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Learn R

As a Language

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Preface

“Suppose that you want to teach the ‘cat’ concept to a very young child. Do you explain that a cat is a relatively small, primarily carnivorous mammal with retractable claws, a distinctive sonic output, etc.? I’ll bet not. You probably show the kid a lot of different cats, saying ‘kitty’ each time, until it gets the idea. To put it more generally, generalizations are best made by abstraction from experience.”

R. P. Boas

Can we make mathematics intelligible?, 1981

Why have I chosen the title “*Learn R: As a Language*”? This book is based on exploration and practice that aims at teaching how to express various operations on data using the R language. It focuses on the language, rather than on specific types of data analysis, and exposes the reader to current usage and does not spare the quirks of the language. When we use our native language in everyday life, we do not think about grammar rules or sentence structure, except for the trickier or unfamiliar situations. My aim is for this book to help readers grow to use R in this same way, i.e., to become fluent in R. The book is structured around the elements of languages with chapter titles that highlight the parallels between natural languages like English and the R language.

Nowadays, many students of biological and environmental sciences learn R in courses about statistics or data analysis. However, frequently not in enough depth to effectively use it in scripts for automating data analyses or documenting the whole data analysis workflow to ensure reproducibility. Students in the humanities and also in other fields, may find it easier to learn the R language separately from data analysis and statistics. There are also many who are already familiar with statistical principles and willing to switch from other software to R. *Learn R: As a Language* is written with these readers in mind to serve both as a text book and as a reference.

A language is a system of communication. Basic concepts and operations are based on abstractions that are shared across programming languages and relevant to programs of all sizes and complexities; these abstractions are explained in the book together their implementation in the R language. Other abstractions and programming concepts, outside the scope of this book, are relevant to large and complex pieces of software meant to be widely distributed. In other words, *Learn R: As a Language* aims at teaching and supporting *programming in the small*: the

use of R to automate the drudgery of data manipulation, including the different steps spanning from data input and exploration to the production of publication-quality illustrations and their documentation.

Using a language actively is the most efficient way of learning it. By using it, I mean actually reading, writing, and running scripts or programs. *Learn R: As a Language* supports learning the R language in a way comparable to how children learn to speak: they work out what the rules are, simply by listening to people speak and trying to utter what they want to tell their parents. Of course, small children receive some guidance, but they are not taught a prescriptive set of rules like when learning a second language at school. Instead of listening, readers will read and run code, and instead of speaking, readers will write and try to execute R code statements on a computer. I do provide explanations and guidance, but the idea of this book is for readers to play with the numerous examples by creating new variations upon them, to find out by themselves the patterns behind the R language. Instead of parents being the sounding board for the first utterances of readers new to R, the computer will play this role.

This revised second edition reflects changes that took place in R and packages described. Very few code chunks from the first edition had stopped working but deprecations meant that some examples triggered messages or warnings, and will eventually fail. Recent (> 4.0.0) versions of R have significant enhancements such as the new pipe operator. Packages have also evolved acquiring new features. Feedback from readers and reviewers has highlighted some gaps in the contents and unclear explanations. Re-reading myself the book after some time allowed me to think of other improvements. I have updated the book accordingly. I have added diagrams and flowcharts to facilitate comprehension programming concepts. I edited the text from the first edition to fix all errors and outdated examples or explanations known to me and to improve the clarity of previously unclear explanations.

I encourage you to approach R like a child approaches his or her mother tongue when first learning to speak: do not struggle, just play, and fool around with R! If the going gets difficult and frustrating, take a break! If you get a new insight, take a break to enjoy the victory!

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In many ways this text owes much more to people who are not authors than to myself. However, as I am the one who has written *Learn R: As a Language* and decided what to include and exclude, I take full responsibility for any errors and inaccuracies.

Helsinki, March 9, 2023



Using the book to learn R

Few people like problems. Hence the natural tendency in problem-solving is to pick the first solution that comes to mind and run with it. ... A better strategy ... is to select the most attractive path from many ideas, or concepts.

J. L. Adams
Conceptual blockbusting, 1987

Approach and structure


Depending on previous experience, reading *Learn R: As a Language* will be about exploring a new world or revisiting a familiar one. In both cases *Learn R: As a Language* aims to be a travel guide, neither a traveler's account, nor a cookbook of R recipes. It can be used as a course book, supplementary reading or for self instruction, and also as a reference.


In R, like in most “rich” languages, there are multiple ways of coding the same operations. I have included code examples that aim to strike a balance between execution speed and readability. One could write equivalent R books using substantially different code examples. Keep this in mind when reading the book and using R. Keep also in mind that it is impossible to remember everything about R and as a user you will frequently need to consult the documentation, even while doing the exercises in this book. The R language, in a broad sense, is vast because it can be expanded with independently developed packages. Learning to use R mainly consists of learning the basics plus developing the skill of finding your way in R, its documentation and on-line question and answer forums.


The contents of the book are organized so that it can be used both as a text book for learning R and as a reference. It starts with simple concepts and language elements progressing towards more complex language structures and uses. Along the way readers will find, in each chapter, descriptions and examples for the common (usual) cases and the exceptions. Some books hide the exceptions and counterintuitive features from learners to make the learning easier, I instead have included these but marked using icons and marginal bars. There are two reasons for choosing this approach. First, the boundary between boringly easy and


frustratingly challenging is different for each of us, and varies depending on the subject dealt with. So, I hope the marks will help readers predict what to expect, how much effort to put in each section and even what to read or skip. Second, if I had hidden the tricky bits of the R language, I would have made reader's later use of R more difficult. It would have also made the book less useful as a reference.


The key to the marginal bars and icons is given next. They inform about what content is advanced or included with a specific aim.

 Signals text providing general information not directly related to the R language.

 Signals in-depth explanations of specific points that may require you to spend time thinking, which in general can be skipped on first reading, but to which you should return at a later peaceful time, preferably with a cup of coffee or tea.

 Signals important bits of information that must be remembered when using R—i.e., explain some unusual feature of the language.

 Signals *playground* sections which contain open-ended exercises—ideas and pieces of R code to play with at the R console. Most code chunks show only the R code listing. Readers are expected to run this code both as is and modified, study the output returned by R for each variation.

 Signals *advanced playground* sections which will require more time to play with before grasping concepts than regular *playground* sections.

Readers new to R should read at least chapters ?? to ?? sequentially. Possibly, starting by reading parts and doing exercises not marked as advanced. However, I expect to be most useful to these readers, not to completely skip the description of unusual features and special cases, but rather to skim enough from them so as to get an idea of what special situations they may face as R users. Playground exercises should not be skipped, as they are a key component of the didactic approach used.

Readers already familiar with R will be able to read the chapters in the book in any order, as need arises. In the long run, I expect *Learn R: As a Language* to remain useful as a reference to those using it as a textbook, both for refreshing the mainstream features and to deal with the oddities and quirks of the language. To make its use as a reference easy, I have been thorough with indexing, including many carefully chosen terms, their synonyms and the names of all R objects and constructs discussed, collecting them in three alphabetical indexes: *General index*, *Index of R names by category*, and *Alphabetic index of R names* starting at pages 92, 94 and ??, respectively. I have also included cross references that link related sections.

Readers should not aim at remembering all the details presented in the book. Using this and other books, and documentation effectively as references, depends on a good grasp of the larger picture of R and how to navigate the documentation; i.e., it is more important to remember abstractions and in what situations they are

used, and function names, than the details of how to use them. Developing a sense of when one needs to be careful not to fall in a “language trap” is also important.

Typography and syntax highlighting

R code chunks are typeset in a typewriter font, and using colour to highlight the different elements of the syntax, such as variables, functions, constant values, etc. R code elements embedded in the text are similarly typeset but always black. For example in the “code chunk” below `mean()` and `print()` are functions; 1, 5 and 3 are constant numeric values, and `z` is the name of a variable where the result of the computation done in the first line of code is stored. The line starting with `##` shows what is printed to the screen when executing the second statement: `[1] 1`.

```
z <- mean(1, 5, 3)
print(z)
## [1] 1
```

To describe data objects I use diagrams inspired in Joseph N. Hall’s PEGS (Perl Graphical Structures) (Hall and Schwartz 1997). One difference with the original black and white PEGS is the use of a colour fill to highlight the type of the stored objects. We also distinguish based on the width of the “signal” border the names of whole object and those of its members. When possible, we use horizontal diagrams to help with fitting the objects to the page.

For code structure I use diagrams based on boxes and arrows and to describe control of the flow of code execution, the usual flow charts.

In the different diagrams, I use the notation `<value>`, `<statement>`, `<name>`, etc., as a generic placeholder indicating *any valid value*, *any valid R statement*, *any valid R name*, etc.



1

The R language: “Words” and “sentences”

The desire to economize time and mental effort in arithmetical computations, and to eliminate human liability to error, is probably as old as the science of arithmetic itself.

Howard Aiken

Proposed automatic calculating machine, 1937; reprinted 1964

1.1 Aims of this chapter

In my experience, for those not familiar with computer programming languages, the best first step in learning the R language is to use it interactively by typing textual commands at the *console* or command line. This will teach not only the syntax and grammar rules, but also give you a glimpse at the advantages and flexibility of this approach to data analysis.

In the first part of the chapter we will use R to do everyday calculations that should be so easy and familiar that you will not need to think about the operations themselves. This easy start will give you a chance to focus on learning how to issue textual commands at the command prompt.

Later in the chapter, you will gradually need to focus more on the R language and its grammar and less on how commands are entered. By the end of the chapter you will be familiar with most of the kinds of “words” used in the R language and you will be able to write simple “sentences” in R.

Along the chapter, I will occasionally show the equivalent of the R code in mathematical notation. If you are not familiar with the mathematical notation, you can safely ignore it, as long as you understand the R code.

1.2 Natural and computer languages

Computer languages have strict rules and interpreters and compilers are unforgiving about errors. They will issue error messages, but in contrast to human readers or listeners, will not guess your intentions and continue. However, computer languages have a much smaller set of words than natural languages, such as English. If you are new to computer programming, understanding the parallels between computer and natural languages may be useful.

One can think of constant values and variables (values stored under a name) as nouns and of operators and functions as verbs. A complete command, or statement, is the equivalent of a natural language sentence: “a comprehensible utterance.” The simple statement `a + 1` has three components: `a`, a variable, `+`, an operator and `1` a constant. The statement `sqrt(4)` has two components, a function `sqrt()` and a numerical constant `4`. We say that “to compute $\sqrt{4}$ we *call* `sqrt()` with `4` as its *argument*.”

Although all values manipulated in a digital computer are stored as *bits* in memory, multiple interpretations are possible. Numbers, letters, logical values, etc., can be encoded into bits and decoded as long as their type or *mode* is known. The concept of `class` is not directly related to how values are encoded when stored in computer memory, but instead their interpretation as part of a computer program. We can have, for example, RGB color values, stored as three numbers such as `0, 0, 255`, as hexadecimal numbers stored as characters `#0000FF`, or even use fancy names stored as character strings like `"blue"`. We could create a `class` for colors using any of these representations, based on two different modes: `numeric` and `character`.

In this chapter we will focus on individual program statements, the equivalent of sentences in natural language. In later chapters you will learn how to combine them to create compound statements, the equivalent of natural-language paragraphs, and scripts, the equivalent of essays. You will also learn how to define new verbs, user-defined functions and operators, and new nouns, user-defined classes.

1.3 Numeric values and arithmetic

When working in R with arithmetic expressions, the normal mathematical precedence rules are respected, but parentheses can be used to alter this order. Parentheses can be nested, but in contrast to the usual practice in mathematics, the same parenthesis symbol is used at all nesting levels.



Both in mathematics and programming languages *operator precedence rules* determine which subexpressions are evaluated first and which later. Contrary to primitive electronic calculators, R evaluates numeric expressions containing operators according to the rules of mathematics. In the expression `3 + 2 × 3`, the product `2 × 3` has precedence over the addition, and is evaluated first, yielding

as the result of the whole expression, 9. In programming languages, similar rules apply to all operators, even those taking as operands non-numeric values.

It is important to keep in mind that in R trigonometric functions interpret numeric values representing angles as being expressed in radians.

The equivalent of the math expression

$$\frac{3 + e^2}{\sin \pi}$$

is, in R, written as follows:

```
(3 + exp(2)) / sin(pi)
## [1] 8.483588e+16
```

It can be seen above that mathematical constants and functions are part of the R language. One thing to remember when translating complex fractions as above into R code, is that in arithmetic expressions the bar of the fraction generates a grouping that alters the normal precedence of operations. In contrast, in an R expression this grouping must be explicitly signaled with additional parentheses.

