method (like in Python)<sup>31</sup>. There, it is *the objects* that are *told* what to do. They are treated as black boxes.

Some popular languages rely on message-passing syntax, where operations are propagated (and written) left-to-right instead of inside-out. For instance, in C++ and Python (amongst many others), “`obj.method1().method2()`” means “call **method1** on `obj` and then call **method2** on the result”.

Since R 4.1.0, there is a *pipe operator*<sup>32</sup>, `|>`. It is merely a syntactic sugar for translating between the message-passing and function-centric notion. In a nutshell, writing:

```
x |> f() |> g(y) |> h()
(x-y) |> square() |> mean()
```

is equivalent, respectively, to:

<sup>30</sup> When methods are parts of particular classes, there can be a lot of duplicated code. Functional OOP can be more developer-friendly as we can provide all methods related to roughly the same functionality in one spot.

<sup>31</sup> See also the concept of extension methods in C# or Kotlin or, to some extent, class inheritance.

<sup>32</sup> It was inspired by `|` in Bash and `|>@` in F# and Julia (which are part of the language specification). Also, there is a `%>` operator (and related ones) in the R package **magrittr**.

```
h(g(f(x), y))
mean(square(x-y))
```

This syntax is developer-centric. It emphasises the order in which the operations are executed, something that could always be achieved with the function-centric form and perhaps a few auxiliary variables.

The placeholder ``_`` can be used on the right-hand side of the pipe operator (only once) to indicate that the left-hand side must be matched to a specific *named* argument of the function to be called. Otherwise, the left side always gets passed as the first argument.

Therefore, the two following expressions are equivalent:

```
x |> median() |> `_`(e1=x, e2=_) |> abs() |> median()
median(abs(x-median(x)))
```

**Example 10.28** *In the above example, a pipe operator version of the `iris` aggregation exercise would look like:*

```
iris_subset |> group_by("Species") |> mean()
```

Expressions on the right-hand side of the pipe operator must always be proper calls. Therefore, the use of round brackets is obligatory. Thus, when passing anonymous functions, we must write:

```
runif(10) |> (function(x) mean((x-mean(x))^2))() # note the "()" at the end
## [1] 0.078184
```

Peculiarly, in R 4.1.0, a “shorthand” notation for creating functions was introduced. We can save seven keystrokes and scribble “`\(...) expr`” instead of “`function(...)` `expr`”.

```
runif(10) |> (\(x) mean((x-mean(x))^2))() # again: "()" at the end
## [1] 0.078184
```

There is nothing that cannot be achieved without the pipe operator. As this book is minimalist by design, we will be refraining<sup>33</sup> ourselves from using it.

---

**Note** When writing code interactively, we may sometimes benefit from using the rightward ``->`` operator. Suffice it to say that “`name <- value`” and “`value -> name`” are synonymous.

This way, we can write some lengthy code, store the result in an intermediate variable, and then continue to the next line (possibly referring to that auxiliary value more than once). In the long run, multiplying entities without necessity is unsustainable.

---

<sup>33</sup> Which some readers would name an *uncool* (old-school) approach, but we do not care. Remember that the functional syntax is the native one. We have to be able to understand it anyway.

For instance:

```
runif(10) -> .; mean((.-mean(.))^2)
## [1] 0.078184
```

or:

```
iris[, c("Sepal.Width", "Petal.Length", "Species")] -> .
.[ .[, "Species"] %in% c("versicolor", "virginica"), ] -> .
mean(group_by(., "Species"))
##      Species      x Mean
## 1 versicolor Sepal.Width 2.770
## 2 versicolor Petal.Length 4.260
## 3 virginica  Sepal.Width 2.974
## 4 virginica  Petal.Length 5.552
```

`.` is as valid a variable name as any other one.

---

## 10.6 Exercises

**Exercise 10.29** Answer the following questions:

- How to display the source code of the default methods for **head** and **tail**?
- Can there be, at the same time, one object of the class `c("A", "B")` and another one of the class `c("B", "A")`?
- If `f` is a factor, what are the relationships between `as.character(f)`, `as.numeric(f)`, `as.character(as.numeric(f))`, and `as.numeric(as.character(f))`?
- If `x` is a named vector and `f` is a factor, is `x[f]` equivalent to `x[as.character(f)]` or rather `x[as.numeric(f)]`?

**Exercise 10.30** A user calls:

```
plot(x, y, col="red", ylim=c(1, max(x)), log="y")
```

where `x` and `y` are numeric vectors. Consult `help("plot")` for the meaning of the `ylim` and `log` arguments. Was that straightforward?

**Exercise 10.31** Explain why the two following calls return significantly different results.

```
c(Sys.Date(), "1970-01-01")
## [1] "2023-05-18" "1970-01-01"
c("1970-01-01", Sys.Date())
## [1] "1970-01-01" "19495"
```

*Propose a workaround.*

**Exercise 10.32** Write methods **head** and **tail** for our example *categorical* class.

**Exercise 10.33** (\*) Write an R package that defines S3 class *categorical*. Add a few methods for this class. Note the need to use the *S3method* directive in the *NAMESPACE* file; see [62].

**Exercise 10.34** Inspect the result of a call to **binom.test**(79, 100). Find the method responsible for such objects' pretty printing.

**Exercise 10.35** Inspect the result of a call to **rle**(**c**(1, 1, 1, 4, 3, 3, 3, 3, 2, 2)). Find the method responsible for such objects' pretty printing.

**Exercise 10.36** Read more about the *connection* class. In particular, see the *Value* section in **help**("connections").

**Exercise 10.37** Read about the subsetting operators overloaded for the *package\_version* class; see **help**("numeric\_version").

**Exercise 10.38** There are *xtfrm* methods overloaded for classes such as *numeric\_version*, *difftime*, *Date*, and *factor*. Find out how they work and where they might be of service (especially in relation to **order** and **sort**; see also Section 12.3.1).

**Exercise 10.39** Give an example where **split**(*x*, **list**(*y1*, *y2*)) (with default arguments) will fail to generate the correct result.

**Exercise 10.40** Write a function that determines the mode, i.e., the most frequently occurring value in a given object of the class *factor*. If the mode is not unique, return a randomly chosen one (each with the same probability).

**Exercise 10.41** Implement your version of the **gl** function.

**Exercise 10.42** Check out which built-in date-time functions the *stringx* package replaces with more portable ones.

---

# 11

---

## Matrices and other arrays

---

When we equip an atomic or generic vector with the `dim` attribute, it automatically becomes an object of the S3 class `array`. In particular, two-dimensional arrays (primary S3 class `matrix`) allow us to represent *tabular* data where items are aligned into rows and columns:

```
structure(1:6, dim=c(2, 3)) # a matrix with 2 rows and 3 columns
##      [,1] [,2] [,3]
## [1,]  1   3   5
## [2,]  2   4   6
```

Combined with the fact that there are many built-in functions overloaded for the `matrix` class, we have just opened up a whole world of new possibilities. We explore them in this chapter.

In particular, we discuss how to perform basic algebraic operations such as matrix multiplication, transpose, finding eigenvalues, and performing various decompositions. We also cover data wrangling operations such as array subsetting and column- and rowwise aggregation.

---

**Important** Oftentimes, a numeric matrix with  $n$  rows and  $m$  columns is used to represent  $n$  points (samples) in an  $m$ -dimensional space (with  $m$  numeric features or variables),  $\mathbb{R}^m$ .

---

Furthermore, in the next chapter, we will introduce data frames: matrix-like objects whose columns can be of any (not necessarily the same) type.

---

### 11.1 Creating arrays

#### 11.1.1 `matrix` and `array`

A matrix can be conveniently created using the `matrix` function.

```
(A <- matrix(1:6, byrow=TRUE, nrow=2))
##      [,1] [,2] [,3]
```

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

The above converted an atomic vector of length six into a matrix with two rows. The number of columns was determined automatically (`ncol=3` could have been passed to get the same result).

---

**Important** By default, the elements of the input vector are read columnwisely:

```
matrix(1:6, ncol=3) # byrow=FALSE
##      [,1] [,2] [,3]
## [1,] 1 3 5
## [2,] 2 4 6
```

A matrix can be equipped with dimension names, being a list of two character vectors of appropriate sizes, labelling each row and column in this order:

```
matrix(1:6, byrow=TRUE, nrow=2, dimnames=list(c("x", "y"), c("a", "b", "c")))
##   a b c
## x 1 2 3
## y 4 5 6
```

Alternatively, to create a matrix, we can use the **array** function, which requires the number of rows and columns to be specified explicitly.

```
array(1:6, dim=c(2, 3))
##      [,1] [,2] [,3]
## [1,] 1 3 5
## [2,] 2 4 6
```

The elements are consumed in a column-major manner.

Arrays of dimensionality other than 2 are also possible. Here is a one-dimensional array. When printed, it is indistinguishable from an atomic vector (but the `class` attribute is still set to `array`):

```
array(1:6, dim=6)
## [1] 1 2 3 4 5 6
```

And now for something completely different: a three-dimensional array of size  $3 \times 4 \times 2$ :

```
array(1:24, dim=c(3, 4, 2))
## , , 1
##
##      [,1] [,2] [,3] [,4]
```

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```
## [1,]    1    4    7   10
## [2,]    2    5    8   11
## [3,]    3    6    9   12
##
## , , 2
##
##      [,1] [,2] [,3] [,4]
## [1,]   13   16   19   22
## [2,]   14   17   20   23
## [3,]   15   18   21   24
```

which can be thought of as two matrices of size  $3 \times 4$  (because how else can we print out a 3D object on a 2D console?).

The **array** function can be fed with the `dimnames` argument too. For instance, the above three-dimensional hypertable would require a list of three character vectors of sizes 3, 4, and 2, respectively.

**Exercise 11.1** *The readers are encouraged to try out themselves that 10-dimensional arrays are also possible.*

### 11.1.2 Promoting and stacking vectors

We can promote an ordinary vector to a column vector, i.e., a matrix with one column, by calling:

```
as.matrix(1:2)
##      [,1]
## [1,]    1
## [2,]    2
cbind(1:2)
##      [,1]
## [1,]    1
## [2,]    2
```

and to a row vector:

```
t(1:3) # transpose
##      [,1] [,2] [,3]
## [1,]    1    2    3
rbind(1:3)
##      [,1] [,2] [,3]
## [1,]    1    2    3
```

Actually, **cbind** and **rbind** stand for column- and row-bind; they allow multiple vectors and matrices to be stacked one after/below another:

```

rbind(1:4, 5:8, 9:10, 11) # row bind
##      [,1] [,2] [,3] [,4]
## [1,]    1    2    3    4
## [2,]    5    6    7    8
## [3,]    9   10    9   10
## [4,]   11   11   11   11
cbind(1:4, 5:8, 9:10, 11) # column bind
##      [,1] [,2] [,3] [,4]
## [1,]    1    5    9   11
## [2,]    2    6   10   11
## [3,]    3    7    9   11
## [4,]    4    8   10   11
cbind(1:2, 3:4, rbind(11:13, 21:23)) # vector, vector, 2x3 matrix
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    3   11   12   13
## [2,]    2    4   21   22   23

```

and so forth.

Unfortunately, the *generalised* recycling rule is not implemented in full:

```

cbind(1:4, 5:8, cbind(9:10, 11)) # different from cbind(1:4, 5:8, 9:10, 11)
## Warning in cbind(1:4, 5:8, cbind(9:10, 11)): number of rows of result is
##      not a multiple of vector length (arg 1)
##      [,1] [,2] [,3] [,4]
## [1,]    1    5    9   11
## [2,]    2    6   10   11

```

The first two arguments are of length four.

### 11.1.3 Simplifying lists

**simplify2array** is an extension of the **unlist** function. Given a list of atomic vectors, each of length one, it will return a flat atomic vector. However, if a list of equisized vectors of greater lengths is given, these will be converted to a matrix.

```

simplify2array(list(1, 11, 21)) # each of length 1
## [1]  1 11 21
simplify2array(list(1:3, 11:13, 21:23, 31:33)) # each of length 3
##      [,1] [,2] [,3] [,4]
## [1,]    1   11   21   31
## [2,]    2   12   22   32
## [3,]    3   13   23   33
simplify2array(list(1, 11:12, 21:23)) # no can do
## [[1]]
## [1] 1

```

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```
##
## [[2]]
## [1] 11 12
##
## [[3]]
## [1] 21 22 23
```

In the second example, each vector becomes a separate column of the resulting matrix<sup>1</sup>.

See Section 12.3.7 for a few more examples.

**Example 11.2** Quite a few functions call the above automatically (compare the *simplify* or *SIMPLIFY* (sic!) argument in **sapply**, **tapply**, **mapply**, **replicate**, etc.).

For instance:

```
min_mean_max <- function(x) c(Min=min(x), Mean=mean(x), Max=max(x))
sapply(split(iris[["Sepal.Length"]], iris[["Species"]]), min_mean_max)
##      setosa versicolor virginica
## Min   4.300      4.900      4.900
## Mean  5.006      5.936      6.588
## Max   5.800      7.000      7.900
```

Take note of what constitutes the columns of the return matrix.

**Exercise 11.3** Inspect the behaviour of **as.matrix** on list arguments. Write your version of **simplify2array** named **as.matrix.list** that always returns a matrix. If a list of non-equisized vectors is given, fill the missing cells with NAs.

---

**Important** Sometimes a call to **do.call(cbind, x)** might be a better idea than a referral to **simplify2array**. Provided that *x* is a list of atomic vectors, it *always* returns a matrix: shorter vectors are recycled (which might be welcome, but not necessarily).

```
do.call(cbind, list(a=c(u=1), b=c(v=2, w=3), c=c(i=4, j=5, k=6)))
## Warning in (function (... , deparse.level = 1) : number of rows of result
## is not a multiple of vector length (arg 2)
##   a b c
## i 1 2 4
## j 1 3 5
## k 1 2 6
```

---

**Example 11.4** Consider a named toy list of numeric vectors:

---

<sup>1</sup> Which can easily be explained by the fact that matrix elements are stored in a columnwise order.

```
x <- list(a=runif(10), b=rnorm(15))
```

Compare the results generated by **sapply** (which calls **simplify2array**):

```
sapply(x, function(e) c(Mean=mean(e)))
##      a.Mean  b.Mean
## 0.57825 0.12431
sapply(x, function(e) c(Min=min(e), Max=max(e)))
##           a           b
## Min 0.045556 -1.9666
## Max 0.940467  1.7869
```

with its version based on **do.call** and **cbind**:

```
sapply2 <- function(...)
  do.call(cbind, lapply(...))

sapply2(x, function(e) c(Mean=mean(e)))
##           a           b
## Mean 0.57825 0.12431
sapply2(x, function(e) c(Min=min(e), Max=max(e)))
##           a           b
## Min 0.045556 -1.9666
## Max 0.940467  1.7869
```

Notice that **sapply** may return an atomic vector with somewhat surprising names.

#### 11.1.4 Beyond numeric arrays

Arrays built on atomic vectors other than numeric ones are possible too. For instance, we will later stress that comparisons featuring matrices are performed elementwisely. They spawn logical matrices:

```
A >= 3
##      [,1] [,2] [,3]
## [1,] FALSE FALSE TRUE
## [2,] TRUE  TRUE TRUE
```

Furthermore, matrices of character strings can be useful too:

```
matrix(strep(LETTERS[1:6], 1:6), ncol=3)
##      [,1] [,2] [,3]
## [1,] "A"  "CCC" "EEEE"
## [2,] "BB" "DDD" "FFFF"
```

And, of course, complex matrices:

```
A + 1i
##      [,1] [,2] [,3]
## [1,] 1+1i 2+1i 3+1i
## [2,] 4+1i 5+1i 6+1i
```

We are not limited to *atomic* vectors: lists can be a basis for arrays as well:

```
matrix(list(1, 11:21, "A", list(1, 2, 3)), nrow=2)
##      [,1]      [,2]
## [1,] 1      "A"
## [2,] integer,11 list,3
```

Some elements are not displayed correctly, but they are still there.

### 11.1.5 Internal representation

An object of the S3 class `array` is an atomic vector or a list equipped with the `dims` attribute being a vector of nonnegative integers. Interestingly, we do not have to set the `class` attribute explicitly: the accessor function `class` will return an implicit<sup>2</sup> class anyway (compare Section 4.4.3).

```
class(1) # atomic vector
## [1] "numeric"
class(structure(1, dim=rep(1, 1))) # 1D array (vector)
## [1] "array"
class(structure(1, dim=rep(1, 2))) # 2D array (matrix)
## [1] "matrix" "array"
class(structure(1, dim=rep(1, 3))) # 3D array
## [1] "array"
```

Note that a two-dimensional array is additionally of the `matrix` class.

Optional dimension names are represented by means of the `dimnames` attribute, which is a list of  $d$  character vectors, where  $d$  is the array's dimensionality.

```
(A <- structure(1:6, dim=c(2, 3), dimnames=list(letters[1:2], LETTERS[1:3])))
##   A B C
## a 1 3 5
## b 2 4 6
dim(A) # or attr(A, "dim")
## [1] 2 3
dimnames(A) # or attr(A, "dimnames")
## [[1]]
## [1] "a" "b"
##
```

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<sup>2</sup> Calling `unclass` on a matrix has no effect.

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```
## [[2]]
## [1] "A" "B" "C"
```

---

**Important** Internally, elements in an array are always stored in the columnwise (column-major, Fortran) order:

```
as.numeric(A) # drop all attributes to reveal the underlying numeric vector
## [1] 1 2 3 4 5 6
```

Setting `byrow=TRUE` in a call to the `matrix` only affects the order in which this function reads a given source vector, not the column/row-majority.

```
(B <- matrix(1:6, ncol=3, byrow=TRUE))
##      [,1] [,2] [,3]
## [1,]    1    2    3
## [2,]    4    5    6
as.numeric(B)
## [1] 1 4 2 5 3 6
```

---

The two said special attributes can be modified through the replacement functions ``dim<-`` and ``dimnames<-`` (and, of course, ``attr<-`` as well). In particular, changing `dim` does not alter the underlying atomic vector; it only affects how other functions, including the corresponding `print` method, interpret their placement on a virtual grid:

```
`dim<-`(A, c(3, 2)) # not the same as transpose of A
##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
## [3,]    3    6
```

We obtained a different *view* of the same *flat* data vector. Also, the `dimnames` attribute was dropped as its size became incompatible with the newly requested dimensionality.

**Exercise 11.5** Study the source code of the `nrow`, `NROW`, `ncol`, `NCOL`, `rownames`, `row.names`, and `colnames` functions.

Interestingly, for one-dimensional arrays, the `names` function returns a reasonable value (based on the `dimnames` attribute, which is a list featuring one character vector), despite the `names` attribute's not being set.

What is more, `dimnames` itself can be named:

```
names(dimnames(A)) <- c("ROWS", "COLUMNS")
print(A)
```

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```
##      COLUMNS
## ROWS A B C
##    a 1 3 5
##    b 2 4 6
```

It is still a numeric matrix, but the presentation thereof is slightly prettified.

**Exercise 11.6** `outer` applies an elementwisely vectorised function on each pair of elements from two vectors, forming a two-dimensional result grid. Based on two calls to `rep`, implement it yourself.

Some examples:

```
outer(c(x=1, y=10, z=100), c(a=1, b=2, c=3, d=4), "*") # multiplication
##      a  b  c  d
## x    1  2  3  4
## y   10 20 30 40
## z  100 200 300 400
outer(c("A", "B"), 1:8, paste, sep="-") # concatenate strings
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
## [1,] "A-1" "A-2" "A-3" "A-4" "A-5" "A-6" "A-7" "A-8"
## [2,] "B-1" "B-2" "B-3" "B-4" "B-5" "B-6" "B-7" "B-8"
```

**Exercise 11.7** Show how `match(y, z)` can be expressed using `outer`. Is its time and memory complexity optimal, though?

**Exercise 11.8** `table` creates a contingency matrix/array that counts the number of unique pairs of corresponding elements from one or more vectors of equal lengths. Implement its one- and two-argument version based on `tabulate`.

For example:

```
tips <- read.csv(paste0("https://github.com/gagolews/teaching-data/raw/",
  "master/other/tips.csv"), comment.char="#") # a data.frame (list)
table(tips[["day"]])
##
##  Fri  Sat  Sun  Thur
##   19   87   76   62
table(tips[["smoker"]], tips[["day"]])
##
##      Fri Sat Sun Thur
## No     4  45  57   45
## Yes    15  42  19   17
```

## 11.2 Array indexing

Array subsetting can be performed by means of an overloaded<sup>3</sup> `[]` method, which we will usually provide with many indexers: two in the matrix case; see `help("[]")`.

Throughout this section, we refer to the two following example matrices:

```
(A <- matrix(1:12, byrow=TRUE, nrow=3))
##      [,1] [,2] [,3] [,4]
## [1,]    1    2    3    4
## [2,]    5    6    7    8
## [3,]    9   10   11   12
B <- A
dimnames(B) <- list(
  c("a", "b", "c"), # row labels
  c("x", "y", "z", "w") # column labels
)
B
##   x  y  z  w
## a 1  2  3  4
## b 5  6  7  8
## c 9 10 11 12
```

Subsetting higher-dimensional arrays will be covered at the end.

### 11.2.1 Arrays are built on basic vectors

Subsetting based on one indexer (as in [Chapter 5](#)) will refer to the underlying flat vector.

For instance:

```
A[6]
## [1] 10
```

It is the element in the third row, second column. Recall that values are stored in the column-major order.

### 11.2.2 Selecting individual elements

Mathematically, we say that our example  $3 \times 4$  real matrix  $\mathbf{A} \in \mathbb{R}^{3 \times 4}$  is like:

$$\mathbf{A} = \begin{bmatrix} a_{1,1} & a_{1,2} & a_{1,3} & a_{1,4} \\ a_{2,1} & a_{2,2} & a_{2,3} & a_{2,4} \\ a_{3,1} & a_{3,2} & a_{3,3} & a_{3,4} \end{bmatrix} = \begin{bmatrix} 1 & 2 & 3 & 4 \\ 5 & 6 & 7 & 8 \\ 9 & 10 & 11 & 12 \end{bmatrix}.$$

<sup>3</sup> Hidden deeply at the C language level.

Matrix elements are aligned in a two-dimensional grid. They are organised into rows and columns. Hence, we can pinpoint a cell using two indexes:  $a_{i,j}$  refers to the  $i$ -th row and the  $j$ -th column.

Similarly in R:

```
A[3, 2] # 3rd row, 2nd column
## [1] 10
B["c", "y"] # using dimnames == B[3, 2]
## [1] 10
```

### 11.2.3 Selecting rows and columns

Some textbooks, and we are fond of this notation here as well, mark with  $\mathbf{a}_{i, \cdot}$  a vector that consists of all the elements in the  $i$ -th row and with  $\mathbf{a}_{\cdot, j}$  all items in the  $j$ -th column.

In R, these will correspond to one of the indexers being left out.

```
A[3, ] # 3rd row
## [1] 9 10 11 12
A[, 2] # 2nd column
## [1] 2 6 10
B["c", ] # or B[3, ]
## x y z w
## 9 10 11 12
B[, "y"] # or B[, 2]
## a b c
## 2 6 10
```

Let us stress that  $A[1]$ ,  $A[1, ]$ , and  $A[, 1]$  have all different meanings. Also, we see that the results' `dimnames` are adjusted accordingly; see also `unname`, which can take care of them once and for all.

**Exercise 11.9** Use  *duplicated* to remove repeating rows in a given numeric matrix (see also *unique*).

### 11.2.4 Dropping dimensions

Extracting an individual element or a single row/column from a matrix brings about an atomic vector. If the `dim` attribute consists of 1s only, it will be removed whatsoever.

In order to obtain proper row and column vectors, we can request the preservation of the dimensionality of the output object (and, more precisely, the length of `dim`). It can be done by passing `drop=FALSE` to ``[``.

```
A[1, 2, drop=FALSE] # 1st row, 2nd columns
##      [,1]
## [1,]    2
```

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```

A[1, , drop=FALSE] # 1st row
##      [,1] [,2] [,3] [,4]
## [1,]    1    2    3    4
A[ , 2, drop=FALSE] # 2nd column
##      [,1]
## [1,]    2
## [2,]    6
## [3,]   10

```

---

**Important** Unfortunately, the `drop` argument defaults to `TRUE`. Many bugs could be avoided otherwise, primarily when the indexers are generated programmatically.

---

See also the **`drop`** function, which removes the dimensions with only one level.

---

**Note** For list-based matrices, we can also use a multi-argument version of ``[[`` to extract the individual elements.

---

```

C <- matrix(list(1, 11:12, 21:23, 31:34), nrow=2)
C[1, 2] # for `[`, input type is the same as the output type, hence a list
## [[1]]
## [1] 21 22 23
C[1, 2, drop=FALSE]
##      [,1]
## [1,] integer,3
C[[1, 2]] # extract
## [1] 21 22 23

```

### 11.2.5 Selecting submatrices

Indexing based on two vectors, both of length two or more, extracts a sub-block of a given matrix:

```

A[1:2, c(1, 2, 4)] # rows 1 and 2, columns 1, 2, and 4
##      [,1] [,2] [,3]
## [1,]    1    2    4
## [2,]    5    6    8
B[c("a", "b"), -3]
##      x y w
## a 1 2 4
## b 5 6 8

```



Note again that `drop=TRUE` is the default, which affects the behaviour if one of the indexes is a scalar.

```
A[c(1, 3), 3]
## [1] 3 11
A[c(1, 3), 3, drop=FALSE]
##      [,1]
## [1,]    3
## [2,]   11
```

**Exercise 11.10** Overload the `split` function for the `matrix` class so that, given a matrix with  $n$  rows and an object of the class `factor` of length  $n$  (or a list of such objects), a list of  $n$  matrices is returned. For example:

```
split.matrix <- ...to.do...
A <- matrix(1:12, nrow=3) # matrix whose rows are to be split
s <- factor(c("a", "b", "a")) # determines the grouping of rows
split(A, s)
## $a
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    7   10
## [2,]    3    6    9   12
##
## $b
##      [,1] [,2] [,3] [,4]
## [1,]    2    5    8   11
```

### 11.2.6 Selecting elements based on logical vectors

Logical vectors can also be used as indexers, with consequences that are not hard to guess:

```
A[c(TRUE, FALSE, TRUE), -1] # select 1st and 3rd row, all but 1st column
##      [,1] [,2] [,3]
## [1,]    4    7   10
## [2,]    6    9   12
B[B[, "x"]>1 & B[, "x"]<=9, ] # all rows where x is in (1, 9]
##   x y z w
## b 5 6 7 8
## c 9 10 11 12
A[2, colMeans(A)>6, drop=FALSE] # 2nd row of the columns with means > 6
##      [,1] [,2]
## [1,]    8   11
```

**Note** Section 11.3 notes that comparisons involving matrices are performed in an elementwise manner, for example:

```
A>7
##      [,1] [,2] [,3] [,4]
## [1,] FALSE FALSE FALSE TRUE
## [2,] FALSE FALSE TRUE TRUE
## [3,] FALSE FALSE TRUE TRUE
```

Such logical matrices can be used to index other matrices of the same size. This kind of indexing always gives rise to a (flat) vector:

```
A[A>7]
## [1] 8 9 10 11 12
```

It is nothing else than the single-indexer subsetting involving two flat vectors (a numeric and a logical one); the `dim` attributes are not considered here.

---

**Exercise 11.11** Implement your versions of `max.col`, `lower.tri`, and `upper.tri`.

### 11.2.7 Selecting based on two-column numeric matrices

We can also index a matrix `A` with a two-column matrix of positive integers `I`, for instance:

```
(I <- cbind(
  c(1, 3, 2, 1, 2),
  c(2, 3, 2, 1, 4)
))
##      [,1] [,2]
## [1,] 1 2
## [2,] 3 3
## [3,] 2 2
## [4,] 1 1
## [5,] 2 4
```

Now `A[I]` gives easy access to:

- `A[I[1, 1], I[1, 2]]`,
- `A[I[2, 1], I[2, 2]]`,
- `A[I[3, 1], I[3, 2]]`,
- ...

and so forth. In other words, each row of `I` gives the coordinates of the elements to extract.

```
A[I]
## [1] 4 9 5 1 11
```

This is exactly  $A[1, 2]$ ,  $A[3, 3]$ ,  $A[2, 2]$ ,  $A[1, 1]$ ,  $A[2, 4]$ . The result is always a flat vector.

---

**Note** `which` can also return a list of index matrices:

```
which(A>7, arr.ind=TRUE)
##      row col
## [1,]  2   3
## [2,]  3   3
## [3,]  1   4
## [4,]  2   4
## [5,]  3   4
```

Moreover, `arrayInd` can be used to convert flat indexes to multidimensional ones.

---

**Exercise 11.12** Implement your version of `arrayInd` and a function performing the inverse operation.

**Exercise 11.13** Write your version of `diag`.

### 11.2.8 Higher-dimensional arrays

For  $d$ -dimensional arrays, indexing can involve up to  $d$  indexes. It is particularly valuable for arrays with the `dimnames` attribute set representing contingency tables over a Cartesian product of multiple factors. The built-in `datasets::Titanic` object is an example of this:

```
str(dimnames(Titanic)) # for reference (note that dimnames are named)
## List of 4
## $ Class : chr [1:4] "1st" "2nd" "3rd" "Crew"
## $ Sex   : chr [1:2] "Male" "Female"
## $ Age   : chr [1:2] "Child" "Adult"
## $ Survived: chr [1:2] "No" "Yes"
Titanic["Crew", "Male", "Adult", "Yes"]
## [1] 192
```

gives the number of adult male crew members who survived the accident. Also:

```
Titanic["Crew", , "Adult", ]
##      Survived
## Sex      No Yes
## Male    670 192
## Female    3  20
```

and so on.

**Exercise 11.14** Check if the above four-dimensional array can be indexed using matrices with four columns.

### 11.2.9 Replacing elements

There is also a multidimensional version of the replacement subsetting function, ``[<-``.

Generally, subsetting drops all attributes except `names`, `dim`, and `dimnames` (unless it does not make sense otherwise). The replacement variant of the index operator modifies vector values but generally preserves all the attributes.

This enables transforming matrix elements like:

```
B[B<10] <- A[B<10]^2
print(B)
##      x  y  z  w
## a 1 16 49 100
## b 4 25 64 121
## c 9 10 11 12
B[] <- rep(seq_len(NROW(B)), NCOL(B)) # NOT the same as B <- ...
print(B)
##      x y z w
## a 1 1 1 1
## b 2 2 2 2
## c 3 3 3 3
```

Take note of the preservation of `dim` and `dimnames`.

**Exercise 11.15** Given a character matrix with entities that can be interpreted as numbers like:

```
(X <- rbind(x=c(a="1", b="2"), y=c("3", "4")))
##      a  b
## x "1" "2"
## y "3" "4"
```

convert it to a numeric matrix with a single line of code. Preserve all attributes.

---

## 11.3 Common operations

### 11.3.1 Matrix transpose

The matrix *transpose*, mathematically denoted with  $A^T$ , is available via a call to `t`:

```
(A <- matrix(1:6, byrow=TRUE, nrow=2))
##      [,1] [,2] [,3]
## [1,]  1   2   3
## [2,]  4   5   6
t(A)
##      [,1] [,2]
## [1,]  1   4
## [2,]  2   5
## [3,]  3   6
```

Hence, if  $\mathbf{B} = \mathbf{A}^T$ , then it is a matrix such that  $b_{i,j} = a_{j,i}$ . In other words, in the transposed matrix, rows become columns, and columns become rows.

For higher-dimensional arrays, a generalised transpose can be achieved with `aperm` (try permuting the dimensions of `Titanic`). Also, the conjugate transpose of a complex matrix  $\mathbf{A}$  is done via `Conj(t(A))`.

### 11.3.2 Vectorised mathematical functions

Vectorised functions such as `sqrt`, `abs`, `round`, `log`, `exp`, `cos`, `sin`, etc., operate on each array element<sup>4</sup>.

```
A <- matrix(1/(1:6), nrow=2)
round(A, 2) # rounds every element in A
##      [,1] [,2] [,3]
## [1,] 1.0 0.33 0.20
## [2,] 0.5 0.25 0.17
```

**Exercise 11.16** Using a single call to `matplot`, which accepts the `y` argument to be a matrix, draw a plot of  $\sin(x)$ ,  $\cos(x)$ ,  $|\sin(x)|$ , and  $|\cos(x)|$  for  $x \in [-2\pi, 6\pi]$ .

### 11.3.3 Aggregating rows and columns

When we call an aggregation function on an array, it will reduce all elements to a single number:

```
(A <- matrix(1:12, byrow=TRUE, nrow=3))
##      [,1] [,2] [,3] [,4]
## [1,]  1   2   3   4
## [2,]  5   6   7   8
## [3,]  9  10  11  12
mean(A)
## [1] 6.5
```

<sup>4</sup> They are simply applied on each element of the underlying flat vector. Section 5.5 mentioned that unary functions preserve *all* attributes of their inputs, hence also `dim` and `dimnames`.

The **apply** function may be used to summarise individual rows or columns in a matrix:

- **apply**(A, 1, f) applies a given function **f** on each *row* of a matrix A;
- **apply**(A, 2, f) applies **f** on each *column* of A.

For instance:

```
apply(A, 1, mean) # synonym: rowMeans(A)
## [1] 2.5 6.5 10.5
apply(A, 2, mean) # synonym: colMeans(A)
## [1] 5 6 7 8
```

The function being applied does not have to return a single number:

```
apply(A, 2, range) # min and max
##      [,1] [,2] [,3] [,4]
## [1,]    1    2    3    4
## [2,]    9   10   11   12
apply(A, 1, function(row) c(Min=min(row), Mean=mean(row), Max=max(row)))
##      [,1] [,2] [,3]
## Min   1.0  5.0  9.0
## Mean  2.5  6.5 10.5
## Max   4.0  8.0 12.0
```

Take note of the columnwise order of the output values.

**apply** works on higher-dimensional arrays:

```
apply(Titanic, 1, mean) # 1st dimension - Class
##      1st      2nd      3rd      Crew
## 40.625 35.625 88.250 110.625
apply(Titanic, c(1, 3), mean) # w.r.t. Class (1st) and Age (3rd)
##      Age
## Class Child Adult
## 1st   1.50 79.75
## 2nd   6.00 65.25
## 3rd  19.75 156.75
## Crew  0.00 221.25
```

### 11.3.4 Binary operators

In [Section 5.5](#), we stated that binary elementwise operations, such as addition or multiplication, preserve the attributes of the longer input or both (with the first argument preferred to the second) if they are of equal sizes.

Taking into account that:

- an array is simply a flat vector equipped with the `dim` attribute, and

- we refer to the respective *default* methods when applying binary operators
- allows us to deduce how ``+``, ``<=>`, ``&``, etc. behave in several different contexts.

**Array-Array.** First, let us note what happens when we operate on two arrays of identical dimensionalities.

```
(A <- rbind(c(1, 10, 100), c(-1, -10, -100)))
##      [,1] [,2] [,3]
## [1,]    1  10 100
## [2,]   -1 -10 -100
(B <- matrix(1:6, byrow=TRUE, nrow=2))
##      [,1] [,2] [,3]
## [1,]    1    2    3
## [2,]    4    5    6
A + B # elementwise addition
##      [,1] [,2] [,3]
## [1,]    2  12 103
## [2,]    3   -5  -94
A * B # elementwise multiplication (not: algebraic matrix multiply)
##      [,1] [,2] [,3]
## [1,]    1  20 300
## [2,]   -4 -50 -600
```

They are simply the addition and multiplication of the corresponding elements of two given matrices.

**Array-Scalar.** Second, we can apply scalar-matrix operations:

```
(-1)*B
##      [,1] [,2] [,3]
## [1,]   -1   -2   -3
## [2,]   -4   -5   -6
A^2
##      [,1] [,2] [,3]
## [1,]    1  100 10000
## [2,]    1  100 10000
```

They multiplied each element in B by -1 and squared every element in A, respectively. The behaviour of relational operators is similar:

```
A >= 1 & A <= 100
##      [,1] [,2] [,3]
## [1,]  TRUE  TRUE  TRUE
## [2,] FALSE FALSE FALSE
```

**Array-Vector.** Next, based on the recycling rule and the fact that elements are ordered columnwisely, we get that:

```
B * c(10, 100)
##      [,1] [,2] [,3]
## [1,]   10   20   30
## [2,]  400  500  600
```

It multiplied every element in the first row by 10 and each element in the second row by 100.

If we wish to multiply each element in the first, second, ..., etc. *column* by the first, second, ..., etc. value in a vector, we should *not* call:

```
B * c(1, 100, 1000)
##      [,1] [,2] [,3]
## [1,]    1 2000  300
## [2,]  400    5 6000
```

but rather:

```
t(t(B) * c(1, 100, 1000))
##      [,1] [,2] [,3]
## [1,]    1  200 3000
## [2,]    4  500 6000
```

or:

```
t(apply(B, 1, `*`, c(1, 100, 1000)))
##      [,1] [,2] [,3]
## [1,]    1  200 3000
## [2,]    4  500 6000
```

**Exercise 11.17** Write a function that standardises the values in each column of a given matrix: for each column, from every element, subtract the mean and then divide it by the standard deviation. Try to do it in a few different ways, including via a call to **apply**, **sweep**, **scale**, or based solely on arithmetic operators.

---

**Note** Some sanity checks are done on the `dim` attributes, so not every configuration is possible. Notice the following peculiarities:

```
getOption("error")
## NULL
A + t(B) # dim==c(2, 3) vs dim==c(3, 2)
## Error in A + t(B): non-conformable arrays
A * cbind(1, 10, 100) # this is too good to be true
## Error in A * cbind(1, 10, 100): non-conformable arrays
```

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```

A * rbind(1, 10) # but A * c(1, 10) works...
## Error in A * rbind(1, 10): non-conformable arrays
A + 1:12
## Error in eval(expr, envir, enclos): dims [product 6] do not match the
##   length of object [12]
A + 1:5 # partial recycling is okay
## Warning in A + 1:5: longer object length is not a multiple of shorter
##   object length
##      [,1] [,2] [,3]
## [1,]    2   13  105
## [2,]    1   -6  -99

```

## 11.4 Numerical matrix algebra (\*)

Many data analysis and machine learning algorithms, in their essence, involve quite simple matrix algebra and numerical mathematics. Suffice it to say that anyone serious about data science and scientific computing should learn the necessary theory; see, for example, [30] and [31].

R is a convenient interface to the well-tested and stable algorithms from, amongst others, **LAPACK** and **BLAS**<sup>5</sup>. Below we mention only a few of them. Many third-party packages feature hundreds of algorithms tackling differential equations, constrained and unconstrained optimisation, etc. Exploring the relevant CRAN Task Views<sup>6</sup> can give a comprehensive overview.

### 11.4.1 Matrix multiplication

``*`` performs elementwise multiplication. For what we call (algebraic) matrix multiplication, we use the ``%*`` operator.

Here is a quick refresher from a basic linear algebra course. The matrix multiplication can only be performed on two matrices of *compatible sizes*: the number of columns in the left matrix must match the number of rows in the right operand.

Given  $\mathbf{A} \in \mathbb{R}^{n \times p}$  and  $\mathbf{B} \in \mathbb{R}^{p \times m}$ , their multiply is a matrix  $\mathbf{C} = \mathbf{AB} \in \mathbb{R}^{n \times m}$  such that  $c_{i,j}$  is the dot product of the  $i$ -th row in  $\mathbf{A}$  and the  $j$ -th column in  $\mathbf{B}$ :

$$c_{i,j} = \mathbf{a}_{i,\cdot} \cdot \mathbf{b}_{\cdot,j} = \sum_{k=1}^p a_{i,k} b_{k,j},$$

<sup>5</sup> (\*) We can select the underlying implementation of **BLAS** at R's compile time; see Section A.3 in [64]. Some of them are faster than others.

<sup>6</sup> <https://cran.r-project.org/web/views/>

for  $i = 1, \dots, n$  and  $j = 1, \dots, m$ .

For instance:

```
(A <- rbind(c(1, 1, 1), c(-1, 1, 0)))
##      [,1] [,2] [,3]
## [1,]    1    1    1
## [2,]   -1    1    0
(B <- rbind(c(3, -1), c(1, 2), c(6, 1)))
##      [,1] [,2]
## [1,]    3   -1
## [2,]    1    2
## [3,]    6    1
A %*% B
##      [,1] [,2]
## [1,]   10    2
## [2,]   -2    3
```

---

**Note** When applying `%*%` on one or more flat vectors, their dimensionality will be promoted automatically to make the operation possible. However, `c(a, b) %*% c(c, d)` gives a scalar  $ac + bd$ , and not a  $2 \times 2$  matrix.

---

Further, `crossprod(A, B)` yields  $\mathbf{A}^T \mathbf{B}$  and `tcrossprod(A, B)` determines  $\mathbf{AB}^T$  more efficiently than relying on `%*%`. We can omit the second argument and get  $\mathbf{A}^T \mathbf{A}$  and  $\mathbf{AA}$ , respectively.

```
crossprod(c(1, 1)) # Euclidean norm squared
##      [,1]
## [1,]    2
crossprod(c(1, 1), c(-1, 1)) # dot product of two vectors
##      [,1]
## [1,]    0
crossprod(A) # same as t(A) %*% A, i.e., dot products of all column pairs
##      [,1] [,2] [,3]
## [1,]    2    0    1
## [2,]    0    2    1
## [3,]    1    1    1
```

Recall that if the dot product of two vectors equals 0, we say that they are orthogonal (perpendicular).

**Exercise 11.18** (\*) Write your versions of `cov` and `cor`: functions to compute the covariance and correlation matrices. Make use of the fact that the former can be determined with `crossprod` based on a centred version of an input matrix.

### 11.4.2 Solving systems of linear equations

The **solve** function can be used to solve  $m$  systems of  $n$  linear equations of the form  $\mathbf{AX} = \mathbf{B}$ , where  $\mathbf{A} \in \mathbb{R}^{n \times n}$  and  $\mathbf{X}, \mathbf{B} \in \mathbb{R}^{n \times m}$  (via the LU decomposition with partial pivoting and row interchanges).

### 11.4.3 Norms and metrics

Given an  $n \times m$  matrix  $\mathbf{A}$ , calling **norm**( $\mathbf{A}$ , "1"), **norm**( $\mathbf{A}$ , "2"), and **norm**( $\mathbf{A}$ , "I"), we can compute the operator norms:

$$\begin{aligned}\|\mathbf{A}\|_1 &= \max_{j=1,\dots,m} \sum_{i=1}^n |a_{i,j}|, \\ \|\mathbf{A}\|_2 &= \sigma_1(\mathbf{A}) = \sup_{\mathbf{x} \in \mathbb{R}^m} \frac{\|\mathbf{Ax}\|_2}{\|\mathbf{x}\|_2}, \\ \|\mathbf{A}\|_I &= \max_{i=1,\dots,n} \sum_{j=1}^m |a_{i,j}|,\end{aligned}$$

where  $\sigma_1$  gives the largest singular value (see below).

Also, passing "F" as the second argument yields the Frobenius norm,  $\|\mathbf{A}\|_F = \sqrt{\sum_{i=1}^n \sum_{j=1}^m a_{i,j}^2}$ , and "M" computes the max norm,  $\|\mathbf{A}\|_M = \max_{i,j=1,\dots,n} |a_{i,j}|$ .

If  $\mathbf{A}$  is a column vector, then  $\|\mathbf{A}\|_F$  and  $\|\mathbf{A}\|_2$  are equivalent. They are referred to as the Euclidean norm. Moreover,  $\|\mathbf{A}\|_M = \|\mathbf{A}\|_I$  give the supremum norm and outputs  $\|\mathbf{A}\|_1$  the Manhattan (taxicab) one.

**Exercise 11.19** Given an  $n \times m$  matrix  $\mathbf{A}$  representing  $m$  vectors in  $\mathbb{R}^n$ , normalise each column so that you obtain  $m$  unit vectors, i.e., whose Euclidean norm equals 1.

Further, **dist** determines all pairwise distances between a set of  $n$  vectors in  $\mathbb{R}^m$ , written as an  $n \times m$  matrix.

For example, let us consider three vectors in  $\mathbb{R}^2$ :

```
(X <- rbind(c(1, 1), c(1, -2), c(0, 0)))
##      [,1] [,2]
## [1,]    1    1
## [2,]    1   -2
## [3,]    0    0
as.matrix(dist(X, "euclidean"))
##      1      2      3
## 1 0.0000 3.0000 1.4142
## 2 3.0000 0.0000 2.2361
## 3 1.4142 2.2361 0.0000
```

Thus, the distance between the first and the third vector is roughly 1.41421. Euclidean, maximum, Manhattan, and Canberra distances/metrics are available, amongst others.

**Exercise 11.20** **dist** returns an object of S3 class *dist*. Inspect how it is represented.

**Example 11.21** **adist** implements a couple of string metrics. For example:

```
x <- c("spam", "bacon", "eggs", "spa", "spams", "legs")
names(x) <- x
(d <- adist(x))
##      spam bacon eggs spa spams legs
## spam    0     5   4   1     1   4
## bacon    5     0   5   5     5   5
## eggs     4     5   0   4     4   2
## spa      1     5   4   0     2   4
## spams    1     5   4   2     0   4
## legs     4     5   2   4     4   0
```

gives the Levenshtein distances between each pair of strings. In particular, we need two edit operations (character insertions, deletions, or replacements) to turn "eggs" into "legs" (add l and remove g).

**Example 11.22** Objects of the class `dist` can be used to perform hierarchical clusterings of data-sets. For example:

```
h <- hclust(as.dist(d), method="average") # see also: plot(h, labels=x)
cutree(h, 3)
##  spam bacon  eggs   spa spams  legs
##    1     2     3     1     1     3
```

determines three clusters using the average linkage strategy ("legs" and "eggs" are grouped together, "spam", "spa", "spams" form another cluster, and "bacon" is a singleton).

#### 11.4.4 Eigenvalues and eigenvectors

**eigen** returns a sequence of eigenvalues ( $\lambda_1, \dots, \lambda_n$ ) (ordered nondecreasingly w.r.t.  $|\lambda_i|$ ) and a matrix **V** whose columns define the corresponding eigenvectors (scaled to unit length) of a given matrix **X**. To recall, by definition, it holds that  $\mathbf{X}\mathbf{v}_{\cdot,i} = \lambda_i\mathbf{v}_{\cdot,i}$ .

Here are the eigenvalues and the corresponding eigenvectors of an example matrix (defining rotation in 2D by  $\pi/3$ ):

```
(R <- rbind(c(cos(pi/3), -sin(pi/3)), c(sin(pi/3), cos(pi/3))))
##      [,1]      [,2]
## [1,] 0.50000 -0.86603
## [2,] 0.86603  0.50000
eigen(R)
## eigen() decomposition
## $values
## [1] 0.5+0.86603i 0.5-0.86603i
##
## $vectors
##      [,1]      [,2]
```

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```
## [1,] 0.70711+0.00000i 0.70711+0.00000i
## [2,] 0.00000-0.70711i 0.00000+0.70711i
```

**Example 11.23** Consider a pseudorandom sample from a bivariate<sup>7</sup> normal distribution; see Figure 11.1.

```
Z <- matrix(rnorm(2000), ncol=2) # independent N(0, 1)
Z <- Z %%% rbind(c(1, 0), c(0, sqrt(5))) # scaling
Z <- Z %%% R # rotation
Z <- t(c(10, -5) + t(Z)) # translation
plot(Z, asp=1)
```

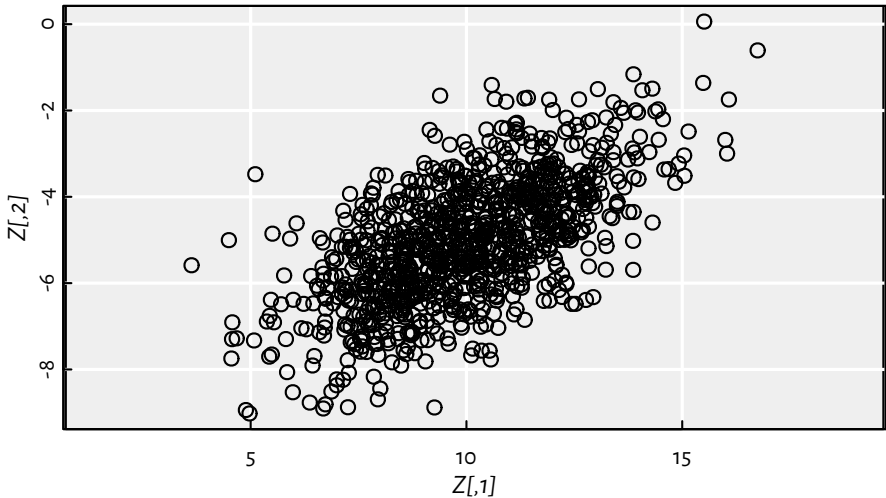


Figure 11.1: Example bivariate normal sample

It is known that eigenvectors of the covariance matrix correspond to the principal components of the original dataset. Furthermore, the eigenvalues give the variance explained by them.

```
eigen(cov(Z))
## eigen() decomposition
## $values
## [1] 5.18609 0.98386
##
## $vectors
##      [,1]      [,2]
```

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<sup>7</sup> For drawing random samples from any multivariate distribution, refer to the theory of copulas, e.g., [48]. There are a few R packages on CRAN that implement the most popular models.

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```
## [1,] -0.86715  0.49804
## [2,] -0.49804 -0.86715
```

this roughly corresponds to the principal directions  $[\sin(\pi/3), \cos(\pi/3)]$  and the thereto-orthogonal  $[\cos(\pi/3), -\sin(\pi/3)]$  with variances of 5 and 1, respectively. Still, this method of performing a PCA is not particularly numerically stable; see below for an alternative.

### 11.4.5 QR decomposition

We say that a real  $n \times m$  matrix  $\mathbf{Q}$ ,  $n \geq m$ , is orthogonal whenever  $\mathbf{Q}^T \mathbf{Q} = \mathbf{I}$  (identity matrix). This is equivalent to  $\mathbf{Q}$ 's being orthogonal unit vectors (if  $\mathbf{Q}$  is a square matrix, then  $\mathbf{Q}^T = \mathbf{Q}^{-1}$  if and only if  $\mathbf{Q}^T \mathbf{Q} = \mathbf{Q} \mathbf{Q}^T = \mathbf{I}$ ).

Let  $\mathbf{A}$  be a real<sup>8</sup>  $n \times m$  matrix with  $n \geq m$ . Then  $\mathbf{A} = \mathbf{Q}\mathbf{R}$  is its QR decomposition (in the so-called narrow form), if  $\mathbf{Q}$  is an orthogonal  $n \times m$  matrix and  $\mathbf{R}$  is an upper triangular  $m \times m$  one.

The `qr` function returns an object of S3 class `qr` from which we can extract the two components; see the `qr.Q` and `qr.R` functions.

**Example 11.24** Let  $\mathbf{X}$  be an  $n \times m$  data matrix, representing  $n$  points in  $\mathbb{R}^m$ , and a vector  $\mathbf{y} \in \mathbb{R}^n$  of the desired outputs corresponding to each input. For fitting a linear model  $\mathbf{x}^T \boldsymbol{\theta}$ , where  $\boldsymbol{\theta}$  is a vector of  $m$  parameters, we can use the method of least squares, which minimises

$$\mathcal{L}(\boldsymbol{\theta}) = \sum_{i=1}^n (\mathbf{x}_{i,\cdot}^T \boldsymbol{\theta} - y_i)^2 = \|\mathbf{X}\boldsymbol{\theta} - \mathbf{y}\|_2^2$$

It might be shown that if  $\mathbf{X} = \mathbf{Q}\mathbf{R}$ , then  $\boldsymbol{\theta} = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{y} = \mathbf{R}^{-1} \mathbf{Q}^T \mathbf{y}$ , which can conveniently be determined via a call to `qr.coef`.

In particular, we can fit a simple linear regression model  $y = ax + b$  by considering  $\mathbf{X} = [x, 1]$  and  $\boldsymbol{\theta} = [a, b]$ , for example (see Figure 11.2):

```
x <- cars[["speed"]]
y <- cars[["dist"]]
X <- cbind(x, 1) # the model is theta[1]*x + theta[2]*1
qrX <- qr(X)
(theta <- solve(qr.R(qrX)) %*% t(qr.Q(qrX)) %*% y) # or: qr.coef(qrX, y)
##      [,1]
## x      3.9324
##      -17.5791
plot(x, y, xlab="speed", ylab="dist") # scatter plot
abline(theta[2], theta[1], lty=2) # add the regression line
```

`solve` with one argument determines the inverse of a given matrix. The fitted model is  $y = 3.93241x - 17.5791$ .

<sup>8</sup>  $\mathbf{A}$  can also be a complex matrix. In this case, its QR decomposition spawns  $\mathbf{Q}$  that is a unitary matrix.

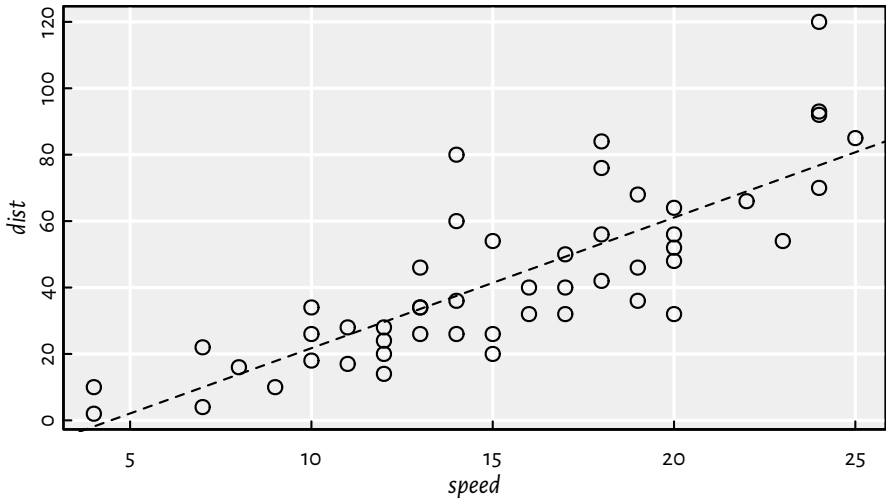


Figure 11.2: The built-in cars dataset and the fitted regression line

The same approach is used by `lm.fit`, the workhorse behind the `lm` method accepting an R formula (which some readers might be familiar with; compare Section 17.6).

```
lm.fit(cbind(x, 1), y)[["coefficients"]] # also: lm(dist~speed, data=cars)
##           x
##    3.9324 -17.5791
```

#### 11.4.6 SVD decomposition

Given a real  $n \times m$  matrix  $\mathbf{X}$ , its singular value decomposition (SVD) is given by  $\mathbf{X} = \mathbf{U}\mathbf{D}\mathbf{V}^T$ , where  $\mathbf{D}$  is a  $p \times p$  diagonal matrix (featuring the so-called singular values of  $\mathbf{X}$ ,  $d_{1,1} \geq \dots \geq d_{p,p} \geq 0$ ,  $p = \min\{n, m\}$ ), and  $\mathbf{U}$  and  $\mathbf{V}$  are orthogonal matrices of dimension  $n \times p$  and  $m \times p$ , respectively.

`svd` may not only be used to determine the solution to linear regression<sup>9</sup> but also to perform the principal component analysis<sup>10</sup>. Namely,  $\mathbf{V}$  gives the eigenvectors of  $\mathbf{X}^T\mathbf{X}$ . Assuming that  $\mathbf{X}$  is centred at 0, the latter is precisely its scaled covariance matrix.

**Example 11.25** Continuing the PCA example above, we can determine the principal directions also by calling:

```
Zc <- apply(Z, 2, function(x) x-mean(x)) # centred version of Z
svd(Zc)[["v"]]
```

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<sup>9</sup> As the pseudoinverse  $\mathbf{X}^+ = (\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T = \mathbf{V}\mathbf{D}^+\mathbf{U}^T = \mathbf{R}^{-1}\mathbf{Q}^T$ , with  $\mathbf{X}^+\mathbf{X} = \mathbf{I}$ . Here  $\mathbf{D}^+$  is a transposed version of  $\mathbf{D}$  featuring the reciprocals of its non-zero elements.

<sup>10</sup> See the source code of `getS3method("prcomp", "default")`.

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```
##           [,1]      [,2]
## [1,] -0.86715  0.49804
## [2,] -0.49804 -0.86715
```

## 11.5 S4 classes (\*)

The concept of the S3-style object-oriented programming is based on a brilliantly simple idea (see [Chapter 10](#)): calling a generic `f(x)` dispatches automatically to a method `f.class_of_x(x)` or `f.default(x)` in the case where the former does not exist. Naturally, it has some inherent limitations:

- classes cannot be formally defined; the `class` attribute may be assigned arbitrarily onto any object<sup>11</sup>,
- argument dispatch is performed only<sup>12</sup> with regard to one data type<sup>13</sup>.

In most cases, and with an appropriate level of mindfulness, this is not a problem at all. However, it is a typical condition of programmers who come to our world from more mainstream languages (e.g., C++; yours truly included) until they appreciate the true beauty of R's being somewhat different. Before they fully develop such an acquired taste, though, they grow restless as “R is not a real object-oriented system because it lacks polymorphism, encapsulation, formal inheritance, and so on, and something must be done about it”. The truth is that it had not had to, but with high probability, it would have anyway in one way or another.

And so the fourth version of the S language was introduced in 1998 (see [9]). It brought a new object-oriented system, which we are used to referring to as S4. Its R version is given by the `methods` package. Below we discuss it briefly; for more details, see `help("Classes_Details")` and `help("Methods_Details")` as well as [10] and [11].

**Note** (\*) S4 was loosely inspired by the Common Lisp Object System (with its `def-class`, `defmethod`, etc.; see, e.g., [20]). In the current author's opinion, the S4 system is somewhat of an afterthought. Due to appendages like this, R seems like a patch-work language; suffice it to say that it was not the last attempt to do a somewhat more real OOP in the overall functional R: the story will resume in [Section 16.1.5](#).

<sup>11</sup> A partial solution to this could involve defining a method like `validate.class_name`, which is called frequently and which checks whether a given object enjoys some desired constraints.

<sup>12</sup> Although there are functions featuring some workarounds (see, e.g., `cbind`, which dispatches to `cbind.data.frame` if one argument is a data frame and the remaining ones are vectors or matrices). Also, we said in the previous chapter that binary operators consider the classes of both operands.

<sup>13</sup> Hypothetically, we can imagine an OOP system relying on methods named like `method.class_name1.class_name2` where dispatching is based on two argument types. It would be beautiful, but it is not the case in R.



The main problem with all the OOP approaches is that each of them is *parallel* to S3 which never lost its popularity and is still at the very core of our language. We are thus covering them for the sake of completeness because that's what must be done. After all, with non-zero probability, the reader will sooner or later come across such objects (e.g., below, we explain the meaning of a notation like `x@slot`). Also, yours truly rebelliously suggests taking statements such as “for new projects, it is recommended to use the more flexible and robust S4 scheme provided in the **methods** package” (see `help("UseMethod")`) with a pinch of salt.

---

### 11.5.1 Defining S4 classes

An S4 class can formally be registered through a call to **setClass**. For instance:

```
library("methods") # in the case where it is not auto-loaded
setClass("categorical", slots=c(data="integer", levels="character"))
```

defines a class named `categorical`. It has two slots: `data` and `levels` being integer and character vectors, respectively. This notation is already quite peculiar. There is no assignment suggesting that we have introduced something novel.

An object of the above class can be instantiated by calling **new**:

```
z <- new("categorical", data=c(1L, 2L, 2L, 1L, 1L), levels=c("a", "b"))
print(z)
## An object of class "categorical"
## Slot "data":
## [1] 1 2 2 1 1
##
## Slot "levels":
## [1] "a" "b"
```

That `z` is of the recently-introduced class can be verified as follows:

```
is(z, "categorical")
## [1] TRUE
class(z) # also: attr(z, "class")
## [1] "categorical"
## attr(,"package")
## [1] ".GlobalEnv"
```

---

**Important** Some R packages require the **methods** package only for the sake of being able to access the handy **is** function. It does not mean they are defining new S4 classes.

---



---

**Note** S4 objects are marked as being of the following basic type:

```
typeof(z)
## [1] "S4"
```

See Section 1.12 of [65] for technical details on how they are internally represented. In particular, in our case, all the slots are simply stored as object attributes:

```
attributes(z)
## $data
## [1] 1 2 2 1 1
##
## $levels
## [1] "a" "b"
##
## $class
## [1] "categorical"
## attr(,"package")
## [1] ".GlobalEnv"
```

---

### 11.5.2 Accessing slots

Reading or writing slot contents can be done via the `@` operator and the `slot` function or their replacement versions.

```
z@data # or slot(z, "data")
## [1] 1 2 2 1 1
z@levels <- c("A", "B")
```

---

**Note** The `@` operator can only be used on S4 objects, and some sanity checks are automatically performed:

```
z@unknown <- "spam"
## Error in (function(cl, name, valueClass) : 'unknown' is not a slot in
##   class "categorical"
z@data <- "spam"
## Error in (function(cl, name, valueClass) : assignment of an object of
##   class "character" is not valid for @'data' in an object of class
##   "categorical"; is(value, "integer") is not TRUE
```

---

### 11.5.3 Defining methods

For the S4 counterparts of the S3 generics (Section 10.2), see `help("setGeneric")`. Luckily, there is a reasonable degree of interoperability between the S3 and S4 systems.

Let us start by introducing a new method for the well-known **as.character** generic. Instead of defining **as.character.categorical**, we need to register a new routine with **setMethod**.

```
setMethod(
  "as.character",      # name of the generic
  "categorical",      # class of 1st arg; or: signature=c(x="categorical")
  function(x, ...)    # method definition
    x@levels[x@data]
)
```

Testing:

```
as.character(z)
## [1] "A" "B" "B" "A" "A"
```

**show** is the S4 counterpart of **print**:

```
setMethod(
  "show",
  "categorical",
  function(object)
  {
    x_character <- as.character(object)
    print(x_character) # calls `print.default`
    cat(sprintf("Categories: %s\n",
               paste(object@levels, collapse=", ")))
  }
)
```

Interestingly, it is involved automatically on a call to **print**:

```
print(z) # calls `show` for `categorical`
## [1] "A" "B" "B" "A" "A"
## Categories: A, B
```

Methods that dispatch on the type of multiple arguments are also possible, for example:

```
setMethod(
  "split",
  c(x="ANY", f="categorical"),
  function(x, f, drop=FALSE, ...)
    split(x, as.character(f), drop=drop, ...)
)
```

allows the first argument to be of any type (like a default method), and:

```

setMethod(
  "split",
  c(x="matrix", f="categorical"),
  function (x, f, drop=FALSE, ...)
    lapply(
      split(seq_len(NROW(x)), f, drop=drop, ...), # calls the above
      function(i) x[i, , drop=FALSE])
)

```

is a version tailored for matrices. Testing:

```

A <- matrix(1:35, nrow=5) # whatever
split(A, z) # matrix,categorical
## $A
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7]
## [1,]    1    6   11   16   21   26   31
## [2,]    4    9   14   19   24   29   34
## [3,]    5   10   15   20   25   30   35
##
## $B
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7]
## [1,]    2    7   12   17   22   27   32
## [2,]    3    8   13   18   23   28   33
split(1:5, z) # ANY,categorical
## $A
## [1] 1 4 5
##
## $B
## [1] 2 3

```

**Exercise 11.26** Overload the ``[`` operator for the categorical class.

### 11.5.4 Defining constructors

We can also overload the `initialize` method, which is automatically called by `new`:

```

setMethod(
  "initialize", # class name
  "categorical", # method name
  function(.Object, x)
  { # the method itself
    x <- as.character(x) # see above
    xu <- unique(sort(x)) # drops NAs

    .Object@data <- match(x, xu)
    .Object@levels <- xu
  }
)

```

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```

        .Object # return value - a modified object
    }
)

```

This allows for constructing new objects of the class `categorical` based on an object like `x` above, for instance:

```

w <- new("categorical", c("a", "c", "a", "a", "d", "c"))
print(w)
## [1] "a" "c" "a" "a" "d" "c"
## Categories: a, c, d

```

We have not set the two slots directly. They were automatically taken care of by **initialize** (note the American spelling).

**Exercise 11.27** Set up a validating method for our class; see `help("setValidity")`.

### 11.5.5 Inheritance

New S4 classes can be derived from existing ones, for instance:

```
setClass("binary", contains="categorical")
```

is a child class inhering all slots from its parent. We can, for example, overload the initialisation method for it:

```

setMethod(
  "initialize",
  "binary",
  function(.Object, x)
  {
    x <- as.character(as.integer(as.logical(x)))
    xu <- c("0", "1")
    .Object@data <- match(x, xu)
    .Object@levels <- xu
    .Object
  }
)

```

Testing:

```

new("binary", c(TRUE, FALSE, TRUE, FALSE, NA, TRUE))
## [1] "1" "0" "1" "0" NA "1"
## Categories: 0, 1

```

We still used the **show** method of the parent class.

### 11.5.6 A note on the **Matrix** package

The **Matrix** package is perhaps the most widely known showcase of the S4 object orientation (and that is the reason why we cover S4 in this very chapter). It defines classes and methods for dense and sparse matrices, including rectangular, symmetric, triangular, band, and diagonal ones.

For instance, large graph (e.g., in network sciences) or preference (e.g., in recommender systems) data can be represented using sparse matrices (those which feature many 0s; after all, it is extremely more common for two vertices in a network *not* to be joined by an edge than to be connected).

For example:

```
library("Matrix")
(A <- Diagonal(x=1:5))
## 5 x 5 diagonal matrix of class "ddiMatrix"
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    .    .    .    .
## [2,]    .    2    .    .    .
## [3,]    .    .    3    .    .
## [4,]    .    .    .    4    .
## [5,]    .    .    .    .    5
```

It created a real diagonal matrix. Moreover:

```
B <- as(A, "sparseMatrix")
B[1, 2] <- 7
B[4, 1] <- 42
print(B)
## 5 x 5 sparse Matrix of class "dgCMatrix"
##
## [1,]  1 7 . . .
## [2,]  . 2 . . .
## [3,]  . . 3 . .
## [4,] 42 . . 4 .
## [5,]  . . . . 5
```

yields a general sparse real matrix in the CRC (compressed, sparse, column-oriented) format.

For more information on the package, see **vignette**(package="Matrix").

## 11.6 Exercises

**Exercise 11.28** Let  $X$  be a matrix with *dimnames* set, e.g.:

```

X <- matrix(1:12, byrow=TRUE, nrow=3)      # example matrix
dimnames(X)[[2]] <- c("a", "b", "c", "d") # set column names
print(X)
##      a  b  c  d
## [1,] 1  2  3  4
## [2,] 5  6  7  8
## [3,] 9 10 11 12

```

Explain (in your own words) the meaning of the following expressions involving matrix subsetting. Note that not each of them is valid.

- `X[1, ]`,
- `X[, 3]`,
- `X[, 3, drop=FALSE]`,
- `X[3]`,
- `X[, "a"]`,
- `X[, c("a", "b", "c")]`,
- `X[, -2]`,
- `X[X[,1] > 5, ]`,
- `X[X[,1]>5, c("a", "b", "c")]`,
- `X[X[,1]>=5 & X[,1]<=10, ]`,
- `X[X[,1]>=5 & X[,1]<=10, c("a", "b", "c")]`,
- `X[, c(1, "b", "d")]`.

**Exercise 11.29** Assuming that `X` is an array, what are the differences between the following indexing schemes?

- `X["1", ]` vs `X[1, ]`,
- `X[, "a", "b", "c"]` vs `X["a", "b", "c"]` vs `X[, c("a", "b", "c")]` vs `X[c("a", "b", "c")]`,
- `X[1]` vs `X[, 1]` vs `X[1, ]`,
- `X[X>0]` vs `X[X>0, ]` vs `X[, X>0]`,
- `X[X[, 1]>0]` vs `X[X[, 1]>0, ]` vs `X[, X[, 1]>0]`,
- `X[X[, 1]>5, X[, 1]<10]` vs `X[X[1, ]>5, X[, 1]<10]`.

**Exercise 11.30** Give a few ways to create a matrix like:

```

##      [,1] [,2]
## [1,]    1    1

```

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

and one like:

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

**Exercise 11.31** For a given real  $n \times m$  matrix  $\mathbf{X}$ , determine the bounding hyperrectangle of thusly encoded  $n$  input points in an  $m$ -dimensional space. Return a  $2 \times m$  matrix  $\mathbf{B}$  with  $b_{1,j} = \min_i x_{i,j}$  and  $b_{2,j} = \max_i x_{i,j}$ .

**Exercise 11.32** Let  $\mathbf{t}$  be a vector of  $n$  integers in  $\{1, \dots, k\}$ . Write a function to one-hot-encode each  $t_i$ : return a 0–1 matrix  $\mathbf{R}$  of size  $n \times k$  such that  $r_{i,j} = 1$  if and only if  $j = t_i$ . For example, if  $\mathbf{t} = [1, 2, 3, 2, 4]$  and  $k = 4$ , then:

$$\mathbf{R} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}.$$

On a side note, such a representation is beneficial when solving, e.g., a multiclass classification problem by means of  $k$  binary classifiers.

Then, compose another function, but this time setting  $r_{i,j} = 1$  if and only if  $j \geq t_i$ , e.g.:

$$\mathbf{R} = \begin{bmatrix} 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 1 \\ 0 & 0 & 1 & 1 \\ 0 & 1 & 1 & 1 \\ 0 & 0 & 0 & 1 \end{bmatrix}.$$



**Important** Kind reminder: as usual, try to solve all the exercises without using explicit **for** and **while** loops (provided that it is possible).

**Exercise 11.33** Given an  $n \times k$  real matrix, apply the softmax function on each row, i.e., map  $x_{i,j}$  to  $\frac{\exp(x_{i,j})}{\sum_{l=1}^k \exp(x_{i,l})}$ . Then, one-hot decode the values in each row, i.e., find the column number with the greatest value. Return a vector of size  $n$  with elements in  $\{1, \dots, k\}$ .

**Exercise 11.34** Assume that an  $n \times m$  real matrix  $\mathbf{X}$  represents  $n$  points in  $\mathbb{R}^m$ . Write a function (but do not refer to **dist**) that determines the pairwise distances between all the  $n$  points and a given  $\mathbf{y} \in \mathbb{R}^m$ . Return a vector  $\mathbf{d}$  of length  $n$  with  $d_i = \|\mathbf{x}_{i,\cdot} - \mathbf{y}\|_2$ .

**Exercise 11.35** Let  $\mathbf{X}$  and  $\mathbf{Y}$  be two real-valued matrices of sizes  $n \times m$  and  $k \times m$ , respectively, representing two sets of points in  $\mathbb{R}^m$ . Return an integer vector  $\mathbf{r}$  of length  $k$  such that  $r_i$  indicates the index of the point in  $\mathbf{X}$  with the least distance to (the closest to) the  $i$ -th point in  $\mathbf{Y}$ , i.e.,  $r_i = \arg \min_j \|\mathbf{x}_{j,\cdot} - \mathbf{y}_{i,\cdot}\|_2$ .

**Exercise 11.36** Write your version of the built-in `utils::combn`.

**Exercise 11.37** Time series are vectors or matrices of the class `ts` equipped with the `ts` attribute, amongst others. Refer to `help("ts")` for more information about how they are represented and what `S3` methods have been overloaded for them.

**Exercise 11.38** (\*) Numeric matrices can be stored in a CSV file, amongst others. Usually, we will be loading them via `read.csv`, which returns a data frame (see Chapter 12), for example:

```
X <- as.matrix(read.csv(
  paste0(
    "https://github.com/gagolews/teaching-data/",
    "raw/master/marek/eurxxx-20200101-20200630.csv"
  ),
  comment.char="#",
  sep=","
))
```

Write a function `read_numeric_matrix(file_name, comment, sep)` which is based on a few calls to `scan` instead. Use `file` to establish a file connection so that you can ignore the comment lines and fetch the column names before reading the actual numeric values.

**Exercise 11.39** (\*) Using `readBin`, read the `t10k-images-idx3-ubyte.gz` from the [MNIST database homepage](https://www Yann LeCun's MNIST database homepage)<sup>14</sup>. The output object should be a three-dimensional,  $10000 \times 28 \times 28$  array with real elements between 0 and 255. Refer to the File Formats section therein for more details.

**Exercise 11.40** (\*\*) Circular convolution of discrete-valued multidimensional signals can be performed by means of `fft` and matrix multiplication, whereas affine transformations require only the latter. Apply various image transformations such as sharpening, shearing, and rotating on the MNIST digits and plot the results using the `image` function.

<sup>14</sup> <https://web.archive.org/web/20211107114045/http://yann.lecun.com/exdb/mnist/>

**Exercise 11.41** (\*) Using **constrOptim**, find the minimum of the Constrained Betts Function  $f(x_1, x_2) = 0.01x_1^2 + x_2^2 - 100$  with linear constraints  $2 \leq x_1 \leq 50$ ,  $-50 \leq x_2 \leq 50$ , and  $10x_1 \geq 10 + x_2$ . (\*\*) Also, use **solve.QP** from the **quadprog** package to find the minimum.

---

# 12

## Data frames

Most matrices are built on top of atomic vectors. Hence, they only allow items of the same type to be arranged into rows and columns. Data frames (objects of S3 class `data.frame`, first introduced in [13]), on the other hand, are collections of vectors of the same lengths or matrices with identical row counts, hence allowing to represent structured<sup>1</sup> data of possibly heterogeneous types. For instance:

```
class(iris) # `iris` is an example built-in data frame
## [1] "data.frame"
iris[c(1, 51, 101), ] # 3 chosen rows from `iris`
##      Sepal.Length Sepal.Width Petal.Length Petal.Width  Species
## 1           5.1         3.5         1.4         0.2    setosa
## 51          7.0         3.2         4.7         1.4 versicolor
## 101         6.3         3.3         6.0         2.5  virginica
```

It is a mix of numeric and factor-type data.

The good news is that not only are data frames built on named lists (e.g., to extract a column, we can refer to ``[ ]``), but also many functions recognise them to be matrix-like (e.g., to select specific rows and columns, two indexes can be passed to ``[ ]`` like in the example above). Hence, it will soon turn out that we already know a lot about how to perform basic data wrangling activities, even if we do not fully realise it now.

---

**Important** Some readers will approach this chapter biased by what they know from elsewhere, including their experience with some popular third-party packages for data frame processing. The art is to filter out that information as noise (for the time being, at least). We will show how robust base R vocabulary is and how much can be implied from the material covered in the preceding chapters.

Yes, this book is like a breathtaking thriller/drama/love story: it is meant to be read from the beginning to the end. Please go back to the start of this comprehensive course if you happened to pop in here by accident or driven by “but I need to know *now*”. Good morning.

---

---

<sup>1</sup> We are already highly skilled in dealing with unstructured data and turning them into something that is much more regular: the numerous functions that we have covered in the first part of this book, allow us to extract meaningful data from text, handle missing values, engineer features, and so forth.

## 12.1 Creating data frames

### 12.1.1 `data.frame` and `as.data.frame`

Most frequently, data frames are based on a series of logical, numeric, or characters vectors of identical lengths. In such a scenario, the `data.frame` function is particularly worthwhile.

```
(x <- data.frame(
  a=c(TRUE, FALSE),
  b=1:6,
  c=runif(6),
  d=c("spam", "spam", "eggs")
))
##      a b      c      d
## 1 TRUE 1 0.77437 spam
## 2 FALSE 2 0.19722 spam
## 3 TRUE 3 0.97801 eggs
## 4 FALSE 4 0.20133 spam
## 5 TRUE 5 0.36124 spam
## 6 FALSE 6 0.74261 eggs
```

The shorter vectors were recycled. We can verify that the diverse column types were retained and no coercion was made, by calling:

```
str(x)
## 'data.frame':      6 obs. of  4 variables:
## $ a: logi  TRUE FALSE TRUE FALSE TRUE FALSE
## $ b: int   1  2  3  4  5  6
## $ c: num   0.774 0.197 0.978 0.201 0.361 ...
## $ d: chr   "spam" "spam" "eggs" "spam" ...
```

We can also fetch the class of each column directly by calling (compare Section 12.3):

```
sapply(x, class) # the same as unlist(Map(class, x))
##           a           b           c           d
## "logical" "integer" "numeric" "character"
```

---

**Important** For many reasons (see, e.g., Section 12.1.5 and Section 12.1.6), we recommend having the type of each column always checked, e.g., by calling the `str` function.

---

Many objects, such as matrices, can easily be coerced to data frames using particular `as.data.frame` methods.

Here is an example matrix:

```
(A <- matrix(1:6, nrow=3,
  dimnames=list(
    NULL,      # no row labels
    c("u", "v") # some column labels
  )))
##      u v
## [1,] 1 4
## [2,] 2 5
## [3,] 3 6
```

Let us convert it to a data frame:

```
as.data.frame(A) # as.data.frame.matrix
##      u v
## 1 1 4
## 2 2 5
## 3 3 6
```

Note that a matrix with no row labels is printed slightly differently than a data frame with (as it will soon turn out) the default `row.names`.

Named lists are amongst other candidates for a meaningful conversion. Consider an example list where each element is a vector of the same length as the other ones:

```
(l <- Map(
  function(x) {
    c(Min=min(x), Median=median(x), Mean=mean(x), Max=max(x))
  },
  split(iris[["Sepal.Length"]], iris[["Species"]])
))
## $setosa
##      Min Median   Mean   Max
## 4.300  5.000  5.006  5.800
##
## $versicolor
##      Min Median   Mean   Max
## 4.900  5.900  5.936  7.000
##
## $virginica
##      Min Median   Mean   Max
## 4.900  6.500  6.588  7.900
```

Each list element will be turned into a separate column:

```
as.data.frame(l) # as.data.frame.list
##          setosa versicolor virginica
## Min      4.300      4.900      4.900
## Median    5.000      5.900      6.500
## Mean      5.006      5.936      6.588
## Max       5.800      7.000      7.900
```

Sadly, **as.data.frame.list** is not particularly fond of lists of vectors of incompatible lengths:

```
as.data.frame(list(a=1, b=11:12, c=21:23))
## Error in (function (..., row.names = NULL, check.rows = FALSE, check.names
##      = TRUE, : arguments imply differing number of rows: 1, 2, 3
```

The above vectors could have been recycled with a warning. But they were not.

```
as.data.frame(list(a=1:4, b=11:12, c=21)) # recycling rule okay
##   a  b  c
## 1 1 11 21
## 2 2 12 21
## 3 3 11 21
## 4 4 12 21
```

The method for the S3 class `table` (mentioned in [Chapter 11](#)) can be helpful as well. Here is an example contingency table together with its *unstacked* version.

```
(t <- table(mtcars[["vs"]], mtcars[["cyl"]]))
##
##      4  6  8
## 0   1  3 14
## 1 10  4  0
as.data.frame(t) # as.data.frame.table; see the stringsAsFactors note below!
##   Var1 Var2 Freq
## 1    0    4    1
## 2    1    4   10
## 3    0    6    3
## 4    1    6    4
## 5    0    8   14
## 6    1    8    0
```

**as.data.frame.table** is so handy that we might want to call it directly on any array. This way, we can convert it from the so-called *wide* format to the *long* one; see [Section 12.3.6](#) for more details.

---

**Note** The above method is based on **expand.grid**, which determines all combinations of a given series of vectors.

```
expand.grid(1:2, c("a", "b", "c")) # see the stringsAsFactors note below!
##   Var1 Var2
## 1    1    a
## 2    2    a
## 3    1    b
## 4    2    b
## 5    1    c
## 6    2    c
```

Overall, many classes of objects can be included<sup>2</sup> in a data frame; the popular choices include `Date`, `POSIXct`, and `factor`. It is worth noting that the `data.frame` function calls the corresponding `as.data.frame` method. Also, `format` is used whilst printing the columns.

**Example 12.1** Here are two custom methods for what we would like to call from now on an `S3` class `spam`:

```
as.data.frame.spam <- function(x, ...)
  structure(
    list(x),
    class="data.frame",
    row.names=seq_along(x)
  )
format.spam <- function(x, ...)
  paste0("*", x, "*")
```

Testing data frame creation and printing:

```
data.frame(
  a=structure(c("a", "b", "c"), class="spam"),
  b=factor(c("spam", "bacon", "spam")),
  c=Sys.Date()+1:3
)
##      a      b      c
## 1 *a*  spam 2023-05-20
## 2 *b*  bacon 2023-05-21
## 3 *c*  spam 2023-05-22
```

### 12.1.2 `cbind.data.frame` and `rbind.data.frame`

There are data frame-specific versions of `cbind` or `rbind` (which we discussed in the context of stacking matrices; Section 11.1.2). They are used quite eagerly:

<sup>2</sup> The attributes of objects stored as matrix columns will generally be preserved (even if they are not displayed by `print`; see `str` though).

`help("cbind")` states that they will be referred to if at least<sup>3</sup> one of its arguments is a data frame, and the other arguments are atomic vectors or lists (possibly with the `dim` attribute).

For example:

```
x <- iris[c(1, 51, 101), c("Sepal.Length", "Species")] # whatever
cbind(Yummy=c(TRUE, FALSE, TRUE), x)
##      Yummy Sepal.Length Species
## 1      TRUE          5.1   setosa
## 51     FALSE          7.0 versicolor
## 101    TRUE          6.3  virginica
```

It added a new column to a data frame `x`. Moreover:

```
rbind(x, list(42, "virginica"))
##      Sepal.Length Species
## 1              5.1   setosa
## 51             7.0 versicolor
## 101            6.3  virginica
## 11            42.0  virginica
```

It added a new row. Note that columns are of different types. Hence, the values to row-bind were provided as a generic vector. The list can also be named. It can consist of vectors of length greater than one, given in any order:

```
rbind(x, list(
  Species=c("virginica", "setosa"),
  Sepal.Length=c(42, 7)
))
##      Sepal.Length Species
## 1              5.1   setosa
## 51             7.0 versicolor
## 101            6.3  virginica
## 11            42.0  virginica
## 2              7.0   setosa
```

Sometimes a direct referral to these methods will be necessary. Consider an example list of atomic vectors:

```
x <- list(a=1:3, b=11:13, c=21:23)
```

First, we call the generic, which dispatches to the default method:

<sup>3</sup> This is a clear violation of the rule that an S3 generic dispatches on the type of only one argument (usually: the first). It is an exception made for the sake of the questionable user *convenience*. Also, note that there is no `cbind.default` method available: it is hardcoded at the C language level.



```
do.call(cbind, x)
##      a  b  c
## [1,] 1 11 21
## [2,] 2 12 22
## [3,] 3 13 23
```

If we want to ensure we garner a data frame as a result, we need to write:

```
do.call(cbind.data.frame, x)
##   a  b  c
## 1 1 11 21
## 2 2 12 22
## 3 3 13 23
```

This is particularly useful for fetching outputs from **Map** and its friends, which are wrapped inside a list. For instance:

```
l <- unname(Map(
  function(x) list(
    Sepal.Length=mean(x[["Sepal.Length"]]),
    Sepal.Width=mean(x[["Sepal.Width"]]),
    Species=x[["Species"]][1]
  ),
  split(iris, iris[["Species"]]) # split.data.frame; see below
))
str(l)
## List of 3
## $ :List of 3
## ..$ Sepal.Length: num 5.01
## ..$ Sepal.Width : num 3.43
## ..$ Species      : Factor w/ 3 levels "setosa","versicolor",...: 1
## $ :List of 3
## ..$ Sepal.Length: num 5.94
## ..$ Sepal.Width : num 2.77
## ..$ Species      : Factor w/ 3 levels "setosa","versicolor",...: 2
## $ :List of 3
## ..$ Sepal.Length: num 6.59
## ..$ Sepal.Width : num 2.97
## ..$ Species      : Factor w/ 3 levels "setosa","versicolor",...: 3
```

It is nothing more than a fancy way to obtain an illustrative list, which we may now turn into a data frame by calling:

```
do.call(rbind.data.frame, l)
##   Sepal.Length Sepal.Width Species
## 1         5.006         3.428  setosa
```

(continues on next page)

(continued from previous page)

```
## 2      5.936      2.770 versicolor
## 3      6.588      2.974 virginica
```

On the other hand, `do.call(rbind, l)` does not return an amiable object type:

```
do.call(rbind, l)
##      Sepal.Length Sepal.Width Species
## [1,] 5.006        3.428        setosa
## [2,] 5.936        2.77         versicolor
## [3,] 6.588        2.974        virginica
```

Despite the pretty face, it is a matrix... over a list:

```
str(do.call(rbind, l))
## List of 9
## $ : num 5.01
## $ : num 5.94
## $ : num 6.59
## $ : num 3.43
## $ : num 2.77
## $ : num 2.97
## $ : Factor w/ 3 levels "setosa","versicolor",...: 1
## $ : Factor w/ 3 levels "setosa","versicolor",...: 2
## $ : Factor w/ 3 levels "setosa","versicolor",...: 3
## - attr(*, "dim")= int [1:2] 3 3
## - attr(*, "dimnames")=List of 2
## ..$ : NULL
## ..$ : chr [1:3] "Sepal.Length" "Sepal.Width" "Species"
```

### 12.1.3 Reading data frames

Structured data can be imported from external sources, such as CSV/TSV (comma/tab-separated values) or HDF5 files, relational databases supporting SQL (see [Section 12.1.4](#)), web APIs (e.g., through the `curl` and `jsonlite` packages), spreadsheets [63], and so on.

In particular, `read.csv` and the like fetch data from plain text files consisting of records, where commas, semicolons, tabs, etc. separate the fields.

For instance:

```
x <- data.frame(a=runif(3), b=c(TRUE, FALSE, TRUE)) # example data frame
f <- tempfile() # temporary file name
write.csv(x, f, row.names=FALSE) # export
```

It created a CSV file that looks like:

```
cat(readLines(f), sep="\n") # print file contents
## "a", "b"
## 0.287577520124614, TRUE
## 0.788305135443807, FALSE
## 0.4089769218117, TRUE
```

The above can be read by calling:

```
read.csv(f)
##           a      b
## 1 0.28758 TRUE
## 2 0.78831 FALSE
## 3 0.40898 TRUE
```

**Exercise 12.2** Check out `help("read.table")` for a long list of tunable parameters, especially: `sep`, `dec`, `quote`, `header`, `comment.char`, and `row.names`. Further, note that reading from compressed files is supported directly.

---

**Important** CSV is the most portable and user-friendly format for exchanging matrix-like objects between different programs and computing languages (Python, Julia, LibreOffice Calc, etc.). Such files can be opened in any text editor.

---



---

**Note** As mentioned in [Section 8.3.5](#), we can process data frames on a chunk-by-chunk basis. This is beneficial especially when data do not fit into memory (compare the `nrows` argument to `read.csv`).

---

#### 12.1.4 Interfacing relational databases and querying with SQL (\*)

The **DBI** package provides a universal interface for particular database management systems whose drivers are in additional add-ons such as **RSQLite**, **RMariaDB**, **RPostgreSQL**, etc., or, more generally, **RODBC** or **odbc**. For more details, see Section 4 of [63].

**Example 12.3** Let us play with an in-memory (volatile) instance of an SQLite database.

```
library("DBI")
con <- dbConnect(RSQLite::SQLite(), ":memory:")
```

It returned an object representing a database connection which we can refer to in further communication.

An easy way to create a database table is to call:

```
dbWriteTable(con, "mtcars", mtcars) # `mtcars` is a toy built-in data frame
```

Alternatively, **dbExecute** could have been called to send SQL statements such as `CREATE TABLE ...` followed by a series of `INSERT INTO ...`.

Some data retrieval can now follow:

```
dbGetQuery(con, "
  SELECT cyl, vs, AVG(mpg) AS mpg_ave, AVG(hp) AS hp_ave
  FROM mtcars
  GROUP BY cyl, vs
")
##   cyl vs mpg_ave hp_ave
## 1   4  0  26.000  91.00
## 2   4  1  26.730  81.80
## 3   6  0  20.567 131.67
## 4   6  1  19.125 115.25
## 5   8  0  15.100 209.21
```

It gave us an ordinary R data frame. We can process it in the same fashion as any other object of this kind.

At the end, the database connection must be closed.

```
dbDisconnect(con)
```

**Exercise 12.4** Database passwords must never be stored in plain text files, let alone in R scripts in version-controlled repositories. Consider a few ways to fetch credentials programmatically:

- using environment variables (see `help("Sys.getenv")`),
- using the **keyring** package,
- calling **system2** (Section 7.3.2) to retrieve it from the system keyring (e.g., the **keyring** package for Python provides a platform-independent command-line utility).

### 12.1.5 Strings as factors?

The following is so critical that we devote a separate section to discuss it so we always remain vigilant (such is life: maintaining some level of mindfulness is often a good idea).

---

**Important** Some functions related to data frames automatically convert character vectors to factors. This behaviour is frequently controlled by the `stringsAsFactors` argument.

---

This is particularly problematic because, when printed, factor and character columns look identical:

```
(x <- data.frame(a=factor(c("U", "V")), b=c("U", "V")))
##   a b
## 1 U U
## 2 V V
```

We recall from Section 10.3.2 that factors can be nasty. For example, passing factors as indexers in `[` or converting them with `as.numeric` might give counterintuitive (for the uninformed) results. Also, when we want to extend factors by previously unobserved data, new levels must manually be added. This can cause some unexpected behaviour in contexts such as:

```
rbind(x, c("W", "W"))
## Warning in `[<-.factor`(`*tmp*`, ri, value = "W"): invalid factor level,
##      NA generated
##      a b
## 1    U U
## 2    V V
## 3 <NA> W
```

Therefore, always having the data types checked is a praiseworthy habit. For instance:

```
str(x)
## 'data.frame':      2 obs. of  2 variables:
##  $ a: Factor w/ 2 levels "U","V": 1 2
##  $ b: chr  "U" "V"
```

Before R 4.0, some functions, including `data.frame` and `read.csv` had the `stringsAsFactors` argument defaulting to `TRUE`. It is no longer the case for many of them.

However, exceptions to this rule still exist, e.g., including `as.data.frame.table` and `expand.grid`. Besides, some built-in example data frames have factor-typed columns inherited from the old days, e.g.:

```
class(iris[["Species"]])
## [1] "factor"
```

We observe that the `Species` column in `iris` is not of the type character. Thence, adding a new variety might be oblique:

```
iris2 <- iris[c(1, 51, 101), ] # example subset
levels(iris2[["Species"]]) <- c(levels(iris2[["Species"]]), "croatica")
rbind(iris2, c(6, 3, 3, 2, "croatica"))
##      Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1           5.1         3.5         1.4         0.2    setosa
## 51           7         3.2         4.7         1.4 versicolor
## 101          6.3         3.3          6         2.5  virginica
## 4           6         3         3         2    croatica
```

Alternatively, we could have simply converted the `Species` column to the type `character`.

### 12.1.6 Internal representation

Objects of S3 class `data.frame` are built on lists of vectors of the same length or matrices with identical row counts. Such lists define their consecutive columns. Apart from class, they must be equipped with the following special attributes:

- `names` – a character vector (as usual in any named list) labelling the columns or their groups,
- `row.names` – a character or integer vector with no duplicates nor missing values, doing what is advertised.

Therefore, a data frame can be created from scratch by calling, for example:

```
structure(
  list(a=11:13, b=21:23), # sets the `names` attribute already
  row.names=1:3,
  class="data.frame"
)
##      a  b
## 1 11 21
## 2 12 22
## 3 13 23
```

Here is a data frame based on a length-5 list, a matrix with five rows, and a length-5 numeric vector with some fancy row names on top:

```
structure(
  list(
    a=list(1, 1:2, 1:3, numeric(0), -(4:1)),
    b=cbind(u=11:15, v=21:25),
    c=runif(5)
  ),
  row.names=c("spam", "bacon", "eggs", "ham", "aubergine"),
  class="data.frame"
)
##              a b.u b.v      c
## spam              1 11 21 0.28758
## bacon            1, 2 12 22 0.78831
## eggs            1, 2, 3 13 23 0.40898
## ham              14 24 0.88302
## aubergine -4, -3, -2, -1 15 25 0.94047
```

In general, the columns of the type `list` can contain anything, e.g., other lists or R

functions. Including atomic vectors of varying lengths, just like above, allows for creating something à la *ragged arrays* – a pretty handy scenario.

The issue with matrix entries, on the other hand, is that they appear as if they were many. Still, as it will turn out in the sequel, they are often treated as a single complex column, e.g., by the index operator (see Section 12.2). Therefore, from this perspective, the above data frame has three columns, not four. Such compound columns can be output by **aggregate** (see Section 12.3), amongst others. They are valuable in certain contexts: the *column groups* can be easily accessed as a whole and batch-processed in the same way.

---

**Important** Unfortunately, data frames with list or matrix columns cannot be normally created with the **data.frame** nor **cbind** functions. This might explain why they are less popular. This behaviour is dictated by the underlying **as.data.frame** methods, which they both call. As a curiosity, see **help("I")**, though.

---

**Exercise 12.5** Verify that if a data frame has a matrix column, the matrix does not need to have any column names (the second *dimnames*).

The **names** and **row.names** attributes are special in the sense of Section 4.4.3. In particular, they can be accessed or modified by the corresponding functions.

It is worth noting that **row.names(df)** always returns a character vector, even when **attr(df, "row.names")** is an integer vector. Further, calling “**row.names(df) <- NULL**” will reset<sup>4</sup> this attribute to the most commonly desired case of consecutive natural numbers, for example:

```
(x <- iris[c(1, 51, 101), ]) # comes with some sad row names
##      Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1           5.1         3.5         1.4         0.2    setosa
## 51          7.0         3.2         4.7         1.4 versicolor
## 101         6.3         3.3         6.0         2.5  virginica
row.names(x) <- NULL # reset to seq_len(NROW(x))
print(x)
##      Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1           5.1         3.5         1.4         0.2    setosa
## 2           7.0         3.2         4.7         1.4 versicolor
## 3           6.3         3.3         6.0         2.5  virginica
```

**Exercise 12.6** What is the name of the replacement version of the **row.names** method for the **data.frame** class?

**Exercise 12.7** Implement your version of **expand.grid**.

---

<sup>4</sup> **attr<-"**(df, "row.names") does not feature the same sanity checks as **row.names<-"**(df) does. For instance, it is easy to corrupt a data frame by setting too short a **row.names** attribute.

**Exercise 12.8** Write a version of `xtabs` that does not rely on a formula interface (compare Section 10.3.4). Allow three parameters: a data frame, the name of the “counts” column, and the names of the cross-classifying variables. Hence, `my_xtabs(x, "Freq", c("Var1", "Var2"))` should be equivalent to `xtabs(Freq~Var1+Var2, x)`.

## 12.2 Data frame subsetting

### 12.2.1 Data frames are lists

Data frames are named lists, where each element represents an individual column. Therefore<sup>5</sup>, `length` yields the number of columns and `names` gives their respective labels.

Let us play with the following data frame:

```
(x <- data.frame(
  a=runif(6),
  b=rnorm(6),
  c=LETTERS[1:6],
  d1=c(FALSE, TRUE, FALSE, NA, FALSE, NA),
  d2=c(FALSE, TRUE, FALSE, TRUE, FALSE, TRUE)
))
##           a           b c    d1    d2
## 1 0.287578 0.070508 A FALSE FALSE
## 2 0.788305 0.129288 B  TRUE  TRUE
## 3 0.408977 1.715065 C FALSE FALSE
## 4 0.883017 0.460916 D    NA  TRUE
## 5 0.940467 -1.265061 E FALSE FALSE
## 6 0.045556 -0.686853 F    NA  TRUE
typeof(x) # each data frame is a list
## [1] "list"
length(x) # the number of columns
## [1] 5
names(x)  # column labels
## [1] "a" "b" "c" "d1" "d2"
```

The one-argument versions of extract and index operators behave as expected. `[[` fetches (looks inside) the contents of a given column:

<sup>5</sup> This is a strong word. This implication relies on an implicit assumption that the primitive functions `length` and `names` have not been contaminated by treating data frames differently than named lists. Luckily, that is indeed not the case. Although we have the index operators specially overloaded for the `data.frame` class, they behave quite reasonably. As we will see, they allow for a mix of list- and matrix-like behaviours.



```
x[["a"]] # or x[[1]]
## [1] 0.287578 0.788305 0.408977 0.883017 0.940467 0.045556
```

``[`` returns a data frame (a list with extras) comprised of the specified elements:

```
x["a"] # or x[1]
##      a
## 1 0.287578
## 2 0.788305
## 3 0.408977
## 4 0.883017
## 5 0.940467
## 6 0.045556
x[c(TRUE, TRUE, FALSE, TRUE, FALSE)]
##      a      b      d1
## 1 0.287578 0.070508 FALSE
## 2 0.788305 0.129288  TRUE
## 3 0.408977 1.715065 FALSE
## 4 0.883017 0.460916  NA
## 5 0.940467 -1.265061 FALSE
## 6 0.045556 -0.686853  NA
```

Just like with lists, the replacement versions of the said operators can be used to add new or replace existing columns.

```
y <- head(x, 1) # for a more compact display
y[["a"]] <- round(y[["a"]], 1) # replaces the column with new content
y[["b"]] <- NULL # removes the column, like, totally
y[["e"]] <- 10*y[["a"]]^2 # adds a new column at the end
print(y)
##      a c      d1      d2      e
## 1 0.3 A FALSE FALSE 0.9
```

**Example 12.9** Some spam for thought to show how much we already know. Here are a few common use cases of indexing using some popular vectorised functions.

```
y <- head(x, 1) # example data frame (more compact display)
```

Move the column *a* to the end:

```
y[unique(c(names(y), "a"), fromLast=TRUE)]
##      b c      d1      d2      a
## 1 0.070508 A FALSE FALSE 0.28758
```

Remove the columns *a* and *c*:

```
y[-match(c("a", "c"), names(y))]  
##           b      d1      d2  
## 1 0.070508 FALSE FALSE
```

Select all columns between *a* and *c*:

```
y[match("a", names(y)):match("c", names(y))]  
##           a           b c  
## 1 0.28758 0.070508 A
```

Fetch the columns with names starting with *d*:

```
y[grep("^d", names(y))]  
##           d1      d2  
## 1 FALSE FALSE
```

Change the name of column *c* to *z*:

```
names(y)[names(y) == "c"] <- "z"  
print(y)  
##           a           b z      d1      d2  
## 1 0.28758 0.070508 A FALSE FALSE
```

Change names: *d2* to *u* and *d1* to *v*:

```
names(y)[match(c("d2", "d1"), names(y))] <- c("v", "u")  
print(y)  
##           a           b z      u      v  
## 1 0.28758 0.070508 A FALSE FALSE
```

---

**Note** Some R users might prefer the ``$`` operator over ``[[``, but we do not. By default, the former supports partial matching of column names which might be appealing when R is used interactively. Nonetheless, it does not work on matrices nor it allows for programmatically generated names. It is also trickier to use on not syntactically valid labels; compare [Section 9.4.1](#).

---

**Exercise 12.10** Write a function `names_replace` that changes the names of columns based on a translation table given in a *from=to* fashion, for instance:

```
names_replace <- function(x, ...) ...to.do...  
x <- data.frame(a=1, b=2, c=3)  
names_replace(x, c="new_c", a="new_a")  
##   new_a b new_c  
## 1     1 2     3
```

### 12.2.2 Data frames are matrix-like

Data frames can be considered “generalised” matrices. They store data of any kind (possibly mixed) organised in a tabular fashion. Some functions mentioned in the previous chapter will be overloaded for the data frame case. These include: `dim` (despite the lack of the `dim` attribute), `NROW`, `NCOL`, and `dimnames` (which is, of course, based on `row.names` and `names`).

For example:

```
(x <- data.frame(
  a=runif(6),
  b=rnorm(6),
  c=LETTERS[1:6],
  d1=c(FALSE, TRUE, FALSE, NA, FALSE, NA),
  d2=c(FALSE, TRUE, FALSE, TRUE, FALSE, TRUE)
))
##           a           b c    d1    d2
## 1 0.287578 0.070508 A FALSE FALSE
## 2 0.788305 0.129288 B  TRUE  TRUE
## 3 0.408977 1.715065 C FALSE FALSE
## 4 0.883017 0.460916 D   NA  TRUE
## 5 0.940467 -1.265061 E FALSE FALSE
## 6 0.045556 -0.686853 F   NA  TRUE
dim(x) # the number of rows and columns
## [1] 6 5
dimnames(x) # it is not a matrix, but a matrix-like object
## [[1]]
## [1] "1" "2" "3" "4" "5" "6"
##
## [[2]]
## [1] "a" "b" "c" "d1" "d2"
```

In addition to the list-like behaviour, which only allows for dealing with particular columns or groups thereof, the ``[`` operator was also equipped with the ability to take two indexers:

```
x[1:2, ] # first two rows
##           a           b c    d1    d2
## 1 0.28758 0.070508 A FALSE FALSE
## 2 0.78831 0.129288 B  TRUE  TRUE
x[x[["a"]] >= 0.3 & x[["a"]] <= 0.8, -2] # or use x[, "a"]
##           a c    d1    d2
## 2 0.78831 B  TRUE  TRUE
## 3 0.40898 C FALSE FALSE
```

Recall the `drop` argument to ``[`` and its effects on matrix indexing. In the current case, its behaviour will be similar with regard to the operations on individual columns:

```
x[, 1]           # synonym: x[[1]] as drop=TRUE
## [1] 0.287578 0.788305 0.408977 0.883017 0.940467 0.045556
x[, 1, drop=FALSE] # synonym: x[1]
##           a
## 1 0.287578
## 2 0.788305
## 3 0.408977
## 4 0.883017
## 5 0.940467
## 6 0.045556
```

When we extract a single row and more than one column, `drop` does not apply. It is because columns (unlike in matrices) can potentially be of different types:

```
x[1, 1:2] # two numeric columns but the result is still a numeric
##           a           b
## 1 0.28758 0.070508
```

However:

```
x[1, 1]
## [1] 0.28758
x[1, 1, drop=FALSE]
##           a
## 1 0.28758
```

---

**Note** Once again, let us take note of logical indexing featuring missing values:

```
x[x[["d1"]], ]
##           a           b           c           d1           d2
## 2      0.78831 0.12929           B TRUE TRUE
## NA           NA           NA <NA> NA NA
## NA.1         NA           NA <NA> NA NA
x[which(x[["d1"]]), ] # drops missing values
##           a           b c           d1           d2
## 2 0.78831 0.12929 B TRUE TRUE
```

The default behaviour is consistent with many other R functions: it explicitly indicates that something is missing (we are selecting a “don’t know”; hence, the result is “don’t know” as well). Regrettably, this comes with no warning. As we rarely manually check missing values in the outputs, our absent-mindedness can lead to code bugs.