If you are in doubt about how precedence rules work, you can add parentheses to make sure the order of computations is the one you intend. Redundant parentheses have no effect.

```
1 + 2 * 3
## [1] 7

1 + (2 * 3)
## [1] 7

(1 + 2) * 3
## [1] 9
```

The number of opening (left side) and closing (right side) parentheses must be balanced, and they must be located so that each enclosed term is a valid mathematical expression, i.e., code that can be evaluated to return a value, a value that can be inserted in place of the expression enclosed in parenthesis before evaluating the remaining of the expression. For example, $(1 + 2) * 3$ after evaluating $(1 + 2)$ becomes $3 * 3$ yielding 9. In contrast, $(1 +) 2 * 3$ is a syntax error as $1 +$ is incomplete and does not yield a number.



Here results are not shown. These are examples for you to type at the command prompt. In general you should not skip them, as in many cases, as with the statements highlighted with comments in the code chunk below, they have something to teach or demonstrate. You are strongly encouraged to *play*, in other words, create new variations of the examples and execute them to explore how R works.


```

1 + 1
2 * 2
2 + 10 / 5
(2 + 10) / 5
10^2 + 1
sqrt(9)
pi # whole precision not shown when printing
print(pi, digits = 22)
sin(pi) # oops! Read on for explanation.
log(100)
log10(100)
log2(8)
exp(1)

```

Variables are used to store values. After we *assign* a value to a variable, we can use in our code the name of the variable in place of the stored value. The “usual” assignment operator is `<-`. In R, all names, including variable names, are case sensitive. Variables `a` and `A` are two different variables. Variable names can be long in R although it is not a good idea to use very long names. Here I am using very short names, something that is usually also a very bad idea. However, in the examples in this chapter where the stored values have no connection to the real world, simple names emphasize their abstract nature. In the chunk below, `a` and `b` are arbitrarily chosen variable names; I could have used names like `my.variable.a` or `outside.temperature` if they had been useful to convey information.

```

a <- 1
a + 1
## [1] 2

a
## [1] 1

b <- 10
b <- a + b
b
## [1] 11

3e-2 * 2.0
## [1] 0.06

```

Entering the name of a variable *at the R console* implicitly calls function `print()` displaying the stored value on the console. The same applies to any other statement entered *at the R console*: `print()` is implicitly called with the result of executing the statement as its argument.

```


a
## [1] 1

print(a)
## [1] 1


a + 1
## [1] 2

print(a + 1)
## [1] 2

```

 There are some syntactically legal assignment statements that are not very frequently used, but you should be aware that they are valid, as they will not trigger error messages, and may surprise you. The most important thing is to write code consistently. The “backwards” assignment operator `->` and resulting code like `1 -> a` are valid but less frequently used. The use of the equals sign (`=`) for assignment in place of `<=` although valid is discouraged. Chaining assignments as in the first statement below can be used to signal to the human reader that `a`, `b` and `c` are being assigned the same value.

```
a <- b <- c <- 0.0
a
b
c
1 -> a
a
a = 3
a
```

 In R, all numbers belong to mode `numeric` (we will discuss the concepts of *mode* and *class* in section 1.8 on page 26). We can query if the mode of an object is `numeric` with function `is.numeric()`.

```
mode(1)
## [1] "numeric"

a <- 1
is.numeric(a)
## [1] TRUE
```

Because numbers can be stored in different formats, requiring different amounts of computer memory per value, most computing languages implement several different types of numbers. In most cases R’s `numeric()` can be used everywhere that a number is expected. However, in some cases it has advantages to explicitly indicate that we will store or operate on whole numbers, in which case we can use class `integer`, with integer constants indicated by a trailing capital “L,” as in `32L`.

```
is.numeric(1L)
## [1] TRUE

is.integer(1L)
## [1] TRUE

is.double(1L)
## [1] FALSE
```

Real numbers are a mathematical abstraction, and do not have an exact equivalent in computers. Instead of Real numbers, computers store and operate on numbers that are restricted to a broad but finite range of values and have a finite resolution. They are called, *floats* (or *floating-point* numbers); in R they go by the name of `double` and can be created with the constructor `double()`.

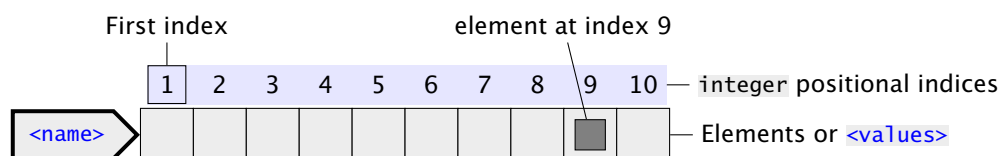
```
is.numeric(1)
## [1] TRUE

is.integer(1)
## [1] FALSE

is.double(1)
## [1] TRUE
```

The name `double` originates from the C language, in which there are different types of floats available. With the name `double` used to mean “double-precision floating-point numbers.” Similarly, the use of `L` stems from the `long` type in C, meaning “long integer numbers.”

R’s vectors are one-dimensional, of varying length and used to store similar values, e.g., numbers. They are different to the vectors, commonly used in Physics for describing directional forces, which are symbolized with an arrow as an “accent,” such as \vec{F} . In R numeric values and other atomic values are always **vector s** that can contain zero, one or more elements. The diagram below exemplifies a vector containing ten elements. These elements can be extracted using integer numbers as positional indices, and manipulated as described in more detail in section 1.12 on page 46.



Vectors, in mathematical notation, are similarly represented using positional indexes as subscripts,

$$a_{1\dots n} = a_1, a_2, \dots, a_i, \dots, a_n, \quad (1.1)$$

where $a_{1\dots n}$ is the whole vector and a_1 its first member. The length of $a_{1\dots n}$ is n as it contains n members. In the diagram above $n = 10$.

As you have seen above, the results of calculations were printed preceded with `[1]`. This is the index or position in the vector of the first number (or other value) displayed at the head of the current line. As single values are vectors of length one, when they are printed, they are also preceded with `[1]`.

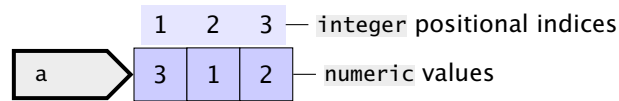
One can use `c()` “concatenate” to create a vector from other vectors, including vectors of length 1, or even vectors of length 0, such as the `numeric` constants in the statements below. The first example shows an anonymous vector created, printed, and then automatically discarded.

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

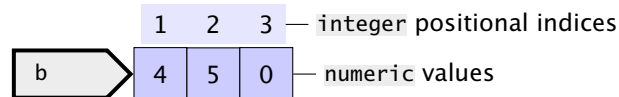
To be able to reuse the vector, we assign it to a variable, giving a name to it. The length of a vector can be queried with method `length()`. We show below R code followed by a diagram depicting the vector created.

```
a <- c(3, 1, 2)
length(a)
## [1] 3

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



```
b <- c(4, 5, 0)
b
## [1] 4 5 0
```



```
c <- c(a, b)
c
## [1] 3 1 2 4 5 0
```



```
d <- c(b, a)
d
## [1] 4 5 0 3 1 2
```



As shown earlier, values can be also printed at the R console. Here we show concatenation with a vector of the same class but with length zero.

```
c(d, numeric())
## [1] 4 5 0 3 1 2
```

Method `c()` accepts as arguments two or more vectors and concatenates them, one after another. Quite frequently we may need to insert one vector in the middle of another. For this operation, `c()` is not useful by itself. One could use indexing combined with `c()`, but this is not needed as R provides a function capable of directly doing this operation. Although it can be used to “insert” values, it is named `append()`, and by default, it indeed appends one vector at the end of another.

```
append(a, b)
## [1] 3 1 2 4 5 0
```

The output above is the same as for `c(a, b)`, however, `append()` accepts as an argument an index position after which to “append” its second argument. This results in an *insert* operation when the index points at any position different from the end of the vector.

```
append(a, values = b, after = 2L)
## [1] 3 1 4 5 0 2
```

Both `c()` and `append()` can also be used with lists (described in section 2.3 on page 54).



One can create sequences using function `seq()` or the operator `:`, or repeat values using function `rep()`. In this case, I leave to the reader to work out the rules by running these and his/her own examples, with the help of the documentation, available through `help(seq)` and `help(rep)`.

```
a <- -1:5
a
b <- 5:-1
b
c <- seq(from = -1, to = 1, by = 0.1)
c
d <- rep(-5, 4)
d
```

Next, something that makes R different from most other programming languages: vectorized arithmetic. Operators and functions that are vectorized accept, as arguments, vectors of arbitrary length, in which case the result returned is equivalent to having applied the same function or operator individually to each element of the vector.

```
a + 1 # we add one to vector a defined above
## [1] 4 2 3

(a + 1) * 2
## [1] 8 4 6

a + b
## [1] 7 6 2

a - a
## [1] 0 0 0
```

As it can be seen in the first line above, another peculiarity of R, is what is frequently called “recycling” of arguments: as vector `a` is of length 6, but the constant 1 is a vector of length 1, this short constant vector is extended, by recycling its value, into a vector of six ones—i.e., a vector of the same length as the longest vector in the statement, `a`.


Make sure you understand what calculations are taking place in the chunk above, and also the one below.

```
a <- rep(1, 6)
a
## [1] 1 1 1 1 1 1

a + 1:2
## [1] 2 3 2 3 2 3

a + 1:3
## [1] 2 3 4 2 3 4

a + 1:4
## Warning in a + 1:4: longer object length is not a multiple of shorter object
length
## [1] 2 3 4 5 2 3
```

 As mentioned above, a vector can have a length of zero or more member values. Vectors of length zero may seem at first sight quite useless, but in fact they are very useful. They allow the handling of “no input” or “nothing to do” cases as normal cases, which in the absence of vectors of length zero would require to be treated as special cases. Constructors for R classes like `numeric()` return vectors of a length given by their first argument, which defaults to zero. I describe here a useful function, `length()` which returns the length of a vector or list.

```
z <- numeric(0)
z
## numeric(0)

length(z)
## [1] 0
```

```
z1 <- numeric()
z1
## numeric(0)

z2 <- numeric(length = 0)
z2
## numeric(0)
```

Vectors (and lists) of length zero, behave in most cases, as expected—e.g., they can be concatenated as shown here.

```
length(c(a, numeric(0), b))
## [1] 9

length(c(a, b))
## [1] 9
```

Many functions, such as R’s maths functions and operators, will accept numeric vectors of length zero as valid input, returning also a vector of length zero, issuing neither a warning nor an error message. In other words, *these are valid operations* in R.

```
log(numeric(0))
## numeric(0)

5 + numeric(0)
## numeric(0)
```

Even when of length zero, vectors do have to belong to a class acceptable for the operation: `5 + character(0)` is an error.

Passing as argument to parameter `length` a value larger than zero creates a longer vector filled with zeros in the case of `numeric()`.

```
numeric(5)
## [1] 0 0 0 0 0
```

The length of a vector can be explicitly increased, with missing values filled automatically with `NA`, the marker for not available.

```
z <- 1:5
z
## [1] 1 2 3 4 5

length(z) <- 10
z
## [1] 1 2 3 4 5 NA NA NA NA NA
```

If the length is decreased, the values in the *tail* of the vector are discarded.

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

length(z) <- 5
z
## [1] 1 2 3 4 5
```

It is possible to *remove* variables from the workspace with `rm()`. Function `ls()` returns a *list* of all objects visible in the current environment, or by supplying a `pattern` argument, only the objects with names matching the `pattern`. The pattern is given as a regular expression, with `[]` enclosing alternative matching characters, `^` and `$`, indicating the extremes of the name (start and end, respectively). For example, `"^z$"` matches only the single character ‘z’ while `"^z"` matches any name starting with ‘z’. In contrast `"^[zy]$"` matches both ‘z’ and ‘y’ but neither ‘zy’ nor ‘yz’, and `"^[a-z]"` matches any name starting with a lowercase ASCII letter. If you are using RStudio, all objects are listed in the Environment pane, and the search box of the panel can be used to find a given object.

```
ls(pattern="^z$")
## [1] "z"

rm(z)
ls(pattern="^z$")
## character(0)
```

There are some special values available for numbers. `NA` meaning “not available” is used for missing values. Calculations can also yield the following values `NaN` “not a number”, `Inf` and `-Inf` for ∞ and $-\infty$. As you will see below, calculations yielding these values do **not** trigger errors or warnings, as they are arithmetically valid. `Inf` and `-Inf` are also valid numerical values for input and constants.

```
a <- NA
a
## [1] NA

-1 / 0
## [1] -Inf

1 / 0
## [1] Inf

Inf / Inf
## [1] NaN

Inf + 4
## [1] Inf

b <- -Inf
b * -1
## [1] Inf
```

Not available (`NA`) values are very important in the analysis of experimental data, as frequently some observations are missing from an otherwise complete data set due to “accidents” during the course of an experiment. It is important to understand how to interpret `NA`’s. They are simple placeholders for something that is unavailable, in other words, *unknown*.

```
A <- NA
A
## [1] NA

A + 1
## [1] NA

A + Inf
## [1] NA
```



When to use vectors of length zero, and when `NA`s? Make sure you understand the logic behind the different behavior of functions and operators with respect to `NA` and `numeric()` or its equivalent `numeric(0)`. What do they represent? Why `NA` s are not ignored, while vectors of length zero are?

```
123 + numeric()
123 + NA
```

Model answer: `NA` is used to signal a value that “was lost” or “was expected” but is unavailable because of some accident. A vector of length zero, represents no values, but within the normal expectations. In particular, if vectors are expected

to have a certain length, or if index positions along a vector are meaningful, then using `NA` is a must.

Any operation, even tests of equality, involving one or more `NA`'s return an `NA`. In other words, when one input to a calculation is unknown, the result of the calculation is unknown. This means that a special function is needed for testing for the presence of `NA` values.

```
is.na(c(NA, 1))
## [1] TRUE FALSE
```

In the example above, we can also see that `is.na()` is vectorized, and that it applies the test to each of the two elements of the vector individually, returning the result as a logical vector of length two.

One thing to be aware of are the consequences of the fact that numbers in computers are almost always stored with finite precision and/or range: the expectations derived from the mathematical definition of Real numbers are not always fulfilled. See the box on page 19 for an in-depth explanation.

```
1 - 1e-20
## [1] 1
```

When comparing `integer` values these problems do not exist, as integer arithmetic is not affected by loss of precision in calculations restricted to integers. Because of the way integers are stored in the memory of computers, within the representable range, they are stored exactly. One can think of computer integers as a subset of whole numbers restricted to a certain range of values.

```
1L + 3L
## [1] 4

1L * 3L
## [1] 3

1L %/% 3L
## [1] 0

1L %% 3L
## [1] 1

1L / 3L
## [1] 0.3333333
```

The last statement in the example immediately above, using the “usual” division operator yields a floating-point `double` result, while the integer division operator `%/%` yields an `integer` result, and `%%` returns the remainder from the integer division. If as a result of an operation the result falls outside the range of representable values, the returned value is `NA`.

```
1000000L * 1000000L
## warning in 1000000L * 1000000L: NAs produced by integer overflow
## [1] NA
```

Both doubles and integers are considered numeric. In most situations, conversion is automatic and we do not need to worry about the differences between these two types of numeric values. The next chunk shows returned values that are either `TRUE` or `FALSE`. These are `logical` values that will be discussed in the next section.

```
is.numeric(1L)
## [1] TRUE

is.integer(1L)
## [1] TRUE

is.double(1L)
## [1] FALSE

is.double(1L / 3L)
## [1] TRUE

is.numeric(1L / 3L)
## [1] TRUE
```



Study the variations of the previous example shown below, and explain why the two statements return different values. Hint: `1` is a `double` constant. You can use `is.integer()` and `is.double()` in your explorations.

```
1 * 1000000L * 1000000L
1000000L * 1000000L * 1
```

Both when displaying numbers or as part of computations, we may want to decrease the number of significant digits or the number of digits after the decimal marker. Be aware that in the examples below, even if printing is being done by default, these functions return `numeric` values that are different from their input and can be stored and used in computations. Function `round()` is used to round numbers to a certain number of decimal places after or before the decimal marker, while `signif()` rounds to the requested number of significant digits.

```
round(0.0124567, digits = 3)
## [1] 0.012

signif(0.0124567, digits = 3)
## [1] 0.0125

round(1789.1234, digits = 3)
## [1] 1789.123


signif(1789.1234, digits = 3)
## [1] 1790

round(1789.1234, digits = -1)
## [1] 1790

a <- 0.12345
b <- round(a, digits = 2)
a == b
## [1] FALSE

a - b
## [1] 0.00345


b
## [1] 0.12
```

 Being `digits`, the second parameter of these functions, the argument can also be passed by position. However, code is usually easier to understand for humans when parameter names are made explicit.

```
round(0.0124567, digits = 3)
## [1] 0.012

round(0.0124567, 3)
## [1] 0.012
```

Functions `trunc()` and `ceiling()` return the non-fractional part of a numeric value as a new numeric value. They differ in how they handle negative values, and neither of them rounds the returned value to the nearest whole number.

 What does value truncation mean? Function `trunc()` truncates a numeric value, but it does not return an `integer`.

- Explore how `trunc()` and `ceiling()` differ. Test them both with positive and negative values.
- **Advanced** Use function `abs()` and operators `+` and `-` to reproduce the output of `trunc()` and `ceiling()` for the different inputs.
- Can `trunc()` and `ceiling()` be considered type conversion functions in R?

1.4 Logical values and Boolean algebra

What in Mathematics are usually called Boolean values, are called `logical` values in R. They can have only two values `TRUE` and `FALSE`, in addition to `NA` (not available). They are vectors as all other atomic types in R (by *atomic* we mean that each value is not composed of “parts”). There are also logical operators that allow Boolean algebra. In the chunk below we operate on `logical` vectors of length one.

```
a <- TRUE
b <- FALSE
mode(a)
## [1] "logical"

a
## [1] TRUE

!a # negation
## [1] FALSE

a && b # logical AND
## [1] FALSE

a || b # logical OR
## [1] TRUE

xor(a, b) # exclusive OR
## [1] TRUE
```

As with arithmetic operators, vectorization is available with *some* logical operators. The availability of two kinds of logical operators is one of the most troublesome aspects of the R language for beginners. Pairs of “equivalent” logical operators behave differently, use similar syntax and use similar symbols! The vectorized operators have single-character names `&` and `|`, while the non-vectorized ones have double-character names `&&` and `||`. There is only one version of the negation operator `!` that is vectorized. In recent versions of R, an error is triggered when a non-vectorized operator is used with a vector with length > 1 .

```
a <- c(TRUE,FALSE)
b <- c(TRUE,TRUE)
a
## [1] TRUE FALSE

b
## [1] TRUE TRUE

a & b # vectorized AND
## [1] TRUE FALSE

a | b # vectorized OR
## [1] TRUE TRUE
```

Functions `any()` and `all()` take zero or more logical vectors as their arguments, and return a single logical value “summarizing” the logical values in the vectors. Function `all()` returns `TRUE` only if all values in the vectors passed as arguments are `TRUE`, and `any()` returns `TRUE` unless all values in the vectors are `FALSE`.

```
any(a)
## [1] TRUE

all(a)
## [1] FALSE

any(a & b)
## [1] TRUE

all(a & b)
## [1] FALSE
```

Another important thing to know about logical operators is that they “short-cut” evaluation. If the result is known from the first part of the statement, the rest of the statement is not evaluated. Try to understand what happens when you enter the following commands. Short-cut evaluation is useful, as the first condition can be used as a guard protecting a later condition from being evaluated when it would trigger an error.

```
TRUE || NA
## [1] TRUE

FALSE || NA
## [1] NA

TRUE && NA
```

```
## [1] NA

FALSE && NA
## [1] FALSE

TRUE && FALSE && NA
## [1] FALSE


TRUE && TRUE && NA
## [1] NA
```

When using the vectorized operators on vectors of length greater than one, ‘short-cut’ evaluation still applies for the result obtained at each index position.

```
a & b & NA
## [1] NA FALSE

a & b & c(NA, NA)
## [1] NA FALSE

a | b | c(NA, NA)
## [1] TRUE TRUE
```

 Based on the description of “recycling” presented on page 8 for numeric operators, explore how “recycling” works with vectorized logical operators. Create logical vectors of different lengths (including length one) and *play* by writing several code statements with operations on them. To get you started, one example is given below. Execute this example, and then create and run your own, making sure that you understand why the values returned are what they are. Sometimes, you will need to devise several examples or test cases to tease out of R an understanding of how a certain feature of the language works, so do not give up early, and make use of your imagination!

```
x <- c(TRUE, FALSE, TRUE, NA)
x & FALSE
x | c(TRUE, FALSE)
```

1.5 Comparison operators and operations

Comparison operators return vectors of `logical` values as results.

```
1.2 > 1.0
## [1] TRUE

1.2 >= 1.0
## [1] TRUE

1.2 == 1.0 # be aware that here we use two = symbols
```

```
## [1] FALSE

1.2 != 1.0
## [1] TRUE

1.2 <= 1.0
## [1] FALSE

1.2 < 1.0
## [1] FALSE

a <- 20
a < 100 && a > 10
## [1] TRUE
```

These operators can be used on vectors of any length, returning as a result a logical vector as long as the longest operand. In other words, they behave in the same way as the arithmetic operators described on page 8: their arguments are recycled when needed. Hint: if you do not know what to expect as a value for the vector returned by `1:10`, execute the statement `print(a)` after the first code statement below, or, alternatively, `1:10` without saving the result to a variable.

```
a <- 1:10
a > 5
## [1] FALSE FALSE FALSE FALSE FALSE TRUE TRUE TRUE TRUE TRUE

a < 5
## [1] TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE

a == 5
## [1] FALSE FALSE FALSE FALSE TRUE FALSE FALSE FALSE FALSE FALSE

all(a > 5)
## [1] FALSE

any(a > 5)
## [1] TRUE

b <- a > 5
b
## [1] FALSE FALSE FALSE FALSE FALSE TRUE TRUE TRUE TRUE TRUE

any(b)
## [1] TRUE

all(b)
## [1] FALSE
```

Precedence rules also apply to comparison operators and they can be overridden by means of parentheses.

```
a > 2 + 3
## [1] FALSE FALSE FALSE FALSE FALSE TRUE TRUE TRUE TRUE TRUE

(a > 2) + 3
## [1] 3 3 4 4 4 4 4 4 4 4
```



Use the statement below as a starting point in exploring how precedence works when logical and arithmetic operators are part of the same statement. *Play* with the example by adding parentheses at different positions and based on the returned values, work out the default order of operator precedence used for the evaluation of the example given below.

```
a <- 1:10
a > 3 | a + 2 < 3
```

Again, be aware of “short-cut evaluation”. If the result does not depend on the missing value, then the result, `TRUE` or `FALSE` is returned. If the presence of the `NA` makes the end result unknown, then `NA` is returned.

```
c <- c(a, NA)
c > 5
## [1] FALSE FALSE FALSE FALSE FALSE TRUE TRUE TRUE TRUE TRUE NA

all(c > 5)
## [1] FALSE

any(c > 5)
## [1] TRUE

all(c < 20)
## [1] NA

any(c > 20)
## [1] NA

is.na(a)
## [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE

is.na(c)
## [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE TRUE

any(is.na(c))
## [1] TRUE

all(is.na(c))
## [1] FALSE
```

The behavior of many of base-R’s functions when `NA`s are present in their input arguments can be modified. `TRUE` passed as an argument to parameter `na.rm`, results in `NA` values being *removed* from the input **before** the function is applied.

```
all(c < 20)
## [1] NA

any(c > 20)
## [1] NA

all(c < 20, na.rm=TRUE)
## [1] TRUE

any(c > 20, na.rm=TRUE)
## [1] FALSE
```



Here I give some examples for which the finite resolution of computer machine floats, as compared to Real numbers as defined in mathematics, can cause serious problems. In R, numbers that are not integers are stored as *double-precision floats*. In addition to having limits to the largest and smallest numbers that can be represented, the precision of floats is limited by the number of significant digits that can be stored. Precision is usually described by “epsilon” (ϵ), abbreviated *eps*, defined as the largest value of ϵ for which $1 + \epsilon = 1$. The finite resolution of floats can lead to unexpected results when testing for equality. In the second example below, the result of the subtraction is still exactly 1 due to insufficient resolution.

```
0 - 1e-20
## [1] -1e-20

1 - 1e-20
## [1] 1
```

The finiteness of floats also affects tests of equality, which is more likely to result in errors with important consequences.

```
1e20 == 1 + 1e20
## [1] TRUE

1 == 1 + 1e-20
## [1] TRUE

0 == 1e-20
## [1] FALSE
```

As R can run on different types of computer hardware, the actual machine limits for storing numbers in memory may vary depending on the type of processor and even compiler used to build the R program executable. However, it is possible to obtain these values at run time from the variable `.Machine`, which is part of the R language. Please see the help page for `.Machine` for a detailed and up-to-date description of the available constants.

```
.Machine$double.eps
## [1] 2.220446e-16

.Machine$double.neg.eps
## [1] 1.110223e-16

.Machine$double.max
## [1] 1024

.Machine$double.min
## [1] -1022
```