---

By far, we might have already noted that the index operator adjusts (not: resets) the `row.names` attribute. For instance:

```
(xs <- x[head(order(x[["a"]], decreasing=TRUE), 3), ])  
##           a           b c    d1    d2  
## 5 0.94047 -1.26506 E FALSE FALSE  
## 4 0.88302  0.46092 D    NA  TRUE  
## 2 0.78831  0.12929 B    TRUE TRUE
```

It is a version of `x` comprised of only the top three values in the `u` column. Indexing by means of character vectors will refer to `row.names` and `names`:

```
xs["5", c("a", "b")]  
##           a           b  
## 5 0.94047 -1.2651
```

This is not the same as `xs[5, c("a", "b")]`, even though `row.names` is formally an integer vector here.

---

**Note** If a data frame features a matrix, we need to use the index/extract operator twice in order to access a specific sub-column:

```
(x <- aggregate(iris[1], iris[5], function(x) c(Min=min(x), Max=max(x))))  
##           Species Sepal.Length.Min Sepal.Length.Max  
## 1      setosa           4.3           5.8  
## 2 versicolor           4.9           7.0  
## 3 virginica           4.9           7.9  
x[["Sepal.Length"]][, "Min"]  
## [1] 4.3 4.9 4.9
```

In other words, neither `x[["Sepal.Length.Min"]]` nor `x[, "Sepal.Length.Min"]` works.

Regarding the replacement version of the index operator, it is a quite flexible tool. It allows the new content to be a vector, a data frame, a list, or even a matrix.

**Exercise 12.11** Write two replacement functions<sup>6</sup>. First, `set_row_names` which replaces the `row.names` of a data frame with the contents of a specific column, for example:

```
(x <- aggregate(iris[1], iris[5], mean)) # some data frame  
##           Species Sepal.Length  
## 1      setosa           5.006  
## 2 versicolor           5.936
```

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---

<sup>6</sup> (\*) Compare `pandas.DataFrame.set_index` and `pandas.DataFrame.reset_index` in Python.

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```
## 3 virginica      6.588
set_row_names(x) <- "Species"
print(x)
##           Sepal.Length
## setosa      5.006
## versicolor  5.936
## virginica   6.588
```

Second, **reset\_row\_names** which converts *row.names* to a standalone column of a given name, for instance:

```
reset_row_names(x) <- "Type"
print(x)
## Sepal.Length      Type
## 1      5.006      setosa
## 2      5.936 versicolor
## 3      6.588 virginica
```

These two functions may be handy as they allow for writing “*x[something, ]*” instead of “*x[x[["column"]] %in% something, ]*”.

---

## 12.3 Common operations

Below we review the most commonly applied operations related to data frame wrangling. We have a few dedicated functions or methods overloaded for the *data.frame* class. However, we have already mastered the necessary skills to deal with such objects through our hard work: in particular, by solving all the exercises listed in the preceding chapters. Let us repeat: data frames are just lists exhibiting matrix-like behaviour.

### 12.3.1 Ordering rows

Ordering rows in a data frame with respect to different criteria can be easily achieved through the **order** function and the two-argument version of ``[`, ``.

For instance, here are the top six cars in terms of the time (in seconds) to complete a 402-metre race:

```
mtcars6 <- mtcars[order(mtcars[["qsec"]])[1:6], ]
mtcars6[["model"]] <- row.names(mtcars6)
row.names(mtcars6) <- NULL
print(mtcars6)
```

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```
##      mpg cyl disp  hp drat   wt  qsec vs am gear carb      model
## 1 15.8   8  351 264 4.22 3.17 14.50 0  1   5   4 Ford Pantera L
## 2 15.0   8  301 335 3.54 3.57 14.60 0  1   5   8 Maserati Bora
## 3 13.3   8  350 245 3.73 3.84 15.41 0  0   3   4 Camaro Z28
## 4 19.7   6  145 175 3.62 2.77 15.50 0  1   5   6 Ferrari Dino
## 5 14.3   8  360 245 3.21 3.57 15.84 0  0   3   4 Duster 360
## 6 21.0   6  160 110 3.90 2.62 16.46 0  1   4   4 Mazda RX4
```

**order** uses a stable sorting algorithm. Therefore, any sorting with respect to a different criterion will not break the *relative* ordering of `qsec` in row groups with ties:

```
mtcars6[order(mtcars6[["cyl"]]), ]
##      mpg cyl disp  hp drat   wt  qsec vs am gear carb      model
## 4 19.7   6  145 175 3.62 2.77 15.50 0  1   5   6 Ferrari Dino
## 6 21.0   6  160 110 3.90 2.62 16.46 0  1   4   4 Mazda RX4
## 1 15.8   8  351 264 4.22 3.17 14.50 0  1   5   4 Ford Pantera L
## 2 15.0   8  301 335 3.54 3.57 14.60 0  1   5   8 Maserati Bora
## 3 13.3   8  350 245 3.73 3.84 15.41 0  0   3   4 Camaro Z28
## 5 14.3   8  360 245 3.21 3.57 15.84 0  0   3   4 Duster 360
```

**Example 12.12** Notice the difference between ordering by `cyl` and `gear` vs `gear` and `cyl`:

```
mtcars6[order(mtcars6[["cyl"]], mtcars6[["gear"]]), ]
##      mpg cyl disp  hp drat   wt  qsec vs am gear carb      model
## 6 21.0   6  160 110 3.90 2.62 16.46 0  1   4   4 Mazda RX4
## 4 19.7   6  145 175 3.62 2.77 15.50 0  1   5   6 Ferrari Dino
## 3 13.3   8  350 245 3.73 3.84 15.41 0  0   3   4 Camaro Z28
## 5 14.3   8  360 245 3.21 3.57 15.84 0  0   3   4 Duster 360
## 1 15.8   8  351 264 4.22 3.17 14.50 0  1   5   4 Ford Pantera L
## 2 15.0   8  301 335 3.54 3.57 14.60 0  1   5   8 Maserati Bora
mtcars6[order(mtcars6[["gear"]], mtcars6[["cyl"]]), ]
##      mpg cyl disp  hp drat   wt  qsec vs am gear carb      model
## 3 13.3   8  350 245 3.73 3.84 15.41 0  0   3   4 Camaro Z28
## 5 14.3   8  360 245 3.21 3.57 15.84 0  0   3   4 Duster 360
## 6 21.0   6  160 110 3.90 2.62 16.46 0  1   4   4 Mazda RX4
## 4 19.7   6  145 175 3.62 2.77 15.50 0  1   5   6 Ferrari Dino
## 1 15.8   8  351 264 4.22 3.17 14.50 0  1   5   4 Ford Pantera L
## 2 15.0   8  301 335 3.54 3.57 14.60 0  1   5   8 Maserati Bora
```

**Note** Mixing increasing and decreasing ordering is tricky as the decreasing argument to **order** currently does not accept multiple flags in all the contexts. Perhaps the easiest way to change the ordering direction is to use the unary minus operator on the column(s) to be sorted decreasingly.

```
mtcars6[order(mtcars6[["gear"]], -mtcars6[["cyl"]]), ]
##   mpg cyl disp  hp drat   wt  qsec vs am gear carb      model
## 3 13.3   8  350 245 3.73 3.84 15.41 0 0   3   4   Camaro Z28
## 5 14.3   8  360 245 3.21 3.57 15.84 0 0   3   4   Duster 360
## 6 21.0   6  160 110 3.90 2.62 16.46 0 1   4   4   Mazda RX4
## 1 15.8   8  351 264 4.22 3.17 14.50 0 1   5   4 Ford Pantera L
## 2 15.0   8  301 335 3.54 3.57 14.60 0 1   5   8 Maserati Bora
## 4 19.7   6  145 175 3.62 2.77 15.50 0 1   5   6 Ferrari Dino
```

For factor and character columns, **xtfrm** can convert them to sort keys first.

```
mtcars6[order(mtcars6[["cyl"]], -xtfrm(mtcars6[["model"])]), ]
##   mpg cyl disp  hp drat   wt  qsec vs am gear carb      model
## 6 21.0   6  160 110 3.90 2.62 16.46 0 1   4   4   Mazda RX4
## 4 19.7   6  145 175 3.62 2.77 15.50 0 1   5   6 Ferrari Dino
## 2 15.0   8  301 335 3.54 3.57 14.60 0 1   5   8 Maserati Bora
## 1 15.8   8  351 264 4.22 3.17 14.50 0 1   5   4 Ford Pantera L
## 5 14.3   8  360 245 3.21 3.57 15.84 0 0   3   4   Duster 360
## 3 13.3   8  350 245 3.73 3.84 15.41 0 0   3   4   Camaro Z28
```

Both of the above behave like `decreasing=c(FALSE, TRUE)`.

**Exercise 12.13** Write a method **sort.data.frame** that orders a data frame with respect to a given set of columns.

```
sort.data.frame <- function(x, decreasing=FALSE, cols) ...to.do...
sort(mtcars6, cols=c("cyl", "model"))
##   mpg cyl disp  hp drat   wt  qsec vs am gear carb      model
## 4 19.7   6  145 175 3.62 2.77 15.50 0 1   5   6 Ferrari Dino
## 6 21.0   6  160 110 3.90 2.62 16.46 0 1   4   4   Mazda RX4
## 3 13.3   8  350 245 3.73 3.84 15.41 0 0   3   4   Camaro Z28
## 5 14.3   8  360 245 3.21 3.57 15.84 0 0   3   4   Duster 360
## 1 15.8   8  351 264 4.22 3.17 14.50 0 1   5   4 Ford Pantera L
## 2 15.0   8  301 335 3.54 3.57 14.60 0 1   5   8 Maserati Bora
```

Unfortunately, that *decreasing* must be of length one and be placed as the second method argument is imposed by the **sort** S3 generic.

### 12.3.2 Handling duplicated rows

**duplicated**, **anyDuplicated**, and **unique** have methods overloaded for the **data.frame** class. They can be used to indicate, get rid of, or replace the repeating rows.

```
sum(duplicated(iris)) # how many duplicated rows are there?
## [1] 1
```

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```
iris[duplicated(iris), ] # show the duplicated rows
##      Sepal.Length Sepal.Width Petal.Length Petal.Width  Species
## 143           5.8         2.7         5.1         1.9 virginica
```

### 12.3.3 Joining (merging) data frames

The `merge` function can perform the JOIN operation that some readers might know from SQL<sup>7</sup>. It matches the items in the columns that two given data frames somewhat share and then returns their combination.

**Example 12.14** Two calls to `merge` could be used to match data on programmers (each identified by `developer_id` and giving such details as their name, location, main skill, etc.) with the information about the open-source projects (each identified by `project_id` and informing us about its title, scope, web site, and so forth) they are engaged in (based on a third data frame featuring `developer_id` and `project_id` pairs).

As a simple illustration, consider the two following objects:

```
A <- data.frame(
  u=c("b0", "b1", "b2", "b3"),
  v=c("a0", "a1", "a2", "a3")
)

B <- data.frame(
  v=c("a0", "a2", "a2", "a4"),
  w=c("c0", "c1", "c2", "c3")
)
```

The two *common* columns, i.e., storing data of similar nature (a-something strings), are both named `v`.

First, the *inner (natural) join*, where we list only the matching pairs:

```
merge(A, B) # x=A, y=B, by="v", all.x=FALSE, all.y=FALSE
##      v  u  w
## 1 a0 b0 c0
## 2 a2 b2 c1
## 3 a2 b2 c2
```

The common column (or, more generally, columns) is included only once in the result.

<sup>7</sup> JOIN is the reverse operation to data normalisation known from the relational database theory. It reduces data redundancy and increases their integrity. What data scientists need for succeeding with their daily activities (analysis, visualisation, processing) is sometimes the opposite of what the art of data management focuses on (efficient collection and storage). The readers are encouraged to learn about various normalisation forms from, e.g., [16] or any other course covering this topic.

The *left join* guarantees that all elements in the first data frame will be included in the result:

```
merge(A, B, all.x=TRUE) # by="v", all.y=FALSE
##      v      u      w
## 1 a0 b0 c0
## 2 a1 b1 <NA>
## 3 a2 b2 c1
## 4 a2 b2 c2
## 5 a3 b3 <NA>
```

The *right join* includes all records in the second argument:

```
merge(A, B, all.y=TRUE) # by="v", all.x=FALSE
##      v      u      w
## 1 a0 b0 c0
## 2 a2 b2 c1
## 3 a2 b2 c2
## 4 a4 <NA> c3
```

The *full outer join* is their set-theoretic union:

```
merge(A, B, all.x=TRUE, all.y=TRUE) # by="v"
##      v      u      w
## 1 a0 b0 c0
## 2 a1 b1 <NA>
## 3 a2 b2 c1
## 4 a2 b2 c2
## 5 a3 b3 <NA>
## 6 a4 <NA> c3
```

**Exercise 12.15** Show how *match* (Section 5.4.1) can be used to author a very basic version of *merge*.

### 12.3.4 Aggregating and transforming columns

Let us discuss how to perform data aggregation or engineer features. Although we already know how to access individual columns with ``[`` and process them using the many vectorised functions, we still have something interesting to add about the said matter.

It would be tempting to try composing such operations with **apply**. Unfortunately, currently, this function coerces its argument to a matrix. Hence, we should refrain from applying it on data frames whose columns are of mixed types<sup>8</sup>.

However, taking into account that data frames are special lists, we can always call **Map** and its relatives.

<sup>8</sup> Due to this, storing data as matrix columns inside data frames is not such a bad idea.

**Example 12.16** Given an example data frame:

```
(iris_sample <- iris[sample(NROW(iris), 6), ])
```

|        | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width | Species    |
|--------|--------------|-------------|--------------|-------------|------------|
| ## 28  | 5.2          | 3.5         | 1.5          | 0.2         | setosa     |
| ## 80  | 5.7          | 2.6         | 3.5          | 1.0         | versicolor |
| ## 101 | 6.3          | 3.3         | 6.0          | 2.5         | virginica  |
| ## 111 | 6.5          | 3.2         | 5.1          | 2.0         | virginica  |
| ## 137 | 6.3          | 3.4         | 5.6          | 2.4         | virginica  |
| ## 133 | 6.4          | 2.8         | 5.6          | 2.2         | virginica  |

To get the class of each column, we can call:

```
sapply(iris_sample, class) # or unlist(Map(class, iris))
```

| ## | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width | Species  |
|----|--------------|-------------|--------------|-------------|----------|
| ## | "numeric"    | "numeric"   | "numeric"    | "numeric"   | "factor" |

Next, here is a way to compute some aggregates of the numeric columns:

```
unlist(Map(mean, Filter(is.numeric, iris_sample)))
```

| ## | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width |
|----|--------------|-------------|--------------|-------------|
| ## | 6.0667       | 3.1333      | 4.5500       | 1.7167      |

or:

```
sapply(iris_sample[sapply(iris_sample, is.numeric)], mean)
```

| ## | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width |
|----|--------------|-------------|--------------|-------------|
| ## | 6.0667       | 3.1333      | 4.5500       | 1.7167      |

We can also fetch more than a single summary of each column:

```
as.data.frame(Map(
  function(x) c(Min=min(x), Max=max(x)),
  Filter(is.numeric, iris_sample)
))
```

| ##     | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width |
|--------|--------------|-------------|--------------|-------------|
| ## Min | 5.2          | 2.6         | 1.5          | 0.2         |
| ## Max | 6.5          | 3.5         | 6.0          | 2.5         |

or:

```
sapply(iris_sample[sapply(iris_sample, is.numeric)], quantile, c(0, 1))
```

| ##      | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width |
|---------|--------------|-------------|--------------|-------------|
| ## 0%   | 5.2          | 2.6         | 1.5          | 0.2         |
| ## 100% | 6.5          | 3.5         | 6.0          | 2.5         |

The latter called **simplify2array** automatically. Thus, the result is a matrix.

On the other hand, the standardisation of all the numeric features can be performed, e.g., via a call:

```
iris_sample[] <- Map(function(x) {
  if (!is.numeric(x)) x else (x-mean(x))/sd(x)
}, iris_sample)
print(iris_sample)
```

| ##     | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width | Species    |
|--------|--------------|-------------|--------------|-------------|------------|
| ## 28  | -1.70405     | 1.03024     | -1.76004     | -1.65318    | setosa     |
| ## 80  | -0.72094     | -1.49854    | -0.60591     | -0.78117    | versicolor |
| ## 101 | 0.45878      | 0.46829     | 0.83674      | 0.85384     | virginica  |
| ## 111 | 0.85202      | 0.18732     | 0.31738      | 0.30884     | virginica  |
| ## 137 | 0.45878      | 0.74927     | 0.60591      | 0.74484     | virginica  |
| ## 133 | 0.65540      | -0.93659    | 0.60591      | 0.52684     | virginica  |

### 12.3.5 Handling missing values

The `is.na` method for objects of the class `data.frame` returns a logical matrix of the same dimensionality<sup>9</sup>, indicating whether the corresponding items are missing or not. Of course, this function can still be called on individual columns as well.

Further, `na.omit` can be used to get rid of rows with missing values.

**Exercise 12.17** Given a data frame, use `is.na` and other functions such as `apply` or `approx` to:

1. remove all rows that feature at least one missing value,
2. remove all rows that only consist of missing values,
3. remove all columns that feature at least one missing value,
4. for each column, replace all missing values with the column averages,
5. for each column, replace all missing values with values that linearly interpolate between the preceding and succeeding well-defined observations (of use in time series), e.g., the blanks in `c(0.60, 0.62, NA, 0.64, NA, NA, 0.58)` should be filled to obtain `c(0.60, 0.62, 0.63, 0.64, 0.62, 0.60, 0.58)`.

### 12.3.6 Reshaping data frames

Consider an example matrix:

```
A <- matrix(round(runif(6), 2), nrow=3,
  dimnames=list(
    c("X", "Y", "Z"), # row labels
    c("u", "v")        # column labels
  ))
```

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<sup>9</sup> Provided that a data frame does not feature a matrix column.

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```
names(dimnames(A)) <- c("Row", "Col")
print(A)
##      Col
## Row    u    v
## X 0.29 0.88
## Y 0.79 0.94
## Z 0.41 0.05
```

The `as.data.frame` method for the `table` class can be called directly on any array:

```
as.data.frame.table(A, responseName="Val")
##      Row Col  Val
## 1    X   u 0.29
## 2    Y   u 0.79
## 3    Z   u 0.41
## 4    X   v 0.88
## 5    Y   v 0.94
## 6    Z   v 0.05
```

It is an instance of array *reshaping*. More precisely, we call it *stacking*: we converted from a *wide* (okay, in this example, not so wide, as we have only two columns) to a *long* format.

This can be also achieved by means of the `reshape` function which is more flexible and operates directly on data frames (but is harder to use):

```
(df <- `names<-` (
  data.frame(row.names(A), A, row.names=NULL),
  c("Row", "Col.u", "Col.v")))
##      Row Col.u Col.v
## 1    X 0.29 0.88
## 2    Y 0.79 0.94
## 3    Z 0.41 0.05
(stacked <- reshape(df, varying=2:3, direction="long"))
##      Row time Col id
## 1.u    X    u 0.29  1
## 2.u    Y    u 0.79  2
## 3.u    Z    u 0.41  3
## 1.v    X    v 0.88  1
## 2.v    Y    v 0.94  2
## 3.v    Z    v 0.05  3
```

Maybe the default column names are not superb, but we can adjust them manually afterwards.

The reverse operation is called *unstacking*:

```
reshape(stacked, idvar="Row", timevar="time", drop="id", direction="wide")
##      Row Col.u Col.v
## 1.u   X   0.29  0.88
## 2.u   Y   0.79  0.94
## 3.u   Z   0.41  0.05
```

**Exercise 12.18** Given a named numeric vector, convert it to a data frame with two columns, for instance:

```
convert <- function(x) ...to.do...
x <- c(spam=42, eggs=7, bacon=3)
convert(x)
##      key value
## 1  spam    42
## 2  eggs     7
## 3  bacon     3
```

**Exercise 12.19** Reshape (stack) the built-in `WorldPhones` dataset. Then, reshape (unstack) the stacked `WorldPhones` dataset. Further, unstack the stacked set but first remove<sup>10</sup> five random rows from it and then randomly permute all the remaining rows. Fill in the missing entries with NAs.

**Exercise 12.20** Implement a basic version of `as.data.frame.table` manually (using `rep` etc.). Also, write a function `as.table.data.frame` that computes its reverse. Make sure both functions are compatible with each other.

**Exercise 12.21** The built-in `Titanic` is a four-dimensional array. Convert it to a long data frame.

**Exercise 12.22** Perform what follows on the data frame defined below:

1. convert the second column from character to a list of character vectors (split at ",");
2. extract the first elements from each of the vectors;
3. extract the last elements;
4. (\*) unstack the data frame;
5. (\*) stack it back to a data frame featuring a list;
6. convert the list back to a character column (concatenate with ", " as separator).

```
(x <- data.frame(
  name=c("Kat", "Ron", "Jo", "Mary"),
  food=c("buckwheat", "spam,bacon,spam", "", "eggs,spam,spam,lollipops")
))
##      name          food
```

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<sup>10</sup> The original dataset can be thought of as representing a fully crossed design experiment (all combinations of two grouping variables are present). Its truncated version is like an incomplete cross-design.

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```
## 1 Kat buckwheat
## 2 Ron spam,bacon,spam
## 3 Jo
## 4 Mary eggs,spam,spam,lollipops
```

**Exercise 12.23** Write a function that converts all matrix-based columns in a given data frame to separate atomic columns. Furthermore, author a function that does the opposite: one that groups all columns with similar prefixes and turns them into matrices.

### 12.3.7 Aggregating data in groups

We can straightforwardly apply various transforms on data groups determined by a factor-like variable or a combination thereof thanks to the `split.data.frame` method, which returns a list of data frames.

For example:

```
x <- data.frame(
  a=c( 10,    20,    30,    40,    50),
  u=c("spam", "spam", "eggs", "spam", "eggs"),
  v=c( 1,    2,    1,    1,    1)
)
split(x, x["u"]) # i.e., split.data.frame(x, x["u"]) or x[["u"]]
```

```
## $eggs
##   a    u v
## 3 30 eggs 1
## 5 50 eggs 1
##
## $spam
##   a    u v
## 1 10 spam 1
## 2 20 spam 2
## 4 40 spam 1
```

It split `x` with respect to the `u` column, which served as the grouping variable. On the other hand:

```
split(x, x[c("u", "v")]) # sep="."
```

```
## $eggs.1
##   a    u v
## 3 30 eggs 1
## 5 50 eggs 1
##
## $spam.1
##   a    u v
```

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```
## 1 10 spam 1
## 4 40 spam 1
##
## $eggs.2
## [1] a u v
## <0 rows> (or 0-length row.names)
##
## $spam.2
##      a      u v
## 2 20 spam 2
```

It partitioned with respect to a combination of two factor-like sequences. A nonexistent level pair (eggs, 2) resulted in an empty data frame.

**Exercise 12.24** `split.data.frame` (when called explicitly) can also be used to break a matrix into a list of matrices (rowwisely). Given a matrix, perform its train-test split: allocate, say, 70% of the rows at random into one matrix and the remaining 30% into another.

If we need to aggregate grouped data in numeric columns, **sapply** is quite convenient. To recall, it is a combination of **lapply** (one-vector version of **Map**) and **simplify2array** (Section 11.1.3).

```
sapply(split(iris[1:2], iris[5]), sapply, mean)
##           setosa versicolor virginica
## Sepal.Length  5.006      5.936      6.588
## Sepal.Width   3.428      2.770      2.974
```

If the function to apply returns more than a single value, **sapply** will not return too informative a result: the list of matrices converted to a matrix will not have the row.names argument set. As a workaround, we either call **simplify2array** explicitly or pass `simplify="array"` to **sapply**:

```
(res <- sapply(
  split(iris[1:2], iris[5]),
  sapply,
  function(x) c(Min=min(x), Max=max(x)),
  simplify="array"
)) # or simplify2array(lapply or Map etc.)
## , , setosa
##
##      Sepal.Length Sepal.Width
## Min           4.3         2.3
## Max           5.8         4.4
##
## , , versicolor
##
```

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```
##      Sepal.Length Sepal.Width
## Min           4.9         2.0
## Max           7.0         3.4
##
## , , virginica
##
##      Sepal.Length Sepal.Width
## Min           4.9         2.2
## Max           7.9         3.8
```

It produced a three-dimensional array, which is particularly handy if we now wish to access specific results by name:

```
res[, "Sepal.Length", "setosa"]
## Min Max
## 4.3 5.8
```

Also, the previously mentioned **as.data.frame.table** method works on it like a charm (up to the column names):

```
as.data.frame.table(res)
##   Var1      Var2      Var3 Freq
## 1  Min Sepal.Length    setosa  4.3
## 2  Max Sepal.Length    setosa  5.8
## 3  Min Sepal.Width    setosa  2.3
## 4  Max Sepal.Width    setosa  4.4
## 5  Min Sepal.Length versicolor  4.9
## 6  Max Sepal.Length versicolor  7.0
## 7  Min Sepal.Width  versicolor  2.0
## 8  Max Sepal.Width  versicolor  3.4
## 9  Min Sepal.Length  virginica  4.9
## 10 Max Sepal.Length  virginica  7.9
## 11 Min Sepal.Width  virginica  2.2
## 12 Max Sepal.Width  virginica  3.8
```

**Note** If the grouping (by) variable is a list of two or more factors, the combined levels will be concatenated to a single string:

```
as.data.frame.table(as.array(sapply(
  split(ToothGrowth["len"], ToothGrowth[c("supp", "dose")]),
  sapply,
  mean
)))
##      Var1  Freq
```

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```
## 1 OJ.0.5.len 13.23
## 2 VC.0.5.len 7.98
## 3 OJ.1.len 22.70
## 4 VC.1.len 16.77
## 5 OJ.2.len 26.06
## 6 VC.2.len 26.14
```

Also, the name of the aggregated column (len) has been included. This behaviour yields a result that may be deemed convenient in some contexts but not necessarily so in others.

**Exercise 12.25** Many aggregation functions are idempotent, which means that when they are fed with a vector with all the elements being identical, the result is exactly that unique element: **min**, **mean**, **median**, and **max** behave this way.

Overload the **mean** and **median** methods for character vectors and factors. They should return NA when fed with a sequence where not all elements are the same. Otherwise, they are expected to output the unique value.

```
mean.character <- function(x, na.rm=FALSE, ...) ...to.do...
mean.factor <- function(x, na.rm=FALSE, ...) ...to.do...
```

This way, we can also aggregate the grouping variables conveniently:

```
do.call(rbind.data.frame,
  lapply(split(ToothGrowth, ToothGrowth[c("supp", "dose")]), lapply, mean))
##      len supp dose
## OJ.0.5 13.23 OJ 0.5
## VC.0.5 7.98 VC 0.5
## OJ.1 22.70 OJ 1.0
## VC.1 16.77 VC 1.0
## OJ.2 26.06 OJ 2.0
## VC.2 26.14 VC 2.0
```

The built-in **aggregate** method can assist us in when a single function is to be applied on all columns in a data frame.

```
aggregate(iris[-5], iris[5], mean) # not: ...[[5]]
##      Species Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1 setosa      5.006      3.428      1.462      0.246
## 2 versicolor 5.936      2.770      4.260      1.326
## 3 virginica  6.588      2.974      5.552      2.026
aggregate(ToothGrowth["len"], ToothGrowth[c("supp", "dose")], mean)
##      supp dose      len
```

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```
## 1 OJ 0.5 13.23
## 2 VC 0.5 7.98
## 3 OJ 1.0 22.70
## 4 VC 1.0 16.77
## 5 OJ 2.0 26.06
## 6 VC 2.0 26.14
```

The second argument, `by`, must be list-like (this includes data frames). Neither a factor nor an atomic vector are acceptable. Also, if the function being applied returns many values, they will be wrapped into a matrix column:

```
(x <- aggregate(iris[2], iris[5], function(x) c(Min=min(x), Max=max(x))))
##      Species Sepal.Width.Min Sepal.Width.Max
## 1   setosa           2.3           4.4
## 2 versicolor           2.0           3.4
## 3  virginica           2.2           3.8
class(x[["Sepal.Width"]])
## [1] "matrix" "array"
x[["Sepal.Width"]] # not: Sepal.Width.Max, etc.
##      Min Max
## [1,] 2.3 4.4
## [2,] 2.0 3.4
## [3,] 2.2 3.8
```

It is actually handy: by referring to `x[["Sepal.Width"]]`, we have access to all the stats for this column. Further, if many columns are being aggregated simultaneously, we can process all the summaries in the same way.

**Exercise 12.26** Check out the built-in `by` function, which supports some basic split-apply-bind use cases. Note the particularly peculiar behaviour of the `print` method for the `by` class.

The most flexible scenario involves applying a custom function returning any set of aggregates in the form of a list and then row-binding the results to obtain a data frame.

**Example 12.27** The following implements an R version of what we would express in SQL as:

```
SELECT supp, dose, AVG(len) AS ave_len, COUNT(*) AS count
FROM ToothGrowth
GROUP BY supp, dose
```

Ad rem:

```
do.call(rbind.data.frame, lapply(
  split(ToothGrowth, ToothGrowth[c("supp", "dose")]),
  function(df) list(
    supp=df[1, "supp"],
```

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```

dose=df[1, "dose"],
ave_len=mean(df[["len"]]),
count=NROW(df)
)
))
##      supp dose ave_len count
## OJ.0.5  OJ  0.5   13.23    10
## VC.0.5  VC  0.5    7.98    10
## OJ.1    OJ  1.0   22.70    10
## VC.1    VC  1.0   16.77    10
## OJ.2    OJ  2.0   26.06    10
## VC.2    VC  2.0   26.14    10

```

**Example 12.28** As an exercise, let us study a function that takes a named list  $x$  (can be a data frame) and a sequence of  $col=f$  pairs and applies the function  $f$  (or each function from a list of functions  $f$ ) on the named element  $col$  in  $x$ :

```

napply <- function(x, ...)
{
  fs <- list(...)
  stopifnot(is.list(x), !is.null(names(x)))
  stopifnot(all(names(fs) %in% names(x)))
  do.call(
    c, # concatenates lists
    lapply(
      structure(seq_along(fs), names=names(fs)),
      function(i)
      { # always returns a list
        y <- x[[ names(fs)[i] ]]
        if (is.function(fs[[i]]))
          list(fs[[i]](y))
        else
          lapply(fs[[i]], function(f) f(y))
      }
    )
  )
}

```

For example:

```

first <- function(x, ...) head(x, n=1L, ...) # we use it below
napply(ToothGrowth,
  supp=first, dose=first, len=list(ave=mean, count=length)
)
## $supp

```

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```
## [1] VC
## Levels: OJ VC
##
## $dose
## [1] 0.5
##
## $len.ave
## [1] 18.813
##
## $len.count
## [1] 60
```

applies **first** on both `ToothGrowth[["supp"]]` and `ToothGrowth[["dose"]]` as well as **mean** and **length** on `ToothGrowth[["len"]]`. List names are there for a more dramatic effect.

And now:

```
do.call(
  rbind.data.frame,
  lapply(
    split(ToothGrowth, ToothGrowth[c("supp", "dose")]),
    napply,
    supp=first, dose=first, len=list(ave=mean, count=length)
  )
)
##      supp dose len.ave len.count
## OJ.0.5   OJ  0.5   13.23        10
## VC.0.5   VC  0.5    7.98        10
## OJ.1     OJ  1.0   22.70        10
## VC.1     VC  1.0   16.77        10
## OJ.2     OJ  2.0   26.06        10
## VC.2     VC  2.0   26.14        10
```

or even:

```
aaaggg <- function(x, by, ...)
  do.call(rbind.data.frame, lapply(split(x, x[by]), napply, ...))
```

so that:

```
aaaggg(iris, "Species", Species=first, Sepal.Length=mean)
##      Species Sepal.Length
## setosa      setosa      5.006
## versicolor versicolor  5.936
## virginica   virginica   6.588
```

This brings fun back to R programming in the sad times when many things are given to us on a plate.

By the way, the above has not been tested thoroughly. It is a proof of concept. As usual, testing, debugging, and extending are left as an exercise for the reader.

**Example 12.29** Section 10.5 considered an example where we used our own **group\_by** function and an aggregation method overloaded for the object's class it returns.

Here is the function that splits a data frame into a list of data frames with respect to a combination of levels in given named columns:

```
group_by <- function(df, by)
{
  stopifnot(is.character(by), is.data.frame(df))
  df <- droplevels(df) # factors might have unused levels
  structure(
    split(df, df[names(df) %in% by]),
    class="list_dfs",
    by=by
  )
}
```

The next function applies a set of aggregates on every column of each data frame in a given list (two nested **lapply**s plus some cosmetic additions):

```
aggregate.list_dfs <- function(x, FUN, ...)
{
  aggregates <- lapply(x, function(df) {
    is_by <- names(df) %in% attr(x, "by")
    res <- lapply(df[!is_by], FUN, ...)
    res_mat <- do.call(rbind, res)
    if (is.null(dimnames(res_mat)[[2]]))
      dimnames(res_mat)[[2]] <- paste0("f", seq_len(NCOL(res_mat)))
    cbind(
      `row.names`=<`(df[1, is_by, drop=FALSE], NULL),
      x=row.names(res_mat),
      `row.names`=<`(res_mat, NULL)
    )
  })
  combined_aggregates <- do.call(rbind.data.frame, aggregates)
  `row.names`=<`(combined_aggregates, NULL)
}

aggregate(group_by(ToothGrowth, c("supp", "dose")), range)
## supp dose x f1 f2
## 1 OJ 0.5 len 8.2 21.5
## 2 VC 0.5 len 4.2 11.5
## 3 OJ 1.0 len 14.5 27.3
```

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```
## 4 VC 1.0 len 13.6 22.5
## 5 OJ 2.0 len 22.4 30.9
## 6 VC 2.0 len 18.5 33.9
```

We really want our API to be bloated. Hence, let us introduce a convenience function, which is a specialised version of the above:

```
mean.list_dfs <- function(x, ...)
  aggregate.list_dfs(x, function(y) c(Mean=mean(y, ...)))
mean(group_by(iris[51:150, c(2, 3, 5)], "Species"))
##      Species      x Mean
## 1 versicolor Sepal.Width 2.770
## 2 versicolor Petal.Length 4.260
## 3 virginica Sepal.Width 2.974
## 4 virginica Petal.Length 5.552
```

### 12.3.8 Transforming data in groups

Some variables will sometimes need to be transformed relative to what is happening in a dataset's subsets. This is the case, e.g., where we decide that missing values should be replaced by the corresponding within-group averages or want to compute the relative ranks or z-scores.

If the loss of the original ordering of rows is not an issue, the standard split-apply-bind will suffice.

An example data frame:

```
(x <- data.frame(
  a=c( 10, 1, NA, NA, NA, 4),
  b=c( -1, 10, 40, 30, 1, 20),
  c=runif(6),
  d=c("v", "u", "u", "u", "v", "u")
))
##      a b      c d
## 1 10 -1 0.52811 v
## 2  1 10 0.89242 u
## 3 NA 40 0.55144 u
## 4 NA 30 0.45661 u
## 5 NA  1 0.95683 v
## 6  4 20 0.45333 u
```

Some operations:

```
fill_na <- function(x) `[<-` (x, is.na(x), value=mean(x[!is.na(x)]))
standardise <- function(x) (x-mean(x))/sd(x)
```

And now:

```
do.call(rbind.data.frame, lapply(
  split(x, x["d"]),
  function(df) {
    df[["a"]] <- fill_na(df[["a"]])
    df[["b"]] <- rank(df[["b"]])
    df[["c"]] <- standardise(df[["c"]])
    df
  }
))
##           a b           c d
## u.2  1.0 1  1.46357 u
## u.3  2.5 4 -0.17823 u
## u.4  2.5 3 -0.63478 u
## u.6  4.0 2 -0.65057 u
## v.1 10.0 1 -0.70711 v
## v.5 10.0 2  0.70711 v
```

Only the *relative* ordering of rows within groups has been retained. Overall, the rows are in a different order.

If this is an issue, we can use the **unsplit** function:

```
unsplit(
  lapply(
    split(x, x["d"]),
    function(df) {
      df[["a"]] <- fill_na(df[["a"]])
      df[["b"]] <- rank(df[["b"]])
      df[["c"]] <- standardise(df[["c"]])
      df
    }
  ),
  x["d"]
)
##           a b           c d
## 1 10.0 1 -0.70711 v
## 2  1.0 1  1.46357 u
## 3  2.5 4 -0.17823 u
## 4  2.5 3 -0.63478 u
## 5 10.0 2  0.70711 v
## 6  4.0 2 -0.65057 u
```

**Exercise 12.30** Show how we can do the above also via the replacement version of **split**.

**Example 12.31** Reverting to the previous ordering can be done manually too. It is because the



split operation behaves as if we first ordered the data frame with respect to the grouping variable(s) (using a stable sorting algorithm).

Here is some transformation of a sample data frame split by a combination of two factors:

```
(x <- `row.names<-`(ToothGrowth[sample(NROW(ToothGrowth), 10), ], NULL))
##      len supp dose
## 1  23.0   OJ  2.0
## 2  23.3   OJ  1.0
## 3  29.4   OJ  2.0
## 4  14.5   OJ  1.0
## 5  11.2   VC  0.5
## 6  20.0   OJ  1.0
## 7  24.5   OJ  2.0
## 8  10.0   OJ  0.5
## 9   9.4   OJ  0.5
## 10 7.0    VC  0.5
(y <- do.call(rbind.data.frame, lapply(
  split(x, x[c("dose", "supp")]), # two grouping variables
  function(df) {
    df[["len"]] <- df[["len"]] * 100^df[["dose"]] * # whatever
    ifelse(df[["supp"]] == "OJ", -1, 1)           # do not overthink it
    df
  }
)))
##      len supp dose
## 0.5.OJ.8    -100   OJ  0.5
## 0.5.OJ.9     -94   OJ  0.5
## 1.OJ.2     -2330   OJ  1.0
## 1.OJ.4     -1450   OJ  1.0
## 1.OJ.6     -2000   OJ  1.0
## 2.OJ.1    -230000   OJ  2.0
## 2.OJ.3    -294000   OJ  2.0
## 2.OJ.7    -245000   OJ  2.0
## 0.5.VC.5      112   VC  0.5
## 0.5.VC.10     70   VC  0.5
```

Section 5.4.4 mentioned that by calling **order**, we can determine the inverse of a given permutation. Hence, we can call:

```
y[order(order(x[["supp"]], x[["dose"]])), ] # not: dose, supp
##      len supp dose
## 2.OJ.1    -230000   OJ  2.0
## 1.OJ.2     -2330   OJ  1.0
## 2.OJ.3    -294000   OJ  2.0
## 1.OJ.4     -1450   OJ  1.0
## 0.5.VC.5      112   VC  0.5
```

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```
## 1.OJ.6      -2000  OJ  1.0
## 2.OJ.7      -245000 OJ  2.0
## 0.5.OJ.8     -100   OJ  0.5
## 0.5.OJ.9     -94    OJ  0.5
## 0.5.VC.10     70    VC  0.5
```

Additionally, we can manually restore the original *row.names*, et voilà.

### 12.3.9 Metaprogramming-based techniques (\*)

Section 9.5.7 mentioned that R is equipped with the ability to compose programs that manipulate unevaluated expressions. As a consequence, some functions provide us with *convenient*<sup>11</sup> interfaces to a few common operations. These include **transform**, **{commandsubset}**, **with**, and basically every procedure accepting a formula. The popular **data.table** and **dplyr** packages also fall into this class (Section 12.3.10).

However, we have already noted that each method must be studied separately. It can arbitrarily interpret the *form* of the passed arguments without taking into account their *real* meaning. Hence, we avoid<sup>12</sup> them in this course, as we can do perfectly without them.

Withal, they are thought-provoking on their own. Furthermore, they are quite popular in other users' code. Hence the honourable mention. Learning them in more detail is left to the earnest reader as an optional exercise.

**Example 12.32** For instance, let us consider an example call to the **subset** function:

```
subset(iris, Sepal.Length>7.5, -(Sepal.Width:Petal.Width))
##      Sepal.Length Species
## 106           7.6 virginica
## 118           7.7 virginica
## 119           7.7 virginica
## 123           7.7 virginica
## 132           7.9 virginica
## 136           7.7 virginica
```

Neither *Sepal.Length>7.5* nor *-(Sepal.Width:Petal.Width)* make sense as standalone R expressions. We have not defined the named variables used therein:

<sup>11</sup> Furthermore, some third-party packages can sometimes be faster and more memory efficient (on larger datasets), as is usually the case with more specialised tools. However, in many daily programming contexts, the speed of the data wrangling operations is not often an issue. Remember that we always have SQL-supporting relational databases at our disposal.

<sup>12</sup> We are not alone in our calling to refrain from using them. **help("subset")** warns (and **help("transform")** quite similarly): *This is a convenience function intended for use interactively. For programming, it is better to use the standard subsetting functions like `[]`, and in particular the nonstandard evaluation of argument **subset** can have unanticipated consequences. The same in **help("with")**: *For interactive use, this is very effective and nice to read. For programming however, i.e., in one's functions, more care is needed, and typically one should refrain from using **with**, as, e.g., variables in data may accidentally override local variables.**

```
Sepal.Length>7.5           # utter nonsense
## Error in eval(expr, envir, enclos): object 'Sepal.Length' not found
-(Sepal.Width:Petal.Width) # gibberish
## Error in eval(expr, envir, enclos): object 'Sepal.Width' not found
```

Only from `help("subset")` we can learn that this tool generously decides that the second expression plays the role of a row selector. Moreover, the third one removes all the columns between the two given ones.

In our course, we pay attention to developing transferable skills. Assuming that R is not the only language we are going to learn during our long and happy lives, it is much more likely that in the next environment, we will be writing something more of the more basic form instead:

```
between <- function(x, from, to) (which(from == x):which(to == x))
iris[iris[["Sepal.Length"]]>7.5,
      -between(names(iris), "Sepal.Width", "Petal.Width")]
##   Sepal.Length Species
## 106          7.6 virginica
## 118          7.7 virginica
## 119          7.7 virginica
## 123          7.7 virginica
## 132          7.9 virginica
## 136          7.7 virginica
```

Let us stress again that this is a book on how to become a great chef who proudly uses sustainably-sourced produce, not how to order ultra-processed food from [DeliverNoodlesQuickly.com](#).

**Example 12.33** `transform` can be used to add, modify, and remove columns in a data frame with the possibility of referring to existing features as if they were ordinary variables:

```
head(transform(mtcars, log_hp=log(hp), am=2*am-1, hp=NULL))
##           mpg cyl  disp  drat   wt  qsec vs  am gear carb log_hp
## Mazda RX4      21.0   6  160  3.90 2.620 16.46  0   1    4    4 4.7005
## Mazda RX4 Wag  21.0   6  160  3.90 2.875 17.02  0   1    4    4 4.7005
## Datsun 710      22.8   4  108  3.85 2.320 18.61  1   1    4    1 4.5326
## Hornet 4 Drive  21.4   6  258  3.08 3.215 19.44  1  -1    3    1 4.7005
## Hornet Sportabout 18.7   8  360  3.15 3.440 17.02  0  -1    3    2 5.1648
## Valiant         18.1   6  225  2.76 3.460 20.22  1  -1    3    1 4.6540
```

Similarly, `attach` adds any named list to the search path (see Section 16.2.6) so that the columns can be accessed by name. Nevertheless, we cannot alter their contents. As an alternative, `with` and `within` may be referred to if writing `df[["..."]]` each time is so difficult for us (it should not be):

```
within(head(mtcars), {
  log_hp <- log(hp)
  fuel_economy <- 235/mpg
  am <- factor(am, levels=c(0, 1), labels=c("no", "yes"))
```

(continues on next page)

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```
rm(list=c("mpg", "hp", "vs", "qsec"))
})
```

|                      | cyl | disp | drat | wt    | am  | gear | carb | fuel_economy | log_hp |
|----------------------|-----|------|------|-------|-----|------|------|--------------|--------|
| ## Mazda RX4         | 6   | 160  | 3.90 | 2.620 | yes | 4    | 4    | 11.190       | 4.7005 |
| ## Mazda RX4 Wag     | 6   | 160  | 3.90 | 2.875 | yes | 4    | 4    | 11.190       | 4.7005 |
| ## Datsun 710        | 4   | 108  | 3.85 | 2.320 | yes | 4    | 1    | 10.307       | 4.5326 |
| ## Hornet 4 Drive    | 6   | 258  | 3.08 | 3.215 | no  | 3    | 1    | 10.981       | 4.7005 |
| ## Hornet Sportabout | 8   | 360  | 3.15 | 3.440 | no  | 3    | 2    | 12.567       | 5.1648 |
| ## Valiant           | 6   | 225  | 2.76 | 3.460 | no  | 3    | 1    | 12.983       | 4.6540 |

**Example 12.34** As mentioned in Section 10.3.4 (see Section 17.6 for more details), formulae are special objects that consist of two unevaluated expressions separated by a tilde (~).

Functions can support formulae and do what they please with them, but a popular approach is to allow them to express “something grouped by something else” or “one thing as a function of other things”.

```
do.call(rbind.data.frame, lapply(split(ToothGrowth, ~supp+dose), head, 1))
```

|           | len  | supp | dose |
|-----------|------|------|------|
| ## OJ.0.5 | 15.2 | OJ   | 0.5  |
| ## VC.0.5 | 4.2  | VC   | 0.5  |
| ## OJ.1   | 19.7 | OJ   | 1.0  |
| ## VC.1   | 16.5 | VC   | 1.0  |
| ## OJ.2   | 25.5 | OJ   | 2.0  |
| ## VC.2   | 23.6 | VC   | 2.0  |

```
aggregate(cbind(mpg, log_hp=log(hp))~am:cyl, mtcars, mean)
```

|      | am | cyl | mpg    | log_hp |
|------|----|-----|--------|--------|
| ## 1 | 0  | 4   | 22.900 | 4.4186 |
| ## 2 | 1  | 4   | 28.075 | 4.3709 |
| ## 3 | 0  | 6   | 19.125 | 4.7447 |
| ## 4 | 1  | 6   | 20.567 | 4.8552 |
| ## 5 | 0  | 8   | 15.050 | 5.2553 |
| ## 6 | 1  | 8   | 15.400 | 5.6950 |

```
head(model.frame(mpg+hp~log(hp)+I(1/qsec), mtcars))
```

|                      | mpg + hp | log(hp) | I(1/qsec)    |
|----------------------|----------|---------|--------------|
| ## Mazda RX4         | 131.0    | 4.7005  | 0.060753.... |
| ## Mazda RX4 Wag     | 131.0    | 4.7005  | 0.058754.... |
| ## Datsun 710        | 115.8    | 4.5326  | 0.053734.... |
| ## Hornet 4 Drive    | 131.4    | 4.7005  | 0.051440.... |
| ## Hornet Sportabout | 193.7    | 5.1648  | 0.058754.... |
| ## Valiant           | 123.1    | 4.6540  | 0.049455.... |

If these seem esoteric, it is because that is precisely the case. We need to consult the corresponding functions’ manuals to understand what they do. And, as we do not recommend their use by beginner programmers, we will not explain them here.

**Exercise 12.35** *In the last example, the peculiar printing of the last column is due to which method's being overloaded?*

In the third part of this book, we will return to these functions as they will serve as an amusing illustration of how to indite our own procedures that rely on metaprogramming techniques.

### 12.3.10 A note on the **dplyr** (tidyverse) and **data.table** packages (\*)

The popular third-party packages **data.table** and **dplyr** implement the most common data frame wrangling procedures. Some operations may be much faster for larger datasets.

They both introduce an entirely new API for the operations we already know well how to perform. Furthermore, they are heavily based on metaprogramming (lazy evaluation). A nice way to learn them is by solving some of the exercises listed below.

**dplyr** is part of a vast system of interdependent packages called **tidyverse**, which tend to do things their own way. They became quite invasive over the last few years.

Still, R programmers ought to remember that they are *able* to do without them. What is more, they also *need* to rely on other solutions when processing other prominent data structures is required, e.g., of fancy lists and matrices. Base R always comes first as the most fundamental layer.

---

**Important** Some functions we may find helpful (annoyingly to base R users) return objects of the class **tibble** (**tbl\_df**) (e.g., **haven::read.xpt** that reads **SAS** data files). However, these are, in fact, subclasses of **data.frame**. We can always use **as.data.frame** to get our favourite objects back.

---

Also, we cannot stress enough that it is **SQL** that we recommend learning as perhaps the most powerful interface to more considerable amounts of data. It will give us the skills that can be used later in other programming environments.

Base R (and its predecessor, S) has long ago proven to be a versatile tool for rapid prototyping, calling specialised procedures written in C or Java, and wrangling data that *fit into memory*. For larger problems, techniques for working with batches of data, sampling methods, or aggregating data stored elsewhere are often the way to go, especially when building machine learning models or visualisation<sup>13</sup> is required. Usually, the most recent data will be stored in normalised databases, and we will need to join a few tables to fetch something interesting from the perspective of the current analysis context.

---

<sup>13</sup> For example, drawing a scatter plot of one billion points makes little sense. It may result in unreadable images of large file sizes. They first need to be sampled or summarised somehow (e.g., binned); see Chapter 13.

## 12.4 Exercises

**Exercise 12.36** Answer the following questions:

- What attributes a data frame must be equipped with?
- If `row.names` is an integer vector, how to access rows labelled 1, 7, and 42?
- How to create a data frame that features a column that is a list of character vectors of different lengths?
- How to create a data frame that includes a matrix column?
- How to convert all numeric columns in a data frame to a numeric matrix?
- Assuming that `x` is an atomic vector, what is the difference between “`as.data.frame(x)`” vs “`as.data.frame(as.list(x))`” vs “`as.data.frame(list(a=x))`” vs “`data.frame(a=x)`”?