The last two values refer to the exponents of 10, rather than the maximum and minimum size of numbers that can be handled as objects of class `double`. Values outside these limits are stored as `-Inf` or `Inf` and enter arithmetic as infinite values according the mathematical rules.


```
1e1026
## [1] Inf

1e-1026
## [1] 0

Inf + 1
## [1] Inf

-Inf + 1
## [1] -Inf
```

As `integer` values are stored in machine memory without loss of precision, `epsilon` is not defined for `integer` values.

```
.Machine$integer.max
## [1] 2147483647

2147483699L
## [1] 2147483699
```

In those statements in the chunk below where at least one operand is `double` the `integer` operands are *promoted* to `double` before computation. A similar promotion does not take place when operations are among `integer` values, resulting in *overflow*, meaning numbers that are too big to be represented as `integer` values.

```
2147483600L + 99L

## Warning in 2147483600L + 99L: NAs produced by integer overflow
## [1] NA

2147483600L + 99
## [1] 2147483699

2147483600L * 2147483600L

## Warning in 2147483600L * 2147483600L: NAs produced by integer overflow
## [1] NA


2147483600L * 2147483600
## [1] 4.611686e+18
```

We see next that the exponentiation operator `^` forces the promotion of its arguments to `double`, resulting in no overflow. In contrast, as seen above, the multiplication operator `*` operates on integers resulting in overflow.

```
2147483600L * 2147483600L

## Warning in 2147483600L * 2147483600L: NAs produced by integer overflow
## [1] NA

2147483600L^2L
## [1] 4.611686e+18
```

 In many situations, when writing programs one should avoid testing for equality of floating point numbers ('floats'). Here we show how to gracefully handle rounding errors. As the example shows, rounding errors may accumulate, and in practice `.Machine$double.eps` is not always a good value to safely use in tests for "zero," and a larger value may be needed. Whenever possible according to the logic of the calculations, it is best to test for inequalities, for example using `x <= 1.0` instead of `x == 1.0`. If this is not possible, then the tests should be done replacing tests like `x == 1.0` with `abs(x - 1.0) < eps`. Function `abs()` returns the absolute value, in simpler words, makes all values positive or zero, by changing the sign of negative values, or in mathematical notation $|x| = |-x|$.

```
a == 0.0 # may not always work
## [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE

abs(a) < 1e-15 # is safer
## [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

```
sin(pi) == 0.0 # angle in radians, not degrees!
## [1] FALSE
```

```
sin(2 * pi) == 0.0
## [1] FALSE
```

```
abs(sin(pi)) < 1e-15
## [1] TRUE
```

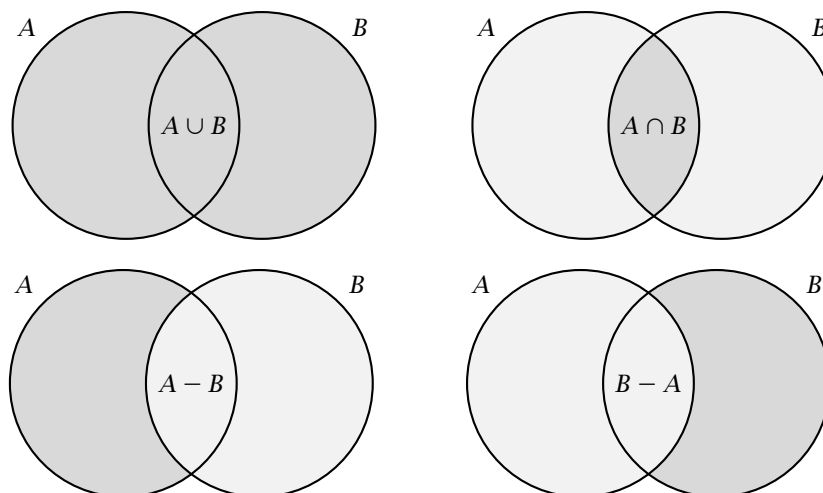
```
abs(sin(2 * pi)) < 1e-15
## [1] TRUE
```

```
sin(pi)
## [1] 1.224606e-16
```

```
sin(2 * pi)
## [1] -2.449213e-16
```

1.6 Sets and set operations

The R language supports set operations on vectors. They can be useful in many different contexts when manipulating and comparing vectors of values. Set algebra operations and their equivalents in mathematical notation and R functions are: *union*, \cup , `union()`; *intersection*, \cap , `intersect()`; *difference (asymmetrical)*, $-$, `setdiff()`; *equality test* `setequal()`; *membership*, `is.element()` and `%in%`. The first three functions return vector of the same mode as their inputs, and the last three a logical vector. The action of the first three operations is most easily illustrated with Venn diagrams.



In Bioinformatics it is usual, for example, to have character vectors of gene tags. We may have a vector for each of a set of different samples, and need to compare them. However, we start by using a more mundane example, everyday shopping, as illustration, followed by explanations.

```
fruits <- c("apple", "pear", "orange", "lemon", "tangerine")
bakery <- c("bread", "buns", "cake", "cookies")
dairy <- c("milk", "butter", "cheese")
shopping <- c("bread", "butter", "apple", "cheese", "orange")
intersect(fruits, shopping)
## [1] "apple" "orange"

intersect(bakery, shopping)
## [1] "bread"

intersect(dairy, shopping)
## [1] "butter" "cheese"

"lemon" %in% dairy
## [1] FALSE

"lemon" %in% fruits
## [1] TRUE

dairy %in% shopping
## [1] FALSE TRUE TRUE

setdiff(union(bakery, dairy), shopping)
## [1] "buns" "cake" "cookies" "milk"
```

For explanations we use abstract (symbolic) examples.


```
my.set <- c("a", "b", "c", "b")
```

To test if a given value belongs to a set, we use operator `%in%` or its function equivalent `is.element()`. In the algebra of sets notation, this is written $a \in A$, where A is a set and a a member. The second statement shows that the `%in%` operator is vectorized on its left-hand-side (lhs) operand, returning a logical vector.

```
is.element("a", my.set)
## [1] TRUE

"a" %in% my.set
## [1] TRUE

c("a", "a", "z") %in% my.set
## [1] TRUE TRUE FALSE
```

 Keep in mind that inclusion is an asymmetrical (not reflective) operation among sets. The rhs argument is interpreted as a set, while the lhs argument is interpreted as a vector of values to test for inclusion. In other words, any duplicate member in the lhs will be retained while the rhs is interpreted as a set of unique values. The returned logical vector has the same length as the lhs.

```
my.set %in% "a"
## [1] TRUE FALSE FALSE FALSE
```


The negation of inclusion is $a \notin A$, and coded in R by applying the negation operator `!` to the result of the test done with `%in%` or function `is.element()`.

```
!is.element("a", my.set)
## [1] FALSE

!"a" %in% my.set
## [1] FALSE

!c("a", "a", "z") %in% my.set
## [1] FALSE FALSE TRUE
```

Although inclusion is a set operation, it is also very useful for the simplification of `if()...else` statements by replacing multiple tests for alternative constant values of the same mode chained by multiple `|` operators. A useful property of `%in%` and `is.element()` is that they never return NA.

 Use operator `%in%` to write more concisely the following comparisons. Hint: see section 1.4 on page 14 for the difference between `|` and `||` operators.

```
x <- c("a", "a", "z")
x == "a" | x == "b" | x == "c" | x == "d"
```

Convert the logical vectors of length 3 into a vector of length one. Hint: see help for functions `all()` and `any()`.

With `unique()` we convert a vector of possibly repeated values into a set of unique values. In the algebra of sets, a certain object belongs or not to a set. Consequently, in a set, multiple copies of the same object or value are meaningless.

```
unique(my.set)
## [1] "a" "b" "c"

c("a", "a", "z") %in% unique(my.set)
## [1] TRUE TRUE FALSE
```

In the notation used in algebra of sets, the set union operator is \cup while the intersection operator is \cap . If we have sets A and B , their union is given by $A \cup B$ —in the next three examples, `c("a", "a", "z")` is a constant, while `my.set` is a variable.

```
union(c("a", "a", "z"), my.set)
## [1] "a" "z" "b" "c"
```

If we have sets A and B , their intersection is given by $A \cap B$.

```
intersect(c("a", "a", "z"), my.set)
## [1] "a"
```



What do you expect to be the difference between the values returned by the three statements in the code chunk below? Before running them, write down your expectations about the value each one will return. Only then run the code. Independently of whether your predictions were correct or not, write down an explanation of what each statement’s operation is.

```
union(c("a", "a", "z"), my.set)
c(c("a", "a", "z"), my.set)
c("a", "a", "z", my.set)
```

In the algebra of sets notation $A \subseteq B$, where A and B are sets, indicates that A is a subset or equal to B . For a true subset, the notation is $A \subset B$. The operators with the reverse direction are \supseteq and \supset . Implement these four operations in four R statements, and test them on sets (represented by R vectors) with different “overlap” among set members.



All set algebra examples above use character vectors and character constants. This is just the most frequent use case. Sets operations are valid on vectors of any atomic class, including `integer`, and computed values can be part of statements. In the second and third statements in the next chunk, we need to use additional parentheses to alter the default order of precedence between arithmetic and set operators.

```
9L %in% 2L:4L
## [1] FALSE

9L %in% ((2L:4L) * (2L:4L))
## [1] TRUE

c(1L, 16L) %in% ((2L:4L) * (2L:4L))
## [1] FALSE TRUE
```

Empty sets are an important component of the algebra of sets, in R they are represented as vectors of zero length. Vectors and lists of zero length, which the R language fully supports, can be used to “encode” emptiness also in other contexts. These vectors do belong to a class such as `numeric` or `character` and must be compatible with other operands in an expression. By default, constructors for vectors, construct empty vectors.

```
length(integer())
## [1] 0

1L %in% integer()
## [1] FALSE

setdiff(1L:4L, union(1L:4L, integer()))
## integer(0)
```

Although set operators are defined for `numeric` vectors, rounding errors in ‘floats’ can result in unexpected results (see section 1.5 on page 19). The next two examples do, however, return the correct answers.

```
9 %in% (2:4)^2
## [1] TRUE

c(1, 5) %in% (1:10)^2
## [1] TRUE FALSE
```


1.7 Character values

Character variables can be used to store any character. Character constants are written by enclosing characters in quotes. There are three types of quotes in the ASCII character set, double quotes `"`, single quotes `'`, and back ticks ```. The first two types of quotes can be used as delimiters of `character` constants.

```
a <- "A"
a
## [1] "A"

b <- 'A'
b
## [1] "A"

a == b
## [1] TRUE
```

 In many computer languages, vectors of characters are distinct from vectors of character strings. In these languages, character vectors store at each index position a single character, while vectors of character strings store at each index position strings of characters of various lengths, such as words or sentences. If you are familiar with C or C++, you need to keep in mind that C’s `char` and R’s `character` are not equivalent and that in R, `character` vectors are vectors of character strings. In contrast to these other languages, in R there is no predefined class for vectors of individual characters and character constants enclosed in double or single quotes are not different.

Concatenating character vectors of length one does not yield a longer character string, it yields instead a longer vector.

```
a <- 'A'
b <- "bcdefg"
c <- "123"
d <- c(a, b, c)
d
## [1] "A"      "bcdefg" "123"
```

Having two different delimiters available makes it possible to choose the type of quotes used as delimiters so that other quotes can be included in a string.

```
a <- "He said 'hello' when he came in"
a
## [1] "He said 'hello' when he came in"

b <- 'He said "hello" when he came in'
b
## [1] "He said \"hello\" when he came in"
```

The outer quotes are not part of the string, they are “delimiters” used to mark the boundaries. As you can see when `b` is printed special characters can be represented using “escape sequences”. There are several of them, and here we will show just four, new line (`\n`) and tab (`\t`), `\` the escape code for a quotation mark within a string and `\\` the escape code for a single backslash `\`. We also show here the different behavior of `print()` and `cat()`, with `cat()` *interpreting* the escape sequences and `print()` displaying them as entered.