**Exercise 12.37** Assuming that `x` is a data frame, what is the meaning of/difference between the following:

- “`x[“u”]`” vs “`x[[“u”]]`” vs “`x[, “u”]`”?
- “`x[“u”][1]`” vs “`x[[“u”]][1]`” vs “`x[1, “u”]`” vs “`x[1, “u”, drop=FALSE]`”?
- “`x[which(x[[1]] > 0), ]`” vs “`x[x[[1]] > 0, ]`”?
- “`x[grep("^foo", names(x))]`”?

**Exercise 12.38** Assume we have a data frame with columns named like: `ID` (character), `checked` (logical, possibly with missing values), `category` (factor), `x0`, ... `x9` (ten separate numeric columns), `y0`, ... `y9` (ten separate numeric columns), `coords` (numeric matrix with two columns named `lat` and `long`), and `features` (list of character vectors of different lengths).

- How to extract the rows where `checked` is `TRUE`?
- How to extract a subset comprised only of `ID` and `x`-something columns?
- How to extract the rows for which `ID` is like three letters and then five digits (e.g., `XYZ12345`)?
- How to select all the numeric columns in one go?
- Assuming that the `IDs` are like three letters and then five digits, how to add two columns: `ID3` (the letters) and `ID5` (the five digits)?
- How to get rid of all the columns between `x3` and `y7`?
- How to check where both `lat` and `long` in `coords` are positive?
- How to add the row indicating the number of features?
- How to extract the rows where “spam” is amongst the features?
- How to convert it to a long data frame with two columns: `ID` and `feature` (individual strings)?

- How to change the name of the ID column to `id`?
- How to make the `y-foo` columns appear before the `x-bar` ones?
- How to order the rows with respect to `checked` (`FALSE` first, then `TRUE`) and IDs (decreasingly)?
- How to remove rows with duplicate IDs?
- How to determine how many entries correspond to each category?
- How to compute the average `lat` and `long` in each category?
- How to compute the average `lat` and `long` for each category and `checked` combined?

**Exercise 12.39** Consider the `flights`<sup>14</sup> dataset. Give some ways to select all rows between March and October (regardless of the year).

**Exercise 12.40** In this task, you will be working with a version of a dataset on 70k+ Melbourne trees (`urban_forest`<sup>15</sup>).

1. Load the downloaded dataset by calling the `read.csv` function.
2. Fetch the IDs (`CoM.ID`) and trunk diameters (`Diameter.Breast.Height`) of five horse chestnuts with the smallest diameters at breast height. The output data frame must be sorted with respect to `Diameter.Breast.Height`, decreasingly.
3. Create a new data frame that gives the number of trees planted each year.
4. Compute the average age (in years, based on `Year.Planted`; using `aggregate`) of the trees of genera (each genus separately): *Eucalyptus*, *Platanus*, *Ficus*, *Acer*, and *Quercus*. Depict the sorted data with `barplot`.

**Exercise 12.41** (\*) Consider the historic data dumps of <https://travel.stackexchange.com/> available [here](#)<sup>16</sup>. Export the CSV files located therein to an SQLite database. Then, write some R code that corresponds to the following SQL queries (use `dbGetQuery` to verify your results):

```

--- 1)
SELECT
  Users.DisplayName,
  Users.Age,
  Users.Location,
  SUM(Posts.FavoriteCount) AS FavoriteTotal,
  Posts.Title AS MostFavoriteQuestion,
  MAX(Posts.FavoriteCount) AS MostFavoriteQuestionLikes
FROM Posts
JOIN Users ON Users.Id=Posts.OwnerUserId
WHERE Posts.PostTypeId=1
GROUP BY OwnerUserId

```

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<sup>14</sup> <https://github.com/gagolews/teaching-data/blob/master/other/flights.csv>

<sup>15</sup> [https://github.com/gagolews/teaching-data/raw/master/marek/urban\\_forest.csv.gz](https://github.com/gagolews/teaching-data/raw/master/marek/urban_forest.csv.gz)

<sup>16</sup> [https://github.com/gagolews/teaching-data/tree/master/travel\\_stackexchange\\_com\\_2017](https://github.com/gagolews/teaching-data/tree/master/travel_stackexchange_com_2017)

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```

ORDER BY FavoriteTotal DESC
LIMIT 10
--- 2)
SELECT
    Posts.ID,
    Posts.Title,
    Posts2.PositiveAnswerCount
FROM Posts
JOIN (
    SELECT
        Posts.ParentID,
        COUNT(*) AS PositiveAnswerCount
    FROM Posts
    WHERE Posts.PostTypeID=2 AND Posts.Score>0
    GROUP BY Posts.ParentID
) AS Posts2
ON Posts.ID=Posts2.ParentID
ORDER BY Posts2.PositiveAnswerCount DESC
LIMIT 10
--- 3)
SELECT
    Posts.Title,
    UpVotesPerYear.Year,
    MAX(UpVotesPerYear.Count) AS Count
FROM (
    SELECT
        PostId,
        COUNT(*) AS Count,
        STRFTIME('%Y', Votes.CreationDate) AS Year
    FROM Votes
    WHERE VoteTypeId=2
    GROUP BY PostId, Year
) AS UpVotesPerYear
JOIN Posts ON Posts.Id=UpVotesPerYear.PostId
WHERE Posts.PostTypeId=1
GROUP BY Year
--- 4)
SELECT
    Questions.Id,
    Questions.Title,
    BestAnswers.MaxScore,
    Posts.Score AS AcceptedScore,
    BestAnswers.MaxScore-Posts.Score AS Difference
FROM (

```

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```

        SELECT Id, ParentId, MAX(Score) AS MaxScore
        FROM Posts
        WHERE PostTypeId==2
        GROUP BY ParentId
    ) AS BestAnswers
JOIN (
    SELECT * FROM Posts
    WHERE PostTypeId==1
) AS Questions
ON Questions.Id=BestAnswers.ParentId
JOIN Posts ON Questions.AcceptedAnswerId=Posts.Id
WHERE Difference>50
ORDER BY Difference DESC
--- 5)
SELECT
    Posts.Title,
    CmtTotScr.CommentsTotalScore
FROM (
    SELECT
        PostID,
        UserID,
        SUM(Score) AS CommentsTotalScore
    FROM Comments
    GROUP BY PostID, UserID
) AS CmtTotScr
JOIN Posts ON Posts.ID=CmtTotScr.PostID
    AND Posts.OwnerUserId=CmtTotScr.UserID
WHERE Posts.PostTypeId=1
ORDER BY CmtTotScr.CommentsTotalScore DESC
LIMIT 10
--- 6)
SELECT DISTINCT
    Users.Id,
    Users.DisplayName,
    Users.Reputation,
    Users.Age,
    Users.Location
FROM (
    SELECT
        Name, UserID
    FROM Badges
    WHERE Name IN (
        SELECT
            Name

```

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```

        FROM Badges
        WHERE Class=1
        GROUP BY Name
        HAVING COUNT(*) BETWEEN 2 AND 10
    )
    AND Class=1
) AS ValuableBadges
JOIN Users ON ValuableBadges.UserId=Users.Id
--- 7)
SELECT
    Posts.Title,
    VotesByAge2.OldVotes
FROM Posts
JOIN (
    SELECT
        PostId,
        MAX(CASE WHEN VoteDate = 'new' THEN Total ELSE 0 END) NewVotes,
        MAX(CASE WHEN VoteDate = 'old' THEN Total ELSE 0 END) OldVotes,
        SUM(Total) AS Votes
    FROM (
        SELECT
            PostId,
            CASE STRFTIME('%Y', CreationDate)
                WHEN '2017' THEN 'new'
                WHEN '2016' THEN 'new'
                ELSE 'old'
            END VoteDate,
            COUNT(*) AS Total
        FROM Votes
        WHERE VoteTypeId=2
        GROUP BY PostId, VoteDate
    ) AS VotesByAge
    GROUP BY VotesByAge.PostId
    HAVING NewVotes=0
) AS VotesByAge2 ON VotesByAge2.PostId=Posts.ID
WHERE Posts.PostTypeId=1
ORDER BY VotesByAge2.OldVotes DESC
LIMIT 10

```

**Exercise 12.42** (\*) Generate a CSV file featuring some random data arranged in a few columns of a size at least two times larger than your available RAM. Then, export the CSV file to an SQLite database. Use file connections (Section 8.3.5) and the `nrow` argument to **read.table** to be able to process it on a chunk-by-chunk basis.

Determine whether setting `colClasses` in **read.table** speeds up the reading of large CSV files significantly or not.

**Exercise 12.43** (\*) *Export the whole XML data dump of StackOverflow<sup>17</sup> published at <https://archive.org/details/stackexchange> (see also <https://data.stackexchange.com/>) to an SQLite database.*

---

---

<sup>17</sup> <https://stackoverflow.com>



The R Project homepage advertises our free software as an *environment for statistical computing and graphics*. Hence, had we not dealt with the latter use case, our course would have been incomplete.

R is nowadays equipped with the two following independent (incompatible, yet coexisting) systems for graphics generation; see [Figure 13.1](#).

1. The (historically) newer one, **grid** (e.g., [47]), is very flexible but might seem quite complicated. Some readers might have come across the **lattice** [52] and **ggplot2** [57, 60] packages before. They are built on top of **grid**.
2. On the other hand, its traditional (S-style) counterpart, *base graphics* (e.g., [7]), is much easier to master. It still gives their users complete control over drawing processes. It is simple, fast, and minimalist, which makes it very attractive from the perspective of this course's philosophy.

This is why we only cover the second system here.

---

**Note** All figures in this book were generated using **graphics** and its dependants. They are *sufficiently* aesthetic, aren't they? Form precedes essence.

---

---

### 13.1 Graphics primitives

In **graphics**, we do not choose from a superfluity of virtual objects to be placed on an abstract canvas, letting some algorithm decide how and when to delineate them. We *just draw*. To do so, we call functions that plot the following *graphics primitives* (see, e.g., [36, 44]):

- plotting symbols (e.g., pixels, circles, stars) of different shapes and colours,
- line segments of different styles (e.g., solid, dashed, dotted),
- polygons (optionally filled),
- text (using available fonts),
- raster images (bitmaps; if the output device supports it).

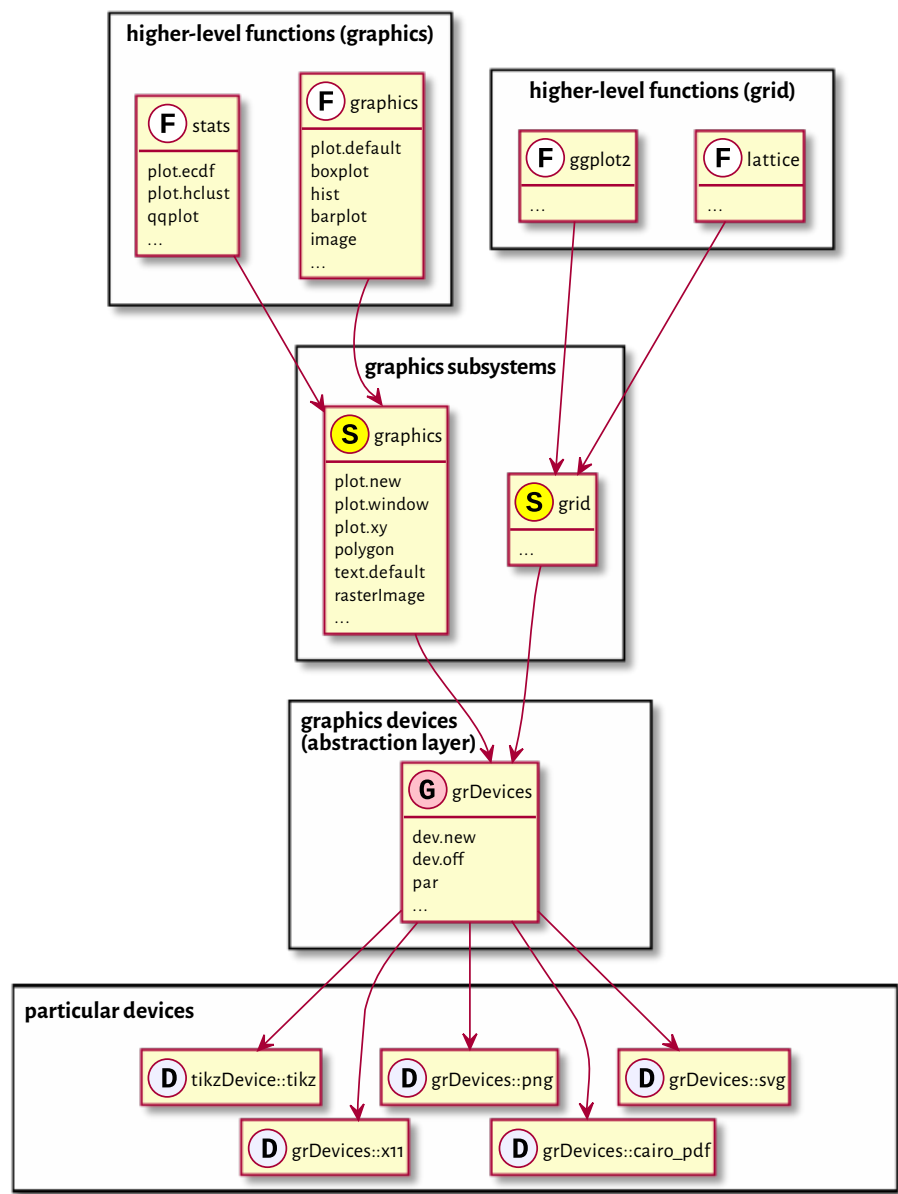


Figure 13.1: Relation between the graphics subsystems

That's it. It will turn out that *all* other shapes (smooth curves, circles) might be easily approximated using the above.

**Example 13.1** Figure 13.2 depicts some graphics primitives, which we plotted using the following program. We will detail the meaning of all the functions in the next sections.

```
par(mar=rep(0.5, 4)) # small plot margins (bottom, left, top, right)
plot.new() # start a new plot
plot.window(c(0, 6), c(0, 2), asp=1) # x range: 0-6, y: 0-2; proportional
x <- c(0, 0, NA, 1, 2, 3, 4, 4, 5, 6)
y <- c(0, 2, NA, 2, 1, 2, 2, 1, 0.25, 0)
points(x[-(1:6)], y[-(1:6)]) # symbols
lines(x, y) # line segments
text(c(0, 6), c(0, 2), c("(0, 0)", "(6, 2)"), col="red") # two text labels
rasterImage(
  matrix(c(1, 0, # 2x3 pixel "image"; 0=black, 1=red
           0, 1,
           0, 0), byrow=TRUE, ncol=2),
  5, 0.5, 6, 2, # position: xleft, ybottom, xright, ytop
  interpolate=FALSE
)
polygon(
  c(4, 5, 5.5, 4), # x coordinates of the vertices
  c(0, 0, 1, 0.75), # y coordinates
  lty="dotted", # border style
  col="#ffff0044" # fill colour: semi-transparent yellow
)
```

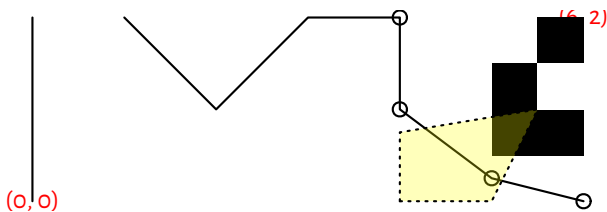


Figure 13.2: Graphics primitives: plotting symbols, line segments, polygons, text labels, and bitmaps; Objects are added one after another, with newer ones drawn over the already existing shapes

---

**Important** In **graphics**, most of the function calls have immediate effects. Objects are drawn on the active plot one by one, and their state cannot be modified later.

---

Of course, in practice, we do not always have to be so low-level. There are many built-in functions that provide the most popular chart types: histograms, bar plots, dendro-

grams, etc. They are expected to suit our basic needs. We will review them in [Section 13.3](#).

The more basic routines we discuss next will still be of service for fine-tuning our figures and adding further details. But, if the prefabricated components are not what we are after, we will be able to create any drawing from scratch.

### 13.1.1 Symbols (points)

The **points** function can draw a series of plotting symbols (by default, circles) on the two-dimensional plot region relative to the user coordinate system.

We specify the points' coordinates using the `x` and `y` arguments (two vectors of equal lengths; no recycling). Alternatively, we may give a matrix or a data frame with two columns: its first column (regardless of how and if it is named) defines the abscissae, and the second column determines the ordinates.

This function allows each point to be plotted differently if this is what we desire. Thus, it is ideal for drawing scatter plots, possibly for grouped data (see [Figure 13.17](#) below). It is vectorised with respect to, amongst others, the `col` (colour; see [Section 13.2.1](#)), `cex` (scale, defaults to 1), and `pch` (plotting character or symbol, defaults to 1, i.e., a circle) arguments.

**Example 13.2** *Figure 13.3 gives an overview of the plotting symbols available. The most often used ones are:*

- `NA_integer_` – no symbol,
- `0, ..., 14` and `15, ..., 18` – unfilled and filled symbols, respectively;
- `19, ..., 25` – filled symbols with a border of width `lwd`; for codes `21–25`, the fill colour is controlled separately by the `bg` parameter,
- `"."` – a tiny point (a “pixel”),
- `"a", "1",` etc. – a single character (not all Unicode characters are available); strings longer than one will be truncated.

```
par(mar=rep(0.5, 4)); plot.new(); plot.window(c(0.9, 9.1), c(0.9, 4.1))
points(
  cbind(1:9, 1), # or x=1:9, y=rep(1, 9)
  col="red",
  pch=c("A", "B", "a", "b", "Spanish Inquisition", "*", "!", ".", "9")
)
xy <- expand.grid(1:9, 4:2)
text(xy, labels=0:(NROW(xy)-1), pos=1, cex=0.89, offset=0.75, col="darkgray")
points(xy, pch=0:(NROW(xy)-1), bg="yellow")
## Warning in plot.xy(xy.coords(x, y), type = type, ...): unimplemented pch
##      value '26'
```



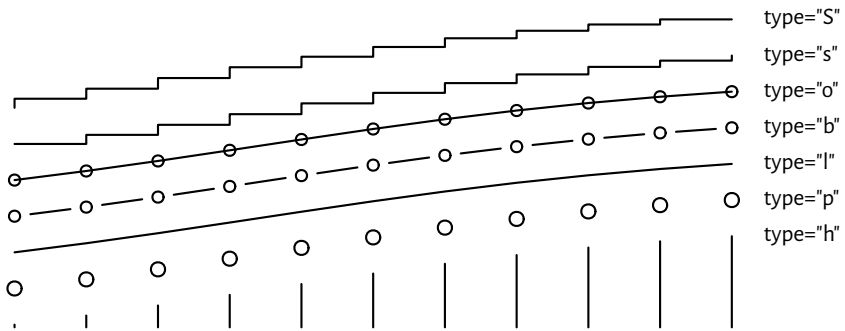
|    |    |    |    |    |    |    |    |    |
|----|----|----|----|----|----|----|----|----|
| □  | ○  | △  | +  | ×  | ◇  | ▽  | ⊠  | *  |
| 0  | 1  | 2  | 3  | 4  | 5  | 6  | 7  | 8  |
| ◊  | ⊕  | ⊗  | ⊞  | ⊗  | ◊  | ■  | ●  | ▲  |
| 9  | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 |
| ◆  | ●  | ●  | ●  | ■  | ◆  | ▲  | ▼  |    |
| 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 |
| A  | B  | a  | b  | S  | *  | !  | .  | 9  |

Figure 13.3: Plotting characters and symbols (pch)

### 13.1.2 Line segments

**lines** can be used to draw connected line segments whose mid- and endpoints are given in a similar manner as in the **points** function. A series of segments can be interrupted by defining an endpoint whose coordinate is a missing value; compare Figure 13.2.

Actually, **points** and **lines** are wrappers around the same function, **plot.xy**, which we usually do not call directly. Their type arguments determine the object to draw; the only difference is that the former uses `type="p"` whilst the latter relies on `type="l"` by default. Changing these to `type="b"` (both) or `type="o"` (overplot) will give their combination. Moreover, `type="s"` and `type="S"` creates step functions (with post- and pre-increments, respectively), and `type="h"` draws bar plot-like vertical lines. See Figure 13.4 for an illustration (implement something similar yourself as an exercise).

Figure 13.4: Different type argument settings in **lines** or **points**

The `col` argument controls the line colour (see Section 13.2.1), and `lwd` determines the line width (1 by default). Six named line types (`lty`) are available, which can also be specified via their respective numeric identifiers, `lty=1, ..., lty=6`; see Figure 13.5 (implementing a similar plot is left as an exercise). Additionally, custom dashes can be defined using strings of up to 8 (hexadecimal) digits. Consecutive digits give the lengths of the dashes and blanks. For instance, `lty="1343"` yields a dash of length 1,

followed by a space of length 3, then a segment of length 4, followed by a blank of length 3. The whole sequence will be recycled for as long as necessary.

|                        |       |                         |       |
|------------------------|-------|-------------------------|-------|
| "solid", or 1          | ————— | "dashed", "44", or 2    | ----- |
| "dotted", "13", or 3   | ..... | "dotdash", "1343", or 4 | ----- |
| "longdash", "73", or 5 | ----- | "twodash", "2262", or 6 | ----- |
| "5515"                 | ----- | "9515"                  | ----- |
| "19"                   | ----- | "4484C4"                | ----- |

Figure 13.5: Line types (lty)

**Example 13.3** `lines` can be used for plotting empirical cumulative distribution functions (we will suggest it as an exercise later), regression models (e.g., lines, splines of different degrees), time series, and any other mathematical functions, even when they are smooth and curvy. The naked eye cannot tell the difference between a densely sampled piecewise linear approximation of an object and its original version.

The code below illustrates this (sad for the high-hearted idealists) truth using the sine function; see Figure 13.6.

```
ns <- c(seq(3, 25, by=2), 50, 100)
par(mar=rep(0.5, 4)); plot.new(); plot.window(c(0, length(ns)*pi), c(-1, 1))
for (i in seq_along(ns)) {
  x <- seq((i-1)*pi, i*pi, length.out=ns[i])
  lines(x, sin(x))
  text((i-0.5)*pi, 0, ns[i], cex=0.89)
}
```



Figure 13.6: Sampling more densely gives the illusion of smoothness

**Exercise 13.4** Implement your version of the `segments` function using a call to `lines`.

**Exercise 13.5** (\*) Implement a simplified version of the `arrows` function, where the length of edges of the arrowhead is given in user coordinates (and not inches; you will be equipped with skills to achieve this later; see Section 13.2.5). Use the `ljoin` and `lend` arguments (see `help("par")` for admissible values) to change the line end and join styles (from the default rounded caps).

### 13.1.3 Polygons

**polygon** draws a polygon with a border of specified colour and line type (*border*, *lty*, *lwd*). If the *col* argument is not missing, the polygon is filled (or hatched; cf. the *density* and *angle* arguments).

**Example 13.6** To demo the above function, let us draw a few regular (equilateral and equiangular) polygons; see Figure 13.7. By increasing the number of sides, we can obtain an approximation to a circle.

```
regular_poly <- function(x0, y0, r, n=101, ...)
{
  theta <- seq(0, 2*pi, length.out=n+1)[-1]
  polygon(x0+r*cos(theta), y0+r*sin(theta), ...)
}

par(mar=rep(0.5, 4)); plot.new(); plot.window(c(0, 9.5), c(-1, 1), asp=1)
regular_poly(1, 0, 1, n=3)
regular_poly(3.5, 0, 1, n=7, density=15, angle=45, col="tan", border="red")
regular_poly(6, 0, 1, n=10, density=8, angle=-60, lty=3, lwd=2)
regular_poly(8.5, 0, 1, n=100, border="brown", col="lightyellow")
```

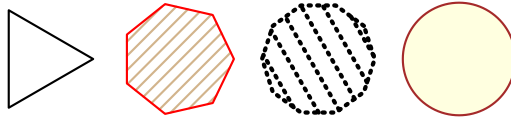


Figure 13.7: Regular polygons drawn using **polygon**

Note the *asp=1* argument to the **plot.window** function (which we detail below) that guarantees the same scaling of the *x*- and *y*-axes. This way, the circle looks like one and not an oval.

Notice that the last vertex adjoins the first one. Also, if we are absent-minded (or particularly creative), we can produce self-intersecting or otherwise degenerate shapes.

**Exercise 13.7** Implement your version of the **rect** function using a call to **polygon**.

### 13.1.4 Text

A call to **text**, draws arbitrary strings (newlines and tabs are allowed) centred at the specified points. Moreover, by setting the *pos* argument, the labels may be placed below, to the left of, etc., the pivots. Some further position adjustments are also possible (*adj*, *offset*); see Figure 13.8.

*col* specifies the colour, *cex* affects the size, and *srt* changes the rotation of the text.

On many default graphics devices, we have little control over the font face used: font family can be chosen using *family* ("sans", "serif", "mono"), and font can be used to

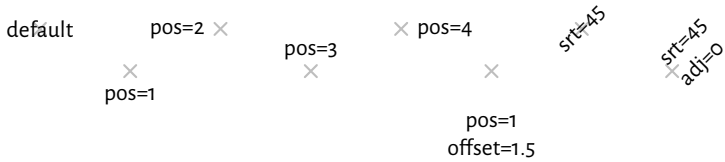


Figure 13.8: The positioning of text with **text** (the plotting symbols were added for reference)

select the normal variant (1), bold (2), italic (3), or bold italic (4). See, however, [Section 13.2.7](#) for some workarounds.

---

**Note** (\*) There is some limited support for basic mathematical symbols and formulae. It relies on some quirky syntax that we enter using unevaluated R expressions ([Chapter 15](#)). Still, it should be enough to meet our most basic needs. For instance, passing “**quote**(beta[i]^j)” as the **labels** argument to **text**, will output “ $\beta_i^j$ ”. See **help**(“plotmath”) for more details.

For more sophisticated mathematical typesetting, see the **tikzDevice** graphics device mentioned in [Section 13.2.7](#). It outputs plot specifications that can be rendered by the LaTeX typesetting system.

---

### 13.1.5 Raster images (bitmaps) (\*)

Most output devices support drawing raster images encoded in the form of bitmaps, i.e., matrices whose elements represent pixels (see [Figure 13.2](#) for an example).

Raster images are helpful for drawing heat maps or backgrounds of contour plots; see [Section 13.3.4](#).

**Example 13.8** *Optionally, bilinear interpolation can be applied if the drawing area is larger than the bitmap size, and we would like to smoothen the colour transitions out. [Figure 13.9](#) presents a very stretched  $4 \times 3$  pixel image, with and without interpolation.*

```
par(mar=rep(0.5, 4)); plot.new(); plot.window(c(0, 9), c(0, 1))
I <- matrix(nrow=4, byrow=TRUE,
  c(  "red", "yellow",  "white",
    "yellow", "yellow", "orange",
    "yellow", "orange", "orange",
    "white", "orange",  "red" )
)
rasterImage(I, 0, 0, 4, 1) # interpolate=TRUE
rasterImage(I, 5, 0, 9, 1, interpolate=FALSE)
```



Figure 13.9: Example bitmaps drawn with **rasterImage**: with (left) and without (right) colour interpolation

## 13.2 Graphics settings

**par** can be used to query and modify (as long as they are not read-only) many graphics settings.

For instance, we have several parameters related to the current page or device settings, e.g., the plot's margins (see [Section 13.2.2](#)) or user coordinates (see [Section 13.2.3](#)).

Moreover, values of some of the parameters set via **par** may be taken by a few functions<sup>1</sup> as settings to use by default. This is the case of, e.g., **col**, **pch**, **lty** in the **points** and **lines** function.

**Exercise 13.9** Study the following (pseudo)code.

```
lines(x, y) # use the default `lty`, i.e., par("lty") == "solid"
old_settings <- par(lty="dashed") # change setting, save old for reference
lines(x, y) # use the default `lty`, i.e., par("lty") == "dashed"
lines(x, y, lty=3) # use the given `lty`
lines(x, y) # lty="dashed"
par(old_settings) # restore previous settings
lines(x, y) # lty="solid"
```

The reference list of available parameters is given in **help("par")**. Below we discuss the most noteworthy ones.

### 13.2.1 Colours

Many functions allow specifying colours of the plotted objects or their parts; compare, e.g., **col** and **border** arguments to **polygon**, or **col** and **bg** to **points**.

There are a few ways to specify colours (see the *Colour Specification* section in **help("par")** for more details).

- A "colour name" string, being one of the 657 predefined tags known to the **colours** function:

<sup>1</sup> Unfortunately, it is not as straightforward as that. For instance, **polygon** is unaffected by the **col** setting, **axis** uses **col.axis** instead, etc. We should always consult the documentation.

```
sample(colours(), 8) # this is just a sample
## [1] "grey23"          "darksalmon"      "tan3"            "violetred4"
## [5] "lightblue1"       "darkorchid3"     "darkseagreen1"   "slategray3"
```

- An "#rrggbb" string, specifying a position in the RGB<sup>2</sup> colour space; three series of hexadecimal numbers of two digits each, i.e., between 00<sub>hex</sub> = 0 (off) and FF<sub>hex</sub> = 255 (full on), giving the intensity of the red, green, and blue channels<sup>3</sup>.

In practice, the `col2rgb` and `rgb` functions can be used to convert between the decimal and hexadecimal representations:

```
C <- c("black", "red", "green", "blue", "cyan", "magenta",
      "yellow", "grey", "lightgrey", "pink") # example colours
(Cmat <- structure(col2rgb(C), dimnames=list(c("R", "G", "B"), C)))
##   black red green blue cyan magenta yellow grey lightgrey pink
## R   0 255   0   0   0   255 255 190   211 255
## G   0   0 255   0 255   0   255 190   211 192
## B   0   0   0 255 255 255   0 190   211 203
structure(rgb(Cmat[1, ], Cmat[2, ], Cmat[3, ], maxColorValue=255),
  names=C)
##   black      red      green      blue      cyan magenta yellow
## "#000000" "#FF0000" "#00FF00" "#0000FF" "#00FFFF" "#FF00FF" "#FFFF00"
##   grey lightgrey pink
## "#BEBE" "#D3D3D3" "#FFC0CB"
```

- An "#rrggbbaa" string, like above, but with the added alpha channel (two additional hexadecimal digits): from 00<sub>hex</sub> = 0 denoting fully transparent, to FF<sub>hex</sub> = 255 indicating fully visible ("lit") colour; see Figure 13.2 for an example.

Semi-transparency (translucency) can significantly enhance the expressivity of our data visualisations; see Figure 13.18 and Figure 13.19.

- An integer index, selecting an item from the *current palette* (with recycling), which we can get or set by a call to `palette`. Moreover, 0 identifies the background colour, `par("bg")`.

Integer colour specifiers are particularly valuable when plotting data in groups, as defined by factors. The underlying integer level codes can be mapped to consecutive colours from any palette; see Figure 13.17 below for an example.

**Example 13.10** We recommend memorising the colours in the default palette:

<sup>2</sup> [https://en.wikipedia.org/wiki/RGB\\_color\\_model](https://en.wikipedia.org/wiki/RGB_color_model)

<sup>3</sup> From school, we probably know the *subtractive* CMY (cyan, magenta, yellow) model, where we obtain, e.g., a green colour by using blue-ish and yellow crayons (subtracting certain wavelengths from white light). The RGB model, on the other hand, corresponds to the three photoreceptor/cone cells in the retinas of the human eyes. Nonetheless, it is *additive* and, therefore, less intuitive: total darkness emerges when we emit no light, yellow emerges when mixing red and green beams, etc.

```
palette() # default palette
## [1] "#000000F0" "#DF536BF0" "#61D04FF0" "#2297E6F0" "#28E2E5F0"
## [6] "#CD0BBCF0" "#F5C710F0" "#999999F0"
```

These are<sup>4</sup>, in order: black, red, green, blue, cyan, magenta, yellow, and grey; see<sup>5</sup> Figure 13.10 for an illustration.

```
k <- length(palette())
par(mar=rep(0.5, 4)); plot.new(); plot.window(c(0, k+1), c(0, 1))
points(1:k, rep(0.5, k), col=1:k, pch=16, cex=3)
text(1:k, 0.5, palette(), pos=rep(c(1, 3), length.out=k), col=1:k, offset=1)
text(1:k, 0.5, 1:k, pos=rep(c(3, 1), length.out=k), col=1:k, offset=1)
```



Figure 13.10: The default colour **palette**

Choosing usable colours requires some talents that most programmers lack. Therefore, we will find ourselves relying on the built-in colour sets. **palette.pals** and **hcl.pals** return the names of the available *discrete* (qualitative) palettes. Then, **palette.colors** and **hcl.colors** (note the American spelling) can generate a given number of colours from a particular named set.

*Continuous* (quantitative) palettes are also available, see **rainbow**, **heat.colors**, **terrain.colors**, **topo.colors**, **cm.colors**, and **gray.colors**. They transition smoothly between some predefined pivot colours, e.g., from blue through green to brown (like in a topographic map with elevation colouring). They may be of use, e.g., when drawing contour plots; compare Figure 13.27.

**Exercise 13.11** Create a demo of the aforementioned built-in palettes in a similar (or nicer) style to that in Figure 13.11.

### 13.2.2 Plot margins and clipping regions

A *device* (page) region represents a single plot window, one raster image file, or a page in a PDF document (see Section 13.2.7 for more information on graphics devices). As we will learn from Section 13.2.6, it is capable of holding many *figures*.

<sup>4</sup> Actually, red-ish, green-ish, etc. The choice is more aesthetic than when pure red, green, etc. was used (before R 4.0.0). It is also expected to be more friendly to people who have some colour vision deficiencies (roughly every 1 in 12 men (8%) and 1 in 200 women (0.5%), especially in the red-green or blue-yellow spectrum; see [49] for more details).

<sup>5</sup> The readers of the printed version of this book should know that its online version displays this figure (and all others) in full colour. See you there.

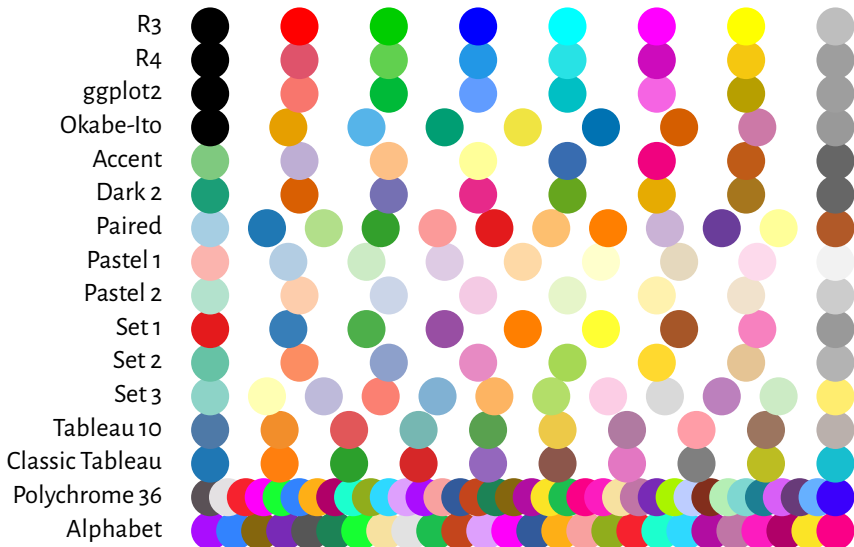


Figure 13.11: Qualitative colour palettes in `palette.pals`; `R4` is the default one, as seen in Figure 13.10

Usually, however, we draw *one figure per page*. In such a case, the device region is divided into the following parts:

- 1) *outer margins*, which can be set using, e.g., the `oma` graphics parameter (in text lines, based on the height of the default font); by default, they equal to 0;
- 2) *figure region*:
  - a) *inner (plot) margins*, by default `mar=c(5.1, 4.1, 4.1, 2.1)` text lines (bottom, left, top, right, respectively); this is where we usually emplace the figure title, axes labels, etc.
  - b) *plot region*, where we draw graphics primitives positioned relative to the user coordinates.

---

**Note** Typically, all drawings are *clipped* to the plot region, but this can be changed with the `xpd` parameter; see also the `clip` function that allows clipping to an arbitrary rectangle.

---

**Example 13.12** Figure 13.12 shows the default page layout. In the code chunk below, note the use of `mtext` to print a text line in the inner margins, `box` to draw a rectangle around the plot or figure region, `axis` to add the two axes (labels and tick marks), and `title` to add some descriptive labels.



```

plot.new(); plot.window(c(-2, 2), c(-1, 1)) # whatever
for (i in 1:4) { # Some text lines on the inner margins
  for (j in seq_len(par("mar")[i]))
    mtext(sprintf("Text line %d", j), side=i, line=j-1, col="lightgray")
}

title(main="Main", sub="sub", xlab="xlab", ylab="ylab")
box("figure", lty="dashed") # a box around the figure region
box("plot") # a box around the plot region
axis(1) # horizontal axis (bottom)
axis(2) # vertical axis (left)

rect(-10, -10, 10, 10, col="lightgray") # rectangle (clipped to plot region)
text(0, 0, "Plot region")
lines(c(-3, 0, 3), c(-2, 2, -2)) # standard clipping (plot region)
lines(c(-3, 0, 3), c(-2, 1.25, -2), xpd=TRUE, lty=3) # clip to figure region

```

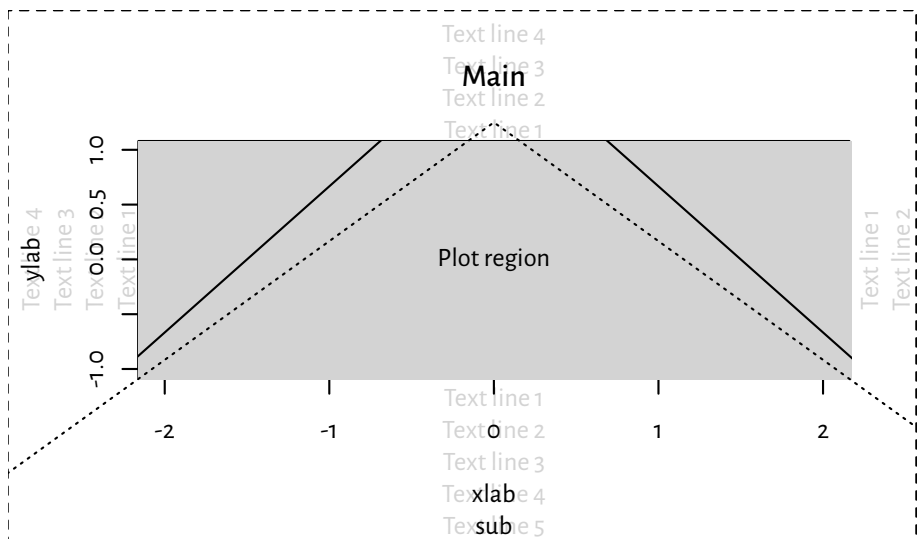


Figure 13.12: Figure layout with default inner (`mar=c(5.1, 4.1, 4.1, 2.1)`) text lines and outer (`oma=c(0, 0, 0, 0)`) margins; We see that a lot of space is wasted and hence some tweaking might be necessary to suit our needs better; Note the clipping of the solid line to the plot region

### 13.2.3 User coordinates

`plot.window` can be used to set the user coordinates. It accepts the following parameters:

- `xlim, ylim` – vectors of length two giving the minimal and maximal ranges on the

respective axes; by default, they are extended by 4% in each direction (for aesthetic reasons; see, e.g., Figure 13.12), but see the `xaxs` and `yaxs` graphics parameters;

- `asp` – aspect ratio ( $y/x$ ); defaults to `NA`, i.e., no adjustment; use `asp=1` for circles to look like ones, and not ovals;
- `log` – switches logarithmic scaling on particular axes: "" (none; default), "x", "y", or "xy".

**Example 13.13** *The graphics parameter `usr` can be used to read (and set) the extremes of the user coordinates in the form  $(x_1, x_2, y_1, y_2)$ .*

```
plot.new()
plot.window(c(-1, 1), c(1, 1000), log="y", yaxs="i")
par("usr")
## [1] -1.08  1.08  0.00  3.00
```

Indeed, the  $x$ -axis range was extended by 4% in each direction. We have turned this behaviour off for the  $y$ -axis, which uses the base-10 logarithmic scale. In this case, its actual range is  $10^{\text{par("usr")[3:4]}}$  because  $\log_{10} 1 = 0$  and  $\log_{10} 1000 = 3$ .

**Exercise 13.14** *Implement your version of the `abline` function.*

#### 13.2.4 Axes

Even though axes (labels and tick marks) can be drawn manually using the aforementioned graphics primitives, it is usually too tedious a work.

This is why we tend to rely on the `axis` function, which draws the object on one of the plot sides (as usual, 1=bottom, ..., 4=right).

Once `plot.window` is called, `axTicks` can be called to guesstimate some tasteful (round) locations for the tick marks based on the current plot size. By default, they are based on the `xaxp` and `yaxp` graphics parameters, which give the axis ranges and the number of intervals between the tick marks.

```
plot.new(); plot.window(c(-0.9, 1.05), c(1, 11))
par("usr") # (x1, x2, y1, y2)
## [1] -0.978  1.128  0.600 11.400
par("yaxp") # (y1, y2, n)
## [1]  2 10  4
axTicks(2) # left y-axis
## [1]  2  4  6  8 10
par("xaxp") # (x1, x2, n)
## [1] -0.5  1.0  3.0
axTicks(1) # bottom x-axis
## [1] -0.5  0.0  0.5  1.0
par(xaxp=c(-0.9, 1.0, 5)) # change
```

(continues on next page)

(continued from previous page)

```
axTicks(1)
## [1] -0.90 -0.52 -0.14  0.24  0.62  1.00
```

**axis** relies on the same algorithm as **axTicks**. Alternatively, we can provide our own tick locations and labels.

**Example 13.15** Most of the plots in this book use the following graphics settings (except *las=1* to **axis(2)**); see Figure 13.13. Check out **help("par")**, **help("axis")**, etc. and tune them up to suit your needs.

```
par(mar=c(2.2, 2.2, 1.2, 0.6))
par(tcl=0.25) # the length of the tick marks (fraction of text line height)
par(mgp=c(1.1, 0.2, 0)) # axis title, axis labels, and axis line location
par(cex.main=1, font.main=2) # bold, normal size - main in title
par(cex.axis=0.8889)
par(cex.lab=1, font.lab=3) # bold italic, normal size
plot.new(); plot.window(c(0, 1), c(0, 1))
# a "grid":
rect(par("usr")[1], par("usr")[3], par("usr")[2], par("usr")[4],
     col="#00000010")
abline(v=axTicks(2), col="white", lwd=1.5, lty=1)
abline(h=seq(0, 1, length.out=4), col="white", lwd=1.5, lty=1)
# set up axes:
axis(2, at=seq(0, 1, length.out=4), c("0", "1/3", "2/3", "1"), las=1)
axis(1)
title(xlab="xlab", ylab="ylab")
box()
```

### 13.2.5 Plot dimensions (\*)

Certain sizes can be read or specified in inches (1 inch (1") is exactly 25.4 mm):

- **pin** – plot dimensions (width, height),
- **fin** – figure region dimensions,
- **din** – page (device) dimensions,
- **mai** – plot (inner) margin size,
- **omi** – outer margins,
- **cin** – the size of the “default” character (width, height).

If the figure is scaled, the *virtual* inch (the one reported by R) will not match the physical one (e.g., the actual size in the printed version of this book or on the computer screen).

---

**Important** Most objects’ positions are specified in *virtual* user coordinates, as given by

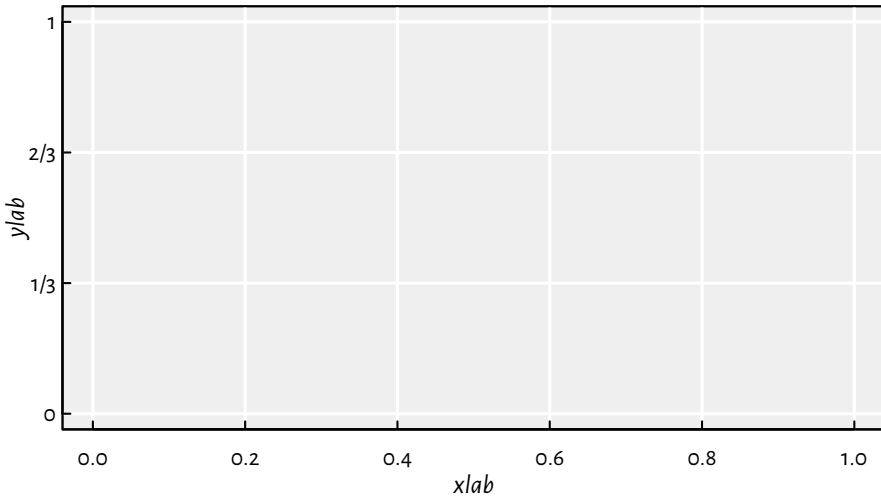


Figure 13.13: Custom axes and other settings

`usr`. They are automatically mapped to the *physical* device region, taking into account the page size, outer and inner margins, etc.

Knowing the above, some basic scaling can be used to convert between the user and physical sizes (in inches). It is based on the ratios  $(usr[2]-usr[1])/pin[1]$  and  $(usr[4]-usr[3])/pin[2]$ ; compare the `xinch` and `yinch` functions.

**Example 13.16** (\*) *Figure 13.14 shows how we can pinpoint the edges of the figure and device region in user coordinates.*

**Exercise 13.17** (\*) *We cannot use `mtext` to print text on the right inner margin rotated by 180 degrees compared to what we see in Figure 13.12. Write your version of this function that will allow you to do so. Hint: use `text`, the `c` in graphics parameter, and what you can read from Figure 13.14.*

### 13.2.6 Many figures on one page (subplots)

It is possible to create many figures on one page. In such a case, each of them has its own inner margins and a plot region.

A call to `par(mfrow=c(nr, nc))` or `par(mfcol=c(nr, nc))` splits the page into a regular grid with `nr` rows and `nc` columns. Each invocation of `plot.new` starts a new figure. Consecutive figures are either placed in a rowwise manner (`mfrow`) or the columnwise one (`mfcol`). Alternatively, the `mfg` parameter can be used to enforce a custom order.

**Example 13.18** *Figure 13.15 depicts an example page with four figures aligned on a  $2 \times 2$  grid.*

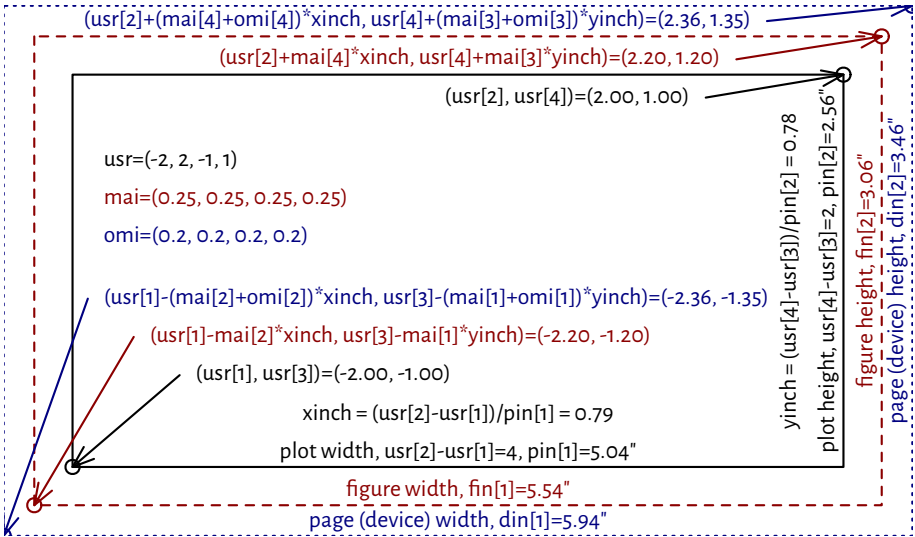


Figure 13.14: User vs device coordinates

```

par(oma=rep(1.2, 4)) # outer margins (default 0)
par(mfrow=c(2, 2)) # a 2x2 plot grid

for (i in 1:4) {
  plot.new()
  par(mar=c(3, 3, 2, 2)) # each plot can have different inner margins
  plot.window(c(i-1, i+1), c(-1, 1)) # separate user coordinates for each

  text(i, 0, sprintf("Plot region (plot %d)\n(%d, %d)", i,
    par("mfgr")[1], par("mfgr")[2]))

  box("figure", lty="dashed") # a box around the figure region
  box("plot") # a box around the plot region
  axis(1) # horizontal axis (bottom)
  axis(2) # vertical axis (left)
}

box("outer", lty="dotdash") # a box around the whole page
for (i in 1:4)
  mtext(sprintf("Outer margin %d", i), side=i, outer=TRUE)

```

Thanks to `mfrow` and `mfcol`, we can create a scatter plot matrix or different trellis plots. If a non-regular grid is required, we can call the slightly more sophisticated `layout` function (which is incompatible with `mfrow` and `mfcol`). Examples will follow later; see Figure 13.26 and Figure 13.24.

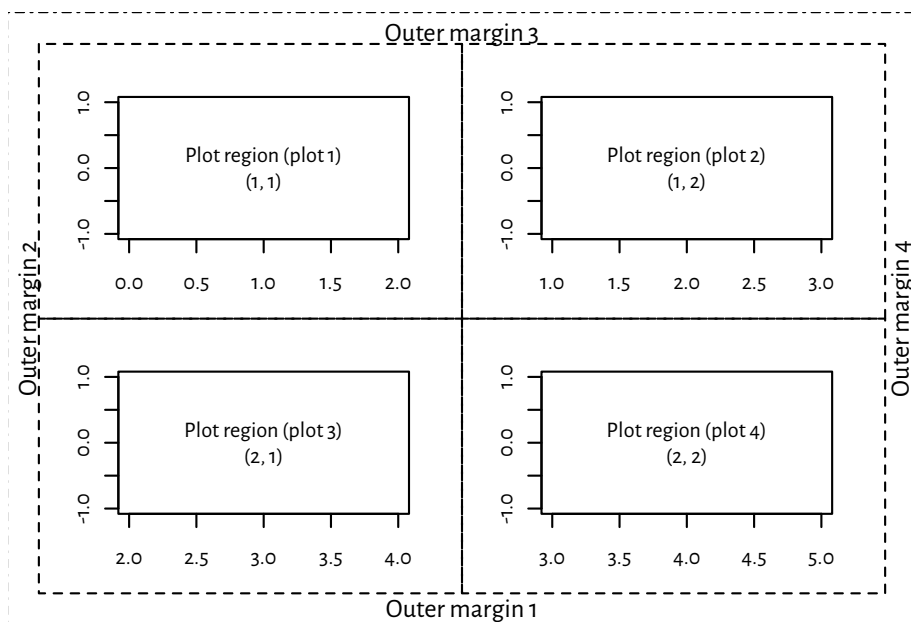


Figure 13.15: A page with four figures created using `par(mfrow=c(2, 2))`

Certain grid sizes might affect the `mex` and `cex` parameters and hence the default font sizes (amongst others). Refer to the documentation of `par` for more details.

### 13.2.7 Graphics devices

Where our plots are *displayed* depends on our development environment (Section 1.2). Users of **JupyterLab** see the plots embedded into the current notebook, consumers of **RStudio** display them in a dedicated *Plots* pane, working from the console opens a new graphics window (unless we work in a text-only environment), whereas compiling `utils::Sweave` or `knitr` markup files brings about an image included in the output document.

In practice, we might be interested in exercising our creative endeavours on different devices. For instance:

```
cairo_pdf("figure.pdf", width=6, height=3.5) # open "device"
# ... calls to plotting functions...
dev.off() # save file, close device
```

This draws something in a PDF file. Similarly, a call to `png` or `svg` would create a PNG or a SVG file. In both cases, as we rely on the **Cairo** library, we can customise the font family by calling `Cairo::CairoFonts`.

**Note** Typically, web browsers can display JPEG, PNG, and SVG files. However, JPEG

uses a lossy compression method. Therefore, it is not a particularly fortunate file format for data visualisations. It does not support transparency either.

PDF is a popular choice in printed publications (e.g., articles or books).

It is worth knowing that PNG and JPEG are raster graphics formats, i.e., they store figures as bitmaps (pixel matrices). They are fast to render, but the file sizes might become immense if we want decent image quality (high resolution). Most importantly, they should not be scaled: it is best to display them at their original widths and heights.

On the other hand, SVG and PDF files store vector graphics, i.e., all primitives are described geometrically. This way, the image can be redrawn at any size and is always expected to be aesthetic. Unfortunately, scatter plots featuring millions of points will result in considerable files size and relatively slow rendition times (but there are tricks to remedy this).

---

Users of TeX might be interested in `tikzDevice::tikz`, which creates TikZ files that can be compiled in the form of standalone PDF files or embedded in LaTeX documents (and its variants). This allows typesetting beautiful equations using the standard `"$. . $"` syntax within any R string.

A list of many built-in devices is available in `help("Devices")`.

---

**Note** (\*) The opened graphics devices form a stack; calling `dev.off` will return to the last opened device (if any). See `dev.list` and other functions listed in its help page for more information.

Each device has its own graphics parameters. When opening a new device, we start with default settings in place.

Also, `dev.hold` and `dev.flush` can be used to suppress the immediate display of the plotted objects, which might increase the drawing speed on certain devices.

The current plot can be copied to another device (e.g., a PDF file) using `dev.print`.

---

**Exercise 13.19** (\*) Create an animated PNG displaying a large point sliding along the sine curve. Generate a series of video frames like in Figure 13.16. Store each frame in a separate PNG file. Then, use *ImageMagick*<sup>6</sup> (compare Section 7.3.2; or rely on some other tool) to combine these files as a single animated PNG.

---

### 13.3 Higher-level functions

Higher-level plotting commands call `plot.new`, `plot.window`, `axis`, `box`, `title`, etc., and draw many graphics primitives on behalf of the user. They provide ready-to-use im-

---

<sup>6</sup> <https://imagemagick.org/>

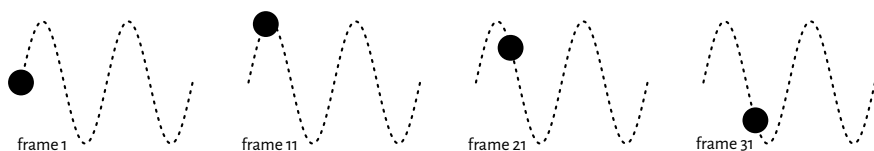


Figure 13.16: Selected frames of an example animation: they can be stored in separate files and then be combined into a single animated PNG

plementations of the most common data visualisation tools, e.g., box-and-whisker plots, histograms, pairs plots, etc.

Below we review some of them. We also show how they can be customised or even rewritten from scratch if we are not completely happy with them. They will inspire us to practice some lower-level graphics programming.

**Exercise 13.20** Check out the meaning of the `ask`, `new`, `xaxt`, `yaxt`, and `ann` graphics parameters and how they affect **plot**, **new**, **axis**, **title**, and so forth.

### 13.3.1 Scatter- and function plots with `plot.default` and `matplot`

The default method for the **plot** S3 generic is a convenient wrapper around **points** and **lines**.

**Example 13.21** **plot** can be used to draw a scatter plot of two numeric variables, possibly grouped by another categorical variable. From Section 10.3.2 we know that a factor is represented as a vector of small natural numbers. Therefore, its underlying level codes can be used directly as `col` or `pch` specifiers; see Figure 13.17 for a demonstration. Take note of a call to the **legend** function.