```
c <- "abc\\ndef\\tx\\"yz\\"\\\\"tm"
print(c)
## [1] "abc\\ndef\\tx\\"yz\\"\\\\"tm"

cat(c)
## abc
## def x"yz"\ m
```

The *escape codes* work only in some contexts, as when using `cat()` to generate the output. For example, the new-line escape (`\n`) can be embedded in strings used for axis-label, title or label in a plot to split them over two or more lines.

1.8 The ‘mode’ and ‘class’ of objects

Variables have a *mode* that depends on what is stored in them. But different from other languages, assignment to a variable of a different mode is allowed and in most cases its mode changes together with its contents. However, there is a restriction that all elements in a vector, array or matrix, must be of the same mode. While this is not required for lists, which can be heterogenous. In practice this means that we can assign an object, such as a vector, with a different *mode* to a name already in use, but we cannot use indexing to assign an object of a different

mode to individual members of a vector, matrix or array. Functions with names starting with `is.` are tests returning a logical value, `TRUE`, `FALSE` or `NA`. Function `mode()` returns the mode of an object, as a character string and `typeof()` returns R’s internal type or storage mode.

```
my_var <- 1:5
mode(my_var) # no distinction of integer or double
## [1] "numeric"

typeof(my_var)
## [1] "integer"

is.numeric(my_var) # no distinction of integer or double
## [1] TRUE

is.double(my_var)
## [1] FALSE

is.integer(my_var)
## [1] TRUE

is.logical(my_var)
## [1] FALSE

is.character(my_var)
## [1] FALSE

my_var <- "abc"
mode(my_var)
## [1] "character"
```

While *mode* is a fundamental property, and limited to those modes defined as part of the R language, the concept of *class*, is different in that new classes can be defined in user code. In particular, different R objects of a given mode, such as `numeric`, can belong to different `classes`. The use of classes for dispatching functions is discussed in section ?? on page ??, in relation to object-oriented programming in R. Method `class()` is used to query the class of an object, and method `inherits()` is used to test if an object belongs to a specific class or not (including “parent” classes, to be later described).

```
class(my_var)
## [1] "character"

inherits(my_var, "character")
## [1] TRUE

inherits(my_var, "numeric")
## [1] FALSE
```


1.9 ‘Type’ conversions

The least-intuitive type conversions are those related to logical values. All others are as one would expect. By convention, functions used to convert objects from one mode to a different one have names starting with `as.`¹.

```
as.character(1)
## [1] "1"

as.numeric("1")
## [1] 1

as.logical("TRUE")
## [1] TRUE

as.logical("NA")
## [1] NA
```

Conversion takes place automatically in arithmetic and logical expressions.

```
TRUE + 10
## [1] 11

1 || 0
## [1] TRUE

FALSE | -2:2
## [1] TRUE TRUE FALSE TRUE TRUE
```




There is some flexibility in the conversion from character strings into `numeric` and `logical` values. Use the examples below plus your own variations to get an idea of what strings are acceptable and correctly converted and which are not. Do also pay attention at the conversion between `numeric` and `logical` values.

```
as.character(3.0e10)
as.numeric("5E+5")
as.numeric("A")
as.numeric(TRUE)
as.numeric(FALSE)
as.logical("T")
as.logical("t")
as.logical("true")
as.logical(100)
as.logical(0)
as.logical(-1)
```



Compare the values returned by `trunc()` and `as.integer()` when applied to a floating point number, such as `12.34`. Check for the equality of values, and for the *class* of the returned objects.

¹Except for some packages in the ‘tidyverse’ that use names starting with `as_` instead of `as.`

 Using conversions, the difference between the length of a `character` vector and the number of characters composing each member “string” within a vector is obvious.

```
f <- c("1", "2", "3")
length(f)
## [1] 3

g <- "123"
length(g)
## [1] 1

as.numeric(f)
## [1] 1 2 3

as.numeric(g)
## [1] 123
```

Other functions relevant to the “conversion” of numbers and other values are `format()`, and `sprintf()`. These two functions return `character` strings, instead of `numeric` or other values, and are useful for printing output. One could think of these functions as advanced conversion functions returning formatted, and possibly combined and annotated, character strings. However, they are usually not considered normal conversion functions, as they are very rarely used in a way that preserves the original precision of the input values. We show here the use of `format()` and `sprintf()` with `numeric` values, but they can also be used with values of other modes.

When using `format()`, the format used to display numbers is set by passing arguments to several different parameters. As `print()` calls `format()` to make numbers *pretty* it accepts the same options.

```
x = c(123.4567890, 1.0)
format(x) # using defaults
## [1] "123.4568" " 1.0000"

format(x[1]) # using defaults
## [1] "123.4568"

format(x[2]) # using defaults
## [1] "1"

format(x, digits = 3, nsmall = 1)
## [1] "123.5" " 1.0"

format(x[1], digits = 3, nsmall = 1)
## [1] "123.5"

format(x[2], digits = 3, nsmall = 1)
## [1] "1.0"

format(x, digits = 3, scientific = TRUE)
## [1] "1.23e+02" "1.00e+00"
```

Function `sprintf()` is similar to C’s function of the same name. The user interface is rather unusual, but very powerful, once one learns the syntax. All the formatting is specified using a character string as template. In this template, placeholders for data and the formatting instructions are embedded using special codes. These codes start with a percent character. We show in the example below the use of some of these: `f` is used for numeric values to be formatted according to a “fixed point,” while `g` is used when we set the number of significant digits and `e` for exponential or *scientific* notation.

```
x = c(123.4567890, 1.0)
sprintf("The numbers are: %4.2f and %.0f", x[1], x[2])
## [1] "The numbers are: 123.46 and 1"

sprintf("The numbers are: %4.4g and %.2g", x[1], x[2])
## [1] "The numbers are: 123.5 and 1"

sprintf("The numbers are: %4.2e and %.0e", x[1], x[2])
## [1] "The numbers are: 1.23e+02 and 1e+00"
```

In the template "The numbers are: %4.2f and %.0f", there are two placeholders for numeric values, %4.2f and %.0f, so in addition to the template, we pass two values extracted from the first two positions of vector `x`. These could have been two different vectors of length one, or even numeric constants. The template itself does not need to be a character constant as in these examples, as a variable can be also passed as argument.



Function `format()` may be easier to use, in some cases, but `sprintf()` is more flexible and powerful. Those with experience in the use of the C language will already know about `sprintf()` and its use of templates for formatting output. Even if you are familiar with C, look up the help pages for both functions, and practice, by trying to create the same formatted output by means of the two functions. Do also play with these functions with other types of data like integer and character.



We have above described `NA` as a single value ignoring modes, but in reality `NA` s come in various flavors. `NA_real_`, `NA_character_`, etc. and `NA` defaults to an `NA` of class `logical`. `NA` is normally converted on the fly to other modes when needed, so in general `NA` is all we need to use.

```
a <- c(1, NA)
is.numeric(a[2])
## [1] TRUE

is.numeric(NA)
## [1] FALSE

b <- c("abc", NA)
is.character(b[2])
## [1] TRUE
```

```
is.character(NA)
## [1] FALSE

class(NA)
## [1] "logical"

class(NA_character_)
## [1] "character"
```

```
c <- NA
c(c, 2:3)
## [1] NA  2  3
```

However, even the statement below works transparently.

```
a[3] <- b[2]
```

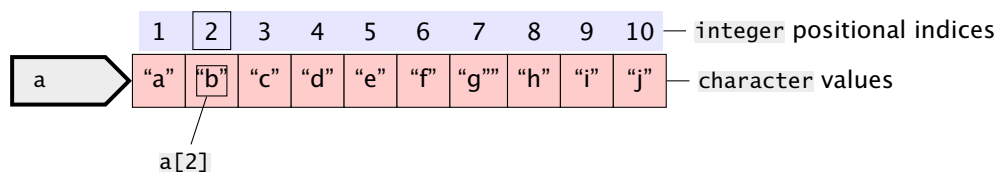
1.10 Vector manipulation

If you have read earlier sections of this chapter, you already know how to create a vector. If not, see pages 6–10 before continuing.


In this section we are going to see how to extract or retrieve, replace, and move elements such as a_2 from a vector $a_{1=1\dots n}$. Elements are extracted using an index enclosed in single square brackets. The index indicates the position in the vector, starting from one, following the usual mathematical tradition. What in maths notation would be a_i , in R is represented as `a[i]` and the whole vector, by excluding the brackets and indexing vector, as `a`.

We extract the first 10 elements of the vector `letters`.


```
a <- letters[1:10]
a
## [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j"
```



```
a[2]
## [1] "b"
```

 Four constant vectors are available in R: `letters`, `LETTERS`, `month.name` and `month.abb`, of which we used `letters` in the example above. These vectors are always for English, irrespective of the locale.


```
month.name[6]
## [1] "June"
```

 In R, indexes always start from one, while in some other programming languages such as C and C++, indexes start from zero. It is important to be aware of this difference, as many computation algorithms are valid only under a given indexing convention.

It is possible to extract a subset of the elements of a vector in a single operation, using a vector of indexes. The positions of the extracted elements in the result (“returned value”) are determined by the ordering of the members of the vector of indexes—easier to demonstrate than to explain.

```
a[c(3, 2)]
## [1] "c" "b"

a[10:1]
## [1] "j" "i" "h" "g" "f" "e" "d" "c" "b" "a"
```

 The length of the indexing vector is not restricted by the length of the indexed vector. However, only numerical indexes that match positions present in the indexed vector can extract values. Those values in the indexing vector pointing to positions that are not present in the indexed vector, result in `NA`s. This is easier to learn by *playing* with R, than from explanations. Play with R, using the following examples as a starting point.

```
length(a)
a[c(3, 3, 3, 3)]
a[c(10:1, 1:10)]
a[c(1, 11)]
a[11]
```

Have you tried some of your own examples? If not yet, do *play* with additional variations of your own before continuing.

Negative indexes have a special meaning; they indicate the positions at which values should be excluded. Be aware that it is *illegal* to mix positive and negative values in the same indexing operation.

```
a[-2]
## [1] "a" "c" "d" "e" "f" "g" "h" "i" "j"

a[-c(3,2)]
## [1] "a" "d" "e" "f" "g" "h" "i" "j"

a[-3:-2]
## [1] "a" "d" "e" "f" "g" "h" "i" "j"
```



Results from indexing with special values and zero may be surprising. Try to build a rule from the examples below, a rule that will help you remember what to expect next time you are confronted with similar statements using “subscripts” which are special values instead of integers larger or equal to one—this is likely to happen sooner or later as these special values can be returned by different R expressions depending on the value of operands or function arguments, some of them described earlier in this chapter.

```
a[ ]
a[0]
a[numeric(0)]
a[NA]
a[c(1, NA)]
a[NULL]
a[c(1, NULL)]
```

Another way of indexing, which is very handy, but not available in most other programming languages, is indexing with a vector of `logical` values. The `logical` vector used for indexing is usually of the same length as the vector from which elements are going to be selected. However, this is not a requirement, because if the `logical` vector of indexes is shorter than the indexed vector, it is “recycled” as discussed above in relation to other operators.

```
a[TRUE]
## [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j"

a[FALSE]
## character(0)

a[c(TRUE, FALSE)]
## [1] "a" "c" "e" "g" "i"

a[c(FALSE, TRUE)]
## [1] "b" "d" "f" "h" "j"

a > "c"
## [1] FALSE FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE

a[a > "c"]
## [1] "d" "e" "f" "g" "h" "i" "j"
```

Indexing with logical vectors is very frequently used in R because comparison operators are vectorized. Comparison operators, when applied to a vector, return a `logical` vector, a vector that can be used to extract the elements for which the result of the comparison test was `TRUE`.




The examples in this text box demonstrate additional uses of logical vectors: 1) the logical vector returned by a vectorized comparison can be stored in a variable, and the variable used as a “selector” for extracting a subset of values from the same vector, or from a different vector.

```
a <- letters[1:10]
b <- 1:10
selector <- a > "c"
selector
a[selector]
b[selector]
```

Numerical indexes can be obtained from a logical vector by means of function `which()`.

```
indexes <- which(a > "c")
indexes
a[indexes]
b[indexes]
```

Make sure to understand the examples above. These constructs are very widely used in R because they allow for concise code that is easy to understand once you are familiar with the indexing rules. However, if you do not command these rules, many of these terse statements will be unintelligible to you.

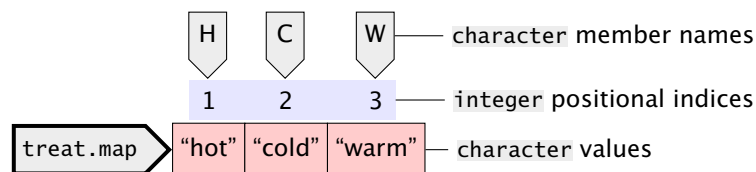
 In all earlier examples we have used integer valued indices for extraction of elements. In the vectors used as examples above the elements were anonymous or nameless. In R the elements can be assigned names, and these names used in place of numeric indices to extract the named elements. There is one situation where this is very useful: the mapping of values between two representations.

Let’s assume we have a long vector encoding treatments using single letter codes and we want to replace these codes with clearer names.

```
treat <- c("H", "C", "H", "W", "C", "H", "H", "W", "W")
```

We can create a named vector to *map* the single letter codes into some other codes, in this case full words that are easier to understand.

```
treat.map <- c(H = "hot", C = "cold", W = "warm")
treat.map
##      H      C      W
## "hot" "cold" "warm"
```



As `treat.map` is a named vector, we can use the element names as indices for element extraction.

```
treat.map["H"]
##      H
## "hot"
```

The indexing vector can be of a different length than the indexed vector, and that the returned value is a new vector of the same length as the indexing vector.

```
treat.new <- treat.map[treat]
treat.new
##      H      C      H      W      C      H      H      W      W
## "hot" "cold" "hot" "warm" "cold" "hot" "hot" "warm" "warm"
```

where `treat.new` is a named vector, from which we will frequently want to remove the names.

```
treat.new <- unname(treat.new)
treat.new
## [1] "hot" "cold" "hot" "warm" "cold" "hot" "hot" "warm" "warm"
```

It is more common to use named members with lists than with vectors, but in R, in both cases it is possible to use both numeric positional indices and names.

Indexing can be used on either side of an assignment expression. In the chunk below, we use the extraction operator on the left-hand side of the assignments to replace values only at selected positions in the vector. This may look rather esoteric at first sight, but it is just a simple extension of the logic of indexing described above. It works, because the low precedence of the `<-` operator results in both the left-hand side and the right-hand side being fully evaluated before the assignment takes place. To make the changes to the vectors easier to follow, we use identical vectors with different names for each of these examples.

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

a[1] <- 99
a
## [1] 99 2 3 4 5 6 7 8 9 10

b <- 1:10
b[c(2,4)] <- -99 # recycling
b
## [1] 1 -99 3 -99 5 6 7 8 9 10

c <- 1:10
c[c(2,4)] <- c(-99, 99)
c
## [1] 1 -99 3 99 5 6 7 8 9 10

d <- 1:10
d[TRUE] <- 1 # recycling
d
## [1] 1 1 1 1 1 1 1 1 1 1

e <- 1:10
e <- 1 # no recycling
e
## [1] 1
```


We can also use subscripting on both sides of the assignment operator, for example, to swap two elements.

```
a <- letters[1:10]
a[1:2] <- a[2:1]
a
## [1] "b" "a" "c" "d" "e" "f" "g" "h" "i" "j"
```



Do play with subscripts to your heart's content, really grasping how they work and how they can be used, will be very useful in anything you do in the future with R. Even the contrived example below follows the same simple rules, just study it bit by bit. Hint: the second statement in the chunk below, modifies `a`, so, when studying variations of this example you will need to recreate `a` by executing the first statement, each time you run a variation of the second statement.

```
a <- letters[1:10]
a[5:1] <- a[c(TRUE, FALSE)]
a
```



In R, indexing with positional indexes can be done with `integer` or `numeric` values. Numeric values can be floats, but for indexing, only integer values are meaningful. Consequently, `double` values are converted into `integer` values when used as indexes. The conversion is done invisibly, but it does slow down computations slightly. When working on big data sets, explicitly using `integer` values can improve performance.

```
b <- LETTERS[1:10]
b
## [1] "A" "B" "C" "D" "E" "F" "G" "H" "I" "J"

b[1]
## [1] "A"

b[1.1]
## [1] "A"

b[1.9999] # surprise!!
## [1] "A"

b[2]
## [1] "B"
```

From this experiment, we can learn that if positive indexes are not whole numbers, they are truncated to the next smaller integer.

```
b <- LETTERS[1:10]
b
## [1] "A" "B" "C" "D" "E" "F" "G" "H" "I" "J"

b[-1]
## [1] "B" "C" "D" "E" "F" "G" "H" "I" "J"

b[-1.1]
## [1] "B" "C" "D" "E" "F" "G" "H" "I" "J"

b[-1.9999]
## [1] "B" "C" "D" "E" "F" "G" "H" "I" "J"

b[-2]
## [1] "A" "C" "D" "E" "F" "G" "H" "I" "J"
```

From this experiment, we can learn that if negative indexes are not whole numbers, they are truncated to the next larger (less negative) integer. In conclusion, double index values behave as if they were sanitized using function `trunc()`.

This example also shows how one can tease out of R its rules through experimentation.

A frequent operation on vectors is sorting them into an increasing or decreasing order. The most direct approach is to use `sort()`.

```
my.vector <- c(10, 4, 22, 1, 4)
sort(my.vector)
## [1] 1 4 4 10 22


sort(my.vector, decreasing = TRUE)
## [1] 22 10 4 4 1
```

An indirect way of sorting a vector, possibly based on a different vector, is to generate with `order()` a vector of numerical indexes that can be used to achieve the ordering.

```
order(my.vector)
## [1] 4 2 5 1 3

my.vector[order(my.vector)]
## [1] 1 4 4 10 22

another.vector <- c("ab", "aa", "c", "zy", "e")
another.vector[order(my.vector)]
## [1] "zy" "aa" "e" "ab" "c"
```

 A problem linked to sorting that we may face is counting how many copies of each value are present in a vector. We need to use two functions `sort()` and `rle()`. The second of these functions computes *run length* as used in *run length encoding* for which *rle* is an abbreviation. A *run* is a series of consecutive identical values. As the objective is to count the number of copies of each value present, we need first to sort the vector.

```
my.letters <- letters[c(1,5,10,3,1,4,21,1,10)]
my.letters
## [1] "a" "e" "j" "c" "a" "d" "u" "a" "j"

sort(my.letters)
## [1] "a" "a" "a" "c" "d" "e" "j" "j" "u"

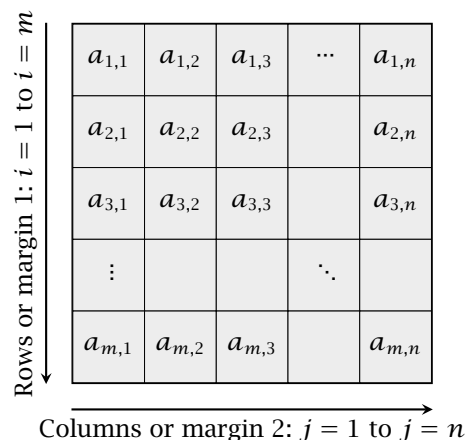
rle(sort(my.letters))
## Run Length Encoding
##  lengths: int [1:6] 3 1 1 1 2 1
##  values  : chr [1:6] "a" "c" "d" "e" "j" "u"
```


The second and third statements are only to demonstrate the effect of each step. The last statement uses nested function calls to compute the number of copies of each value in the vector.

1.11 Matrices and multidimensional arrays

Matrices have two dimensions, rows and columns, and like vectors all their members share the same mode, and are atomic, i.e., they are homogeneous. Most commonly, matrices are used to store `numeric`, `integer` or `logical` values. The number of rows and columns can differ, so matrices can be either square or rectangular in shape, but never ragged.

In R, the first index always denotes rows and the second index always denotes columns. The diagram below depicts a matrix, A , with m rows and n columns and size equal to $m \times n$ “cells”, with individual values denoted by $a_{i,j}$. Here we use a simpler representation than that used for vectors on page 6 above, but the same concepts apply.



 In R documentation and in function parameters, the individual dimensions of matrices and arrays are sometimes called *margins*, numbered in the same order as the indices are given.

In mathematical notation the same generic matrix is represented as

$$A_{m \times n} = \begin{bmatrix} a_{1,1} & a_{1,2} & \cdots & a_{1,j} & \cdots & a_{1,n} \\ a_{2,1} & a_{2,2} & \cdots & a_{2,j} & \cdots & a_{2,n} \\ \vdots & \vdots & \ddots & \vdots & & \vdots \\ a_{i,1} & a_{i,2} & \cdots & a_{i,j} & \cdots & a_{i,n} \\ \vdots & \vdots & & \vdots & \ddots & \vdots \\ a_{m,1} & a_{m,2} & \cdots & a_{m,j} & \cdots & a_{m,n} \end{bmatrix}$$

where A represents the whole matrix, $m \times n$ its dimensions, and $a_{i,j}$ its elements, with i indexing rows and j indexing columns. The lengths of the two dimensions of the matrix are given by m and n , for rows and columns.

Vectors have a single dimension, and, as described on page 6 above, we can query this dimension, their length, with method `length()`. Matrices have two dimensions, which can be queried individually with `ncol()` and `nrow()`, and jointly with method `dim()`. As expected method `is.matrix()` can be used to query the class.

We can create a matrix using the `matrix()` or `as.matrix()` constructors. The first argument of `matrix()` must be a vector. Method `as.matrix()` is a conversion constructor, with specializations accepting as argument objects belonging to a few other classes.

```
matrix(1:15, ncol = 3)
##      [,1] [,2] [,3]
## [1,]  1   6  11
## [2,]  2   7  12
## [3,]  3   8  13
## [4,]  4   9  14
## [5,]  5  10  15

matrix(1:15, nrow = 3)
##      [,1] [,2] [,3] [,4] [,5]
## [1,]  1   4   7  10  13
## [2,]  2   5   8  11  14
## [3,]  3   6   9  12  15
```

When a matrix is printed in R the row and column indexes are indicated on the edges left and top margins, in the same way as they would be used to extract whole rows and columns.

When a vector is converted to a matrix, R's default is to allocate the values in the vector to the matrix starting from the leftmost column, and within the column, down from the top. Once the first column is filled, the process continues from the top of the next column, as can be seen above. This order can be changed as you will discover in the playground below.



Check in the help page for the `matrix` constructor how to use the `byrow` parameter to alter the default order in which the elements of the vector are allocated to columns and rows of the new matrix.

```
help(matrix)
```

While you are looking at the help page, also consider the default number of columns and rows.

```
matrix(1:15)
```

And to start getting a sense of how to interpret error and warning messages, run the code below and make sure you understand which problem is being reported. Before executing the statement, analyze it and predict what the returned value will be. Afterwards, compare your prediction, to the value actually returned.

```
matrix(1:15, ncol = 2)
```

Subscripting of matrices and arrays is consistent with that used for vectors; we only need to supply an indexing vector, or leave a blank space, for each dimension. A matrix has two dimensions, so to access an element or group of elements, we use two indices. The first index value selects rows, and the second one, columns.

```
A <- matrix(1:20, ncol = 4)
A
##      [,1] [,2] [,3] [,4]
## [1,]    1    6   11   16
## [2,]    2    7   12   17
## [3,]    3    8   13   18
## [4,]    4    9   14   19
## [5,]    5   10   15   20

A[1, 1]
## [1] 1
```

Remind yourself of how indexing of vectors works in R (see section 1.10 on page 31). We will now apply the same rules in two dimensions to extract and replace values. The first or leftmost indexing vector corresponds to rows and the second one to columns, so R uses a rows-first convention for indexing. Missing indexing vectors are interpreted as meaning *extract all rows* and *extract all columns*, respectively.


```
A[1, ]
## [1] 1 6 11 16

A[ , 1]
## [1] 1 2 3 4 5

A[2:3, c(1,3)]
##      [,1] [,2]
## [1,]    2   12
## [2,]    3   13

A[3, 4] <- 99
A
##      [,1] [,2] [,3] [,4]
## [1,]    1    6   11   16
## [2,]    2    7   12   17
## [3,]    3    8   13   99
## [4,]    4    9   14   19
## [5,]    5   10   15   20
```

```
A[4:3, 2:1] <- A[3:4, 1:2]
A
##      [,1] [,2] [,3] [,4]
## [1,]    1    6   11   16
## [2,]    2    7   12   17
## [3,]    9    4   13   99
## [4,]    8    3   14   19
## [5,]    5   10   15   20
```

 Vectors are simpler than matrices, and by default when possible the “slice” extracted from a matrix it is simplified into a vector by dropping one dimension. By passing `drop = FALSE`, we can prevent this.

```
is.matrix(A[1, ])
## [1] FALSE

is.matrix(A[1:2, 1:2])
## [1] TRUE

is.vector(A[1, ])
## [1] TRUE

is.vector(A[1:2, 1:2])
## [1] FALSE

is.matrix(A[1, , drop = FALSE])
## [1] TRUE

is.matrix(A[1:2, 1:2, drop = FALSE])
## [1] TRUE
```