```
plot(
  jitter(iris[["Sepal.Length"]]), # x (it is a numeric vector)
  jitter(iris[["Petal.Width"]]),  # y (it is a numeric vector)
  col=as.numeric(iris[["Species"]]), # colours (integer codes)
  pch=as.numeric(iris[["Species"]]), # plotting symbols (integer codes)
  xlab="Sepal length",
  ylab="Petal width",
  asp=1 # y/x aspect ratio
)
legend(
  "bottomright",
  legend=levels(iris[["Species"]]),
  col=seq_along(levels(iris[["Species"]])),
  pch=seq_along(levels(iris[["Species"]])),
  bg="white"
)
```



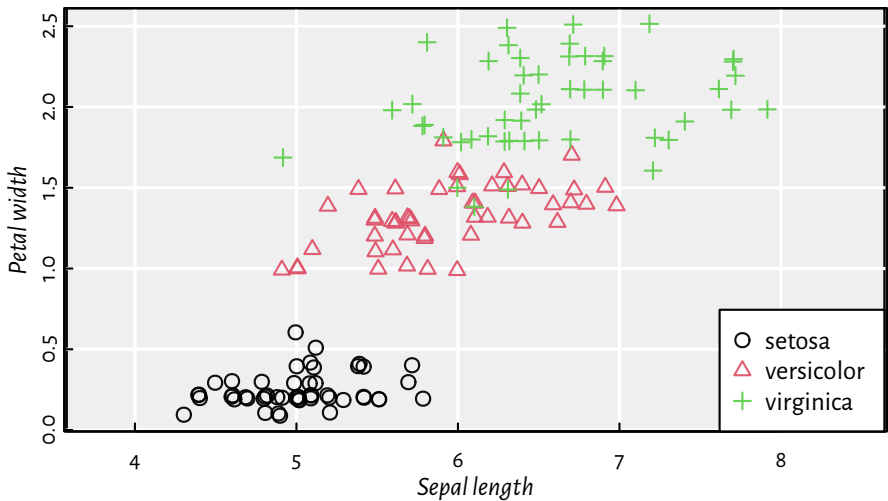


Figure 13.17: `as.numeric` on factors can be used to define different plotting styles for each factor level

**Exercise 13.22** Pass `ann=FALSE` and `axes=FALSE` to `plot` to suppress the addition of axes and labels. Then, draw them manually using the functions discussed in the previous section.

**Exercise 13.23** Draw a plot of the  $y = \sin x$  function using a call to `plot`. Then, call `lines` to depict  $y = \cos x$ . Add a legend. Later, do the same using a single call to `matplot`.

**Example 13.24** Semi-transparency may convey additional information. Figure 13.18 shows two scatter plots of adult females' weight vs height. If the points are fully opaque, we cannot judge the density around them. On the other hand, translucent symbols somewhat imitate the two-dimensional histograms that we depict later in Figure 13.29.

```
nhanes <- read.csv( # see https://github.com/gagolews/teaching-data
  file=~ /Projects/teaching-data/marek/nhanes_adult_female_bmx_2020.csv",
  comment.char="#", col.names=c("weight", "height", "armlen", "leglen",
    "armcirc", "hipcirc", "waistcirc"))
par(mfrow=c(1, 2))
for (col in c("black", "#00000010"))
  plot(nhanes[["height"]], nhanes[["weight"]], col=col,
    pch=16, xlab="Height", ylab="Weight")
```

**Example 13.25** Figure 13.19 depicts the average monthly temperatures in Warsaw, Poland (a time series). Note that the translucent ribbon representing the low-high average temperature intervals was added using a call to `polygon`.

```
# Warsaw monthly temperatures; source: https://en.wikipedia.org/wiki/Warsaw
high <- c( 0.6, 1.9, 6.6, 13.6, 19.5, 21.9,
```

(continues on next page)

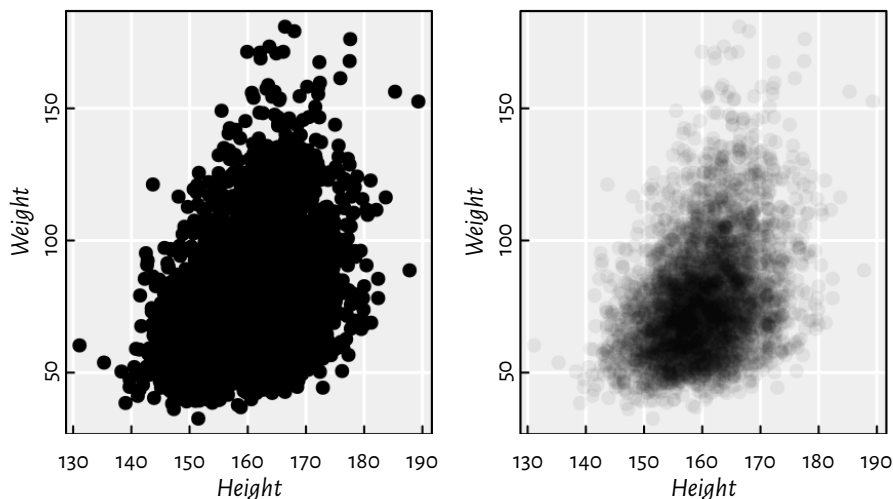


Figure 13.18: Semi-transparent symbols can give the idea of the points' distribution density

(continued from previous page)

```

      24.4, 23.9, 18.4, 12.7,  5.9,  1.6)
mean <- c(-1.8, -0.6,  2.8,  8.7, 14.2, 17.0,
      19.2, 18.3, 13.5,  8.5,  3.3, -0.7)
low  <- c(-4.2, -3.6, -0.6,  3.9,  8.9, 11.8,
      13.9, 13.1,  9.1,  4.8,  0.6, -3.0)
matplot(1:12, cbind(high, mean, low), type="o", col=c(2, 1, 4), lty=1,
      xlab="month", ylab="temperature [°C]", xaxt="n", pch=16, cex=0.5)
axis(1, at=1:12, labels=month.abb, line=-0.25, lwd=0, lwd.ticks=1)
polygon(c(1:12, rev(1:12)), c(high, rev(low)), border=NA, col="#ffff0011")
legend("bottom", c("average high", "mean", "average low"),
      lty=1, col=c(1, 2, 4), bg="white")

```

**Example 13.26** Figure 13.20 depicts a scatter plot similar to Figure 13.18, but now with the points' hue being a function of a third variable.

```

midpoints <- function(x) 0.5*(x[-1]+x[-length(x)])
layout(matrix(c(1, 2), nrow=1), # 2 plots in 1 page
      widths=c(1, lcm(3))) # the 2nd one of fixed width "3cm" (scaled)
z <- nhanes[["waistcirc"]]
breaks <- seq(min(z), max(z), length.out=10)
zf <- cut(z, breaks, include.lowest=TRUE)
col <- hcl.colors(nlevels(zf), "Viridis", alpha=0.5)
plot(nhanes[["height"]], nhanes[["weight"]], col=col[as.numeric(zf)],

```

(continues on next page)

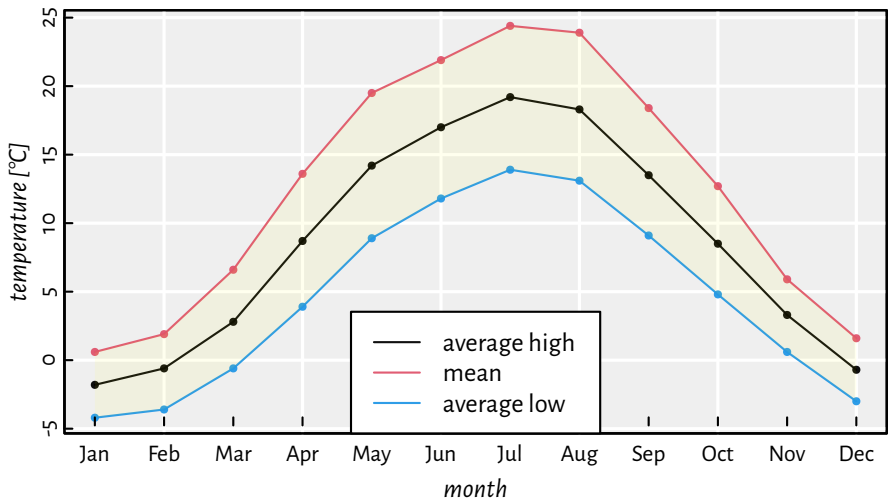


Figure 13.19: A semi-transparent ribbon was added by calling `polygon` to highlight the area between the low-high ranges (intervals)

(continued from previous page)

```
pch=16, xlab="Height", ylab="Weight")
par(mar=c(2.2, 0.6, 2.2, 0.6))
plot.new(); plot.window(c(0, 1), c(0, nlevels(zf)))
rasterImage(as.matrix(rev(col)), 0, 0, 1, nlevels(zf), interpolate=FALSE)
text(0.5, 1:nlevels(zf)-0.5, sprintf("%3.0f", midpoints(breaks)))
mtext("Waist 0", side=3)
```

**Exercise 13.27** Implement your version of the function to draw a scatter plot matrix (a pairs plot), `pairs`.

**Exercise 13.28** `ecdf` returns an object of S3 classes `c("ecdf", "stepfun")`. There are `plot` methods overloaded for these classes. Inspect their source code. Then, inspired by this, create your own function to compute and display the empirical cumulative distribution function corresponding to a given numeric vector.

**Exercise 13.29** `spline` performs cubic spline interpolation, whereas `smooth.spline` determines a smoothing spline of a given two-dimensional dataset. Plot different splines for `cars[["dist"]]` as a function of `cars[["speed"]]`. Which of these two functions is more appropriate for depicting this dataset?

### 13.3.2 Bar plots and histograms

A bar plot is drawn using a series of rectangles (i.e., some polygons) of different heights (or widths, if we request horizontal alignment).

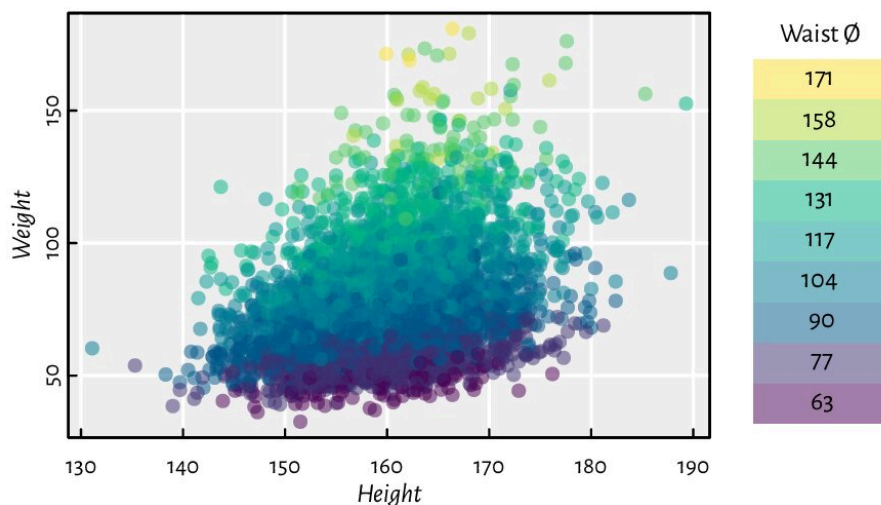


Figure 13.20: A 2D scatter plot with a third variable represented by colours

**Example 13.30** Let us visualise the *dataset*<sup>7</sup> listing the most frequent causes of medication errors (data are fabricated):

```
cat_med = c(
  "Unauthorised drug", "Wrong IV rate", "Wrong patient", "Dose missed",
  "Underdose", "Wrong calculation", "Wrong route", "Wrong drug",
  "Wrong time", "Technique error", "Duplicated drugs", "Overdose"
)
counts_med = c(1, 4, 53, 92, 7, 16, 27, 76, 83, 3, 9, 59)
```

A Pareto chart combines a bar plot with bars of decreasing heights with a cumulative percentage curve; see Figure 13.21. Note that **barplot** returns the midpoints of the bars and that the function sets the *xaxis* graphics parameter and thus does not extend the x-axis range by 4% on both sides (which does not make us happy here).

```
o <- order(counts_med)
cato_med <- cat_med[o]
pcto_med <- counts_med[o]/sum(counts_med)*100
cumpcto_med <- rev(cumsum(rev(pcto_med)))
# bar plot of %s
par(mar=c(2.2, 0.6, 2.2, 6.6)) # wide left margin
midp <- barplot(pcto_med, horiz=TRUE, xlab="%",
  col="white", xlim=c(0, 25), xaxs="r", yaxs="r", yaxt="n",
  width=3/4, space=1/3)
```

(continues on next page)

<sup>7</sup> <https://www.cec.health.nsw.gov.au/CEC-Academy/quality-improvement-tools/pareto-charts>

(continued from previous page)

```

text(pcto_med, midp, sprintf("%.1f%%", pcto_med), pos=4, cex=0.89)
axis(4, at=midp, labels=cato_med, las=1)
box()
# cumulative % curve in a new coordinate system
par(usr=c(-4, 104, par("usr")[3], par("usr")[4])) # 0-100 with 4% addition
lines(cumpcto_med, midp, type="o", col=4, pch=18)
axis(3, col=4)
mtext("cumulative %", side=3, line=1.2, col=4)
text(cumpcto_med, midp, sprintf("%.1f%%", cumpcto_med), cex=0.89, col=4,
     pos=c(4, 2)[(cumpcto_med>80)+1], offset=0.5)

```

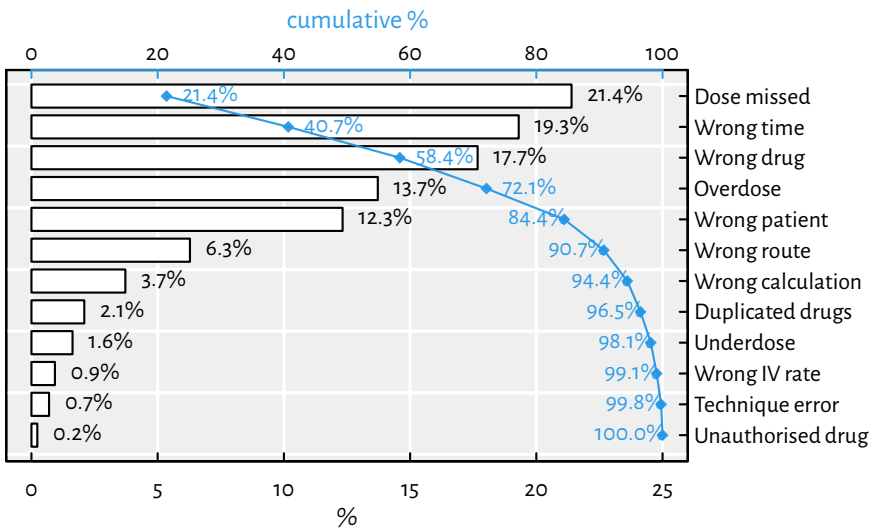


Figure 13.21: An example Pareto chart (a fancy bar plot); double axes have a general tendency to confuse the reader

**Exercise 13.31** Draw a bar plot summarising, for each passenger Class and Sex, the number of adults who did not survive the sinking of the deadliest 1912 cruise; see Figure 13.22 and the built-in *Titanic* dataset.

**Exercise 13.32** Implement your version of **barplot**, but where the bars are placed precisely at the positions specified by the user, e.g., allowing the bar midpoints to be consecutive integers.

We will definitely not cover the (in)famous pie charts in our book. The human brain is not very skilled at judging the relative differences between the areas of geometric objects.

Moving on: a histogram is a simple density estimator for continuous data. It can be thought of as a bar plot with bars of heights proportional to the number of observa-

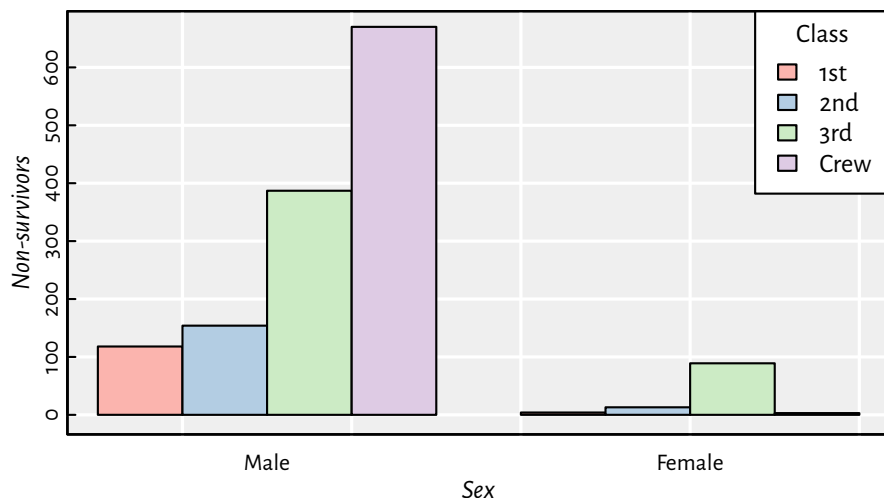


Figure 13.22: An example bar plot representing a two-way contingency table

tions falling into the corresponding disjoint intervals. Most often, there is no space between the bars to emphasise that the intervals cover the whole data range.

A histogram can be computed and drawn using the high-level function **hist**; see Figure 13.23.

```
par(mfrow=c(1, 2))
for (breaks in list("Sturges", 25)) {
  # Sturges (a heuristic) is the default; any value is merely a suggestion
  hist(iris[["Sepal.Length"]], probability=TRUE, xlab="Sepal length",
       main=NA, breaks=breaks, col="white")
  box() # weirdly we need to add it manually
}
```

**Exercise 13.33** Study the source code of **hist.default**. Note the (invisibly returned) list (of S3 class *histogram*). Then, study **graphics::plot.histogram**. Implement similar functions yourself.

**Exercise 13.34** Modify your function to draw a scatterplot matrix so that it gives the histograms of the marginal distributions on its diagonal.

**Example 13.35** Using **layout** mentioned in Section 13.2.6, we can draw a scatterplot with marginal histograms; see Figure 13.24. Note that we split the page into four plots of unequal sizes, but the upper right part of the grid is unused. We use **hist** for binning only (**plot=FALSE**). Then, **barplot** is utilised for drawing as it gives greater control over the process (e.g., allows vertical layout).

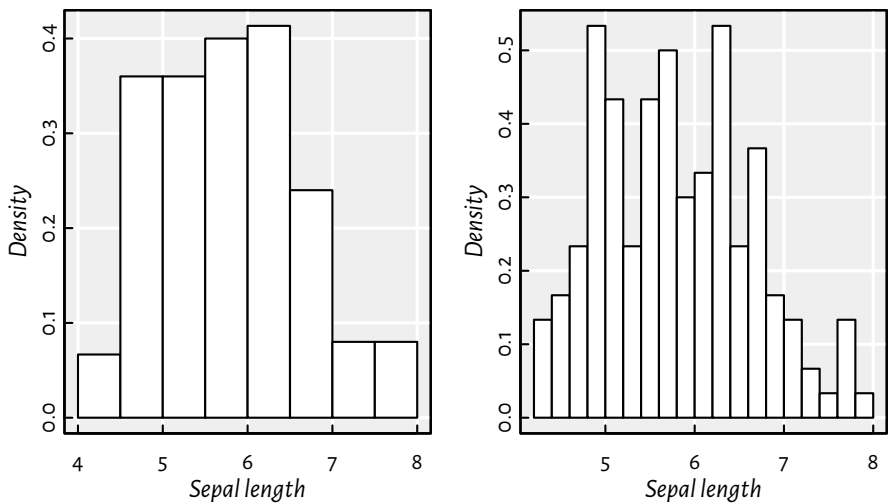


Figure 13.23: Example histograms: The same dataset, but different bin numbers

```
layout(matrix(
  c(1, 1, 0, # first row: plot no. 1 of width 3 and nothing
    3, 3, 3, 2, # three rows: square plot no. 3 and a thin but long no. 2
    3, 3, 3, 2,
    3, 3, 3, 2), nrow=4, byrow=TRUE))
par(mex=1, cex=1) # the layout function changed this!
x <- jitter(iris[["Sepal.Length"]])
y <- jitter(iris[["Sepal.Width"]])
# subplot 1
par(mar=c(0.2, 2.2, 0.6, 0.2), ann=FALSE)
hx <- hist(x, plot=FALSE, breaks=seq(min(x), max(x), length.out=20))
barplot(hx[["density"]], space=0, axes=FALSE, col="#00000011")
# subplot 2
par(mar=c(2.2, 0.2, 0.2, 0.6), ann=FALSE)
hy <- hist(y, plot=FALSE, breaks=seq(min(y), max(y), length.out=20))
barplot(hy[["density"]], space=0, axes=FALSE, horiz=TRUE, col="#00000011")
# subplot 3
par(mar=c(2.2, 2.2, 0.2, 0.2), ann=TRUE)
plot(x, y, xlab="Sepal length", ylab="Sepal width",
      xlim=range(x), ylim=range(y)) # default xlim, ylim
```

**Example 13.36** (\*) Kernel density estimators (KDEs) are another way to guesstimate the data distribution. The `density` function, for a given numeric vector, returns a list that features, amongst others, the `x` and `y` coordinates of the points that we can pass directly to the `lines` function. Below we depict the KDEs of data split into three groups; see Figure 13.25.



Figure 13.24: Three (four) plots on one page, but on a nonuniform grid created using **layout**: A scatter plot with marginal histograms

```
adjust_transparency <- function(col, alpha)
  rgb(t(col2rgb(col)/255), alpha=alpha) # alpha in [0, 1]

pal <- adjust_transparency(palette(), 0.2)
kdes <- lapply(split(iris[["Sepal.Length"]], iris[["Species"]]), density)
matplot(sapply(kdes, `[`, "x"), sapply(kdes, `[`, "y"),
  type="l", xlab="Sepal length", ylab="density", lwd=1.5)
for (i in seq_along(kdes))
  polygon(kdes[[i]][["x"]], kdes[[i]][["y"]], col=pal[i], border=NA)
legend("topright", legend=levels(iris[["Species"]]), bg="white", lwd=1.5,
  col=seq_along(levels(iris[["Species"]])),
  lty=seq_along(levels(iris[["Species"]])))
```



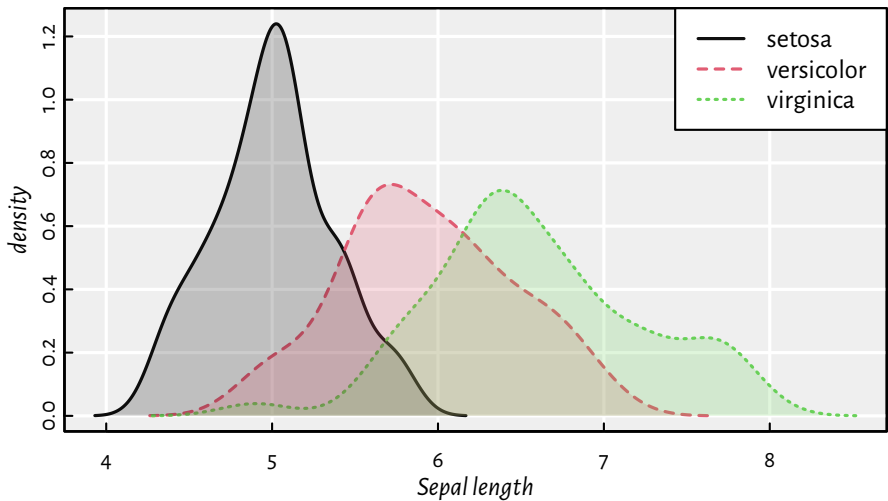


Figure 13.25: Kernel density estimators of sepal length split by species in the Iris data-set; Note the semi-transparent polygons (again)

**Exercise 13.37** (\*) Implement a function `grid_kde`, which draws kernel density estimators for a given numeric variable split by a combination of three factor levels; see Figure 13.26 for an example.

```
grid_kde <- function(data, values, x, y, hue) ...to.do...

tips <- read.csv("~/Projects/teaching-data/other/tips.csv", comment.char="#",
  stringsAsFactors=TRUE) # see https://github.com/gagolews/teaching-data
head(tips, 3) # preview an example dataset
## total_bill tip sex smoker day time size
## 1 16.99 1.01 Female No Sun Dinner 2
## 2 10.34 1.66 Male No Sun Dinner 3
## 3 21.01 3.50 Male No Sun Dinner 3
grid_kde(tips, values="tip", x="smoker", y="time", hue="sex")
```

### 13.3.3 Box-and-whisker plots

We have already seen a chart generated by `boxplot` in Figure 5.1. Tinkering with it will give us some robust practice, which in turn shall make us perfect.

**Exercise 13.38** Modify the code generating Figure 5.1 so that:

1. same doses are grouped together (more space between different doses; also, on the x-axis, only unique doses are printed),
2. different supps have different colours (add a legend explaining them).

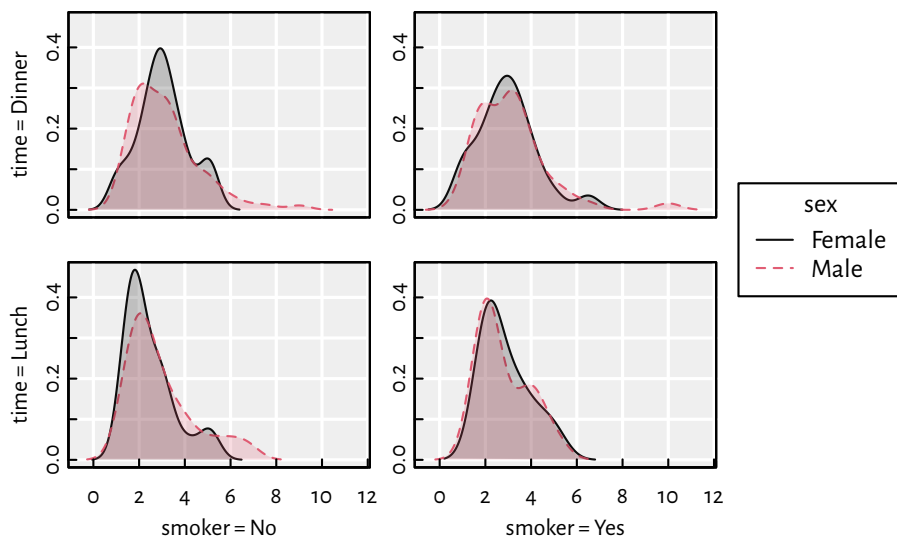


Figure 13.26: An example grid plot (also known as a trellis, panel, conditioning, or lattice plot) featuring kernel density estimators for a numeric variable (amount of tip in a US restaurant) split by a combination of three factor levels (smoker, time, sex)

**Exercise 13.39** Write a function for drawing box plots using graphics primitives.

**Exercise 13.40** (\*) Write a function for drawing violin plots. They are similar to box plots but use kernel density estimators.

**Exercise 13.41** (\*) Implement a bag plot, which is a two-dimensional version of a box plot. Use `chull` to compute the convex hull of a point set.

### 13.3.4 Contour plots and heat maps

When plotting a function of two variables like  $z = f(x, y)$ , the magnitude of the  $z$  component can be expressed using colour brightness or hue.

`image` is a convenient wrapper around `rasterImage`, which can be used to draw contour plots, two-dimensional histograms, heatmaps, etc.

**Example 13.42** Figure 13.27 presents a filled contour plot of Himmelblau's function,  $f(x, y) = (x^2 + y - 11)^2 + (x + y^2 - 7)^2$ , for  $x \in [-5, 5]$  and  $y \in [-4, 4]$ . A call to `contour` adds labelled contour lines (which is actually a nontrivial operation).

```
x <- seq(-5, 5, length.out=250)
y <- seq(-4, 4, length.out=200)
z <- outer(x, y, function(xg, yg) (xg^2 + yg - 11)^2 + (xg + yg^2 - 7)^2)
image(x, y, z, col=grey(seq(1, 0, length.out=16)))
contour(x, y, z, nlevels=16, add=TRUE)
```

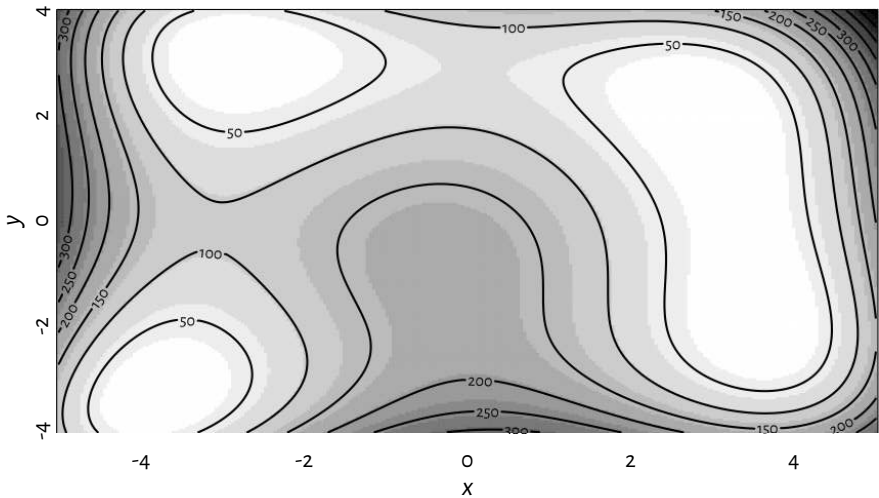


Figure 13.27: A filled contour plot of Himmelblau's function with labelled contour lines

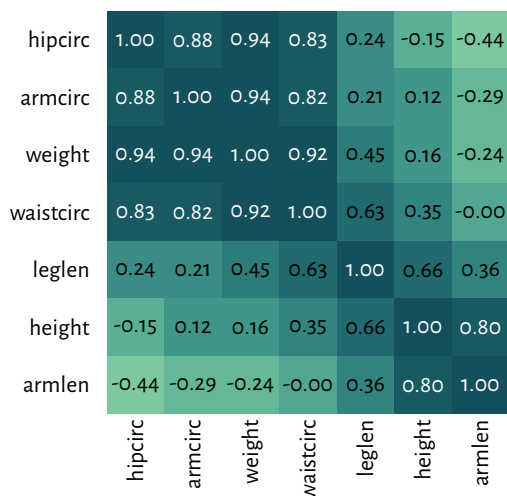
In **image**, the number of rows in **z** matches the length of **x**, whereas the number of columns therein is equal to the size of **y**. This might be counterintuitive; if **z** is printed, the image is its 90-degree rotated version.

**Example 13.43** Figure 13.28 presents an example heatmap depicting Pearson's correlations between all pairs of variables in the *nhanes* dataset which we loaded some time ago.

```
o <- c(6, 5, 1, 7, 4, 2, 3) # order of rows/cols (by similarity)
R <- cor(nhanes[o, o])
par(mar=c(2.8, 7.6, 1.2, 7.6), ann=FALSE)
image(1:NROW(R), 1:NCOL(R), R,
      ylim=c(NROW(R)+0.5, 0.5),
      xlim=c(-1, 1),
      col=hcl.colors(20, "BluGrn", rev=TRUE),
      xlab=NA, ylab=NA, asp=1, axes=FALSE)
axis(1, at=1:NROW(R), labels=dimnames(R)[[1]], las=2, line=FALSE, tick=FALSE)
axis(2, at=1:NCOL(R), labels=dimnames(R)[[2]], las=1, line=FALSE, tick=FALSE)
text(arrayInd(seq_along(R), dim(R)),
      labels=sprintf("%.2f", R),
      col=c("white", "black")[abs(R<0.8)+1],
      cex=0.89)
```

**Exercise 13.44** Check out the **heatmap** function, which uses hierarchical clustering to find an aesthetic reordering of the matrix's items.

**Example 13.45** Figure 13.29 depicts a two-dimensional histogram. It approaches the idea of reflecting the points' density quite differently from the semi-transparent symbols in Figure 13.18.

Figure 13.28: A correlation heatmap drawn using `image`

```

histogram_2d <- function(x, y, k=25, ...)
{
  breaksx <- seq(min(x), max(x), length.out=k)
  fx <- cut(x, breaksx, include.lowest=TRUE)
  breaksy <- seq(min(y), max(y), length.out=k)
  fy <- cut(y, breaksy, include.lowest=TRUE)
  C <- table(fx, fy)
  image(midpoints(breaksx), midpoints(breaksy), C,
        xaxs="r", yaxs="r", ...)
}

par(mfrow=c(1, 2))
for (k in c(25, 50))
  histogram_2d(nhanes[["height"]], nhanes[["weight"]], k=k,
              xlab="Height", ylab="Weight",
              col=c("#ffffff00", hcl.colors(25, "Viridis", rev=TRUE))
  )

```

**Exercise 13.46** (\*) Implement some two-dimensional kernel density estimator and plot it using `contour`.

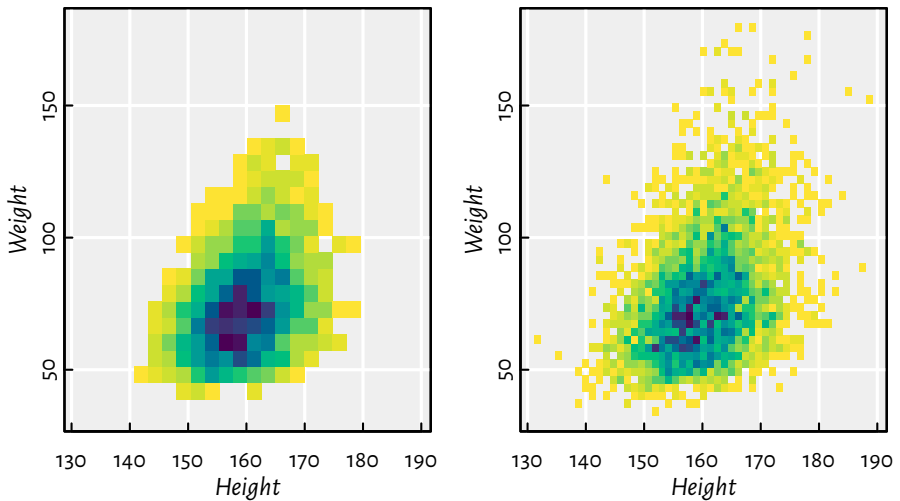


Figure 13.29: Two-dimensional histograms with different numbers of bins, where the bin count is reflected by the colour

## 13.4 Exercises

**Exercise 13.47** Answer the following questions:

- Can functions from the **graphics** package be used to adjust the plots generated by **lattice** and **ggplot2**?
- List the most common graphics primitives.
- Can all high-level functions be implemented using low-level ones? As an example, discuss the key ingredients used in **barplot**.
- Some high-level functions discussed in this chapter feature the `add` parameter. What is its purpose?
- What are the admissible values of `pch` and `lty`? Also, in the default palette, what is the meaning of colours 1, 2, ..., 16? Can their meaning be changed?
- Can all graphics parameters be changed?
- What is the difference between passing `xaxt="n"` to **plot.default** vs setting it with **par**, and then calling **plot.default**?
- Which graphics parameters are set by **plot.window**?
- What is the meaning of the `usr` parameter when using the logarithmic scale on the x-axis?

- (\*) How to place a plotting symbol exactly 1 centimetre from the top-left corner of the current page (following the page's diagonal)?
- Semi-transparent polygons are nice, right?
- Can an ellipse be drawn using `polygon`?
- What happens when we set the graphics parameter `mfrow=c(2, 2)`?
- How to export the current plot to a PDF file?

**Exercise 13.48** Draw the 2022 BTC-to-USD close rates<sup>8</sup> time series. Then, add the 7- and 30-day moving averages.

(\*) Also, fit a local polynomial (moving) regression model using the Savitzky–Golay filter (see `loess`).

**Exercise 13.49** (\*) Draw (from scratch) a candlestick plot for the 2022 BTC-to-USD rates<sup>9</sup>.

**Exercise 13.50** (\*) Create a function to draw a normal quantile-quantile (Q-Q) plot, i.e., for inspecting whether a numeric sample might come from some normal distribution.

**Exercise 13.51** (\*) Draw a map of the world, where each country is filled with a colour whose brightness or hue is linked to its Gini index of income inequality. You can easily find the data on Wikipedia. Try to find an open dataset that gives the borders of each country as vertices of a polygon (e.g., in the form of a (geo)JSON file).

**Exercise 13.52** Next time you see a pleasant data visualisation somewhere, try to reproduce it using base **graphics**.

For further information on graphics generation in R, see, e.g., Chapter 12 of [56], [47], and [51]. In this chapter, we were only interested in *static* graphics, e.g., for use in printed publications or plain websites. Interactive plots that a user might tinker with in a web browser are a different story.

And so the second part of our course is ended.

<sup>8</sup> [https://github.com/gagolews/teaching-data/raw/master/marek/btcusd\\_close\\_2022.csv](https://github.com/gagolews/teaching-data/raw/master/marek/btcusd_close_2022.csv)

<sup>9</sup> [https://github.com/gagolews/teaching-data/raw/master/marek/btcusd\\_ohlc\\_2022.csv](https://github.com/gagolews/teaching-data/raw/master/marek/btcusd_ohlc_2022.csv)

## **Part III**

# **Deepest**





## *Interfacing compiled code (\*\*)*

---

R is an effective *glue* language. It is suitable for composing whole data wrangling pipelines: from data import through processing, analysis, and visualisation to export. It makes using and connecting larger *building blocks* very convenient.

R is also a competent tool for developing quick and dirty prototypes of standalone, general-purpose algorithms, especially if they are of *numerical* nature. Nevertheless, for performance reasons, we may<sup>1</sup> consider moving computing-intensive tasks to the C or C++ level<sup>2</sup>. It is particularly the case when we need a method that:

- has higher memory or time complexity than its straightforward implementation when it is programmed using vectorised R functions,
- has an *iterative* or *recursive* nature, e.g., involving unvectorisable *for* or *while* loops,
- relies on complicated dynamic data structures (e.g., hash maps, linked lists, or trees),
- needs methods provided elsewhere and not available in R (e.g., other C or C++ libraries).

In the current chapter, we will demonstrate that R works very well as a user-friendly interface to compiled code.

This topic is overall very technical. The definitive reference is [62]; but see also Chapter 11 of [10]. Furthermore, R's source code provides many working examples of how to deal with R objects in C.

Here, we will only cover the most important basics. We will focus on writing or interfacing *portable*<sup>3</sup> function libraries that only rely on *simple*<sup>4</sup> data structures (e.g., arrays

---

<sup>1</sup> C and C++ are as fast as we can get without applying fancy CPU-specific optimisations and similar hacks. Nevertheless, D.E. Knuth once said: *The real problem is that programmers have spent far too much time worrying about efficiency in the wrong places and at the wrong times; premature optimisation is the root of all evil (or at least most of it) in programming* [39].

<sup>2</sup> Fortran is also supported but will not be covered in this book because of its smaller popularity. Some third-party packages are gateways to other languages, such as Java.

<sup>3</sup> Hence, we are not interested in the overall very convenient **Rcpp** or **cpp11** packages. They define C++ classes that make interacting with R objects more pleasant for some users. (\*\*) If you have time and skills to help write a lightweight, more abstract version of **Rcpp** that would also work with Python and other popular languages, please contact yours truly.

<sup>4</sup> Thus, we will not discuss the ALTREP [54] representation of objects, ways to deal with environments or pairlists, etc. This chapter might be extended in the future if the diligent reader expresses interest in such additions.

of the type `double` and `int`). Thanks to this, we will be able to reuse them in other environments such as Python (e.g., via Cython) or Julia. Let us remember that R is one of *many* languages out there.

We assume basic knowledge of the C language; see [38]. The reader can skip this chapter now and return to it later. The remaining material is not contingent on the current one.

From now on, we take for granted that our environment can successfully build a source package with C code, as mentioned in Section 7.3.1. In particular, `W***ws` and `m**OS` should have, respectively, `RTools` and `Xcode` installed.

---

**Note** To avoid ambiguity, in the main text, calls to C functions will be prefixed with “`C::`”; e.g., `C::spanish_inquisition()`.

---

## 14.1 C and C++ code in R

### 14.1.1 Source files for compiled code in R packages

Perhaps the most versatile way to interact with portable C code is via standalone R packages. For the purpose of the current chapter, we created a demo project available at <https://github.com/gagolews/cpackagedemo>.

**Exercise 14.1** *Inspect the structure of `cpackagedemo`. Note that C source files are located in the `src/` subdirectory. Build and install the package. Call `my_sum` in R on some numeric vector.*

The package provides an R interface to one function, `C::my_c_sum`, written in the most portable fashion possible. Its declaration is included in the `src/cfuncs.h` file:

```
#ifndef __CFUNS_H
#define __CFUNS_H
#include <stddef.h>

double my_c_sum(const double* x, size_t n);

#endif
```

The function accepts a pointer to the start of a numeric sequence and its size, which is a standard<sup>5</sup> way of representing an array of doubles.

---

<sup>5</sup> (\*) A slightly more sophisticated representation (used, e.g., in GNU GSL and `numpy`) deals with a *sliced* array, where we additionally store the so-called *stride*. Instead of inspecting elements one after another, we advance the iterator by a given step size. This way, we could apply the same function on selected rows of a matrix (if it is in the column-major order).

Its definition is given in `src/cfuncs.c`. We see that it is nothing more than a simple sum of all the elements in an array:

```
#include "cfuncs.h"

/* computes the sum of all elements in an array x of size n */
double my_c_sum(const double* x, size_t n)
{
    double s = 0.0;
    for (size_t i = 0; i < n; ++i) {
        /* this code does not treat potential missing values specially
           (they are kinds of NaNs); to fix this, add:
           if (ISNA(x[i])) return NA_REAL; // #include <R.h> */
        s += x[i];
    }
    return s;
}
```

To make `C::my_c_sum` available in R, we will have to introduce a wrapper around it that works with the data structures from the first part of this jolly book. We know that an R function accepts objects of *any* kind on input and yields *anything* as a result. In the next section, we will explain that we get access to R objects via special pointers of the type SEXP (S expressions).

And so we declare our R-callable wrapper in `src/rfuncs.h`:

```
#ifndef __RFUNS_H
#define __RFUNS_H
#include <R.h>
#include <Rinternals.h>
#include <Rmath.h>

SEXP my_c_sum_wrapper(SEXP x);

#endif
```

The actual definition is included in `src/rfuncs.c`:

```
#include "rfuncs.h"
#include "cfuncs.h"

/* a wrapper around my_c_sum callable from R */
SEXP my_c_sum_wrapper(SEXP x)
{
    double s;
```

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```

if (!Rf_isReal(x)) {
    /* the caller is expected to prepare the arguments
       (doing it at the C level is tedious work) */
    Rf_error("`x` should be a vector of type 'double'");
}

/* Exercise: consider missing value (NA) checking
   as my_c_sum doesn't do it */

s = my_c_sum(REAL(x), (size_t)XLENGTH(x));

return Rf_ScalarReal(s);
}

```

The arguments can be, technically speaking, prepared at the C level. For instance, if ``x`` turned out to be an integer vector, we could convert it to the double one (these are two different types; see [Section 6.4.1](#)). Nevertheless, overall, it is very burdensome. It is better to use pure R code to ensure that the arguments are of the correct form and to beautify the outputs.

This explains why we only assert the enjoyment of `C::Rf_isReal(x)`. It guarantees that the `C::REAL` and `C::XLENGTH` functions correctly return the pointer to the start of the sequence and its length, respectively.

Once `C::my_c_sum` is called, we must convert it to an R object. Here, it is a newly allocated numeric vector of length one. It can be done easily by calling `C::Rf_ScalarReal`.

Although optional (see [Section 5.4](#) of [62]), we will register `C::my_c_sum_wrapper` as a callable function explicitly. This way, R will not struggle to find the specific entry point in the resulting dynamically linked library (DLL). We do this in `src/cpackagedemo.c`:

```

#include <R_ext/Rdynload.h>
#include "rfuns.h"

/* the list of functions available in R via a call to .Call():
   each entry is like {exported_name, fun_pointer, number_of_arguments} */
static const R_CallMethodDef cCallMethods[] = {
    {"my_c_sum_wrapper", (DL_FUNC)&my_c_sum_wrapper, 1},
    {NULL, NULL, 0} // the end of the list
};

/* registers the list of callable functions */
void R_init_cpackagedemo(DllInfo *dll)
{
    R_registerRoutines(dll, NULL, cCallMethods, NULL, NULL);
}

```

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```
R_useDynamicSymbols(dll, FALSE);
}
```

The function can be invoked from R using `.Call`. We do it in `R/my_sum.R`:

```
my_sum <- function(x)
{
  # prepare input data:
  if (!is.double(x))
    x <- as.double(x)

  s <- .Call("my_c_sum_wrapper", x, PACKAGE="cpackagedemo")

  # some rather random postprocessing:
  attr(s, "what") <- deparse(substitute(x))
  s
}
```

And, finally, here is the package `NAMESPACE` file responsible for registering the exported R names and indicating the DLL to use:

```
export(my_sum)
useDynLib(cpackagedemo)
```

Once the package is built and installed (e.g., by running “R CMD INSTALL <pkgdir>” in the terminal), we can test it by calling:

```
library("cpackagedemo")
my_sum(runif(100)/100)
## [1] 0.49856
## attr(,"what")
## [1] "runif(100)/100"
```

**Exercise 14.2** *Extend the package (locally) by adding a function to compute the index of the greatest element in a numeric vector. Note that C uses 0-based array indexing, whereas, in R, the first element is at index 1. Compare its run time against `which.max` using `proc.time`.*

#### 14.1.2 R CMD SHLIB

The “R CMD SHLIB <files>” command compiles one or more source files without the need for turning them into standalone packages; see [62]. Then, `dyn.load` loads the resulting DLL.

**Exercise 14.3** (\*) Compile `src/cfuncs.c` and `src/rfuncs.c` from our demo package using “R CMD SHLIB <files>”. Call **dyn.load**. Write an R function that uses **.Call** to invoke C: `my_c_sum_wrapper` from the second source file.

The direct SHLIB approach is convenient for learning C programming, including running simple examples. We will thus use it for didactic reasons in this chapter. The `inst/examples/csource.R` file in our demo package includes the implementation of an R function called **csource**. It compiles a given C source file, loads the resulting DLL, and extracts and executes a designated R code chunk (preferably defining a function that refers to **.Call**).

Here is an example source file, `inst/examples/helloworld.c` in the **cpackagedemo** source code repository:

```
// the necessary header files are automatically included by `csource`

SEXP C_hello()
{
    Rprintf("The mill's closed. There's no more work. We're destitute.\n"
           "I'm afraid I've no choice but to sell you all "
           "for scientific experiments.\n");
    return R_NilValue;
}

/* R
# this chunk will be extracted and executed by `csource`.

hello <- function()
    invisible(.Call("C_hello", PACKAGE="helloworld"))

R */
```

Let us compile it and call the R function defined above.