Matrices, like vectors, can be assigned names that function as “nicknames” for indices for assignment and extraction. Matrices can have row names and/or column names.

```
colnames(A)
## NULL

rownames(A)
## NULL

colnames(A) <- c("a", "b", "c", "d")
A
##      a  b  c  d
## [1,] 1  6 11 16
## [2,] 2  7 12 17
## [3,] 9  4 13 99
## [4,] 8  3 14 19
## [5,] 5 10 15 20

A[, c("b", "a")]
##      b  a
## [1,] 6  1
## [2,] 7  2
## [3,] 4  9
## [4,] 3  8
## [5,]10  5
```

```
colnames(A) <- NULL
```

```
A
##      [,1] [,2] [,3] [,4]
## [1,]    1    6   11   16
## [2,]    2    7   12   17
## [3,]    9    4   13   99
## [4,]    8    3   14   19
## [5,]    5   10   15   20
```



Matrices can be indexed as vectors, without triggering an error or warning.

```
A <- matrix(1:20, ncol = 4)
```

```
A
##      [,1] [,2] [,3] [,4]
## [1,]    1    6   11   16
## [2,]    2    7   12   17
## [3,]    3    8   13   18
## [4,]    4    9   14   19
## [5,]    5   10   15   20
```

```
dim(A)
```

```
## [1] 5 4
```

```
A[10]
```

```
## [1] 10
```

```
A[5, 2]
```

```
## [1] 10
```

The next code example demonstrates that indexing as a vector with a single index, always works column-wise even if matrix **B** was created by assigning vector elements by row.

```
B <- matrix(1:20, ncol = 4, byrow = TRUE)
```

```
B
##      [,1] [,2] [,3] [,4]
## [1,]    1    2    3    4
## [2,]    5    6    7    8
## [3,]    9   10   11   12
## [4,]   13   14   15   16
## [5,]   17   18   19   20
```

```
dim(B)
```

```
## [1] 5 4
```

```
B[10]
```

```
## [1] 18
```

```
B[5, 2]
```

```
## [1] 18
```



In R, a **matrix** can have a single row, a single column, a single element or no elements. However, in all cases, a **matrix** will have a *dimensions* attribute of length two defined.

```

my.vector <- 1:6
dim(my.vector)
## NULL

one.col.matrix <- matrix(1:6, ncol = 1)
dim(one.col.matrix)
## [1] 6 1

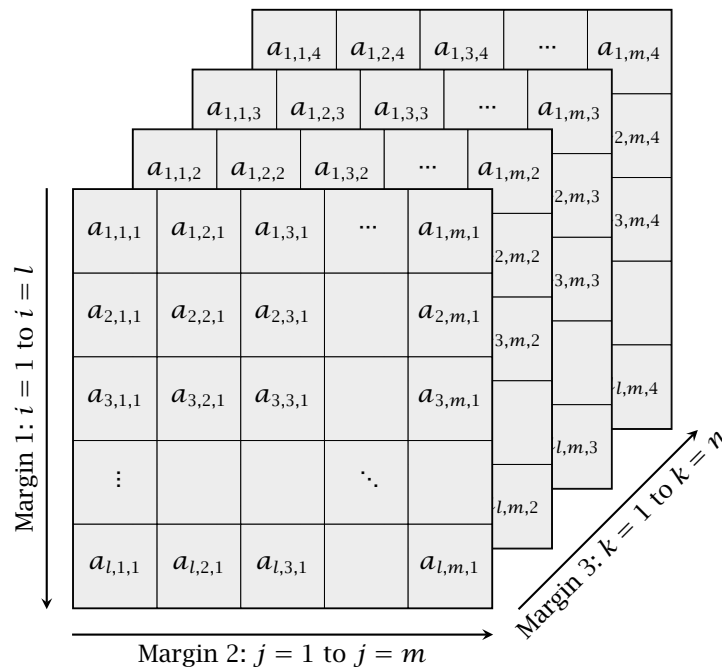
two.col.matrix <- matrix(1:6, ncol = 2)
dim(two.col.matrix)
## [1] 3 2

one.elem.matrix <- matrix(1, ncol = 1)
dim(one.elem.matrix)
## [1] 1 1

no.elem.matrix <- matrix(numeric(), ncol = 0)
dim(no.elem.matrix)
## [1] 0 0

```

Arrays are similar to matrices, but can have one or more dimensions. The dimensions of an array can be queried with method `dim()`, similarly as with matrices. Whether an R object is an array can be found out with function `is.array()`. The diagram below depicts an array, A with three dimensions giving a size equal to $l \times m \times n$, and individual values denoted by $a_{i,j,k}$.



When calling the constructor `array()`, dimensions are specified with the argument passed to parameter `dim`.


```

B <- array(1:27, dim = c(3, 3, 3))
B
## , , 1
##
##      [,1] [,2] [,3]
## [1,]    1    4    7
## [2,]    2    5    8
## [3,]    3    6    9
##
## , , 2
##
##      [,1] [,2] [,3]
## [1,]   10   13   16
## [2,]   11   14   17
## [3,]   12   15   18
##
## , , 3
##
##      [,1] [,2] [,3]
## [1,]   19   22   25
## [2,]   20   23   26
## [3,]   21   24   27
B[2, 2, 2]
## [1] 14

```

In the chunk above, the length of the supplied vector is the product of the dimensions, $27 = 3 \times 3 \times 3 = 3^3$. Arrays are printed in slices, with slices across 3rd and higher dimensions printed separately, with their corresponding indexes above each slice and the first two dimensions on the margins of the individual slices, similarly to how matrices are displayed.



How do you use indexes to extract the second element of the original vector, in each of the following matrices and arrays?

```

v <- 1:10
m2c <- matrix(v, ncol = 2)
m2cr <- matrix(v, ncol = 2, byrow = TRUE)
m2r <- matrix(v, nrow = 2)
m2rc <- matrix(v, nrow = 2, byrow = TRUE)

v <- 1:10
a2c <- array(v, dim = c(5, 2))
a2c <- array(v, dim = c(5, 2), dimnames = list(NULL, c("c1", "c2")))
a2r <- array(v, dim = c(2, 5))

```

Be aware that vectors and one-dimensional arrays are not the same thing, while two-dimensional arrays are matrices.

1. Use the different constructors and query methods to explore this, and its consequences.
2. Convert a matrix into a vector using `unlist()` and `as.vector()` and compare the returned values.

Operators for matrices are available in R, as matrices are used in many statistical algorithms. We will not describe them all here, only `t()` and some specializations of arithmetic operators. Function `t()` transposes a matrix, by swapping columns and rows.

```
A <- matrix(1:20, ncol = 4)
A
##      [,1] [,2] [,3] [,4]
## [1,]    1    6   11   16
## [2,]    2    7   12   17
## [3,]    3    8   13   18
## [4,]    4    9   14   19
## [5,]    5   10   15   20

t(A)
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    2    3    4    5
## [2,]    6    7    8    9   10
## [3,]   11   12   13   14   15
## [4,]   16   17   18   19   20
```

As with vectors, recycling applies to arithmetic operators when applied to matrices.

```
A + 2
##      [,1] [,2] [,3] [,4]
## [1,]    3    8   13   18
## [2,]    4    9   14   19
## [3,]    5   10   15   20
## [4,]    6   11   16   21
## [5,]    7   12   17   22

A * 0:1
##      [,1] [,2] [,3] [,4]
## [1,]    0    6    0   16
## [2,]    2    0   12    0
## [3,]    0    8    0   18
## [4,]    4    0   14    0
## [5,]    0   10    0   20

A * 1:0
##      [,1] [,2] [,3] [,4]
## [1,]    1    0   11    0
## [2,]    0    7    0   17
## [3,]    3    0   13    0
## [4,]    0    9    0   19
## [5,]    5    0   15    0
```

In the examples above with the usual multiplication operator `*`, the operation described is not a matrix product, but instead, the products between individual elements of the matrix and vectors. Matrix multiplication is indicated by operator `%*%`.

```
B <- matrix(1:16, ncol = 4)
B * B
##      [,1] [,2] [,3] [,4]
```

```
## [1,]    1   25   81  169
## [2,]    4   36  100  196
## [3,]    9   49  121  225
## [4,]   16   64  144  256

B %*% B
##      [,1] [,2] [,3] [,4]
## [1,]   90  202  314  426
## [2,]  100  228  356  484
## [3,]  110  254  398  542
## [4,]  120  280  440  600
```

Other operators and functions for matrix algebra like cross-product (`crossprod()`), extracting or replacing the diagonal (`diag()`) are available in base R. Packages, including ‘matrixStats’, provide additional functions and operators for matrices.

1.12 Factors

Factors are very important in R. In contrast to other statistical software in which the role of a variable is set when defining a model to be fitted or when setting up a test, in R, models are specified exactly in the same way for ANOVA and regression analysis, both as *linear models*. The type of model that is fitted is decided by whether the explanatory variable is a factor (giving ANOVA) or a numerical variable (giving regression). This makes a lot of sense, because in most cases, considering an explanatory variable as categorical or not, depends on the quantity stored and/or the design of the experiment or survey. In other words, being categorical is a property of the data. The order of the levels in an unordered `factor` does not affect simple calculations or the values plotted, but as we will see in chapters ?? and ??, it does affect how the output is printed, the order of the levels in the scales and keys of plots, and in some cases how contrasts are applied in significance tests.

In a factor, values indicate discrete unordered categories, most frequently the treatments in an experiment, or categories in a survey. They can be created either from numerical or character vectors. The different possible values are called *levels*. Factors created with `factor()` are always unordered or categorical. R also supports ordered factors, created with function `ordered()` with identical user interface. The distinction, however, only affects how they are interpreted in statistical tests as discussed in chapter ??.

When using `factor()` or `ordered()` we create a factor from a vector, but this vector can be created on-the-fly and anonymous as shown in this example. When the vector is `numeric` and no labels are supplied, level labels are character strings matching the numbers. The default ordering of the levels is alphanumerical.

```
factor(x = c(1, 2, 2, 1, 2, 1, 1))
## [1] 1 2 2 1 2 1 1
## Levels: 1 2

ordered(x = c(1, 2, 2, 1, 2, 1, 1))
```

```
## [1] 1 2 2 1 2 1 1
## Levels: 1 < 2

factor(x = c(1, 2, 2, 1, 2, 1, 1), ordered = TRUE)
## [1] 1 2 2 1 2 1 1
## Levels: 1 < 2
```



When the pattern of levels is regular, it is possible to use function `gl()`, *generate levels*, to construct a factor. Nowadays, it is usual to read data into R from files in which the treatment codes are already available as character strings or numeric values, however, when we need to create a factor within R, `gl()` can save some typing. In this case instead of passing a vector as argument, we pass a *recipe* to create it: `n` is the number of levels, and `k` the number of contiguous repeats (called “replicates” in R documentation) and `length` the length of the factor to be created.

```
gl(n = 2, k = 5, labels = c("A", "B"))
## [1] A A A A A B B B B B
## Levels: A B

gl(n = 2, k = 1, length = 10, labels = c("A", "B"))
## [1] A B A B A B A B A B
## Levels: A B
```

It is always preferable to use meaningful labels for levels, even if R does not require it. Here the vector is stored in a variable named `my.vector`. In a real data analysis situation in most cases the vector would have been read from a file on disk and would be longer.

```
my.vector <- c("treated", "treated", "control", "control", "control", "treated")
factor(my.vector)
## [1] treated treated control control control treated
## Levels: control treated
```

The ordering of levels is established at the time a factor is created, and by default is alphabetical. This default ordering of levels is frequently not the one needed. We can pass an argument to parameter `levels` of function `factor()` to set a different ordering of the levels.

```
factor(x = my.vector, levels = c("treated", "control"))
## [1] treated treated control control control treated
## Levels: treated control
```

The labels (“names”) of the levels can be set when calling `factor()`. Two vectors are passed as arguments to parameters `levels` and `labels` with levels and matching labels in the same position. The argument passed to `levels` determines the order of the levels based on their old names or values, and the argument passed to `labels` gives new names to the levels.

```
factor(x = c(1, 1, 0, 0, 0, 1), levels = c(1, 0), labels = c("treated", "control"))
## [1] treated treated control control control treated
## Levels: treated control
```

In the examples above we passed a numeric vector or a character vector as an argument for parameter `x` of function `factor()`. It is also possible to pass a `factor` as an argument to parameter `x`. This makes it possible to modify the ordering of levels or replace the labels in a factor.

```
my.factor <- factor(x = my.vector)
my.factor
## [1] treated treated control control control treated
## Levels: control treated

factor(x = my.factor, levels = c("treated", "control"))
## [1] treated treated control control control treated
## Levels: treated control

factor(x = my.factor, labels = c(control = "cooled", treated = "heated"))
## [1] heated heated cooled cooled cooled heated
## Levels: cooled heated

factor(x = my.factor,
       levels = c("treated", "control"),
       labels = c("heated", "cooled"))
## [1] heated heated cooled cooled cooled heated
## Levels: heated cooled
```



Merging factor levels. We use `factor()` as shown below, setting the same label for the levels we want to merge.

```
my.factor1 <- gl(4, 3, labels = c("A", "F", "B", "Z"))
my.factor1
## [1] A A A F F F B B B Z Z Z
## Levels: A F B Z

factor(my.factor1,
       levels = c("A", "B", "F", "Z"),
       labels = c("A", "B", "C", "C"))
## [1] A A A C C C B B B C C C
## Levels: A B C
```

We can use indexing on factors in the same way as with vectors. In the next example, we use a test returning a logical vector to extract all “controls.” We use function `levels()` to look at the levels of the factors, as with vectors, `length()` to query the number of values stored.

```
my.factor
## [1] treated treated control control control treated
## Levels: control treated

levels(my.factor)
## [1] "control" "treated"

length(my.factor)
## [1] 6

control.factor <- my.factor[my.factor == "control"]
control.factor
```

```
## [1] control control control
## Levels: control treated

levels(control.factor) # same as in my.factor
## [1] "control" "treated"

length(control.factor) # shorter than my.factor
## [1] 3

control.factor <- factor(control.factor)
levels(control.factor) # the unused level was dropped
## [1] "control"
```

It can be seen above that subsetting does not drop unused factor levels, and that `factor()` can be used to explicitly drop the unused factor levels.