```
source("~/R/cpackagedemo/inst/examples/csource.R") # defines csource
csource("~/R/cpackagedemo/inst/examples/helloworld.c")
hello()
## The mill's closed. There's no more work. We're destitute.
## I'm afraid I've no choice but to sell you all for scientific experiments.
```

**Exercise 14.4** (\*) C++ is also supported. It can be thought of as a superset of the C language, but the devil is in the detail. Change the name of the above file to `helloworld2.cpp`, add “extern “C” before the function declaration, and compile it.

**Exercise 14.5** (\*) Verify that C and C++ source files can coexist in R packages.

**Example 14.6** (\*) It might be very educative to study the implementation of **csource**. By now, we should be able to author such functions ourselves (a few hours’ worth of work), let alone read with understanding.

```

# compiles a C or C++ source file using R CMD SHLIB,
# loads the resulting DLL, and executes the embedded R code
csource <- function(
  fname,
  libname=regmatches(basename(fname),
    regexp("[^.]*(?=|\\.*)", basename(fname), perl=TRUE)),
  shlibargs=character(),
  headers=paste0(
    "#include <R.h>\n",
    "#include <Rinternals.h>\n",
    "#include <Rmath.h>\n"
  ),
  R=file.path(R.home(), "bin/R")
) {
  stopifnot(file.exists(fname))
  stopifnot(is.character(libname), length(libname) == 1)
  stopifnot(is.character(shlibargs))
  stopifnot(is.character(headers))
  stopifnot(is.character(R), length(R) == 1)

  # read the source file:
  f <- paste(readLines(fname), collapse="\n")

  # set up output file names:
  tmpdir <- normalizePath(tmpdir(), winslash="/") # tmpdir on Win uses \
  dynlib_ext <- .Platform[["dynlib.ext"]]
  libpath <- file.path(tmpdir, sprintf("%s%s", libname, dynlib_ext))
  cfname <- file.path(tmpdir, basename(fname))
  rfname <- sub("\\..*?$", ".R", cfname, perl=TRUE)

  # separate the /* R ... <R code> ... R */ chunk from the source file:
  rpart <- regexec("(?smi)^(\\|* R\\|s?(.*)R \\|*/$", f, perl=TRUE)[[1]]
  rpart_start <- rpart
  rpart_len <- attr(rpart, "match.length")
  if (rpart_start[1] < 0 || rpart_len[1] < 0)
    stop("enclose R code between /* R ... and ... R */")

  rcode <- substr(f, rpart_start[2], rpart_start[2]+rpart_len[2]-1)
  cat(rcode, file=rfname, append=FALSE)

  # write the C/C++ file:
  ccode <- paste(
    headers,
    substr(f, 1, rpart_start[1]-1),
    substr(f, rpart_start[1]+rpart_len[1], nchar(f)),

```

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```

    collapse="\n"
  )
  cat(ccode, file=cfname, append=FALSE)

  # prepare the "R CMD SHLIB ..." command:
  shlibargs <- c(
    "CMD", "SHLIB",
    sprintf("-o %s", libpath),
    cfname,
    shlibargs
  )

  # compile and load the DLL, run the extracted R script:
  retval <- FALSE
  oldwd <- setwd(tmpdir)
  tryCatch({
    if (libpath %in% sapply(getLoadedDLLs(), `[[`, "path"))
      dyn.unload(libpath)
    stopifnot(system2(R, shlibargs) == 0) # 0 == success
    dyn.load(libpath)
    source(rfname)
    retval <- TRUE
  }, error=function(e) {
    cat(as.character(e), file=stderr())
  })
  setwd(oldwd)

  if (!retval) stop("error compiling file")
  invisible(TRUE)
}

```

## 14.2 Handling basic types

### 14.2.1 SEXPTYPES

All R objects are stored as instances of the C language structure `SEXP`. Usually, we access them via pointers, which are of the type `SEXP` (S expression).

C functions referred to via `.Call` take the very generic SEXPs on input. They output some `SEXP`. One of the said structure's fields represents the actual R object type (SEXPTYPE numbers); see Table 14.1 for a selection.



Table 14.1: Basic R types in C

| SEXPTYPE  | Type in R (typeof)                      | Test in C  |
|-----------|---|--|
| NILSXP    | NULL                                    | <b>Rf_isNull</b> (x) ( <i>true for R_NilValue only</i> ) |
| RAWSXP    | raw                                     | <b>TYPEOF</b> (x) == RAWSXP                              |
| LGLSXP    | logical                                 | <b>Rf_isLogical</b> (x)                                  |
| INTSXP    | integer                                 | <b>Rf_isInteger</b> (x)                                  |
| REALSXP   | double                                  | <b>Rf_isReal</b> (x)                                     |
| CPLXSXP   | complex                                 | <b>Rf_isComplex</b> (x)                                  |
| STRSXP    | character                               | <b>Rf_isString</b> (x)                                   |
| VECSXP    | list                                    | <b>Rf_isVectorList</b> (x)                               |
| CHARSXP   | char ( <i>scalar string; internal</i> ) | <b>TYPEOF</b> (x) == CHARSXP                             |
| EXTPTRSXP | externalptr ( <i>internal</i> )         | <b>TYPEOF</b> (x) == EXTPTRSXP                           |

**Example 14.7** To illustrate that any R object is available as a SEXP, let us consider *inst/examples/sexptype.c* from **cpackagedemo**:

```
SEXP C_test_sexptype(SEXP x)
{
    Rprintf("type of x: %s (SEXPTYPE=%d)\n",
           Rf_type2char(TYPEOF(x)),
           (int)TYPEOF(x)
    );
    return R_NilValue;
}

/* R
test_sexptype <- function(x)
  invisible(.Call("C_test_sexptype", x, PACKAGE="sexptype"))
R */
```

Example calls:

```
csource("~/R/cpackagedemo/inst/examples/sexptype.c")
test_sexptype(1:10)
## type of x: integer (SEXPTYPE=13)
test_sexptype(NA)
## type of x: logical (SEXPTYPE=10)
test_sexptype("spam")
## type of x: character (SEXPTYPE=16)
```

We should refer to particular SEXPTYPES via their descriptive names (constants; e.g., STRSXP), not their numeric identifiers (e.g., 16); see Section 1.1 of [65] for the complete list<sup>6</sup>.

<sup>6</sup> src/include/Rinternals.h in R's source code repository; see, e.g., <https://svn.r-project.org/R/trunk/>.

14.2.2 Accessing elements in simple atomic vectors

Table 14.2 gives the most important vector-like SEXPTYPES (atomic and generic), their corresponding C types and the functions to access the underlying array pointers. A call to `C::XLENGTH` returns the length of a given sequence.

We have already seen an example function that processes a numeric vector; see `C::my_c_sum_wrapper` above.

Let us stress that writing functions that accept only `int` and `double` array pointers and their lengths makes them easily reusable in other environments. In many data analysis applications, we do not need much more.

Table 14.2: Basic array-like R types and their elements in C

| SEXPTYPE | Array element type  | Pointer access          |
|----------|---|-------------------------|
| RAWXP    | <code>typedef unsigned char Rbyte;</code>   | <code>RAW(x)</code>     |
| LGLXP    | <code>int</code> (use the <code>FALSE</code> , <code>TRUE</code> , and <code>NA_LOGICAL</code> constants) | <code>LOGICAL(x)</code> |
| INTXP    | <code>int</code>  | <code>INTEGER(x)</code> |
| REALXP   | <code>double</code>   | <code>REAL(x)</code>    |
| CPLXP    | <code>typedef struct { double r; double i; } Rcomplex;</code>   | <code>COMPLEX(x)</code> |
| STRXP    | SEXP (array of SEXPs of type CHARXP)  | (not directly)          |
| VECSXP   | SEXP (array of SEXPs of any SEXPTYPE)   | (not directly)          |
| CHARXP   | <code>const char*</code> (read-only; trailing 0; check encoding)  | <code>CHAR(x)</code>    |

**Important** With raw, logical, integer, floating-point, and complex vectors, we get direct access to data that might be shared amongst many objects (compare Section 16.1.4). SEXPRECS are simply passed by pointers (since SEXPs are exactly them). We must thus refrain<sup>7</sup> from modifying the objects passed as function parameters. See below for ways to create new vectors, e.g., for storing auxiliary or return values.

**Example 14.8** Consider `inst/examples/sharedmem.c`:

```
SEXP C_test_sharedmem(SEXP x)
{
    if (!Rf_isReal(x) || XLENGTH(x) == 0)
        Rf_error("`x` should be a non-empty vector of type 'double'");

    REAL(x)[0] = REAL(x)[0]+1; // never do it; always make a copy;
                               // the underlying array `x` may be shared by many objects

    return R_NilValue;
}
```

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<sup>7</sup> (\*) Unless we know what we are doing, e.g., we are certain that we deal with a local variable in an R function that invokes our `.call`.

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```
/* R
test_sharedmem <- function(x)
  invisible(.Call("C_test_sharedmem", x, PACKAGE="sharedmem"))
R */
```

And now, calling the above function on an example vector:

```
csource("~/R/cpackagedemo/inst/examples/sharedmem.c")
y <- 1
z <- y
test_sharedmem(y)
print(z)
## [1] 2
```

modifies *y* and *z* in place! It is not the same semantics as the one we are used to when interacting with R. Hence, we must always make a copy.

### 14.2.3 Representation of missing values

Most languages do not support the notion of missing values out of the box. Therefore, in R, they have to be emulated. Table 14.3 lists the relevant constants and the conventional ways for testing for missingness.

Table 14.3: Representation of missing values

| SEXPTYPE | Missing value                 | Testing          |
|----------|-------------------------------|------------------|
| RAWSXP   | (none)                        | (none)           |
| LGLSXP   | NA_LOGICAL (equal to INT_MIN) | e1 == NA_LOGICAL |
| INTSXP   | NA_INTEGER (equal to INT_MIN) | e1 == NA_INTEGER |
| REALSXP  | NA_REAL (a special NaN)       | ISNA(e1)         |
| CPLXSXP  | a pair of NA_REALS            | ISNA(e1.r)       |
| STRSXP   | NA_STRING (a CHARSXP object)  | e1 == NA_STRING  |

In logical and integer vectors, NAs are represented as the smallest 32-bit signed integer. Thus, we need to be careful when performing any operations on these types: testing for missingness must be performed first.

The case of doubles is slightly less irksome, for a missing value is represented as a special not-a-number. Many arithmetic operations on NaNs return NaNs as well, albeit there is no guarantee<sup>8</sup> that they will be of precisely the same type as NA\_REAL. Thus, manual testing for the missingness is also advised.

<sup>8</sup> (\*\*) Namely, NAs are encoded as un-signalling NaNs 0x7ff000000000007a2 of type double (the lower 32 payload bits are equal to 1954, decimally); see `src/arithmetic.c` in R's source code. The payload propagation is not fully covered by the current IEEE 754 floating point standard; see [22] for discussion. Reliance on

**Example 14.9** The `inst/examples/mean_naomit.c` file defines a function to compute the arithmetic mean of an `int` or a `double` vector:

```
SEXP C_mean_naomit(SEXP x)
{
    double ret = 0.0;
    size_t k = 0;

    if (Rf_isInteger(x)) {
        const int* xp = INTEGER(x);
        size_t n = XLENGTH(x);
        for (size_t i=0; i<n; ++i)
            if (xp[i] != NA_INTEGER) { // NOT: ISNA(xp[i])
                ret += (double)xp[i];
                k++;
            }
    }
    else if (Rf_isReal(x)) {
        const double* xp = REAL(x);
        size_t n = XLENGTH(x);
        for (size_t i=0; i<n; ++i)
            if (!ISNA(xp[i])) { // NOT: xp[i] == NA_REAL
                ret += xp[i];
                k++;
            }
    }
    else
        Rf_error("`x` should be a numeric vector");

    return Rf_ScalarReal((k>0)?(ret/(double)k):NA_REAL);
}

/* R
mean_naomit <- function(x)
{
    if (!is.numeric(x)) # neither integer nor double
        x <- as.numeric(x) # convert to double
    .Call("C_mean_naomit", x, PACKAGE="mean_naomit")
}
R */
```

There is some inherent code duplication: `int` and `double` are distinct types, and they need to be handled separately. Some tests:

such behaviour will thus make our code platform-dependent. R itself sometimes does that; theoretically, this may cause some NAs to be converted to (other) NaNs.

```

csource("~/R/cpackagedemo/inst/examples/mean_naomit.c")
mean_naomit(c(1L, NA_integer_, 3L, NA_integer_, 5L))
## [1] 3
mean_naomit(rep(NA_real_, 10))
## [1] NA

```

**Exercise 14.10** Implement *all* and *any* in C.

#### 14.2.4 Memory allocation

R features a simple yet effective garbage collector that relies on reference counting. Occasionally<sup>9</sup>, memory blocks deemed no longer reachable are either freed or marked as reusable.

To allocate a new vector of length one and set its only element, we can call `C::ScalarLogical`, `C::ScalarInteger`, `C::ScalarReal`, etc. We have already used these functions for returning R “scalars”.

Vectors of arbitrary lengths can be created using `C::Rf_allocVector(sexptype, size)`. Note that this function does not initialise the elements of logical and numeric sequences (amongst others). They will need to be set manually after creation.

---

**Important** We must protect all allocated vectors from garbage collection when we use them inside our functions. For this purpose, R maintains a stack<sup>10</sup> of objects guarded against premature annihilation. `C::PROTECT(sexp)` pushes a given object pointer onto the top of the list. `C::UNPROTECT(n)` pops the last  $n$  elements therefrom (in a last-in-first-out manner). At the end of a `.Call`, R checks if the number of protects matches that of un-protects. If it is not the case, a warning is generated.

---

Protection is not needed:

- for arguments to functions referred to by `.Call`, as they are already in use and hence protected;
  - for objects assigned as list or character vectors’ elements using `C::SET_VECTOR_ELT` and `C::SET_STRING_ELT` (see below); when the container is protected, so are its components;
  - when we return the allocated vector to R immediately after creating it (like in `return Rf_ScalarReal(val)` in a C function invoked by `.Call`).
- 

**Example 14.11** Here is a function to compute the square of each element in a numeric vector. Note that the new vector must be protected from garbage collection while data are being prepared.

---

<sup>9</sup> A safe strategy is to assume that any call to a function from R’s API may trigger the memory cleanup. On a side note, we may call the `gc` function in R to enforce rubbish removal. It also reports the current memory usage.

<sup>10</sup> (\*\*) `C::R_PreserveObject` protects an arbitrary SEXP until `C::R_ReleaseObject` is called manually. With this mechanism, objects are not automatically released at the end of a `.Call`.

```

SEXP C_square1(SEXP x)
{
    // no need to call PROTECT(x), it is already in use
    if (!Rf_isReal(x)) Rf_error("`x` should be a vector of type 'double'");

    size_t n = XLENGTH(x);
    const double* xp = REAL(x);

    SEXP y = PROTECT(Rf_allocVector(REALSXP, n)); // won't be GC'd
    double* yp = REAL(y);

    for (size_t i=0; i<n; ++i) {
        if (ISNA(xp[i])) yp[i] = xp[i];
        else yp[i] = xp[i]*xp[i];
    }

    UNPROTECT(1); // pops 1 object from the protect stack;
    // does not trigger garbage collection, so we can return `y` now
    return y;
}

/* R
square1 <- function(x)
{
    if (!is.double(x)) x <- as.double(x)
    .Call("C_square1", x, PACKAGE="square1")
}
R */

```

Alternatively, in this case, we may use `C::Rf_duplicate`:

```

SEXP C_square2(SEXP x)
{
    if (!Rf_isReal(x)) Rf_error("`x` should be a vector of type 'double'");

    x = PROTECT(Rf_duplicate(x)); // OK; it's a pointer

    size_t n = XLENGTH(x);
    double* xp = REAL(x);
    for (size_t i=0; i<n; ++i)
        if (!ISNA(xp[i])) xp[i] = xp[i]*xp[i];

    UNPROTECT(1);

    return x;
}

```

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```

}

/* R
square2 <- function(x)
{
  if (!is.double(x)) x <- as.double(x)
  .Call("C_square2", x, PACKAGE="square2")
}
R */

```

Some tests:

```

csource("~/R/cpackagedemo/inst/examples/square1.c")
square1(c(-2, -1, 0, 1, 2, 3, 4, NA_real_))
## [1] 4 1 0 1 4 9 16 NA
csource("~/R/cpackagedemo/inst/examples/square2.c")
square2(c(-2, -1, 0, 1, 2, 3, 4, NA_real_))
## [1] 4 1 0 1 4 9 16 NA

```

We can claim some auxiliary memory from the heap during a function's runtime using the well-known `C::malloc` (or `new` in C++). We are of course fully responsible for releasing it via `C::free` (or `delete`).

There is also `C::R_alloc(n, size)` which allocates  $n \times \text{size}$  bytes. The memory will automatically be garbage-collected at the end of a `.Call`.

**Example 14.12** Here is our version of the *which* function.

```

SEXP C_which1(SEXP x)
{
  if (!Rf_isLogical(x)) Rf_error("`x` should be of type 'logical'");

  size_t n = XLENGTH(x), i, k;
  const int* xp = LOGICAL(x);

  size_t* d = (size_t*)malloc(n*sizeof(size_t)); // conservative size
  if (!d) Rf_error("memory allocation error");

  for (i=0, k=0; i<n; ++i)
    if (xp[i] != NA_LOGICAL && xp[i])
      d[k++] = i;

  SEXP y = PROTECT(Rf_allocVector(REALSXP, k));
  double* yp = REAL(y); // yes, type is double - ready for long vectors
  for (i=0; i<k; ++i)

```

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```

        yp[i] = (double)d[i]+1; // R uses 1-based indexing
    UNPROTECT(1);

    free(d); // we don't want any memory leaks!

    return y;
}

/* R
which1 <- function(x)
{
    if (!is.logical(x)) x <- as.logical(x)
    .Call("C_which1", x, PACKAGE="which1")
}
R */

```

Some tests:

```

csource("~/R/cpackagedemo/inst/examples/which1.c")
which1(c(TRUE, FALSE, TRUE, NA, TRUE))
## [1] 1 3 5

```

Note that R's **which** returns either an `int` or a `double` vector, depending on the size of the input vector (whether it is shorter than  $2^{31} - 1$ ). As an exercise, rewrite the above to take that into account: integer arithmetic is faster.

**Example 14.13** (\*) If we do not like that we are potentially wasting too much memory in the case of sparse logical vectors, we can rely on dynamically growable arrays. Below is a C++ rewrite of the above function using `deque` (double-ended queue) from the language's standard library.

```

#include <deque>

extern "C" SEXP C_which2(SEXP x)
{
    if (!Rf_isLogical(x)) Rf_error("`x` should be of type 'logical'");

    size_t n = XLENGTH(x), i;
    const int* xp = LOGICAL(x);

    std::deque<size_t> d;
    for (i=0; i<n; ++i)
        if (xp[i] != NA_LOGICAL && xp[i])
            d.push_back(i);

    SEXP y = PROTECT(Rf_allocVector(REALSXP, d.size()));

```

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```

double* yp = REAL(y); // ready for long vectors
i=0;
for (size_t k : d)
    yp[i++] = (double)k+1; // R uses 1-based indexing
UNPROTECT(1);

return y;
}

/* R
which2 <- function(x)
{
    if (!is.logical(x)) x <- as.logical(x)
    .Call("C_which2", x, PACKAGE="which2")
}
R */

```

Example calls:

```

csource("~/R/cpackagedemo/inst/examples/which2.cpp")
x <- (runif(10) > 0.5)
stopifnot(which(x) == which1(x))
stopifnot(which(x) == which2(x))

```

Alternatively, we could use **C::realloc** to extend an initially small buffer allocated using **C::malloc** by, say, 50% whenever it is about to overflow.

### 14.2.5 Lists

For safety reasons<sup>11</sup>, we do not get access to the underlying pointers in lists and character vectors. List items can be read by calling **C::VECTOR\_ELT(x, index)** and can be set with **C::SET\_VECTOR\_ELT(x, index, newval)**.

Note that lists (VECSXPs) are comprised of SEXPs of any type. Hence, after extracting an element, its SEXPTYPE needs to be tested using one of the functions listed in Table 14.1. This is tiresome.

**Example 14.14** Here is a rather useless function that fetches the first and the last element in a given numeric vector or a list. However, if the latter case, we apply the function recursively on all its elements.

```

SEXP C_firstlast(SEXP x)
{

```

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<sup>11</sup> To get the object reference counting right. **C::SET\_VECTOR\_ELT** needs to un-protect the old element and start protecting the new one.

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```

if (!Rf_isVector(x) || XLENGTH(x) == 0)
  Rf_error("`x` must be a non-empty vector (atomic or generic)");
else if (Rf_isReal(x)) {
  SEXP y = PROTECT(Rf_allocVector(REALSXP, 2));
  REAL(y)[0] = REAL(x)[0];           // first
  REAL(y)[1] = REAL(x)[XLENGTH(x)-1]; // last
  UNPROTECT(1);
  return y;
}
else if (Rf_isVectorList(x)) {
  SEXP y = PROTECT(Rf_allocVector(VECSXP, 2));
  // VECTOR_ELT(x, i) is PROTECTED by the container;
  // SET_VECTOR_ELT does not trigger GC, so no need to call PROTECT
  // on the result of C_firstlast(...) in this context
  SET_VECTOR_ELT(y, 0, C_firstlast(VECTOR_ELT(x, 0)));
  SET_VECTOR_ELT(y, 1, C_firstlast(VECTOR_ELT(x, XLENGTH(x)-1)));
  UNPROTECT(1);
  return y;
}
else
  Rf_error("other cases left as an exercise");

return R_NilValue; // avoid compiler warning
}

/* R
firstlast <- function(x)
  .Call("C_firstlast", x, PACKAGE="firstlast")
R */

```

Testing:

```

csource("~/R/cpackagedemo/inst/examples/firstlast.c")
firstlast(c(1, 2, 3))
## [1] 1 3
firstlast(list(c(1, 2, 3), c(4, 5), 6))
## [[1]]
## [1] 1 3
##
## [[2]]
## [1] 6 6
firstlast(list(c(1, 2, 3), 4, 5, list(6, c(7, 8), c(9, 10, 11))))
## [[1]]
## [1] 1 3
##

```

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```
## [[2]]
## [[2]][[1]]
## [1] 6 6
##
## [[2]][[2]]
## [1] 9 11
```

**Exercise 14.15** Implement a C function that returns the longest vector in a given list. Use `C::Rf_isVector` to check whether a given object is an atomic or a generic vector, and hence if `C::XLENGTH` can be called thereon.

**Exercise 14.16** Inscribe your version of `unlist`. Consider scanning the input list twice. First, determine the size of the output vector. Second, fill the return object with un-listed values.

**Exercise 14.17** Write a C function that takes a list of numeric vectors of identical lengths on input. Return their elementwise sum: the first element of the output should be the sum of the first elements in every vector, and so forth.

### 14.2.6 Character vectors and individual strings (\*)

Character vectors (STRSXPs) are similar to VECSXPs except that they only feature individual strings. The latter are represented using a separate data type, CHARXP. `C::STRING_ELT(x, index)` and `C::SET_STRING_ELT(x, index, newval)` work as the element getters and setters.

---

**Important** If we are not interested in text processing but rather in handling *categorical* data or defining grouping variables, we should consider converting character vectors to *factors* before issuing a `.Call`. Comparing small integers is much faster than strings; see below for more details.

---

Because of R's string cache, there are no duplicate strings in the memory. However, this feature could only be guaranteed by making data in CHARSXPs *read-only*. We can access the underlying `const char*` pointer by calling `C::CHAR(s)`. As typical in C, a string is terminated by byte 0.

---

**Note** R strings may be of different encodings; compare [Section 6.1.1](#). For portability and peace of mind, it is best to preprocess the arguments to `.Call` using `enc2utf8`, which converts all strings to UTF-8<sup>12</sup>.

Despite being the most universal encoding, UTF-8 does not represent a single code point using a fixed number of bytes. For instance, computing the string length re-

---

<sup>12</sup> Take care when using `C::Rprintf`, though. It should only be used to output messages in the *native* encoding, which does not necessarily have to be UTF-8, although this landscape is slowly changing. Sticking to ASCII is the riskless choice.

quires iterating over all its elements. For CHARSXPs, `C::XLENGTH` returns the number of bytes, not including the trailing `\0`.

It is thus best to leave the processing of strings to the dedicated libraries, e.g., ICU<sup>13</sup> or rely on functions from the `stringi` package [27] at the R level.

C strings can be converted to CHARSXPs by calling `C::Rf_mkCharCE(stringbuf, CE_UTF8)` or `C::Rf_mkCharLenCE(stringbuf, buflen, CE_UTF8)`. If we are sure that a string is in ASCII (a subset of UTF-8), we can also call `C::Rf_mkChar(stringbuf)`.

We should never return CHARSXPs as results to R. They are for internal use only. They must be wrapped inside a character vector, e.g., using `C::Rf_ScalarString`.

### 14.2.7 Calling R functions from C (\*\*)

Section 5.11 of [62] discusses ways to call R functions in C. To understand them, we will first need to study the material from the remaining chapters of our book, i.e., environments and the related evaluation model. They can be useful, e.g., when calling optimisation algorithms implemented in C on objective functions written in R.

### 14.2.8 External pointers (\*\*)

There is a separate basic R type for storing arbitrary C pointers, `externalptr` (SEXPTYPE of `EXTPTRXP`); see Section 5.13 of [62] for more details.

We can use them to maintain dynamic data structures or resource handlers between calls to R functions. The problem with these is that pointers are passed as... pointers. They can easily break R's pass-by-value semantics, where changes to the state of the referenced object will be visible outside the call.

Furthermore, pointers are not serialisable. They cannot be saved for use in another R session.

**Example 14.18** (\*\*) *inst/examples/stack.cpp provides a C++ implementation of the stack data structure, being a last-in-first-out container of arbitrary R objects:*

```
#include <deque>

class S : public std::deque<SEXP>
{
public: ~S()
{ // destructor: release all SEXPs so that they can be GC'd
  while (!this->empty()) {
    SEXP obj = this->front();
    this->pop_front();
    R_ReleaseObject(obj);
  }
}
```

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<sup>13</sup> <https://icu.unicode.org/>

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```

    }
}
};

S* get_stack_pointer(SEXP s, bool check_zero=true) // internal function
{
    if (typeof(s) != EXTPTRSXP)
        Rf_error("not an external pointer");

    SEXP tag = R_ExternalPtrTag(s); // our convention, this can be anything
    if (typeof(tag) != CHARSXP || strcmp(CHAR(tag), "stack") != 0 )
        Rf_error("not a stack");

    S* sp = (S*)R_ExternalPtrAddr(s);
    if (check_zero && !sp)
        Rf_error("address is 0");

    return sp;
}

void stack_finaliser(SEXP s) // internal function
{
    // called during garbage collection
    S* sp = get_stack_pointer(s, false);
    if (sp) {
        delete sp; // destruct S, release SEXPs
        R_ClearExternalPtr(s);
    }
}

extern "C" SEXP C_stack_create()
{
    S* sp = new S(); // stack pointer
    SEXP s = PROTECT(
        R_MakeExternalPtr((void*)sp, /*tag*/mkChar("stack"), R_NilValue)
    );
    R_RegisterCFinalizerEx(s, stack_finaliser, TRUE); // auto-called on GC
    UNPROTECT(1);
    return s;
}

extern "C" SEXP C_stack_empty(SEXP s)
{
    S* sp = get_stack_pointer(s);

```

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```

    return Rf_ScalarLogical(sp->empty());
}

extern "C" SEXP C_stack_push(SEXP s, SEXP obj)
{
    S* sp = get_stack_pointer(s);
    R_PreserveObject(obj);
    sp->push_front(obj);
    return R_NilValue;
}

extern "C" SEXP C_stack_pop(SEXP s)
{
    S* sp = get_stack_pointer(s);
    if (sp->empty())
        Rf_error("stack is empty");
    SEXP obj = sp->front();
    sp->pop_front();
    R_ReleaseObject(obj);
    return obj;
}

/* R
stack_create <- function()
  .Call("C_stack_create", PACKAGE="stack")

stack_empty <- function(s)
  .Call("C_stack_empty", s, PACKAGE="stack")

stack_push <- function(s, obj)
  .Call("C_stack_push", s, obj, PACKAGE="stack")

stack_pop <- function(s)
  .Call("C_stack_pop", s, PACKAGE="stack")
R */

```

Note how we preserve R objects from garbage collection.

Some tests:

```

csource("~/R/cpackagedemo/inst/examples/stack.cpp")
s <- stack_create()
print(s)
## <pointer: 0x55fbff912210>
typeof(s)

```

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```
## [1] "externalptr"
for (i in c("one", "two", "Spanish Inquisition"))
  stack_push(s, i)
while (!stack_empty(s))
  print(stack_pop(s))
## [1] "Spanish Inquisition"
## [1] "two"
## [1] "one"
```

## 14.3 Dealing with compound types

### 14.3.1 Reading and setting attributes

From Chapter 10, we know that compound types such as matrices, factors, or data frames are represented using basic data structures. Usually, they are atomic vectors of lists organised in a predefined manner.

`C::Rf_getAttrib(x, attrname)` and `C::Rf_setAttrib(x, attrname, newval)` gets and sets specific attributes of an object `x`. Their second argument, `attrname`, should be a one-element STRSXP. For convenience, the constants `R_ClassSymbol`, `R_DimNamesSymbol`, `R_DimSymbol`, `R_LevelsSymbol`, `R_NamesSymbol`, and `R_RowNamesSymbol` can be used instead of the STRSXP versions of the "class", "dimnames", "dim", "levels", "names", and "row.names" strings.

**Example 14.19** Consider a function for testing whether a given object is of a specific class:

```
#include <string.h>

SEXP C_isofclass(SEXP x, SEXP class)
{
  if (!Rf_isString(class) && XLENGTH(class) != 1)
    Rf_error("`class` must be a single string");

  if (!OBJECT(x)) // is the class attribute set at all?
    return Rf_ScalarLogical(FALSE);

  SEXP xclass = Rf_getAttrib(x, R_ClassSymbol); // STRSXP (guaranteed)
  const char* c = CHAR(STRING_ELT(class, 0)); // class arg as a C string
  size_t n = XLENGTH(xclass);
  for (size_t i=0; i<n; ++i)
    if (strcmp(CHAR(STRING_ELT(xclass, i)), c) == 0)
      return Rf_ScalarLogical(TRUE);
}
```

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```

    return Rf_ScalarLogical(FALSE);
}

/* R
isofclass <- function(x, class)
  .Call("C_isofclass", x, class, PACKAGE="isofclass")
R */

```

Some tests:

```

csource("~/R/cpackagedemo/inst/examples/isofclass.c")
isofclass(Sys.time(), "POSIXct")
## [1] TRUE
isofclass(cbind(1:5, 11:15), "matrix")
## [1] FALSE

```

Note that a matrix has an implicit class (reported by the `class` function), but its `class` attribute does not have to be set. Hence the negative result.

**Example 14.20** Write a function that fetches a particular named element in a list.

### 14.3.2 Factors

Factors (Section 10.3.2) are represented as integer vectors with elements in the set  $\{1, 2, \dots, k, \text{NA\_integer\_}\}$  for some  $k$ . They are equipped with the `levels` attribute, being a character vector of length  $k$ . Their class attribute is set to "factor".

**Example 14.21** An example implementation of a function to compute the number of occurrences of each factor level is given below.

```

SEXP C_table1(SEXP x)
{
    if (!Rf_isFactor(x)) Rf_error("`x` is not an object of class 'factor'");

    size_t n = XLENGTH(x);
    const int* xp = INTEGER(x); // x is INTSXP

    SEXP levels = Rf_getAttrib(x, R_LevelsSymbol); // levels is STRSXP
    size_t k = XLENGTH(levels);

    SEXP y = PROTECT(Rf_allocVector(REALSXP, k));
    double* yp = REAL(y);
    for (size_t i=0; i<k; ++i)
        yp[i] = 0.0;
    for (size_t j=0; j<n; ++j) {
        if (xp[j] != NA_INTEGER) {

```

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```

        if (xp[j] < 1 || xp[j] > k)
            Rf_error("malformed factor"); // better safe than sorry
        yp[xp[j]-1] += 1.0; // levels are 1..k, but C needs 0..k-1
    }
}

Rf_setAttrib(y, R_NamesSymbol, levels); // set names attribute
UNPROTECT(1);
return y;
}

/* R
table1 <- function(x)
{
    if (!is.factor(x)) x <- as.factor(x)
    .Call("C_table1", x, PACKAGE="table1")
}
R */

```

Testing:

```

csource("~/R/cpackagedemo/inst/examples/table1.c")
table1(c("spam", "bacon", NA, "spam", "eggs", "bacon", "spam", "spam"))
## bacon  eggs  spam
##      2      1      4

```

**Exercise 14.22** Create a function to compute the most frequently occurring value (mode) in a given factor. Return a character vector. If a mode is ambiguous, return all the possible candidates.

### 14.3.3 Matrices

Matrices (Chapter 11) are *flat* atomic vectors or lists with the `dim` attribute being a vector of length two. The `class` attribute does not have to be set (but the `class` function returns "matrix" and "array").

Matrices are so important in data analysis that they have been blessed with a few dedicated functions available at the C level. `C::Rf_isMatrix` tests if a given object meets the criteria mentioned above.

R relies on the Fortran order of matrix elements: they are aligned columnwisely. Let `A` be a matrix with  $n$  rows and  $m$  columns (compare `C::Rf_nrows` and `C::Rf_ncols`). Then, the element in the  $i$ -th row and the  $j$ -th column is at `A[i+n*j]`.

`C::Rf_allocMatrix`(sexptype,  $n$ ,  $m$ ) allocates a new matrix. The `dimnames` attributes must be handled manually, though.

**Example 14.23** Here is a function to compute the transpose of a given numeric matrix:

```

SEXP C_transpose(SEXP x)
{
    if (!Rf_isMatrix(x) || !Rf_isReal(x))
        Rf_error("`x` must be a real matrix");

    size_t n = Rf_nrows(x);
    size_t m = Rf_ncols(x);
    const double* xp = REAL(x);

    SEXP y = PROTECT(Rf_allocMatrix(REALSXP, m, n));
    double* yp = REAL(y);
    for (size_t i=0; i<n; ++i)
        for (size_t j=0; j<m; ++j)
            yp[j+m*i] = xp[i+n*j];

    SEXP dimnames = Rf_getAttrib(x, R_DimNamesSymbol);
    if (!Rf_isNull(dimnames)) {
        SEXP tdimnames = PROTECT(Rf_allocVector(VECSXP, 2));
        SET_VECTOR_ELT(tdimnames, 0, VECTOR_ELT(dimnames, 1));
        SET_VECTOR_ELT(tdimnames, 1, VECTOR_ELT(dimnames, 0));
        Rf_setAttrib(y, R_DimNamesSymbol, tdimnames); // set dimnames
        UNPROTECT(1);
        // dimnames might have the names attribute too (left as an exercise)
    }
    UNPROTECT(1);
    return y;
}

/* R
transpose <- function(x)
{
    if (!is.matrix(x)) x <- as.matrix(x)
    .Call("C_transpose", x, PACKAGE="transpose")
}
R */

```

Testing:

```

csource("~/R/cpackagedemo/inst/examples/transpose.c")
transpose(cbind(c(1, 2, 3, 4), c(5, 6, 7, 8)))
##      [,1] [,2] [,3] [,4]
## [1,]    1    2    3    4
## [2,]    5    6    7    8
transpose(Titanic[, "Male", "Adult", ])
##      1st 2nd 3rd Crew

```

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```
## No 118 154 387 670
## Yes 57 14 75 192
```

**Exercise 14.24** Author a C function named `table2` that computes a two-way contingency table.

### 14.3.4 Data frames

Data frames (Chapter 12) are lists of  $m$  vectors of identical lengths  $n$  or matrices of  $n$  rows for some  $n$  and  $m$ . The character vectors stored in the `row.names` and `names` attributes give the  $n$  row and  $m$  column labels. They are objects of S3 class "data.frame".

We process data frames as ordinary lists. However, in many applications, it is enough to write functions that accept ordinary numeric matrices instead. If element grouping is required, they can be accompanied by a factor or a list of factor variables. Do not complicate our lives beyond necessity.

## 14.4 Using existing function libraries

### 14.4.1 Checking for user interrupts

Long computations may lead to R's becoming unresponsive. For instance, the user may request to cancel the evaluation of the current expression by pressing Ctrl+C.

To process the event queue, we should occasionally call `C::R_CheckUserInterrupt()`, e.g., in every iteration of a complex for loop. Note that R might decide never to return to our function. Thus, we have to prevent memory leaks, e.g., by preferring `C::R_alloc` over `C::malloc`.

### 14.4.2 Generating pseudorandom numbers

`C::unif_rand` returns a single pseudorandom deviate from the uniform distribution on the unit interval. It is the basis for generating numbers from all other supported distributions (Section 6.7.1 of [62]).

It uses the same pseudorandom generator as we described in Section 2.1.5. To read and memorise its seed (the `.Random.seed` object in the global environment), we have to call `C::GetRNGstate()` and `C::PutRNGstate()` at the beginning and the end of our function, respectively.

**Example 14.25** Below is a function to generate a pseudorandom bit sequence:

```
SEXP C_randombits(SEXP n)
{
    if (!Rf_isInteger(n) || XLENGTH(n) != 1)
```

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```

    Rf_error("`n` should be a single integer");

    size_t _n = INTEGER(n)[0];
    if (_n == NA_INTEGER || _n < 1)
        Rf_error("incorrect `n`");

    SEXP y = PROTECT(Rf_allocVector(INTSXP, _n));
    int* yp = INTEGER(y);

    GetRNGstate();
    for (size_t i=0; i<_n; ++i)
        yp[i] = (int)(unif_rand()>0.5);
    PutRNGstate();

    UNPROTECT(1);

    return y;
}

/* R
randombits <- function(n)
{
    if (!is.integer(n)) n <- as.integer(n)
    .Call("C_randombits", n, PACKAGE="randombits")
}
R */

```

Let us play with the above:

```

csource("~/R/cpackagedemo/inst/examples/randombits.c")
set.seed(123); randombits(10)
## [1] 0 1 0 1 1 0 1 1 1 0
randombits(10)
## [1] 1 0 1 1 0 1 0 0 0 1
set.seed(123); randombits(20)
## [1] 0 1 0 1 1 0 1 1 1 0 1 0 1 1 0 1 0 0 0 1
set.seed(123); as.integer(runif(20)>0.5) # it's the same "algorithm"
## [1] 0 1 0 1 1 0 1 1 1 0 1 0 1 1 0 1 0 0 0 1

```

**Exercise 14.26** Create a function to compute the most frequently occurring value (mode) in a given factor object. In the case of ambiguity, return a randomly chosen candidate.

### 14.4.3 Mathematical functions from the R API

Section 6.7 of [62] lists the available statistical distribution functions, mathematical routines and constants, and other numerical utilities.

### 14.4.4 Header files from other R packages (\*)

A package may use header files from another package. For this to be possible, it must include the dependency name in the `LinkingTo` field of its `DESCRIPTION` file; see [62] for discussion.

**Exercise 14.27** *The `BH` package on CRAN gives access to Boost, which are header-only C++ libraries defining many algorithms and data structures. Create an R package that calls `C::boost::math::gcd` after issuing the `#include <boost/math/common_factor.hpp>` directive.*

### 14.4.5 Specifying compiler and linker flags (\*\*)

We can pass arbitrary flags to the compiler or linker, e.g., to use any library installed on our system.

Basic configuration can be set via `Makevars` (or `Makevars.win` on `W****ws`), e.g., by setting `PKG_CFLAGS` or `PKG_LIBS` variables.

For maximum portability across different platforms, which is overall challenging to ensure if we do not wish to exclude `W****ws` users, we might be required to write our own `configure` (and `configure.win`) scripts.

For more information, see [62]. In particular, it discusses how to use `OpenMP`<sup>14</sup> in our projects.

---

## 14.5 Exercises

**Exercise 14.28** *Answer the following questions:*

- *What are the most common `SEXPTYPES`?*
- *How are missing values represented?*
- *How can we check if an integer is a missing value? What about a floating-point variable?*
- *How to prevent `SEXPs` from being garbage-collected?*

---

<sup>14</sup> Most functions we use in R are single-threaded by design. It is up to the user to decide whether and how they would like their code to be parallelised. More often than not, computations in the data science domain are naïvely parallelisable (e.g., Monte Carlo simulations, exhaustive grid search, etc.). For serious jobs, running *multiple* single-threaded R instances via, e.g., the `slurm` workload manager might be a better idea than starting a single R process that tries to fork itself or spawn many child threads. Sometimes, the R package `parallel` might be helpful, too: it defines parallel versions of `lapply` and `apply`.

- How are character vectors represented? What is the difference between a *CHARSXP* and a *STRSXP*?
- Why is it better to process factor objects than raw character vectors if we merely would like to define grouping variables?
- How are R matrices handled in C? Does R use the C or Fortran order of matrix elements?
- How are R data frames handled in C?

**Exercise 14.29** Implement the C versions of the *rep*, *seq*, *rle*, *match*, *findInterval*, *sample*, *order*, *unique*, and *split* functions.

**Exercise 14.30** (\*) Read [62] in its entirety.

**Exercise 14.31** (\*) Download R's source code from [CRAN](https://stat.ethz.ch/R/daily/)<sup>15</sup> or its *Subversion*<sup>16</sup> (SVN) repository. Explore the header files in the *src/include/* subdirectory. They are part of the callable API.

---

---

<sup>15</sup> <https://stat.ethz.ch/R/daily/>

<sup>16</sup> <https://svn.r-project.org/R/trunk/>

## Unevaluated expressions (\*)

In this and the remaining chapters, we will learn some hocus-pocus that should only be of interest to the advanced-to-be<sup>1</sup> and open-minded R programmers who would like to understand what is going on under our language's hood. In particular, we will inspect the mechanisms behind why certain functions act differently from what we would expect them to do if a *standard* evaluation scheme was followed (compare **subset** and **transform** mentioned in [Section 12.3.9](#)).

Namely, in *normal* programming languages, when we execute something like:

```
plot(x, exp(x))
```

the expression `exp(x)`, is evaluated *first* and its value<sup>2</sup> (in this case: probably a numeric vector) is only then passed to the `plot` function as the actual parameter. Thus, if `x`` was set to be `seq(0, 10, length.out=1001)`, the above never means anything else than:

```
plot(c(0.00, 0.01, 0.02, 0.03, ...), c(1.0000, 1.0101, 1.0202, 1.0305, ...))
```

But R was heavily inspired by the S language from whom it has taken the notion of lazy arguments ([Chapter 17](#)). It is equipped with the ability to apply a set of techniques referred to as *metaprogramming* (computing on the language, reflection). With it, we can define functions that can peek outside their small world and clearly see the code fragment passed as their arguments. Having access to such *unevaluated expressions*, we can do to them whatever we please: print, modify, evaluate on different data, or ignore whatsoever.

In theory, this enables implementing many *potentially helpful*<sup>3</sup> beginner-friendly features and express certain requests in a more concise manner. For instance, that the y-axis labels in [Figure 2.2](#) could be generated automatically is precisely because `plot` was able to see not only a vector like `c(1.0000, 1.0101, 1.0202, 1.0305, ...)` but also the expression that generated it, `exp(x)`.

<sup>1</sup> Remember that this book is supposed to be read from the beginning to the end. Also, if you have not tested yourself against all the 300-odd exercises suggested so far, please do it before proceeding with the material presented here. Only practice makes perfect, and nothing is built in a day. Give yourself time: you can always come back later.

<sup>2</sup> Or a reference/pointer to an object that stores the said value.

<sup>3</sup> The original authors of R (R. Ihaka and R. Gentleman), in [37], mention: "A policy of *lazy arguments* is very useful because it means that, in addition to the value of an argument, its symbolic form can be made available in the function being called. This can be very useful for specifying functions or models in symbolic form."

Nonetheless, as a form of *untamed freedom of expression*<sup>4</sup>, metaprogramming has the endless potential to arouse chaos, confusion, and division in the user community. In particular, we can introduce a dialect *within* our language that people outside our circle will not be able to understand.

Therefore, cursed be us, for we are about to start eating from the tree of the knowledge of good and evil. But remember: with great power comes great fun (and responsibility).

---

## 15.1 Expressions at a glance

At the most general level, expressions (statements) in a language like R can be classified into two groups:

- *simple expressions*:
  - *constants* (e.g., 3.14, 2i, 42L, NA\_real\_, TRUE, "character string", NULL, -1.3e-16, 0x123abc),
  - *names* (symbols, identifiers),
- *compound expressions* – combinations of  $n + 1$  expressions (simple or compound) of the form:

$$(f, e_1, e_2, \dots, e_n).$$

As we will soon see, compound expressions represent a *call* to  $f$  (an *operator*) on a sequence of arguments  $e_1, e_2, \dots, e_n$  (*operands*). It is why, equivalently, we denote them with  $f(e_1, e_2, \dots, e_n)$ .

On the other hand, *names* such as ``x``, ``iris``, ``sum``, and ``spam`` have no meaning without an explicitly stated context. This will be a topic we will explore in [Chapter 16](#). Prior to that, we treat them as meaning-less.

Hence, for the time being, we are only interested in the *syntax* or *grammar* of our language, not the *semantics*. We are abstract in the sense that, in the expression “`mean(rates)+2`”<sup>5</sup>, neither ``mean``, ``x``, nor even ``+`` have the “usual” sense. Therefore, we should treat them as equivalent to, say, `f(g(x), 2)` or `spam(bacon(spanish_inquisition), 2)`.

---

<sup>4</sup> In the current author’s opinion, R (as a whole, in the sense of *R (GNU S) as a language and an environment*) would be better off if an ordinary programmer was not exposed so much to functions heavily relying on metaprogramming. A healthy user can perfectly do without (and thus refrain from using) them. The fact that we call them *advanced* will not make us *cool* if we start horsing around with nonstandard evaluation. *Perverse* is perhaps a better label.

<sup>5</sup> Which we know that we can equivalently express as “``+` (mean(rates), 2)`”; see Section 9.4.5.



## 15.2 Language objects

There are three types of *language objects* in R:

- `name` (symbol) – stores object names in the sense of *simple expressions: names* in Section 15.1;
- `call` – represents unevaluated function calls in the sense of *compound expressions* above;
- `expression` – quite confusingly, represents a *sequence* of simple or compound expressions (constants, names, or calls).

One way to create a simple or compound expression is by *quoting*, where interpreter is asked to refrain from evaluating a given command:

```
quote(spam) # name (symbol)
## spam
quote(f(x)) # call
## f(x)
quote(1+2+3*pi) # another call
## 1 + 2 + 3 * pi
```

None of the above was executed.

Single strings can be converted to names by calling:

```
as.name("spam")
## spam
```

Calls can be built programmatically by invoking:

```
call("sin", pi/2)
## sin(1.5707963267949)
```

Sometimes we had rather quote the arguments passed:

```
call("sin", quote(pi/2))
## sin(pi/2)
call("c", 1, exp(1), quote(exp(1)), pi, quote(pi))
## c(1, 2.71828182845905, exp(1), 3.14159265358979, pi)
```

Objects of the type `expression` can be thought of as list-like objects that consist of simple or compound expressions.

```
(exprs <- expression(1, spam, mean(x)+2))
## expression(1, spam, mean(x) + 2)
```

All arguments were quoted.

We can select or subset the individual statements using the extraction or index operators:

```
exprs[-1]
## expression(spam, mean(x) + 2)
exprs[[3]]
## mean(x) + 2
```

**Exercise 15.1** Check the type of the object returned by a call to `c(1, "two", sd, list(3, 4:5), expression(3+3))`.

There is also an option to *parse* a given text fragment or a whole source file:

```
parse(text="mean(x)+2")
## expression(mean(x) + 2)
parse(text=" # two code lines (a comment to be ignored by the parser)
  x <- runif(5, -1, 1)
  print(mean(x)+2)
")
## expression(x <- runif(5, -1, 1), print(mean(x) + 2))
parse(text="2+") # syntax error - unfinished business
## Error in parse(text = "2+"): <text>:2:0: unexpected end of input 1: 2+ ^
```

---

**Important** The `deparse` function can be used to convert language objects to character vectors. For instance:

```
deparse(quote(mean(x+2)))
## [1] "mean(x + 2)"
```

This function has the nice side effect of tidying up the code formatting:

```
exprs <- parse(text=
  "`+'(x, 2)->y; if(y>0) print(y**10|>log()) else { y<- -y; print(y)}")
```

Let us print them out:

```
for (e in exprs)
  cat(deparse(e), sep="\n")
## y <- x + 2
## if (y > 0) print(log(y^10)) else {
##   y <- -y
##   print(y)
## }
```

---

---

**Note** Calling `class` on objects of the three aforementioned types yields `name`, `call`, and `expression`, whereas `typeof` returns `symbol`, `language`, and `expression`, respectively.

---

### 15.3 Calls as combinations of expressions

We have mentioned that calls (compound expressions) are combinations of simple or compound expressions of the form  $(f, e_1, \dots, e_n)$ .

The first expression on the list, denoted above with  $f$ , plays a special role. It is precisely seen in the following examples:

```
as.call(expression(f, x))
## f(x)
as.call(expression(`+`, 1, x))
## 1 + x
as.call(expression(`while`, i < 10, i <- i + 1))
## while (i < 10) i <- i + 1
as.call(expression(function(x) x**2, log(exp(1))))
## (function(x) x^2)(log(exp(1)))
as.call(expression(1, x, y, z)) # utter nonsense, but syntactically valid
## 1(x, y, z)
```

Recall from Section 9.4 that operators and language constructs such as `if` and `while` are ordinary functions.

Furthermore:

```
expr <- quote(f(1+2, a=1, b=2))
length(expr)
## [1] 4
names(expr) # NULL if no arguments are named
## [1] "" "" "a" "b"
```

#### 15.3.1 Browsing parse trees

Square brackets give us access to the individual expressions constituting an object of the type `call`. For example:

```
expr <- quote(1+x)
expr[[1]]
## `+`
```

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```
expr[2:3]
## 1(x)
```

A compound expression was defined recursively: it may consist of other compound expressions.

For instance, the following expression:

```
expr <- quote(
  while (i < 10) {
    cat("i =", i, "\n")
    i <- i+1
  }
)
```

can be rewritten using the  $f(\dots)$  notation like:

```
`while`(`<`(i, 10), `{`(`cat`("i =", i, "\n"), `<-`(i, `+`(i, 1))))
```

Equivalently, in the Polish notation (the prefix notation;  $(f, \dots)$ ; traditionally used in Lisp), it will look like:

```
(
  `while`,
  (`<`, i, 10),
  (
    `{`,
    (cat, "i =", i, "\n"),
    (
      `<-`,
      i,
      (`+`, i, 1)
    )
  )
)
```

Thus, for example, we can dig into the sub-expressions using a series of extractions:

```
expr[[2]][[1]] # or expr[[c(2, 1)]]
## `<`
expr[[3]][[2]][[4]] # or expr[[c(3, 2, 4)]]
## [1] "\n"
```

**Example 15.2** We can even compose a recursive function to traverse the whole parse tree:

```
recapply <- function(expr)
```

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```

{
  if (is.call(expr)) lapply(expr, recapply)
  else expr
}

str(recapply(expr))
## List of 3
## $ : symbol while
## $ :List of 3
## ..$ : symbol <
## ..$ : symbol i
## ..$ : num 10
## $ :List of 3
## ..$ : symbol {
## ..$ :List of 4
## .. ..$ : symbol cat
## .. ..$ : chr "i ="
## .. ..$ : symbol i
## .. ..$ : chr "\n"
## ..$ :List of 3
## .. ..$ : symbol <-
## .. ..$ : symbol i
## .. ..$ :List of 3
## .. .. ..$ : symbol +
## .. .. ..$ : symbol i
## .. .. ..$ : num 1

```

### 15.3.2 Manipulating calls

The R language is *homoiconic*: it can treat code as data. This includes the ability to manipulate it on the fly. This is because, just like on lists, we can freely use the replacement versions of ``[`` and ``[[`` on objects of the type `call`.

```

expr[[2]][[1]] <- as.name("<=")
expr[[3]] <- quote(i <- i * 2)
print(expr)
## while (i <= 10) i <- i * 2

```

We are only limited by our imagination.

## 15.4 Inspecting function definitions and arguments thereto

### 15.4.1 Getting the body and formal arguments

Consider the following definition:

```
test <- function(x, y=1)
  x+y # whatever
```

We know from the first part of this book that calling **print** on a function will reveal its source code.

It turns out that we can get access to the list of parameters in the form of a named list<sup>6</sup>:

```
formals(test)
## $x
##
##
## $y
## [1] 1
```

Note that the expressions generating the values of the default arguments are stored as ordinary list elements (for more details, see [Section 17.2](#)).

Furthermore, we can get access to the function's body:

```
body(test)
## x + y
```

It is an object of the now well-known class `call`. Thus, we can customise it as we please:

```
body(test)[[1]] <- as.name("*") # change from `+` to `*`
body(test) <- as.call(list(as.name("{"), quote(cat("spam")), body(test)))
test
## function (x, y = 1)
## {
##   cat("spam")
##   x * y
## }
```

<sup>6</sup> Actually, a special internal datatype called `pairlist`, which is rarely seen in R; see [65] and [62] for information on how to deal with them at the C level. From this course's perspective, seeing pairlists as named lists is perfectly fine.

### 15.4.2 Getting the expression passed as an actual argument

A call to **substitute** allows us to reveal the expression used to generate a function's argument.

```
test <- function(x) substitute(x)
```

Some examples:

```
test(1)
## [1] 1
test(2+spam)
## 2 + spam
test(test(test(!!7)))
## test(test(!!7))
test() # it is not an error
```

Chapter 17 notes that arguments are evaluated only on demand (lazily): **substitute** triggers no computations. This opens the possibility to author functions that interpret their input whichever way they like; see Section 9.5.7, Section 12.3.9, and Section 17.5 for examples.

**Example 15.3** **library** (see Section 7.3.1) allows specifying the name of the package to be loaded both in the form of a character string and a name:

```
library("gsl") # preferred
library(gsl) # discouraged - via as.character(substitute(package))
```

A user saves two keystrokes at the cost of not being able to prepare the package name programmatically before the call:

```
which_package <- "gsl"
library(which_package) # library("which_package")
## Error in library(which_package): there is no package called
## 'which_package'
```

In order to make the above possible, we need to alter the `character.only` argument (which defaults to `FALSE`):

```
library(which_package, character.only=TRUE)
```

**Exercise 15.4** It is quite common to see a call like **deparse(substitute(arg))** or **as.character(substitute(arg))** in many built-in functions. Study the source code of **plot.default**, **hist.default**, **prop.test**, **wilcox.test.default** and the aforementioned **library**. Explain why they do that. Propose a solution to achieve the same functionality without using reflection techniques.

### 15.4.3 Checking if an argument is missing

There is an easy way to check whether an argument was provided at all:

```
test <- function(x) missing(x)

test(1)
## [1] FALSE
test()
## [1] TRUE
```

**Exercise 15.5** Study the source code of `sample`, `seq.default`, `plot.default`, `matplot`, and `t.test.default`. Determine the role of a call to `missing`. Would introducing a default argument `NULL` and testing its value with `is.null` constitute a reasonable alternative?

### 15.4.4 Determining how a function was called

Even though this somewhat touches on the topics discussed in the two following chapters, it is worth knowing that `sys.call` can look at the call stack and determine how the current function was invoked.

Moreover, `match.call` takes us a step further: it returns a call with argument names matched to a function's formal parameters list.

For instance:

```
test <- function(x, y, ..., a="yes", b="no")
{
  print(sys.call()) # sys.call(0)
  print(match.call())
}

x <- "maybe"
test("spam", "bacon", "eggs", u = "ham" < "jam", b=x)
## test("spam", "bacon", "eggs", u = "ham" < "jam", b = x)
## test(x = "spam", y = "bacon", "eggs", u = "ham" < "jam", b = x)
```

Another example where we see that we can access the call stack much more deeply:

```
f <- function(x)
{
  g <- function(y)
  {
    cat("g:\n")
    print(sys.call(0))
    print(sys.call(-1)) # go back one frame
    y
  }
}
```

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```

    cat("f:\n")
    print(sys.call(0))
    g(x+1)
}

f(1)
## f:
## f(1)
## g:
## g(x+1)
## f(1)
## [1] 2

```

**Note** Let us formalise the order of matching function parameters to the passed arguments. As described in Section 4.3 of [66], it proceeds as follows:

1. keyword arguments with names matched exactly, each name matched at most once,
2. remaining keyword arguments, but with the partial matching of names listed before the ellipsis, ``...``, each match must be unambiguous,
3. positional matching to the remaining parameters,
4. all remaining arguments (named or not) will be consumed by the ellipsis (if present).

For instance:

```

test <- function(spam, jasmine, jam, ..., option=NULL)
  print(match.call())

```

Example calls:

```

test(1, 2, 3, 4, option="yes")
## test(spam = 1, jasmine = 2, jam = 3, 4, option = "yes")
test(1, 2, jasmine="no", sp=4, ham=7)
## Warning in test(1, 2, jasmine = "no", sp = 4, ham = 7): partial argument
##   match of 'sp' to 'spam'
## Warning in match.call(definition, call, expand.dots, envir): partial
##   argument match of 'sp' to 'spam'
## test(spam = 4, jasmine = "no", jam = 1, 2, ham = 7)
test(1, 2, ja=7) # ambiguous match
## Warning in test(1, 2, ja = 7): partial argument match of 'ja' to 'jasmine'
## Error in test(1, 2, ja = 7): argument 3 matches multiple formal arguments

```

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```
test(o=7) # partial matching of `option` failed - `option` is after `...`
## test(o = 7)
```

Note again that our environment uses `options(warnPartialMatchArgs=TRUE)`.

**Exercise 15.6** A function can<sup>7</sup> see how it was defined by its maker. Call `sys.function` inside its body to reveal that.

**Exercise 15.7** Execute “`match.call(sys.function(-1), sys.call(-1))`” in the `g` function above.

## 15.5 Exercises

**Exercise 15.8** Answer the following questions:

- What is a simple expression? What is a compound expression? Give a few examples.
- What is the difference between an object of the type `call` and that of the type `expression`?
- What do **formals** and **body** return when called on a function object?
- How to test if an argument to a function was given at all? Provide a use case for such a verification.
- Give a few ways to create an unevaluated call.
- What is the purpose of `deparse(substitute(...))`? Give a few examples of functions that use this technique.
- What is the difference between `sys.call` and `match.call`?

**Exercise 15.9** Write a function that takes the dot-dot-dot argument (Section 9.5.6). Using `match.call` (amongst others), determine the list of all the expressions passed via ``...``; some might be named (just like in one of the above examples). The solution is given in Section 17.3.

**Exercise 15.10** Write a function `check_if_calls(f, fun_list)` that takes another function `{command}fon` input. Then, it verifies iff calls any of the functions (referred to by their names) from a character vector `fun_list`.

<sup>7</sup> Therefore, it is possible to have a function that returns a modified version of itself.

---

## Environments and evaluation (\*)

---

In the first part of our book, we discussed the most crucial *basic* object types: numeric, logical, and character vectors, lists (generic vectors), and functions.

In this chapter, we introduce another basic type: *environments*. Like lists, they can be classified as recursive data structures; compare the diagram in [Figure 17.2](#).

---

**Important** Each object of the type `environment` consists of:

- a *frame*<sup>1</sup> ([Section 16.1](#)), which stores a set of *bindings* that associate variable names with their corresponding values; it can be thought of as a container of named R objects of any type;
  - a reference to an *enclosing environment*<sup>2</sup> ([Section 16.2.2](#)), which might be inspected (recursively!) when a requested named variable is not found in the current frame.
- 

Even though we rarely interact with them directly (unless we need a hash table-like data structure with a quick by-name element lookup), they are crucial for the R interpreter itself. Namely, we shall soon see that they form the basis of the *environment model of evaluation*, which governs how expressions are computed ([Section 16.2](#)).

---

### 16.1 Frames: Environments as object containers

To create a new, empty environment, we can call the `new.env` function:

```
e1 <- new.env()
typeof(e1)
## [1] "environment"
```

In this section, we treat environments merely as containers for named objects of any kind, i.e., we deal with the *frame* part thereof.

---

<sup>1</sup> Not to be confused with a *data frame*, i.e., an object (list) of S3 class `data.frame`; see [Chapter 12](#).

<sup>2</sup> Some also call it a *parent* environment, but we will not. We will try following the nomenclature established in [Section 3.2](#) in [1]. Note that there is a bit of a mess in the R documentation regarding how enclosing environments are referred to.

Let us insert some elements into `e1`:

```
e1[["x"]] <- "x in e1"
e1[["y"]] <- 1:3
e1[["z"]] <- NULL # unlike in the case of lists, creates a new element
```

The ``[[`` operator provides us with a *named list*-like look-and-feel also in the case of element extraction:

```
e1[["x"]]
## [1] "x in e1"
e1[["spam"]] # does not exist
## NULL
(e1[["y"]] <- e1[["y"]]*10) # replace with new content
## [1] 10 20 30
```

### 16.1.1 Printing

Printing an environment leads to a quite awkward result:

```
print(e1) # same with str(e1)
## <environment: 0x55888446baa8>
```

It is the address where `e1` is stored in the computer's memory. It can serve as the environment's unique identifier.

As we have said, these objects are of rather *internal* interest. Thus, such an esoteric message was perhaps a good design choice to ward off novices. However, we can easily get the list of objects stored inside the container by calling `names`:

```
names(e1) # but attr(e1, "names") is not set
## [1] "x" "y" "z"
```

Moreover, `length` gives the number of bindings in the frame:

```
length(e1)
## [1] 3
```

### 16.1.2 Environments vs named lists

Environment frames, in some sense, can be thought of as named lists, but the set of admissible operations is severely restricted. In particular, we cannot extract more than one element at the same time using the index operator:

```
e1[c("x", "y")] # but see the `mget` function
## Error in e1[c("x", "y")]: object of type 'environment' is not subsettable
```

nor can we refer to the elements by position:

```
e1[[1]] <- "bad key"
## Error in e1[[1]] <- "bad key": wrong args for environment subassignment
```

**Exercise 16.1** Check if **`lapply`** and **`Map`** can be applied directly on environments. Also, can we iterate over their elements using a **`for`** loop?

Still, named lists can be converted to environments and vice versa using **`as.list`** and **`as.environment`**.

```
as.list(e1)
## $x
## [1] "x in e1"
##
## $y
## [1] 10 20 30
##
## $z
## NULL
as.environment(list(u=42, whatever="it's not going to be printed anyway"))
## <environment: 0x558884023528>
as.list(as.environment(list(x=1, y=2, x=3))) # no duplicates allowed
## $y
## [1] 2
##
## $x
## [1] 3
```

### 16.1.3 Hash maps: Fast element lookup by name

Environment frames are internally implemented using hash tables (hash maps; see, e.g., [14, 41]) with character string keys.

---

**Important** A *hash table* is a data structure that allows for a very quick<sup>3</sup> lookup and insertion of individual elements *by name*.

---

The above comes at a price, including what we have already observed above:

- the elements are not ordered in any particular way: they cannot be referred to via a numeric index;
- all element names must be unique.

---

**Note** A list may be considered a *sequence*, but an environment frame is only, in fact, a *set* (a bag) of *key-value pairs*. In most numerical computing applications, we would rather

---

<sup>3</sup> In hash tables, element lookup, insertion, and deletion take amortised  $O(1)$  time.

store, iterate over, and process all the elements *in order*, hence the greater prevalence of the former. Lists still allow for an element lookup by name, even though this is slightly slower<sup>4</sup>. Overall, they are much more universal.

**Example 16.2** *A natural use case of manually-created environment frames deals with grouping a series of objects identified by character string keys.*

*Consider a simple pseudocode for counting the number of occurrences of objects in a given container:*

```
for (key in some_container) {
  if (!is.null(counter[["key"]]))
    counter[["key"]] <- counter[["key"]]+1
  else
    counter[["key"]] <- 1
}
```

*Let us assume that `some_container` is large, say, of size  $n$ , e.g., it is generated on the fly by reading some data stream. Then, the run-time of the above algorithm will depend on the data structure used. If the counter is a list, then, theoretically, the worst-case performance will be  $O(n^2)$  (if all keys are unique). On the other hand, for environments, it will be faster by one order magnitude: down to amortised  $O(n)$ .*

**Exercise 16.3** *Implement a test function according to the above pseudocode and benchmark the two data structures using `proc. time` on some example data.*

**Exercise 16.4** (\*) *Determine the number of unique text lines in a huge file (assuming that the set of unique text lines fits into memory, but the file itself does not). Also, determine the five most frequently occurring text lines.*

### 16.1.4 Pass by value, copy on demand: Not for environments

Given any object, say, `x`, when we issue:

```
y <- x
```

its copy<sup>5</sup> is made so that `y` and `x` are independent. In other words, any change to the state of `x` (or `y`) is not reflected in `y` (or `x`).

For instance:

```
x <- list(a=1)
y <- x
y[["a"]] <- y[["a"]]+1
```

(continues on next page)

<sup>4</sup> Accessing elements by position (numeric index) in lists takes  $O(1)$  time. The worst-case scenario for the element lookup by name is linear with respect to the container size: when the item is not found. Also, inserting new elements at the end takes amortised  $O(1)$  time.

<sup>5</sup> Delayed (on demand); see below.

(continued from previous page)

```
print(y)
## $a
## [1] 2
print(x) # not affected: `x` and `y` are independent
## $a
## [1] 1
```

The same happens with arguments that we feed to the functions:

```
mod <- function(y, key) # it is like: local_y <- passed_argument
{
  y[[key]] <- y[[key]]+1
  y
}

mod(x, "a") # returns a modified copy of `x`
## $a
## [1] 2
print(x) # not affected
## $a
## [1] 1
```

We can thus say that R applies the *pass-by-value* strategy here.

---

**Important** Environments are the only<sup>6</sup> objects that follow the assign- and pass-by-reference strategies.

---

In other words, if we perform:

```
x <- as.environment(x)
y <- x
```

then the names `x` and `y` are bound with the same object in the computer's memory:

```
print(x)
## <environment: 0x558883254728>
print(y)
## <environment: 0x558883254728>
```

Therefore:

---

<sup>6</sup> We do not count all the tricks we can do at the C language level (Chapter 14). Also, the distinction between pass-by-value and pass-by-reference is slightly more complicated in R because of the lazy evaluation of arguments (Chapter 17). We make an idealisation for didactic purposes here.

```

y[["a"]] <- y[["a"]]+1
print(y[["a"]])
## [1] 2
print(x[["a"]]) # `x` is `y`, `y` is `x`
## [1] 2

```

The same happens when we pass an environment to a function:

```

mod(y, "a") # pass-by-reference (`y` is `x`, remember?)
## <environment: 0x558883254728>
x[["a"]] # `x` has changed
## [1] 3

```

Thus, any changes we make to an environment passed as an argument to a function will be visible *outside* the call. This minimises time and memory use in certain situations.

---

**Note** (\*) For efficiency reasons, when we write “`y <- x`”, a copy of `x` (unless it is an environment) is created only if it is absolutely necessary.

Here is some benchmarking of the *copy-on-demand* mechanism.

```

n <- 100000000 # like, a lot

```

Creation of a new large numeric vector:

```

t0 <- proc.time(); x <- numeric(n); proc.time() - t0
##      user  system elapsed
## 0.853   1.993   2.852

```

Creation of a (delayed) copy:

```

t0 <- proc.time(); y <- x; proc.time() - t0
##      user  system elapsed
##      0      0      0

```

It was instant. Thus, we definitely did not duplicate the `n` data cells.

Copy-on-demand is implemented using some simple *reference counting*; compare Section 14.2.4. We can inspect that `x` and `y` point to the same address in memory by calling:

```

.Internal(inspect(x)) # internal function - do not use it
## @7efba1134010 14 REALSXP g0c7 [REF(2)] (len=1000000000, tl=0) 0,0,0,0,...
.Internal(inspect(y))
## @7efba1134010 14 REALSXP g0c7 [REF(2)] (len=1000000000, tl=0) 0,0,0,0,...

```

The actual copying is only triggered when we try to modify `x` or `y`. This is when the objects need to be separated.



```
t0 <- proc.time(); y[1] <- 1;      proc.time() - t0
##   user  system elapsed
##  1.227   1.910   3.142
```

Now *x* and *y* are different objects.

```
.Internal(inspect(x))
## @7efba1134010 14 REALSXP g0c7 [MARK,REF(1)] (len=1000000000, tl=0) 0,0,...
.Internal(inspect(y))
## @7ef9c43ce010 14 REALSXP g0c7 [MARK,REF(1)] (len=1000000000, tl=0) 1,0,...
```

The elapsed time is similar to that needed to create *x* from scratch. Further modifications will already be quick:

```
t0 <- proc.time(); y[2] <- 2;      proc.time() - t0
##   user  system elapsed
##  0.000   0.001   0.000
```

### 16.1.5 A note on reference classes (\*\*)

In Section 11.5, we briefly mentioned the S4 system for object-oriented programming.

It turns out that we also have access to its variant, called *reference classes*<sup>7</sup>. It was first introduced in R version 2.12.0.

Reference classes are implemented using S4 classes, with the data part being of the type environment. This gives a more typical object-oriented experience, where methods can modify the data they act on in place.

They are theoretically interesting concepts on their own and quite appealing to package developers with C++ or Java background. Nevertheless, in the current author's opinion, such classes are alien citizens of our environment, violating its *functional* nature. Therefore, we will not be discussing them here.

A curious reader is referred to `help("ReferenceClasses")` and Chapters 9 and 11 of [11] for more details.

---

## 16.2 The environment model of evaluation

In Chapter 15, we said that there are three types of expressions: constants (e.g., 1 and "spam"), names (e.g., ``x`` and ``spam``), and calls (like `f(x, 1)`).

---

<sup>7</sup> Some call them R5, but we will not.

---

**Important** Names (symbols) have no meaning by themselves. The *meaning* of a name always depends on the context, which is specified by some environment.

---

Consider a simple expression merely consisting of a name, ``x``:

```
expr_x <- quote(x)
```

Let us define two environments that bind the name ``x`` with two different constants.

```
e1 <- as.environment(list(x=1))
e2 <- as.environment(list(x="spam"))
```

An expression is evaluated *within* a specific environment. We can do that by calling `eval`:

```
eval(expr_x, envir=e1) # evaluate `x` within environment e1
## [1] 1
eval(expr_x, envir=e2) # evaluate the same `x` within environment e2
## [1] "spam"
```

The very same expression has two different meanings, depending on the context. This is quite like in the so-called real life: “I’m good” can mean “I don’t need anything” but also “My virtues are plentiful”. It all depends on who and when is asking, i.e., in which *environment* we *evaluate* the said sentence.

We call this the *environment model of evaluation*, a notion that R authors have borrowed from a Lisp-like language called Scheme<sup>8</sup> (see Section 3.2 of [1] and Section 6 of [66]).

## 16.2.1 Getting the current environment (here: the global one)

By default, expressions are evaluated in the *current* environment. We can fetch it by calling:

```
sys.frame(sys.nframe()) # get the current environment
## <environment: R_GlobalEnv>
```

We are working *on the R console*. Hence, the current one is the *global* environment (user workspace). We can access it from anywhere by calling `globalenv` or referring to the ``.GlobalEnv`` object.

**Example 16.5** *Calling any operation, for instance*<sup>9</sup>:

---

<sup>8</sup> That is why everyone *serious* about R programming should add the *Structure and Interpretation of Computer Programs* [1] to their reading list. Also, R is not the only known marriage between statistics and Lisp-like languages; see also LISP-STAT [53].

<sup>9</sup> Let us, for now, take for granted that `<-` is accessible from the current context and denotes assignment.

```
x <- "spammy spam"
```

means evaluating it within the current environment:

```
eval(quote(x <- "spammy spam"), envir=sys.frame(sys.nframe()))
```

Here, we bound the string "spammy spam" with the name `x` in the current environment's frame:

```
sys.frame(sys.nframe())[["x"]] # yes, `x` is in the current environment now
## [1] "spammy spam"
globalenv()[["x"]] # because the global environment is the current one here
## [1] "spammy spam"
```

Therefore, when we now refer to `x` (from within the current environment):

```
x # eval(quote(x), envir=sys.frame(sys.nframe()))
## [1] "spammy spam"
```

precisely the above named object is fetched.

**Exercise 16.6 save.image** can be used to save the current workspace, i.e., the global environment, by default, to the file named `.Rdata` in the current working directory. Test this function in combination with **load**.

---

**Note** Names starting with a dot are *hidden*. `ls`, a function to fetch all names registered within a given environment, does not list them by default.

```
.test <- "spam"
ls() # list all names in the current environment, i.e., the global one
## [1] "e1"      "e2"      "expr_x"  "mod"     "x"       "y"
```

Compare the above with:

```
ls(all.names=TRUE)
## [1] ".Random.seed" ".test"      "e1"        "e2"
## [5] "expr_x"      "mod"       "x"         "y"
```

On a side note, `.Random.seed` stores the current pseudorandom number generator's seed; compare Section 2.1.5.

---

### 16.2.2 Enclosures, enclosures thereof, etc.

To show that there is much more to the environment model of evaluation than what we mentioned above, let us try to evaluate an expression featuring two names:

```
e2 <- as.environment(list(x="spam")) # once again (a reminder)
expr_comp <- quote(x < "eggs")
eval(expr_comp, envir=e2)
## Error in x < "eggs": could not find function "<"
```

The meaning of any constant (here, "spam") is context-independent, ``x`` is specified by the environment provided, but the name ``<`` is not mentioned therein. Hence the error.

Nonetheless, we *feel* that we know the meaning of ``<``. It is a relational operator, obviously, isn't it? To increase the confusion, let us highlight that our experience-grounded intuition is true in the following context:

```
e3 <- new.env()
e3[["x"]] <- "bacon"
eval(expr_comp, envir=e3)
## [1] TRUE
```

So where does the name ``<`` come from? It is neither included in `e2` nor `e3`:

```
e2[["<"]]
## NULL
e3[["<"]]
## NULL
```

Is ``<`` hardcoded somewhere? Or is it also dependent on the context? Why is it *visible* when evaluating an expression within `e3` but not in `e2`?

Studying<sup>10</sup> `help("[")` (see the *Environments* section therein), we discover that `e3[["<"]]` is equivalent to a call to `get("<", envir=e3, inherits=FALSE)`.

In `help("get")`, we read that if the `inherits` argument is set to `TRUE` (which is the default in `get`), then *the enclosing frames of the given environment are searched as well*.

Continuing the example from the previous subsection:

```
get("<", envir=e2) # inherits=TRUE
## Error in get("<", envir = e2): object '<' not found
get("<", envir=e3) # inherits=TRUE
## function (e1, e2) .Primitive("<")
```

And indeed, we see that ``<`` is *reachable* from within `e3` but not `e2`. It means that `e3` *points to* another environment where further information should be sought if we the current container is left empty-handed.

---

**Important** The reference (pointer) to the *enclosing environment* is integral to each en-

---

<sup>10</sup> Which we should have done already a long time ago, but most likely, we did not.

vironment (alongside a *frame* of objects). It can be fetched and set using the `parent.env` function.

### 16.2.3 Missing names are sought in enclosing environments

To understand the idea of enclosing environments better, let us create two new environments whose enclosures are explicitly set as follows:

```
(e4 <- new.env(parent=e3))
## <environment: 0x558883a96948>
(e5 <- new.env(parent=e4))
## <environment: 0x558883975f78>
```

To verify that everything is in order, let us inspect the following:

```
print(e3) # this is the address of e3 by the way
## <environment: 0x558884072f90>
parent.env(e4) # e3 is the enclosing environment of e4
## <environment: 0x558884072f90>
parent.env(e5) # e4 is the enclosing environment of e5
## <environment: 0x558883a96948>
```

Also, let us bind two different objects with the name ``y`` in `e5` and `e3`.

```
e5[["y"]] <- "spam"
e3[["y"]] <- function() "a function `y` in e3"
```

The current state of matters is depicted in Figure 16.1.

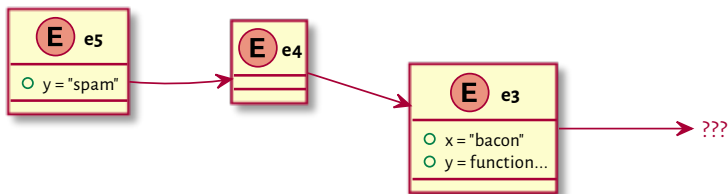


Figure 16.1: Example environments and their enclosures (original setting)

Now, let us consider a simple expression featuring the ``y`` name only and evaluate it in the above environments:

```
expr_y <- quote(y)
eval(expr_y, envir=e3)
## function() "a function `y` in e3"
eval(expr_y, envir=e5)
## [1] "spam"
```

No surprises yet. However, evaluating it in `e4`, which does not feature ``y``, yields:

```
eval(expr_y, envir=e4)
## function() "a function `y` in e3"
```

It returned ``y`` from `e4`'s enclosure, `e3`.

Let us horse around with the enclosures of `e5` and `e4` so that we obtain the setting depicted in Figure 16.2:

```
parent.env(e5) <- e3
parent.env(e4) <- e5
```

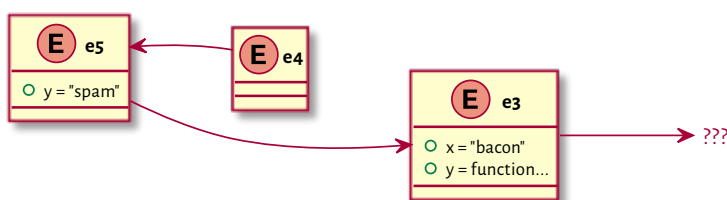


Figure 16.2: Example environments and their enclosures (after the change made)

Evaluating ``y`` again in the same `e4` nourishes a very different result:

```
eval(expr_y, envir=e4)
## [1] "spam"
```

---

**Important** If a name is referred to in an expression but is missing in the current environment, it will be sought in its enclosure(s).

---



---

**Note** There are some functions related to searching within and modifying environments which optionally (see their `inherits` argument) allow for continuing explorations in the enclosures until successful:

---

- `inherits=TRUE` by default:
    - `exists`,
    - `get`,
  - `inherits=FALSE` by default:
    - `assign`,
    - `rm` (remove).
-

### 16.2.4 Looking for functions

Interestingly, if a name is used instead of a function to be called, the object sought is always<sup>11</sup> of the mode function.

Consider a similar expression to the above, but this time including the name ``y`` playing a different role:

```
expr_y2 <- quote(y()) # a call to something named `y`
eval(expr_y2, envir=e4)
## [1] "a function `y` in e3"
```

In other words, what we used here was not:

```
get("y", envir=e4)
## [1] "spam"
```

but:

```
get("y", envir=e4, mode="function")
## function() "a function `y` in e3"
```

---

**Note** `"name()"`, `"`name`()"`, and `"`name`()"` are synonymous. However, the first expression is acceptable only if the name is syntactically valid.

---

### 16.2.5 Inspecting the search path

Going back to our expression involving a relational operator:

```
expr_comp
## x < "eggs"
```

Why does the following work as expected?

```
eval(expr_comp, envir=e3)
## [1] TRUE
```

Well, we gathered all the bits to understand it now. Namely, `<` is a function that is looked up in the following way:

```
get("<", envir=e3, inherits=TRUE, mode="function")
## function(e1, e2) .Primitive("<")
```

It was reachable from `e3`, which means that `e3` also has an enclosing environment.

---

<sup>11</sup> This is why we can write `"c <- c(1, 2)"` and then still be able to call `c` to create another vector.

```
parent.env(e3)
## <environment: R_GlobalEnv>
```

This is our global namespace, which was the current environment when `e3` was created. Still, we did not define ``<`` there. It means that the global environment also has an enclosure.

We can explore the whole *search* path by starting at the global environment and following the enclosures recursively.

```
ecur <- globalenv() # starting point
repeat {
  cat(paste0(format(ecur), " (", attr(ecur, "name"), ")")) # pretty-print

  if (exists("<", envir=ecur, inherits=FALSE))
    cat(strrep(" ", 20), "`<` found here!")
  cat("\n")

  ecur <- parent.env(ecur) # advance to its enclosure
}
## <environment: R_GlobalEnv> ()
## <environment: 0x5588842ab190> (.marekstuff)
## <environment: package:stats> (package:stats)
## <environment: package:graphics> (package:graphics)
## <environment: package:grDevices> (package:grDevices)
## <environment: package:utils> (package:utils)
## <environment: package:datasets> (package:datasets)
## <environment: package:methods> (package:methods)
## <environment: 0x558882343960> (Autoloads)
## <environment: base> ()          `<` found here!
## <environment: R_EmptyEnv> ()
## Error in parent.env(ecur): the empty environment has no parent
```

Underneath the global environment, there is a whole list of attached packages:

1. packages attached by the user (`.marekstuff` is used internally in the process of evaluating code in this book),
2. default packages (Section 7.3.1),
3. **(\*\*)** **Autoloads** (for the promises-to-load R packages; compare `help("autoload")`; it is a technicality we may safely ignore here),
4. the **base** package, which we can access directly by calling `baseenv`; it is where most of the *fundamental* functions from the previous chapters reside,
5. the *empty* environment (`emptyenv`), which is the only one followed by nothing (the loop would turn out endless otherwise).



It comes at no surprise that the `<` operator has been found in the **base** package.

---

**Note** On a side note, the reason why this operation failed:

```
e2 <- as.environment(list(x="span")) # to recall
eval(expr_comp, envir=e2)
## Error in x < "eggs": could not find function "<"
```

is because **as.environment** sets the enclosing environment to:

```
parent.env(e2)
## <environment: R_EmptyEnv>
```

See also **list2env** which gives greater control over this (cf. its **parent** argument).

---

### 16.2.6 Attaching to and detaching from the search path

In Section 7.3.1, we mentioned that we can access the objects exported by a package without attaching them to the search path by using the **pkg::object** syntax (this loads the package if necessary).

For instance:

```
tools::toTitleCase("`tools` not attached to the search path")
## [1] "`tools` not Attached to the Search Path"
```

However:

```
toTitleCase("nope")
## Error in toTitleCase("nope"): could not find function "toTitleCase"
```

It does not work since **toTitleCase** is not reachable from the current environment.

Let us inspect the current search path (yes, there is a built-in function for that):

```
search()
## [1] ".GlobalEnv" ".marekstuff" "package:stats"
## [4] "package:graphics" "package:grDevices" "package:utils"
## [7] "package:datasets" "package:methods" "AutoLoads"
## [10] "package:base"
```

Writing **"pkg::"** might be inconvenient in the long run (for some). Thus, we can call **library** to attach the package to the search path immediately below the global environment.

```
library("tools")
```

The search path becomes (see Figure 16.3 for an illustration):

```
search()
```

```
## [1] ".GlobalEnv"      "package:tools"    ".marekstuff"
## [4] "package:stats"   "package:graphics" "package:grDevices"
## [7] "package:utils"   "package:datasets" "package:methods"
## [10] "Autoloads"       "package:base"
```

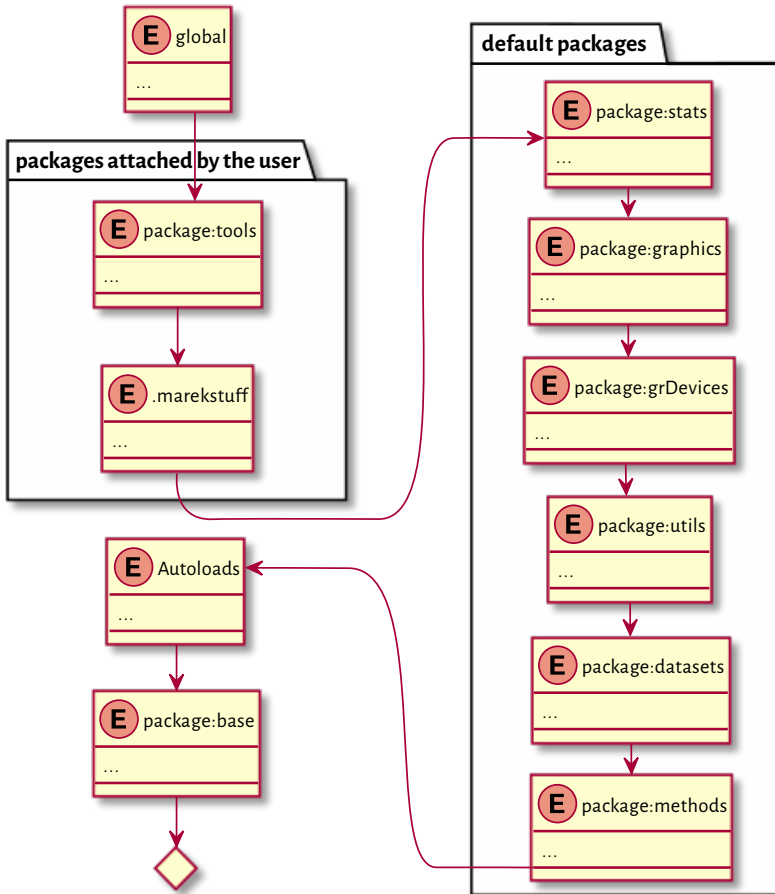


Figure 16.3: The search path after attaching the **tools** package

Therefore, what follows, now works as expected:

```
toTitleCase("Nobody expects the Spanish Inquisition")
## [1] "Nobody Expects the Spanish Inquisition"
```

We can use **detach**<sup>12</sup> to remove an item from the search path.

<sup>12</sup> Which does not unload the package from memory, though; see **unload** (possibly combined with **library.dynam.unload**).

```
detach("package:tools")
"package:tools" %in% search() # not there anymore
## [1] FALSE
```

We use the “package:” prefix for the reasons that we shall describe in [Section 16.3.5](#).

**Note** We can also plug arbitrary environments<sup>13</sup> and named lists into the search path. Recalling that data frames are built on the latter ([Section 12.1.6](#)), some users rely on this technique to free themselves from the onerous burden of typing the object name each time its column is to be referred to:

```
attach(iris)
head(Sepal.Length) # iris[["Sepal.Length"]]
## [1] 5.1 4.9 4.7 4.6 5.0 5.4
```

Here, the `iris` list was converted to an environment, and the necessary enclosures were set accordingly:

```
str(parent.env(globalenv()))
## <environment: 0x558884344860>
## - attr(*, "name")= chr "iris"
str(parent.env(parent.env(globalenv())))
## <environment: 0x5588842ab190>
## - attr(*, "name")= chr ".marekstuff"
```

Overall, attaching data frames is discouraged, especially outside the interactive mode. Let us not be too lazy.

```
detach(iris) # such a relief
```

### 16.2.7 Masking (shadowing) objects from down under

An assignment via `<-` (and **assign**, by default) creates a binding in the *current* environment.

Therefore, even if the name to bind exists somewhere on the search path, it will not be modified. Instead, a new name will be created.

```
expr_comp <- quote("spam" < "eggs")
eval(expr_comp)
## [1] FALSE
```

<sup>13</sup> Or we should rather say, environment frames. When an environment is attached to the search path, it is duplicated so that the changes made to the original environment are not reflected in the copy. Then its previous enclosure is discarded. After all, we want a series of recursive calls to **parent.env** to form the whole search path.

Here, we rely on ``<`` from the base environment. Withal, we can create an object of the same name in the current (global) context:

```
`<` <- function(e1, e2)
{
  warning("This is not the base `<`, mate.")
  NA
}
```

Now we have two different functions of the same name. When we evaluate an expression within the current environment or any of its “descendants”, the new name will *shadow* the base one:

```
eval(expr_comp)
## Warning in "spam" < "eggs": This is not the base `<`, mate.
## [1] NA
eval(expr_comp, envir=e5) # e5's enclosure's enclosure is the global env
## Warning in "spam" < "eggs": This is not the base `<`, mate.
## [1] NA
```

But we can still call the original function directly:

```
base::`<`(1, 2)
## [1] TRUE
```

It is also reachable from within the current environment’s “ancestors”:

```
eval(expr_comp, envir=as.environment("package:utils"))
## [1] FALSE
```

Before proceeding any further, let us clean up after ourselves. Otherwise, we will be asking for trouble.

```
rm("<") # removes `<` from the global environment
```

An attached package may introduce some object names that are also available elsewhere. For instance:

```
library("stringx")
## Attaching package: 'stringx'
## The following objects are masked from 'package:base': casefold, chartr,
##   endsWith, gregexec, gregexpr, grep, grepl, gsub, ISOdate, ISOdatetime,
##   nchar, nzchar, paste, paste0, regexexec, regexpr, sprintf, startsWith,
##   strftime, strptime, strrep, strsplit, strtrim, strwrap, sub, substr,
##   substr<-, substring, substring<-, Sys.time, tolower, toupper, trimws,
##   xtfrm, xtfrm.default
```

Therefore, in the current context, we have what follows:

```
toupper("Groß") # stringx::toupper
## [1] "GROSS"
base::toupper("Groß")
## [1] "GROß"
```

Sometimes<sup>14</sup>, we can use `assign(..., inherits=TRUE)` or its synonym, `<<=`, to modify the *existing* binding (without creating a new one if not necessary).

---

**Note** Let us attach the `iris` data frame (named `list`) to the search path again:

```
attach(iris)
Sepal.Length[1] <- 0
```

It does not modify the original `iris` nor its converted-to-an-environment copy that we can find in the search path. Instead, a new vector named `Sepal.Length` has been created in the current environment:

```
exists("Sepal.Length", envir=globalenv(), inherits=FALSE)
## [1] TRUE
```

We can verify the above statement as follows:

```
rm("Sepal.Length") # removes the one in the global environment
Sepal.Length[1] # `iris` from the search path
## [1] 5.1
iris[["Sepal.Length"]][1] # the original `iris`
## [1] 5.1
```

However, by writing:

```
Sepal.Length[1] <<= 0 # uses assign(..., inherits=TRUE)
```

We changed the state of the environment on the search path.

```
exists("Sepal.Length", envir=globalenv(), inherits=FALSE)
## [1] FALSE
Sepal.Length[1] # `iris` from the search path
## [1] 0
```

Yet, the original `iris` object is left untouched. There is no mechanism in place that would *synchronise* the original data frame and the object in the search path.

---

<sup>14</sup> We normally cannot modify package namespaces. As we will mention in Section 16.3.5, they are automatically locked.

```
iris[["Sepal.Length"]][1] # the original `iris`
## [1] 5.1
```

## 16.3 Closures

So far, we have only covered the rules for evaluating *standalone* R expressions. In this section, we look at what happens *inside* the invoked functions.

### 16.3.1 Local environment

When we call a function, a new temporary environment is created. It is where all arguments<sup>15</sup> and local variables are emplaced. During the function evaluation, this environment becomes the current one. After the call, the environment ceases to exist, and we return to the previous environment from the call stack.

Consider the following function:

```
test <- function(x)
{
  print(ls()) # list object names in the current environment
  y <- x^2 # creates a new variable
  print(sys.frame(sys.nframe())) # get the ID of the current environment
  str(as.list(sys.frame(sys.nframe()))) # display its contents
}
```

First call:

```
test(2)
## [1] "x"
## <environment: 0x558884328378>
## List of 2
## $ y: num 4
## $ x: num 2
```

Second call:

```
test(3)
## [1] "x"
## <environment: 0x5588846da6c0>
## List of 2
```

(continues on next page)

<sup>15</sup> Function arguments are initially unevaluated; see Chapter 17.

*(continued from previous page)*

```
## $ y: num 9
## $ x: num 3
```

Each time, the current environment is different. This is why we do not see the ``y`` variable at the start of the second call. It is a brilliantly simple implementation of the storage for local variables.

### 16.3.2 Lexical scope and function closures

We were able to access the `print` function (amongst others) in the above example. This should make us wonder what the enclosing environment of that local environment is.

```
print_enclosure <- function()
  print(parent.env(sys.frame(sys.nframe()))))

print_enclosure()
## <environment: R_GlobalEnv>
```

It is the global environment. Let us evaluate the same function from within another one:

```
call_print_enclosure <- function()
  print_enclosure()

call_print_enclosure()
## <environment: R_GlobalEnv>
```

It is the global environment again. If R used the so-called *dynamic scoping*, we would see the local environment of the function that invoked the one above. If this were true, we would have access to the caller's local variables from within the callee.

---

**Important** Objects of the type `closure`, i.e., user-defined<sup>16</sup> functions, consist of three components:

- a list of formal arguments (compare **formals** and [Section 15.4.1](#));
- an expression (compare **body** and [Section 15.4.1](#) again);
- a reference to the *associated environment* where the function might store data for further use (see **environment**).

By default, the associated environment is set to the current environment where the function was created.

---

<sup>16</sup> There are two other types of functions: a `special` is an internal function that does not necessarily evaluate its arguments (e.g., `switch`, `if`, or `quote`; compare also [Chapter 17](#)), whereas a `builtin` always evaluates its actual parameters, e.g., `sum`.

A local environment created during a function's call has this associated environment as its closure.

Due to this, we say that R has *lexical (static) scope*.

---

Thence, in the above example, we have:

```
environment(print_enclosure) # print the associated environment
## <environment: R_GlobalEnv>
```

**Example 16.7** Consider the following function that prints out `x`` defined outside of its scope:

```
test <- function() print(x)
```

Now:

```
x <- "x in global"
test()
## [1] "x in global"
```

printed out `x`` from the user workspace as this is precisely the environment associated with the function.

However, setting the associated environment to a different one that also happens to define `x`` will give a different result:

```
e <- new.env()
e[["x"]] <- "x in e"
environment(test) <- e
test()
## [1] "x in e"
```

**Example 16.8** Consider the following example:

```
test <- function()
{
  cat(sprintf("test: current env: %s\n", format(sys.frame(sys.nframe()))))

  subtest <- function()
  {
    e <- sys.frame(sys.nframe())
    cat(sprintf("subtest: enclosing env: %s\n", format(parent.env(e))))
    cat(sprintf("x = %s\n", x))
  }

  x <- "span"
  subtest()
}
```

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```

environment(subtest) <- globalenv()
subtest()
}

x <- "bacon"
test()
## test: current env: <environment: 0x5588840af080>
## subtest: enclosing env: <environment: 0x5588840af080>
## x = spam
## subtest: enclosing env: <environment: R_GlobalEnv>
## x = bacon

```

Here is what happened.

1. A call to **test** creates a local function **subtest**, whose associated environment is set to the local frame of the current call. It is precisely the current environment where **subtest** was created.
2. The above explains why **subtest** can access the local variable `x` inside its maker.
3. Then we change the environment associated with **subtest** to the global one.
4. In the next call to **subtest**, unsurprisingly, we gain access to `x` in the user workspace.

---

**Note** In lexical (static) scoping, which variables a function refers to can be deduced by reading the function's body only and not how it is called in other contexts. This is the theory. Nevertheless, the fact that we can freely modify the associated environment anywhere can complicate the program analysis greatly.

If we find the rules of lexical scoping confusing, we ought to refrain from referring to objects outside of the current scope ("global" or "non-local" variables") except for the functions defined as top-level ones or coming from the external packages. It is what we have been doing so far most of the time.

---

### 16.3.3 Application: Function factories

As closures are functions with associated environments, and the role of environments is to store information, we can consider closures = functions + data.

We have already seen that in [Section 9.5.3](#), where we described the **approxfun** function. To recall:

```

x <- seq(0, 1, length.out=11)
f1 <- approxfun(x, x^2)
print(f1)
## function (v)

```

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```
## .approxfun(x, y, v, method, yleft, yright, f, na.rm)
## <environment: 0x5588845a2050>
```

The variables ``x``, ``y``, etc., that **f1**'s source code refers to, are stored inside its dedicated, associated environment:

```
ls(envir=environment(f1))
## [1] "f"      "method" "na.rm"  "x"      "y"      "yleft"  "yright"
```

We are used to referring to the routines such as **approxfun** as *function factories*. They return functions whose non-local variables are stored in their associated environments.

**Example 16.9** Consider the following function factory:

```
gen_power <- function(p)
  function(x) x^p # p references a non-local variable
```

A call to **gen\_power** creates a local environment that defines one variable, ``p``, where argument's value is stored. Then, we create a function whose associated environment (remember that R uses lexical scoping) is that local one. Therefore, the reference to the non-local ``p`` in its body will be resolved therein. This new function is returned by **gen\_power** to the caller. Normally, the local environment would be destroyed, but it is still used after the call, so it will not be garbage-collected.

Example calls:

```
(square <- gen_power(2))
## function(x) x^p
## <environment: 0x5588828e7548>
(cube <- gen_power(3))
## function(x) x^p
## <environment: 0x558882e5e8e0>
cube(2)
## [1] 8
square(2)
## [1] 4
```

The underlying environment can, of course, be modified:

```
assign("p", 7, envir=environment(cube))
cube(2) # so much for the cube
## [1] 128
```

**Example 16.10** **Negate** is another example of a built-in function factory. Study its source code:

```
print(Negate)
## function (f)
```

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```
## {
##   f <- match.fun(f)
##   function(...) !f(...)
## }
## <environment: namespace:base>
```

**Example 16.11** In [37], the following example is given:

```
account <- function(total)
  list(
    balance = function() total,
    deposit = function(amount) total <- total+amount,
    withdraw = function(amount) total <- total-amount
  )

Robert <- account(1000)
Ross <- account(500)
Robert$deposit(100)
Ross$withdraw(150)
Robert$balance()
## [1] 1100
Ross$balance()
## [1] 350
```

We can now fully understand why the above code does what it does. It somewhat resembles a class with three methods and one data field. No wonder why reference classes (Section 16.1.5) were introduced at some point: they are based on the same concept.

**Exercise 16.12** Write a function factory named **gen\_counter** which implements a simple counter that is increased by one on each call thereto.

```
gen_counter <- function() ...to.do...
c1 <- gen_counter()
c2 <- gen_counter()
c(c1(), c1(), c2(), c1(), c2())
## [1] 1 2 1 3 2
```

Moreover, compose a function that resets a given counter to zero.

```
reset_counter <- function(counter_fun) ...to.do...
reset_counter(c1)
c1()
## [1] 1
```

### 16.3.4 Accessing the calling environment

We know that the environment associated with a function is not necessarily the same as the environment from which the function was called, sometimes quite confusingly referred to as the *parent frame*.

R maintains a whole *frame stack*. The global environment is assigned the number 0. Each call to a function increases the stack by one frame, whereas returning from a call decreases the counter.

To get the current frame number, we call `sys.nframe`. This is why `sys.frame(sys.nframe())` returns the current environment.

We can fetch the calling environment by referring to `parent.frame()` or `sys.frame(sys.parent())`, amongst others<sup>17</sup>.

Thanks to `parent.frame`, we may evaluate arbitrary expressions in (on behalf of) the calling environment. Typically, we should not be doing that. However, some built-in functions rely on this feature, hence our avid interest in it here. We will discuss a few of its use cases below.

### 16.3.5 Package namespaces (\*)

Any R package, say, `pkg`, defines two environments:

- `namespace:pkg` – where all objects are defined (functions, vectors, etc.); this is the enclosing environment of all closures in the package;
- `package:pkg` – can be attached to the search path; contains selected<sup>18</sup> objects from `namespace:pkg` that can be accessed by the user.

We will use our example package discussed in Section 7.3.1. Recall that it is available for download from <https://github.com/gagolews/rpackagedemo/>.

```
library("rpackagedemo") # https://github.com/gagolews/rpackagedemo/
## Loading required package: tools
```

Here is its DESCRIPTION file:

```
Package: rpackagedemo
Type: Package
Title: Just a Demo R Package
Version: 1.0.2
Date: 1970-01-01
Author: Anonymous Llama
Maintainer: Unnamed Kangaroo <roo@inthebush.au>
```

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<sup>17</sup> In `help("sys.parent")`, we read that the parent frame number, as returned by `sys.parent()`, is not necessarily equal to `sys.nframe() - 1`. It is certainly true if we are at the top (global) level.

<sup>18</sup> Exported using the `export` or `exportPattern` directive of the package's `NAMESPACE` file; see Section 1 of [62].

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```

Description: Provides a function named bamboo(), just give it a shot.
License: GPL (>= 2)
Imports: stringx
Depends: tools

```

The Import and Depends fields specify which packages (apart from **base**) ours depends on. As we can see above, all items in the latter list are attached to the search path on a call to **library**.

The NAMESPACE file specifies the names imported from other packages and those that are expected to be visible to the user:

```

importFrom(stringx, sprintf)
importFrom(tools, toTitleCase)
S3method(print, koala)
S3method(print, kangaroo, .a_hidden_method_to_print_a_roo)
export(bamboo)

```

Thus, our package exports one object, a function named **bamboo** (we will discuss the S3 methods in the next section). It is included in the “package:rpackagedemo” environment attached to the search path:

```

ls(envir=as.environment("package:rpackagedemo")) # ls("package:rpackagedemo")
## [1] "bamboo"

```

Let us give it a shot:

```

bamboo("spanish inquisition") # rpackagedemo::bamboo
## G'day, Spanish Inquisition!

```

We did not expect that at all.

Let us inspect its source code:

```

print(bamboo)
## function (x = "world")
## cat(prepare_message(toTitleCase(x)))
## <environment: namespace:rpackagedemo>

```

We see a call to **toTitleCase** (most likely from **tools**, and this is indeed the case) and to **prepare\_message** which is not listed in the package's imports. We definitely cannot access it directly:

```

prepare_message
## Error in eval(expr, envir, enclos): object 'prepare_message' not found

```

It turns out that it is the package's internal function. It is thus included in the “namespace:rpackagedemo” environment.

```
(e <- environment(rpackagedemo::bamboo)) # or getNamespace("rpackagedemo")
## <environment: namespace:rpackagedemo>
ls(envir=e)
## [1] "bamboo"          "prepare_message" "print.koala"
```

We can get it via the `::`` operator:

```
print(rpackagedemo::prepare_message)
## function (x)
## sprintf("G'day, %s!\n", x)
## <environment: namespace:rpackagedemo>
```

All functions defined in a package have the corresponding package namespace as their associated environment. As a consequence, **bamboo** can refer to **prepare\_message** directly.

Now, it will be educative to inspect the enclosure of “namespace:rpackagedemo”:

```
(e <- parent.env(e))
## <environment: 0x558883e3ab38>
## attr(,"name")
## [1] "imports:rpackagedemo"
ls(envir=e)
## [1] "sprintf"      "toTitleCase"
```

It is the environment featuring the bindings to all the imported objects. This is why our package can also refer to **stringx::sprintf** and **tools::toTitleCase**.

Its enclosure is the *namespace* of the **base** package (not to be confused with “package:base”):

```
(e <- parent.env(e))
## <environment: namespace:base>
```

The next enclosure is, interestingly, the global environment:

```
(e <- parent.env(e))
## <environment: R_GlobalEnv>
```

Then, of course, the whole search path follows (Section 16.2.5); see Figure 16.4 for an illustration.

---

**Note** (\*\*) All environments related to packages are locked, which means that we cannot change any bindings within their frames; compare **help**(“lockEnvironment”).

In the extremely rare event of needing to *patch* an existing function within an already loaded package, we can call **unlockBinding** followed by **assign** to change its definition.

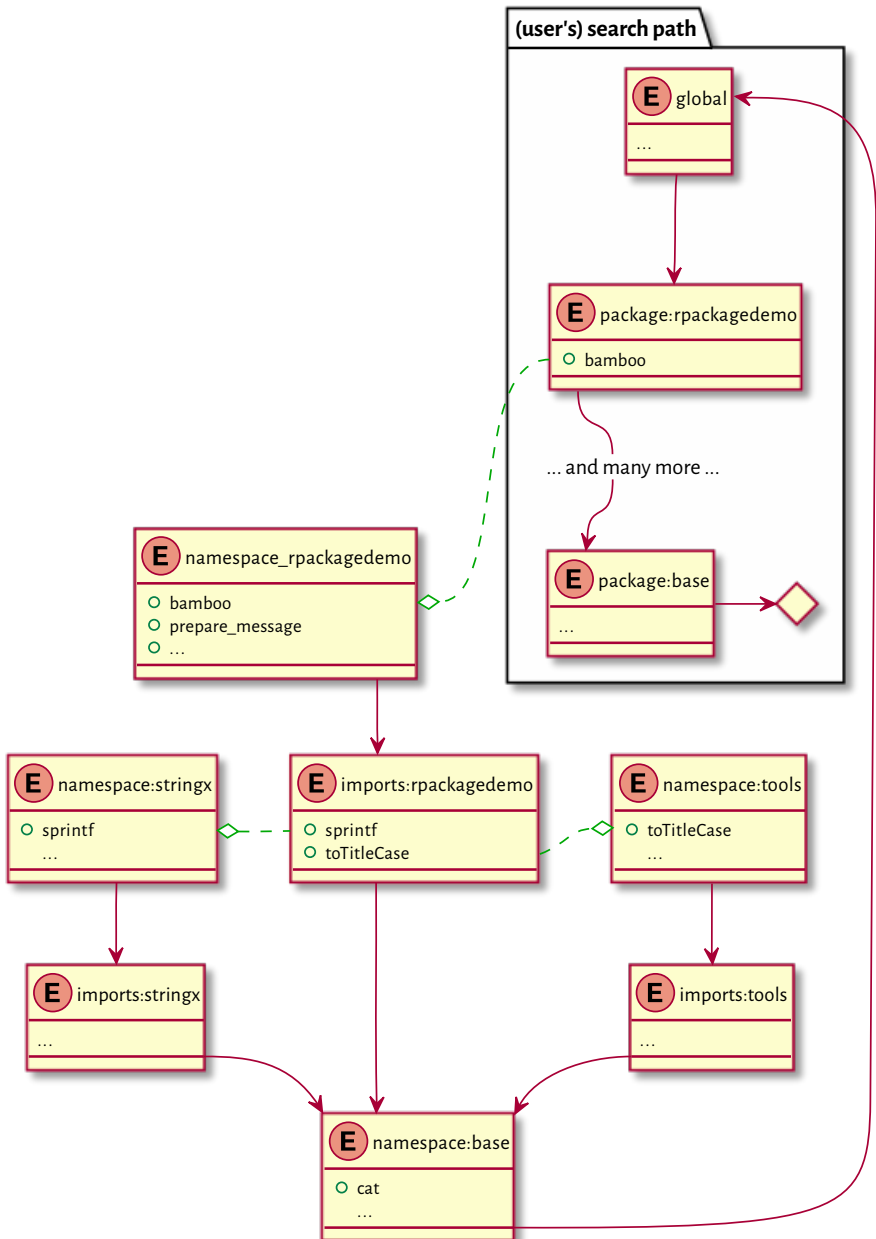


Figure 16.4: A search path for an example package; Dashed lines represent environments associated with closures, whereas solid lines denote enclosing environments; References to objects within each package are resolved inside their respective namespaces

```
new_message <- function (x) sprintf("Nobody expects %s!\n", x)
e <- getNamespace("rpackagedemo")
environment(new_message) <- e # set enclosing environment (very important!)
unlockBinding("prepare_message", e)
assign("prepare_message", new_message, e)
rm("new_message")
bamboo("the spanish inquisition")
## Nobody expects The Spanish Inquisition!
```

R is indeed a quite hackable language (except in the cases where it is not).

**Exercise 16.13** (\*\*) A function or a package might register certain functions (hooks) to be called on various events, e.g., attaching a package to the search path; see `help("setHook")` and `help("onAttach")`.

1. Inspect the source code of `plot.new` and notice a reference to a hook named `"before.plot.new"`. Try setting such a hook yourself (e.g., one that changes some graphics parameters discussed in Section 13.2) and see what happens on each call to a plotting function.
2. Define the `.onLoad`, `.onAttach`, `.onUnload`, and `.onDetach` functions in your own R package and take note of when they are invoked.

**Exercise 16.14** (\*\*) For the purpose of this book, we have registered a custom `"before.plot.new"` hook that sets our favourite graphics parameters that we described in Section 13.2.4. Moreover, we modified `plot.window` slightly to obtain the white grid on a grey background, e.g., in Figure 13.13.

Apply similar hacks to the `graphics` package so that its outputs suit your taste better.

### 16.3.6 S3 method lookup by UseMethod (\*)

Let us go back to the `rpackagedemo` example. Inspecting the `NAMESPACE` file, we see that the package defines two `print` methods: for printing S3 objects of the classes `koala` and `kangaroo`.

The package is attached to the search path. Therefore, we can access these methods via a call to the corresponding generic:

```
print(structure("Tiny Teddy", class="koala"))
## This is a cute koala, Tiny Teddy
print(structure("Moike", class="kangaroo"))
## This is a very naughty kangaroo, Moike
```

However, the package does not make the definitions of these S3 methods available to the user, at least not directly. It is not the first time when we have experienced such an obscuration.

In the first case, the method is simply hidden in the package namespace. It is still available under the expected name:



```

rpackagedemo:::print.koala
## function (x, ...)
## cat(sprintf("This is a cute koala, %s\n", x))
## <environment: namespace:rpackagedemo>

```

In the second case, it appears under a very different identifier:

```

rpackagedemo:::.a_hidden_method_to_print_a_roo
## function (x, ...)
## cat(sprintf("This is a very naughty kangaroo, %s\n", x))
## <environment: namespace:rpackagedemo>

```

Since the base **UseMethod** is still able to find them, we suspect there probably is a global register of all S3 methods. And this is indeed the case.

We can use **getS3method** to get access to what is available via **UseMethod**:

```

getS3method("print", "kangaroo")
## function (x, ...)
## cat(sprintf("This is a very naughty kangaroo, %s\n", x))
## <environment: namespace:rpackagedemo>

```

---

**Important** Overall, the search for methods is performed in two places:

1. in the environment where the generic is called (the current environment); this is why defining **print.kangaroo** in the current scope will use this method instead of the one from the package:

```

print.kangaroo <- function(x, ...) cat("Nobody expects", x, "\n")
print(structure("the Spanish Inquisition", class="kangaroo"))
## Nobody expects the Spanish Inquisition

```

2. in the internal S3 methods table (registration database).

See **help("UseMethod")** for more details. Also, recall that in [Section 10.2.3](#), we said that **UseMethod** is not the only way to perform method dispatching. There are also internal generics (**help("InternalMethods")**) and group generic functions (**help("groupGeneric")**).

---

**Exercise 16.15** (\*) Study the source code of **getS3method**. Note the reference to the `base::__S3MethodsTable__` object which is for R's internal use (we ought not to tinker with it directly). Moreover, study the **registerS3method** function with which we can define new S3 methods not necessarily following the **generic.classname** convention.

## 16.4 Exercises

**Exercise 16.16** *Asking too many questions is not very charismatic, but challenge yourself by trying to find the answer to the following.*

- What is the role of a frame in an environment?
- What is the role of an enclosing environment? How to read it or set it?
- What is the difference between a named list and an environment?
- What functions and operators work on named lists but cannot be applied on environments?
- What do we mean by saying that environments are not passed by value to R functions?
- What do we mean by saying that objects are sometimes copied on demand?
- What happens if a name listed in an expression to be evaluated is not found in the current environment?
- How and what kind of objects can we attach to the search path?
- What happens if we have two identical object names on the search path?
- What do we mean by saying that package namespaces are locked when loaded?
- What is the current environment when we evaluate an expression “on the console”?
- What is the difference between `<-` and `<=<-`?
- Do packages have their own search paths?
- What is a function closure?
- What is the difference between the dynamic and the lexical scope?
- When evaluating a function, how is the enclosure of the current (local) environment determined? Is it the same as the calling environment? How to get it/them programmatically?
- How and why function factories work?
- (\*) What is the difference between the “`package:pkg`” and “`namespace:pkg`” environments?
- How do we fetch the definition of an S3 method that does not seem to be available directly via the standard accessor `generic.classname`?
- (\*) `base::print.data.frame` calls `base::format.data.frame` (directly). Will the introduction of `print.data.frame` in the current environment affect how data frames are printed?
- (\*) On the other hand, `base::format.data.frame` calls the generic `base::format` on all the input data frame’s columns. Will the overloading of the particular methods affect how data frames are printed?

**Exercise 16.17** *Calling:*

```
pkg <- available.packages()
pkg[, "Package"] # a list of the names of available packages
pkg[, "Depends"] # dependencies
```

gives the list of available packages and their dependencies. Convert the dependency lists to a list of character vectors (preferably using regular expressions; see Section 6.2.4).

Then, generate a list of reverse dependencies: what packages depend on each given package.

Use an object of the type *environment* (a hash table) to map the package names to numeric IDs (indexes). It will significantly speed up the whole process (compare it to a named list-based implementation).

**Exercise 16.18** According to [66], compare also Section 9.4.6, a call to:

```
add(x, f(x)) <- v
```

translates to:

```
`*tmp*` <- get(x, envir=parent.env(), inherits=TRUE)
x <- `add<-`(`*tmp*`, f(x), v) # note: not f(`*tmp*`)
rm(`*tmp*`)
```

Given:

```
`add<-` <- function(x, where=TRUE, value)
{
  x[where] <- x[where] + value
  x # the modified object that will replace the original one
}

y <- 1:5
f <- function() { y <- -(1:5); add(y, y== -3) <- 1000; y }
```

explain why we get the following results:

```
f()
## [1] -1 -2 -3 -4 -5
print(y)
## [1] 1 2 1003 4 5
```



# 17

---

## *Lazy evaluation (\*\*)*

---

The ability to create, store, and manipulate unevaluated expressions so that they can be computed later is not particularly special. Many languages enjoy such *metaprogramming* (computing *on* the language, reflection) capabilities, e.g., Lisp, Scheme, Wolfram, Julia, amongst many others.

However, R inherited from its predecessor, the S language, a variation of lazy<sup>1</sup> (non-strict, noneager, delayed) evaluation of function arguments. They are only computed when their *values* are first needed. As we can take the expressions used to generate them (via **substitute**; see [Section 15.4.2](#)), we shall see that we can ignore their meaning in the original (caller's) context and compute them in a very different one.

---

### 17.1 Evaluation of function arguments

We know that calls such as ``if`(test, ifyes, ifno)`, ``||`(mustbe, maybe)`, or ``&&`(mustbe, maybe)` do not have to evaluate all their arguments.

```
{cat(" first "); FALSE} && {cat(" second "); FALSE}
## first
## [1] FALSE
{cat(" first "); TRUE} && {cat(" Spanish Inquisition "); FALSE}
## first Spanish Inquisition
## [1] FALSE
```

We can compose such functions ourselves. For instance:

```
test <- function(a, b, c) a + c # b is unused
test({cat("spam\n"); 1}, {cat("eggs\n"); 10}, {cat("salt\n"); 100})
## spam
## salt
## [1] 101
```

The second argument was not referred to in the function's body. Therefore, it was not evaluated.

---

<sup>1</sup> But without the memoisation of results generated by expressions, which is available, e.g., in Haskell. In other words, in an expression like `c(f(x), f(x))`, the call `f(x)` will still be performed twice.

**Example 17.1** Study the following very carefully.

```
test <- function(a, b, c)
{
  cat("Arguments passed to test (expressions): \n")
  cat("a = ", deparse(substitute(a)), "\n")
  cat("b = ", deparse(substitute(b)), "\n")
  cat("c = ", deparse(substitute(c)), "\n")

  subtest <- function(x, y, z)
  {
    cat("Arguments passed to subtest (expressions): \n")
    cat("x = ", deparse(substitute(x)), "\n")
    cat("y = ", deparse(substitute(y)), "\n")
    cat("z = ", deparse(substitute(z)), "\n")
    cat("Using x and z... ")
    retval <- x + z # does not refer to `y`
    cat("Cheers!\n")
    retval
  }

  cat("Using c... ")
  c # force evaluation; we do not even have to be particularly creative

  subtest(a, ~!~b*2 := headache ->> ha@x$y, c*10) # no evaluation yet!
}

environment(test) <- new.env() # to spice things up

test(
  {testx <- "goulash"; cat("spam\n"); 1},
  {testy <- "kabanos"; cat("eggs\n"); MeAn(egGs+whatever&!!weird[stuff])},
  {testx <- "kransky"; cat("salt\n"); 100}
)

## Arguments passed to test (expressions):
## a = {   testx <- "goulash"   cat("spam\n")   1 }
## b = {   testy <- "kabanos"   cat("eggs\n")   MeAn(egGs + whatever ...
## c = {   testx <- "kransky"   cat("salt\n")   100 }
## Using c... salt
## Arguments passed to subtest (expressions):
## x = a
## y = `:=`(~!~b * 2, ha@x$y <- headache)
## z = c * 10
## Using x and z... spam
## Cheers!
## [1] 1001
```

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```
print(testx)
## [1] "goulash"
print(testy)
## Error in eval(expr, envir, enclos): object 'testy' not found
```

On a side note, the ``~`` (formula) operator will be discussed in [Section 17.6](#). Furthermore, the ``:=`` operator was used in an ancient version of R for assignments. The parser still recognises it, yet now it has no associated meaning.

---

**Important** We note what follows.

- Either the evaluation of an argument does not happen, or is triggered only once (in which case the result is cached).
- Evaluation is *delayed* until the very first request for the underlying value (we call it *lazy evaluation*).
- Evaluation takes place in the calling environment (parent frame).
- Fetching the expression passed as an argument using **substitute** ([Section 15.4.2](#)) or checking if an argument was provided with **missing** ([Section 15.4.3](#)) does not trigger the evaluation.
- Merely passing arguments further to another function *usually* does not trigger the evaluation.

We wrote *usually* because functions of the type builtin (e.g., **c**, **list**, **sum**, ``+``, ``&``, and ``:=``) always evaluate the arguments. There is no lazy evaluation in the case of the arguments passed to group generics; see **help**("groupGeneric") and [Section 10.2.6](#). Furthermore, replacement functions' values arguments ([Section 9.4.6](#)) are computed eagerly.

---

**Exercise 17.2** Study the source code of **system.time** and notice the use of delayed evaluation to measure the duration of the execution of a given expression. Also, **on.exit** ([Section 17.4](#)) reacts to possible exceptions.

**Example 17.3** It turns out that the role of **substitute** is broader than just getting the expression passed as an argument. We can actually replace each occurrence of every name from a given dictionary (a named list or an environment).

For instance:

```
test <- function(x)
{
  subtest <- function(y)
  {
    ex <- substitute(x, env=parent.frame()) # substitute(x) is just `x`
    ey <- substitute(y)
```

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```

    cat("ex =", deparse(ex), "\n")
    cat("ey =", deparse(ey), "\n")
    eval(as.call(list(substitute, ey, list(x=ex))))
  }

  subtest(spam(!x[x](x)))
}

test(eels@hovercraft)
## ex = eels@hovercraft
## ey = spam(!x[x](x))
## spam(!eels@hovercraft[eels@hovercraft](eels@hovercraft))

```

This way, we could fetch the expression passed as the ``x`` argument to the calling function and replace every occurrence of ``x`` in the expression ``ey``.

**substitute** does not evaluate its first argument. Hence, if we called **substitute**(*ey*, ...), we would treat ``ey`` as a quoted name.

**Exercise 17.4** Study the source code of **replicate**:

```

print(replicate)
## function (n, expr, simplify = "array")
## sapply(integer(n), eval.parent(substitute(function(...) expr)),
##   simplify = simplify)
## <environment: namespace:base>

```

**Exercise 17.5** (\*) Implement your version of the **bquote** function.

---

**Note** (\*) Internally, lazy evaluation of arguments is implemented using the so-called *promises* (compare [66]). As such, they consist of:

- an expression (which we can access by calling **substitute**);
- an environment where the expression is to be evaluated (once this happens, it is set to NULL);
- a cached value (computed on demand, once).

This interface is not really visible from within R, but see **help**("delayedAssign").

---

**Exercise 17.6** Inspect the definition of **match.fun**. Why is it called by, e.g., **apply**, **Map**, or **outer**?

Note that it uses **eval.parent(substitute(substitute(FUN)))** to fetch the expression representing the argument passed by the calling function (but it is probably very rarely needed there). Compare:



```
test <- function(x)
{
  subtest <- function(y)
  {
    # NOT: substitute(y)
    # NOT: eval.parent(substitute(y))
    eval.parent(substitute(substitute(y)))
  }

  subtest(x*3)
}

test(1+2)
## (1 + 2) * 3
```

## 17.2 Evaluation of default arguments

As we know from Section 9.5.4, default arguments are special expressions specified in a function's parameter list. When a function's body requires the value of an argument that the caller did not provide, the default expression will be evaluated *in the current (local) environment* of the function. It is thus different from the case of normally passed arguments, which are interpreted in the context of the calling environment.

```
x <- "banana"

test <- function(y={cat("spam\n"); x})
{
  cat(deparse(substitute(y)), "\n")
  cat("bacon\n")
  x <- "rotten potatoes"
  cat(y, y, "\n")
}

test(x)
## x
## bacon
## banana banana
test()
## { cat("spam\n") x }
## bacon
## spam
## rotten potatoes rotten potatoes
```

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```
test({cat("spam\n"); x})
## {      cat("spam\n")      x }
## bacon
## spam
## banana banana
```

As usual, the evaluation is triggered only once, where it is explicitly requested, and only when needed.

**Example 17.7** Consider the following example from [37]:

```
sumsq <- function(y, about=mean(y), na.rm=FALSE)
{
  if (na.rm)
    y <- y[!is.na(y)]
  sum((y - about)^2)
}

sumsq(c(1, NA_real_, NA_real_), na.rm=TRUE)
## [1] 0
```

The nice side effect is that the computation of the mean may take into account the removal of the missing values if requested.

However, as the idea of lazy evaluation of arguments is alien to most programmers (especially those coming from different languages), it might be better to rewrite the above using a call to **missing** (Section 15.4.3):

```
sumsq <- function(y, about, na.rm=FALSE)
{
  if (na.rm)
    y <- y[!is.na(y)]
  if (missing(about))
    about <- mean(y)
  sum((y - about)^2)
}

sumsq(c(1, NA_real_, NA_real_), na.rm=TRUE)
## [1] 0
```

or better even:

```
sumsq <- function(y, about=NULL, na.rm=FALSE)
{
  if (na.rm)
    y <- y[!is.na(y)]
```

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```

    if (is.null(about))
      about <- mean(y)
    sum((y - about)^2)
  }

sumsq(c(1, NA_real_, NA_real_), na.rm=TRUE)
## [1] 0

```

**Exercise 17.8** The default arguments to `do.call`, `list2env`, and `new.env` are set to `parent.frame`. What does that mean?

**Exercise 17.9** Study the source code of the `local` function:

```

print(local)
## function (expr, envir = new.env())
## eval.parent(substitute(eval(quote(expr), envir)))
## <environment: namespace:base>

```

### 17.3 Ellipsis, `...`, revisited

If our function features the dot-dot-dot parameter, `...`, whatever we pass through it is packed into a pairlist of promise expressions. Thus, we can relish the benefits of lazy evaluation. In particular, we can redirect all `...`-fed arguments to another call as-is.

```

test <- function(...)
{
  subtest <- function(x, ...)
  {
    cat("x  = "); str(x)
    cat("... = "); str(list(...))
  }

  subtest(...)
}

test({cat("eggs! "); 1}, {cat("spam! "); 2}, z={cat("rice! "); 3})
## x  = eggs!  num 1
## ... = spam! rice! List of 2
## $ : num 2
## $ z: num 3

```

**Exercise 17.10** In the documentation of `lapply`, we read that this function is called like “lap-

`ply(X, FUN, ...)`, where ``...`` are optional arguments to **FUN**. Verify that whatever is passed via the ellipsis is evaluated only once and not on each application of **FUN** on the elements of *X*.

**Example 17.11** We know from [Chapter 13](#) that many high-level graphics functions rely on multiple calls to more primitive functions that allow for setting a variety of parameters (e.g., via **par**). A common scenario is for a high-level function to submit all the passed arguments to more basic routines. Each underlying procedure can then decide by itself which items it is interested in.

```
test <- function(...)
{
  subtest1 <- function(..., a=1) c(a=a)
  subtest2 <- function(..., b=2) c(b=b)
  subtest3 <- function(..., c=3) c(c=c)

  c(subtest1(...), subtest2(...), subtest3(...))
}

test(a="A", b="B", d="D")
##   a   b   c
## "A" "B" "3"
```

Here, for instance, **subtest1** only consumes the value of ``a`` and ignores all the other arguments whatsoever. **plot.default** (amongst others) relies on such a design pattern.

`...length()` fetches the number of items passed via the ellipsis, `...names()` retrieves their names (in the case they are given as keyword arguments), and `...elt(i)` gives the value of the *i*-th element. Furthermore, `..1`, `..2`, and so forth are synonymous with `...elt(1)`, `...elt(2)`, etc.

```
test <- function(...)
{
  cat("length:", ...length(), "\n")
  cat("names: ", paste(...names(), collapse=" "), "\n")
  for (i in seq_len(...length()))
    cat(i, ":", ...elt(i), "\n")
  print(substitute(...elt(i)))
}

test(u={cat("honey! "); "a"}, {cat("gravy! "); "b"}, w={cat("bacon! "); "c"})
## length: 3
## names: u, , w
## honey! 1 : a
## gravy! 2 : b
## bacon! 3 : c
## ...elt(3L)
```

Note that `...elt(i)` triggers the evaluation of the respective argument. Unfortu-

nately, we cannot use **substitute** to fetch the underlying expression. Instead, we can rely on **match.call** discussed in Section 15.4.4:

```
test <- function(a, b, ..., z=1)
{
  e <- match.call()[-1]
  as.list(e[!(names(e) %in% names(formals(sys.function())))])
}

str(test(1+1, 2+2, 3+3, 4+4, a=2, z=8, w=4))
## List of 4
## $ : language 2 + 2
## $ : language 3 + 3
## $ : language 4 + 4
## $ w: num 4
```

---

**Note** Objects passed via ``...``, even if they are specified as keyword arguments, cannot be referred to by their name as if they were local variables:

```
test <- function(...) zzz
test(zzz=3)
## Error in test(zzz = 3): object 'zzz' not found
```

In other words, no assignment in the local environment is triggered.

---

**Exercise 17.12** *Implement your version of the built-in **switch** function.*

**Exercise 17.13** *Write your version of the **stopifnot** function.*

---

## 17.4 on.exit(\*)

**on.exit** registers an expression to be evaluated at the very end of a call, regardless of whether the function exited due to an error or not. It might be used to reset the temporarily modified graphics parameters (see **par**) and system options (**options**) or clean up the allocated resources (e.g., close all open file connections).

For instance:

```
test <- function(reset=FALSE, error=FALSE)
{
  on.exit(cat("eggs\n"))
  on.exit(cat("bacon\n")) # replace
  on.exit(cat("spam\n"), add=TRUE) # add
```

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```

cat("roti canai\n")

if (reset)
  on.exit() # cancels all (replace by nothing)

if (error)
  stop("aaarrgh!")

cat("end\n")
"return value"
}

test()
## roti canai
## end
## bacon
## spam
## [1] "return value"
test(reset=TRUE)
## roti canai
## end
## [1] "return value"
test(error=TRUE)
## roti canai
## Error in test(error = TRUE): aaarrgh!
## bacon
## spam

```

We can always do without **on.exit**, e.g., by applying proper exception handling techniques; see Section 8.2.

**Exercise 17.14** In the definition of **scan**, notice the call to:

```
on.exit(close(file))
```

Is its purpose to close the file on exit?

**Exercise 17.15** Why does **graphics::barplot.default** call the following expressions?

```

dev.hold()
opar <- if (horiz) par(xaxs="i", xpd=xpd) else par(yaxs="i", xpd=xpd)
on.exit({
  dev.flush()
  par(opar)
})

```

## 17.5 Metaprogramming and laziness in action: Examples (\*)

Due to lazy evaluation, we can define functions that allow any random gibberish as their arguments as long as they are syntactically valid R expressions. Nothing but basic decency stops us from interpreting them in any way we want. Each such function can become a microverse (a microlanguage?) by itself. This will surely confuse<sup>2</sup> our users, as they will have to analyse every procedure's behaviour separately.

In this section, we extend on our notes from [Section 9.5.7](#) and [Section 12.3.9](#). We look at a few built-in functions relying on metaprogramming and laziness, mostly because studying them is a good exercise. It can help extend our programming skills and deepen our understanding of the concepts discussed in this part of the book.

By no means is it an invitation to use them in practice.

Still, R's computing on the language capabilities might interest some advanced programmers (e.g., package developers).

### 17.5.1 `match.arg`

`match.arg` was mentioned in [Section 9.5.7](#). When called normally, it matches a string against a set of possible choices, similarly to `pmatch`:

```
choices <- c("spam", "bacon", "eggs")
match.arg("spam", choices)
## [1] "spam"
match.arg("s", choices) # partial matching
## [1] "spam"
match.arg("eggplant", choices) # no match
## Error in match.arg("eggplant", choices): 'arg' should be one of "spam",
##      "bacon", "eggs"
match.arg(choices, choices) # match first
## [1] "spam"
```

However, skipping the second argument, this function will fetch the choices from the default argument of the function it is enclosed in!

```
test <- function(x=c("spam", "bacon", "eggs"))
  match.arg(x)

test("spam")
## [1] "spam"
test("s")
```

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<sup>2</sup> Novices are prone to overgeneralising when they learn new material that they are still far from comfortable with. Such exceptions go against this natural coping strategy of theirs.

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```
## [1] "spam"
test("eggplant")
## Error in match.arg(x): 'arg' should be one of "spam", "bacon", "eggs"
test()
## [1] "spam"
```

**Exercise 17.16** *Inspect the source code and the documentation of `stats::binom.test`, which looks like:*

```
function(..., alternative = c("two.sided", "less", "greater"))
{
  # ...
  alternative <- match.arg(alternative)
  # ...
}
```

*Note the `alternative` argument and its peculiar default value.*

**Exercise 17.17** *Study the source code of `match.arg`. In particular, notice the following fragment:*

```
if (missing(choices)) {
  formal.args <- formals(sys.function(sysP <- sys.parent()))
  choices <- eval(
    formal.args[[as.character(substitute(arg))]],
    envir=sys.frame(sysP)
  )
}
```

### 17.5.2 curve

The **curve** function can be called, e.g., like:

```
curve(sin(1/x^2), 1/pi, 3, 1001, lty=2)
```

which results in Figure 17.1. Wait a minute... We did not define `x` as a sequence ranging between about 0.3 and 3!

**Exercise 17.18** *Study the source code of `curve`. Take note of the following fragment of its definition:*

```
function(expr, from=NULL, to=NULL, n=101, xlab="x", type="l", ...)
{
  # ...
  expr <- substitute(expr)
  ylab <- deparse(expr)
```

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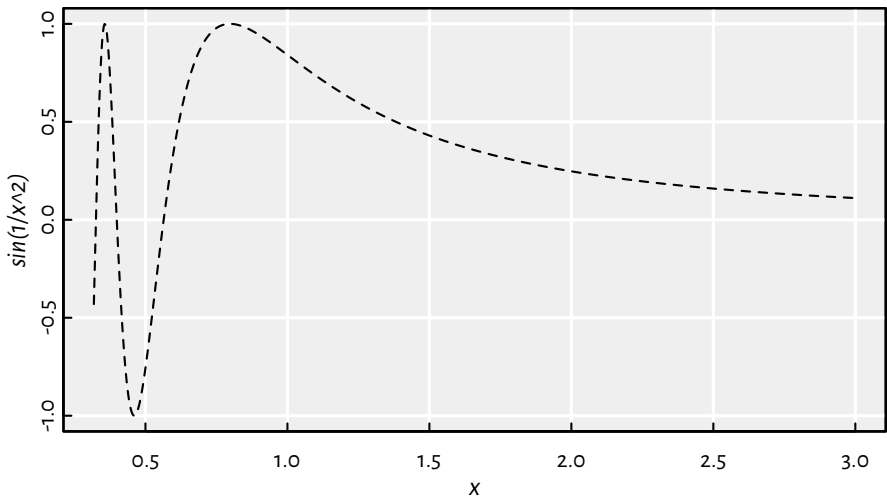


Figure 17.1: An example plot generated by calling **curve**

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```
x <- seq.int(from, to, length.out=n)
ll <- list(x=x)
y <- eval(expr, envir=ll, enclos=parent.frame())
plot(x=x, y=y, type=type, xlab=xlab, ylab=ylab, ...)
# ...
}
```

### 17.5.3 with and within

Environments and named lists (and hence data frames) are similar (Section 16.1.2). Due to this, the **envir** argument to **eval** can be set to either.

Therefore, for instance:

```
eval(quote(head(Sepal.Length)), envir=iris)
## [1] 5.1 4.9 4.7 4.6 5.0 5.4
```

evaluates the given expression in something like **list2env(iris, parent=parent.frame())**. Thus, even though **Sepal.Length** is not a standalone variable, it is treated as one *inside* the **iris** data frame.

The enclosure is set to the calling frame. Hence, we can successfully refer to the **head** function located somewhere on the search path. This is somewhat similar to **attach** (Section 16.2.6) but without modifying the search path.

The **with** function does exactly the above:

```
print(with.default)
## function (data, expr, ...)
## eval(substitute(expr), data, enclos = parent.frame())
## <environment: namespace:base>
```

Example use:

```
with(iris, {
  x <- Sepal.Length # `Sepal.Length` is in `iris`
  mean(x)
})
## [1] 5.8433
```

As we evaluate the above in the local (temporary) environment, we cannot modify the existing columns of the data frame this way. However, the **within** function includes a way to detect and apply any changes made.

```
within(iris, {
  Sepal.Length <- Sepal.Length/1000
  Spam <- "yum!"
}) -> iris2
head(iris2, 3)
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Spam
## 1      0.0051      3.5      1.4      0.2 setosa yum!
## 2      0.0049      3.0      1.4      0.2 setosa yum!
## 3      0.0047      3.2      1.3      0.2 setosa yum!
```

**Exercise 17.19** Study the source code of **within**:

```
print(within.data.frame)
## function (data, expr, ...)
## {
##   parent <- parent.frame()
##   e <- evalq(environment(), data, parent)
##   eval(substitute(expr), e)
##   l <- as.list(e, all.names = TRUE)
##   l <- l[!vapply(l, is.null, NA, USE.NAMES = FALSE)]
##   nl <- names(l)
##   del <- setdiff(names(data), nl)
##   data[nl] <- l
##   data[del] <- NULL
##   data
## }
## <environment: namespace:base>
```

Note that **evalq**(*expr*, ...) is equivalent to **eval**(**quote**(*expr*), ...). Also, **vapply**(*X*, *FUN*, *NA*, ...) is like a call to **sapply**, but it guarantees that the result is a logical vector.

### 17.5.4 transform

We can call **transform** to modify/add columns in a data frame using vectorised functions, for instance:

```
head(transform(mtcars, log_hp=log(hp), am=2*am-1, hp=NULL), 3)
##           mpg cyl disp drat   wt  qsec vs am gear carb log_hp
## Mazda RX4    21.0   6  160 3.90 2.620 16.46  0  1   4    4 4.7005
## Mazda RX4 Wag 21.0   6  160 3.90 2.875 17.02  0  1   4    4 4.7005
## Datsun 710    22.8   4  108 3.85 2.320 18.61  1  1   4    1 4.5326
```

If we suspect that this function evaluates all expressions passed as ``...`` *within* the data frame, we are brilliantly right. Furthermore, there must be some mechanism to detect newly created variables so that new columns can be added.

**Exercise 17.20** Study the source code of **transform**:

```
print(transform.data.frame)
## function (`_data`, ...)
## {
##   e <- eval(substitute(list(...)), `_data`, parent.frame())
##   tags <- names(e)
##   inx <- match(tags, names(`_data`))
##   matched <- !is.na(inx)
##   if (any(matched)) {
##     `_data`[inx[matched]] <- e[matched]
##     `_data` <- data.frame(`_data`)
##   }
##   if (!all(matched))
##     do.call("data.frame", c(list(`_data`), e[!matched]))
##   else `_data`
## }
## <environment: namespace:base>
```

In particular, note that ``e`` is a named list.

### 17.5.5 subset

The **subset** function selects rows and columns of a data frame that meet certain criteria. For instance:

```
subset(airquality, Temp>95 | Temp<57, -(Month:Day))
##      Ozone Solar.R Wind Temp
## 5      NA      NA 14.3  56
## 120    76    203  9.7  97
## 122    84    237  6.3  96
```

The second argument, the row selector, must definitely be evaluated *within* the data

frame. We expect it to reduce itself to a logical vector which then can be passed to the index operator.

The “select all columns except those between the given ones” part can be implemented by assigning each column a consecutive integer and then treating them as numeric indexes.

**Exercise 17.21** Study the source code of `subset`:

```
print(subset.data.frame)
## function (x, subset, select, drop = FALSE, ...)
## {
##   chkDots(...)
##   r <- if (missing(subset))
##     rep_len(TRUE, nrow(x))
##   else {
##     e <- substitute(subset)
##     r <- eval(e, x, parent.frame())
##     if (!is.logical(r))
##       stop("'subset' must be logical")
##     r & !is.na(r)
##   }
##   vars <- if (missing(select))
##     rep_len(TRUE, ncol(x))
##   else {
##     nl <- as.list(seq_along(x))
##     names(nl) <- names(x)
##     eval(substitute(select), nl, parent.frame())
##   }
##   x[r, vars, drop = drop]
## }
## <environment: namespace:base>
```

## 17.5.6 A forward-pipe operator

Section 10.5 mentioned the pipe operator, ``|>``. We can compose its simplified version manually:

```
`%>%` <- function(e1, e2)
{
  e2 <- as.list(substitute(e2))
  e2 <- as.call(c(e2[[1]], substitute(e1), e2[-1]))
  eval(e2, envir=parent.frame())
}
```

This function imputes ``e1`` as the first argument in a call ``e2`` and then evaluates the new expression.

Example calls:

```
x <- c(1, NA_real_, 2, 3, NA_real_, 5)
x %>% mean # mean(x)
## [1] NA
x %>% `-(1) # x-1
## [1] 0 NA 1 2 NA 4
x %>% na.omit %>% mean # mean(na.omit(x))
## [1] 2.75
x %>% mean(na.rm=TRUE) # mean(x, na.rm=TRUE)
## [1] 2.75
```

Moreover, we can memorise the value of ``e1`` under the name, say, ``.`` so that it can be referred to in the right-hand side expression. This comes at the cost of forcing the evaluation of the left-hand side argument and thus losing the potential benefits of laziness, including access to the generating expression.

```
`%.>%` <- function(e1, e2)
{
  env <- list2env(list(.=e1), parent=parent.frame())
  e2 <- as.list(substitute(e2))
  e2 <- as.call(c(e2[[1]], quote(.), e2[-1]))
  eval(e2, envir=env)
}
```

This way, we can refer to the value of the left-hand side multiple times in a single call, for instance:

```
set.seed(123); runif(5) %>% `[`(.>0.5) # x[x>0.5] with x=runif(5)
## [1] 0.78831 0.88302 0.94047
```

This is crazy, I know. I made this. Your author. One more then:

```
# x[x >= 0.5 & x <= 0.9] <- 0.5 with x=round(runif(5), 2):
set.seed(123); runif(5) %>% round(2) %>% `[<`(>=0.5 & <=0.9, value=NA)
## [1] 0.29 NA 0.41 NA 0.94
```

I cannot wait for someone to put this operator into some new R package (it is a brilliant idea, by the way, isn't it?) and then confuse thousands of users ("What is this thing?").

### 17.5.7 Other ideas (\*\*\*)

Why stop ourselves here? We can create way more invasive functions that read some local variables in the calling functions (unless they are primitive; in R, there are always exceptions to general rules...).

Here is an operator, thanks to which we can select a range of columns in a data frame between two given labels:

```
`%:%` <- function(e1, e2)
{
  # get the `x` argument in the caller (hoping its `[`)
  x <- get("x", envir=sys.frame(sys.nframe()-1))
  n <- names(x)
  from <- pmatch(substitute(e1), n)
  to <- pmatch(substitute(e2), n)
  from:to
}

head(iris[, Sepal.W:%Petal.W])
##   Sepal.Width Petal.Length Petal.Width
## 1         3.5         1.4         0.2
## 2         3.0         1.4         0.2
## 3         3.2         1.3         0.2
## 4         3.1         1.5         0.2
## 5         3.6         1.4         0.2
## 6         3.9         1.7         0.4
```

This operator relies on the assumption that it is called in the expression passed as an argument to a non-primitive function which also takes a named vector ``x`` as an actual parameter. So ugly.

**Exercise 17.22** *Make the above more foolproof:*

- if ``%:%`` is used outside of ``[`` or ``[<-``, raise a polite error,
- allow ``x`` to be a matrix (is it possible?),
- prepare better for the case of less expected inputs.

**Exercise 17.23** *Modify the definition of the above operator so that both:*

```
iris[, -Sepal.W:%Petal.W]
iris[, -(Sepal.W:%Petal.W)]
```

mean “select everything except”.

**Exercise 17.24** *Define `%:%` for data frames so that:*

- `x[%:3, ]` means “select the first three rows”,
- `x[3:%, ]` means “select from the third to the end”,
- `x[-3:%, ]` means “select from the third last to the end”,
- `x[%:%-10, ]` means “select all but the last nine”.

The ceiling is the limit. Just please, do not use the above in production.

## 17.6 Processing formulae, `~` (\*)

Formulae were introduced to S in the early 1990s [13]. Their original *raison d'être* was to specify *statistical models*; compare Section 10.3.4.

From the language perspective, they are merely unevaluated calls to the `~` (tilde) operator. When creating them, we do not even have to apply **quote** explicitly. For instance:

```
f <- (y ~ x1 + x2) # or: `~`(y, x1+x2)
mode(f)
## [1] "call"
class(f)
## [1] "formula"
```

Hence, formulae are compound objects in the sense given in Chapter 10.

Usually, formulae are equipped with an additional attribute:

```
attr(f, ".Environment")
## <environment: R_GlobalEnv>
```

**Exercise 17.25** Create a function that generates a list of formulae of the form “ $y \sim x_1 + x_2 + \dots + x_k$ ”, for all possible combinations  $x_1, x_2, \dots, x_k$  (of any cardinality) of elements in a given set of  $x$ s. For instance:

```
formula_allcomb <- function(y, xs, env=parent.frame()) ...to.do...
str(formula_allcomb("len", c("supp", "dose")))
## List of 3
## $ :Class 'formula' language len ~ supp + dose
## .. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
## $ :Class 'formula' language len ~ dose
## .. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
## $ :Class 'formula' language len ~ supp
## .. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
str(formula_allcomb(
  "y",
  c("x1", "x2", "x3"),
  env=NULL
))
## List of 7
## $ :Class 'formula' language y ~ x1 + x2 + x3
## $ :Class 'formula' language y ~ x2 + x3
## $ :Class 'formula' language y ~ x1 + x3
## $ :Class 'formula' language y ~ x3
```

(continues on next page)

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```
## $ :Class 'formula' language y ~ x1 + x2
## $ :Class 'formula' language y ~ x2
## $ :Class 'formula' language y ~ x1
```

As they are unevaluated expressions, functions can assign any fantastic meaning to formulae. We cannot really do anything about it. However, many functions, especially in the **stats** and **graphics** packages, rely on a call to **model.frame** and related routines. Thanks to this, we can at least find some behavioural patterns. In particular, **help("formula")** lists some typical meanings of operators that can be used in a formula.

**Example 17.26** Here are a few examples (executing the expressions below is left as an exercise).

- Draw a box-and-whisker plot for `iris[["Sepal.Length"]]` split by `iris[["Species"]]`:

```
boxplot(Sepal.Length~Species, data=iris)
```

- Draw a box plot for `ToothGrowth[["len"]]` split by a combination of levels in `ToothGrowth[["supp"]]` and `ToothGrowth[["dose"]]`:

```
boxplot(len~supp:dose, data=ToothGrowth)
```

- Split the given data frame by a combination of values in two specified columns therein:

```
split(ToothGrowth, ~supp:dose)
```

- Fit a linear regression model of the form  $y = a + bx$ , where  $y$  is `iris[["Sepal.Length"]]` and  $x$  is `iris[["Petal.Length"]]`:

```
lm(Sepal.Length~Petal.Length, data=iris)
```

- Fit a linear regression model of the form  $z = ax + by$ , where  $z$  is `iris[["Sepal.Length"]]`,  $x$  is `iris[["Petal.Length"]]`, and  $y$  is `iris[["Sepal.Width"]]` (without the intercept term):

```
lm(Sepal.Length~Petal.Length+Sepal.Width+0, data=iris)
```

- Fit a linear regression model of the form  $z = a + bx + cy + dxy$ , where  $z$  is `iris[["Sepal.Length"]]`+`e` (with `e`` fetched from the associated environment), and  $x$  and  $y$  are like above:

```
e <- rnorm(length(iris[["Sepal.Length"]]), 0, 0.05)
lm(I(Sepal.Length+e)~Petal.Length*Sepal.Width, data=iris)
```

- Draw scatter plots of `warpbreaks[["breaks"]]` vs their indexes for data grouped by a combination of `warpbreaks[["wool"]]` and `warpbreaks[["tension"]]`:



```
Index <- seq_len(NROW(warpbreaks))
coplot(breaks ~ Index | wool * tension, data=warpbreaks)
```

From the perspective of this book, which focuses on more universal aspects of the R language, formulae are not interesting enough to describe them in any more detail. However, the tender-hearted reader is now equipped with all the necessary knowledge to solve the following very educative exercises.

**Exercise 17.27** Study the source code of `graphics:::boxplot.formula`, `stats::lm`, and `stats:::t.test.formula` and notice how they prepare and process the calls to `model.frame`, `model.matrix`, `model.response`, `model.weights`, etc.

Note that their main aim is to prepare data to be passed to `boxplot.default`, `lm.fit` (it is just a function with such a name, not an S3 method), and `t.test.default`

**Exercise 17.28** Write a function similar to `curve`, but one that allows to specify the function to plot using a formula.

---

## 17.7 Exercises

**Exercise 17.29** Answer the following questions.

- What is the role of promises?
- Why do we generally discourage the use of functions relying on metaprogramming?
- How are default arguments evaluated?
- Is there anything special about formulae from the language perspective?
- Reevaluates function arguments lazily. Does it mean that “`y[c(length(y)+1, length(y)+1, length(y)+1)] <- list(1, 2, 3)`” extends a list `y` by three elements? Or are there cases where evaluation is eager?

**Exercise 17.30** Given:

```
test <- function(x, y=deparse(substitute(x)), force_first=FALSE)
{
  if (force_first) y # just force the evaluation of y here
  x <- x**2
  print(y)
}

test(1:5)
## [1] "c(1, 4, 9, 16, 25)"
test(1:5, force_first=TRUE)
## [1] "1:5"
```

Why did the two above calls yield different results?

### 17.8 Outro

Recall our first approximation to the classification of R data types that we presented in the *Preface*. To summarise what we have covered in this book, let us contemplate Figure 17.2, which gives a much broader picture.

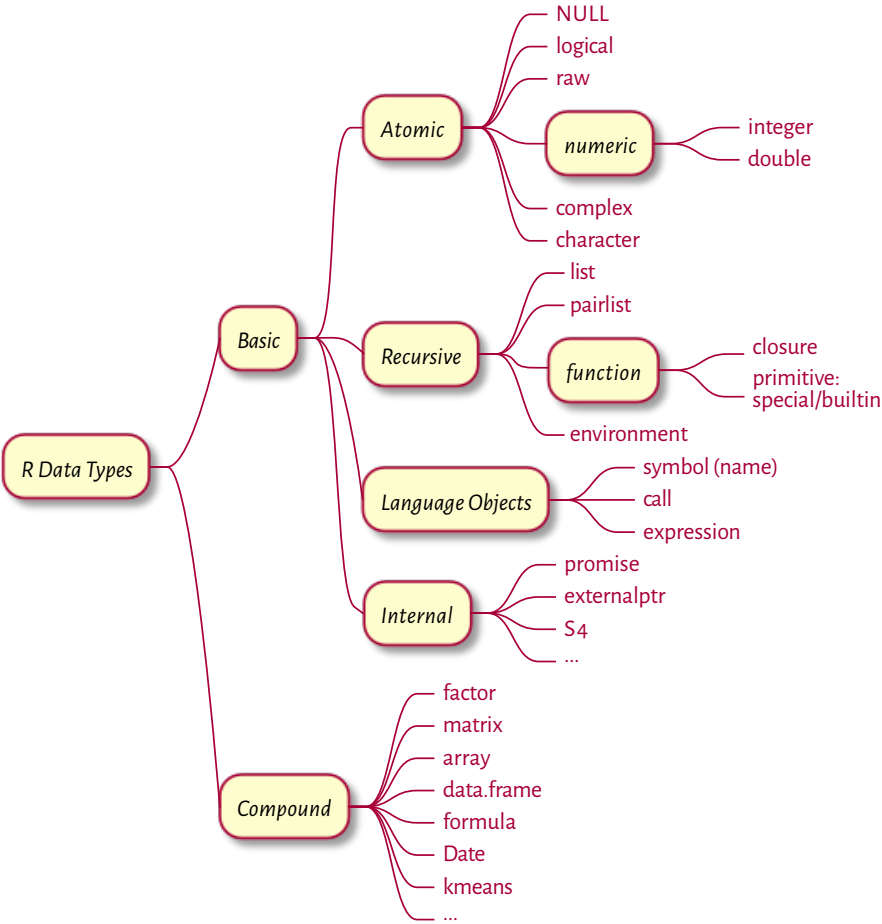


Figure 17.2: R data types

If we omitted something, it was most likely on purpose: either we can now study it on our own easily, it is not really worth our attention, or it violates our *minimalist* design principles that we explained in the *Preface*.

Now that we have reached the end of this course, we might be interested in reading the following materials:

- *R Language Definition* [66],
- *R Internals* [65],
- *Writing R Extensions* [62],
- R's source code available at <https://cran.r-project.org/src/base/>.

What is more, the NEWS files available at <https://cran.r-project.org/doc/manuals/r-release/> will keep us updated with fresh features, bug fixes, and newly deprecated functionality; see also the `news` function.

Please spread the news about this book. Also, check out the other open-access textbook by yours truly, *Minimalist data wrangling with Python*<sup>3</sup> [26]. Thank you.

Good luck with your further projects!

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<sup>3</sup> <https://datawranglingpy.gagolewski.com/>



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# Changelog

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**Important** Any [bug/typos reports/fixes](#)<sup>4</sup> are appreciated.

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The most up-to-date version of this book can be found at <https://deepr.gagolewski.com/>.

Below is the list of the most noteworthy changes:

- **2023-05-19** (v0.9.0):
  - Chapter on interfacing compiled code drafted.
  - Minor extensions.
- **2023-04-27** (v0.2.1):
  - Chapter on graphics drafted.
- **2023-04-09** (v0.2.0):
  - New HTML theme (featuring light and dark modes).
  - Chapter on unevaluated expressions drafted.
  - Chapter on environments and evaluation drafted.
  - Chapter on lazy evaluation drafted.
- **2022-12-29** (v0.1.12):
  - First public release at <https://deepr.gagolewski.com>.
  - Chapters 1–12 (basic and compound types, functions, control flow, etc.) drafted.
  - Preface drafted.
  - ISBN 978-0-6455719-2-9 reserved.
  - Cover.

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<sup>4</sup> <https://github.com/gagolews/deepr/issues>



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