How to convert factors into numeric vectors is not obvious, even when the factor was created from a numeric vector.

```
my.vector2 <- rep(3:5, 4)
my.vector2
## [1] 3 4 5 3 4 5 3 4 5 3 4 5

my.factor2 <- factor(my.vector2)
my.factor2
## [1] 3 4 5 3 4 5 3 4 5 3 4 5
## Levels: 3 4 5

as.numeric(my.factor2)
## [1] 1 2 3 1 2 3 1 2 3 1 2 3

as.numeric(as.character(my.factor2))
## [1] 3 4 5 3 4 5 3 4 5 3 4 5
```



Why is a double conversion needed? Internally, factor values are stored as running integers starting from one, each distinct integer value corresponding to a level. These underlying integer values are returned by `as.numeric()` when applied to a factor instead of the level labels. The labels of the factor levels are always stored as character strings, even when these characters are digits. In contrast to `as.numeric()`, `as.character()` returns the character labels of the levels for each of the values stored in the factor. If these character strings represent numbers, they can be converted, in a second step, using `as.numeric()` into the original numeric values. Use of `class` and `mode` is described on section 1.8 on page 26, and `str()` on page 58.

```
class(my.factor2)
## [1] "factor"

mode(my.factor2)
## [1] "numeric"

str(my.factor2)
## Factor w/ 3 levels "3","4","5": 1 2 3 1 2 3 1 2 3 1 ...
```



Create a factor with levels labeled with words. Create another factor with the levels labeled with the same words, but ordered differently. After this convert both factors to numeric vectors using `as.numeric()`. Explain why the two numeric vectors differ or not from each other.



Safely reordering and renaming factor levels. The simplest approach is to use `factor()` and its `levels` parameter as shown above. In these more advanced examples we use `levels()` to retrieve the names of the levels from the factor itself to protect from possible bugs due to typing mistakes, or for changes in the naming conventions used.

Reverse previous order using `rev()`.

```
my.factor2 <- factor(c("treated", "treated", "control", "control", "control", "treated"))
levels(my.factor2)
## [1] "control" "treated"

my.factor2 <- factor(my.factor2, levels = rev(levels(my.factor2)))
levels(my.factor2)
## [1] "treated" "control"
```

Sort in decreasing order, i.e., opposite to default.

```
my.factor2 <- factor(my.factor2,
                     levels = sort(levels(my.factor2), decreasing = TRUE))
levels(my.factor2)
## [1] "treated" "control"
```

Alter ordering using subscripting; especially useful with three or more levels.

```
my.factor2 <- factor(my.factor2, levels = levels(my.factor2)[c(2, 1)])
levels(my.factor2)
## [1] "control" "treated"
```

Reordering the levels of a factor based on summary quantities from data stored in a numeric vector is very useful, especially when plotting. Function `reorder()` can be used in this case. It defaults to using `mean()` for summaries, but other suitable summary functions, such as `median()` can be supplied in its place.

```
my.factor3 <- gl(2, 5, labels = c("A", "B"))
my.vector3 <- c(5.6, 7.3, 3.1, 8.7, 6.9, 2.4, 4.5, 2.1, 1.4, 2.0)
my.factor3
## [1] A A A A A B B B B B
## Levels: A B

my.factor3ord <- reorder(my.factor3, my.vector3)
levels(my.factor3ord)
## [1] "B" "A"

my.factor3rev <- reorder(my.factor3, -my.vector3) # a simple trick
levels(my.factor3rev)
## [1] "A" "B"
```

In the last statement, using the unary negation operator, which is vectorized, allows us to easily reverse the ordering of the levels, while still using the default function, `mean()`, to summarize the data.



Reordering factor values. It is possible to arrange the values stored in a factor either alphabetically according to the labels of the levels or according to the order of the levels. (The use of `rep()` is explained on page 8.)

```
# gl() keeps order of levels
my.factor4 <- gl(4, 3, labels = c("A", "F", "B", "Z"))
my.factor4
as.integer(my.factor4)
# factor() orders levels alphabetically
my.factor5 <- factor(rep(c("A", "F", "B", "Z"), rep(3,4)))
my.factor5
as.integer(my.factor5)
levels(my.factor5)[as.integer(my.factor5)]
```

We see above that the integer values by which levels in a factor are stored, are equivalent to indices or “subscripts” referencing the vector of labels. Function `sort()` operates on the values’ underlying integers and sorts according to the order of the levels while `order()` operates on the values’ labels and returns a vector of indices that arrange the values alphabetically.

```
sort(my.factor4)
my.factor4[order(my.factor4)]
my.factor4[order(as.integer(my.factor4))]
```

Run the examples in the chunk above and work out why the results differ.

1.13 Further reading

For further reading on the aspects of R discussed in the current chapter, I suggest the books *R Programming for Data Science* (Peng) and *The Art of R Programming: A Tour of Statistical Software Design* (Matloff).



2

The R language: "Collective nouns"

The information that is available to the computer consists of a selected set of *data* about the real world, namely, that set which is considered relevant to the problem at hand, that set from which it is believed that the desired results can be derived. The data represent an abstraction of reality...

Niklaus Wirth
Algorithms + Data Structures = Programs, 1976

2.1 Aims of this chapter

Data-set organization and storage is one of the keys to efficient data analysis. How to keep together all the information that belongs together, say all measurements from an experiment and corresponding metadata such as treatments applied and/or dates. The title “collective nouns” is based on the idea that a data set is a collection of data objects.

In this chapter you will familiarize with how this can be done in R. We will use both abstract examples to emphasize the general properties of data sets and the R classes available for their storage and a few more specific examples to exemplify their use in a more concrete way. While in the previous chapter we focused on atomic data types and objects, like vectors, useful for the storage of collections of values of a given type, like numbers, in the present chapter we will focus on the storage within a single object of heterogeneous data, such as a combination of factors, and character and numeric vectors. Broadly speaking, heterogeneous *data containers*.

As in the previous chapter, we will use diagrams to describe the structure of objects.

2.2 Data from surveys and experiments

The data we plot, summarize and analyze in R, in most cases originate from measurements done as part of experiments or surveys. Data collected mechanically from user interactions with web sites or by crawling through internet content originate from a statistical perspective from surveys. The value of any data comes from knowing their origin, say treatments applied to plants, or country from where web site users connect, sometimes several properties are of interest to describe the origin of the data and in other cases observations consist in the measurement of multiple properties on each subject under study. Consequently, all software designed for data analysis implements ways of dealing with data sets as a whole both during storage and when passing them as arguments to functions. A data set is a usually heterogeneous collection of data with related information.

In R, lists are the most flexible type of objects useful for storing whole data sets. In most cases we do not need this much flexibility, so rectangular collections of observations are most frequently stored in a variation upon lists called data frames. These objects can have as their members the vectors and factors we described in the previous chapter.

Any R object can have attributes, allowing objects to carry along additional bits of information. Some like comments are part of R and aimed at storage of ancillary information or metadata by users. Others are used internally by R and finally users can store data using attributes named *ad hoc*.

2.3 Lists

Lists' main difference from vectors is, in R, that they can be heterogeneous. While the member elements of a vector must be *atomic* values, any R object can be a list member. In R, the members of a list can be considered as following a sequence, and accessible through numerical indexes, the same as members of vectors. Members of a list as well as members of a vector can be named, and retrieved (indexed) through their names. In practice, named lists are more frequently used than named vectors. Lists are created using function `list()` similarly as `c()` is used for vectors. Members of a list can be objects differing both in their class and in their size. Lists can be nested.



In R lists can have as members not only objects storing data on observations and categories, but also function definitions, model formulas, unevaluated expressions, matrices, arrays, and objects of user defined classes.

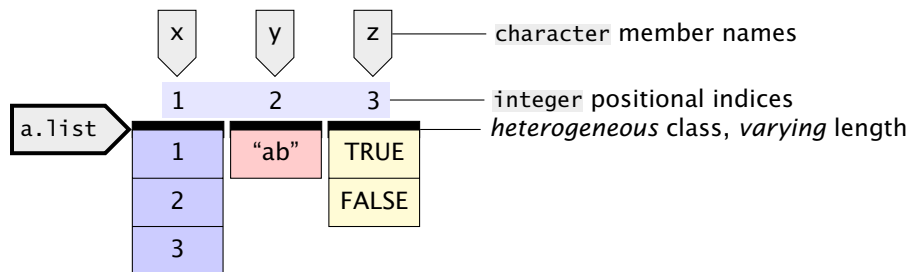
Differently to languages like C, C++ and Pascal, R does not implement memory pointers or linked lists using pointers.

Our first list has as its members three different vectors, each one belonging to a different class: `numeric`, `character` and `logical`. The three vectors also differ in their length: 6, 1, and 2, respectively.

```
a.list <- list(x = 1:3, y = "ab", z = c(TRUE, FALSE))
```

```
str(a.list)
## List of 3
## $ x: int [1:3] 1 2 3
## $ y: chr "ab"
## $ z: logi [1:2] TRUE FALSE

names(a.list)
## [1] "x" "y" "z"
```



⚠ With lists it is best to use informative names for indexing, as their members are heterogeneous usually containing loosely related/connected data. Names make code easier to understand and mistakes more visible. Using names also makes code more robust to future changes in the position of fields in lists created upstream. Below, we use both positional indices and names to highlight the similarities between lists and vectors.

Lists can behave as vectors with heterogeneous elements as members, as we will describe next. Lists can be nested, so tree-like structures are also possible (see section 2.3.2 on page 58).

2.3.1 Member extraction, deletion and insertion

In section 1.10 on page 31 we saw that the extraction operator `[]` applied to a vector, returns a vector, longer or shorter, possibly of length one, or even length zero. Similarly, applying operator `[]` to a list returns a list, possibly of different length: `a.list["x"]` or `a.list[1]` return a list containing only one member, the numeric vector stored at the first position of `a.list`. In the last statement above, `a.list[c(1, 3)]` returns a list of length two as expected.

```
a.list["x"]
## $x
## [1] 1 2 3

a.list$x
## [1] 1 2 3

a.list[1]
## $x
## [1] 1 2 3
```

```
a.list[c(1, 3)]
## $x
## [1] 1 2 3
##
## $z
## [1] TRUE FALSE
```

As with vectors negative positional indices remove members instead of extracting them. See page 57 for a safer approach to deletion of list members.

```
a.list[-1]
## $y
## [1] "ab"
##
## $z
## [1] TRUE FALSE

a.list[c(-1, -3)]
## $y
## [1] "ab"
```

Using operator `[[]]` (double square brackets) for indexing a list extracts the element stored in the list, in its original mode. In the example below, `a.list[["x"]]` and `a.list[["x"]]` return a numeric vector. We might say that extraction operator `[[]]` reaches “deeper” into the list than operator `[]`.

```
a.list$x
## [1] 1 2 3

a.list[["x"]]
## [1] 1 2 3

a.list[[1]]
## [1] 1 2 3
```

The operators can be used together as shown below, with `a.list[[1]]` extracting the vector from `a.list` and `[3]` extracting the member at position 3 of the vector.

```
a.list[[1]][3]
## [1] 3
```




Operators can be used on the lhs as well as on the rhs of an assignment, and lists can be empty, i.e. be of length zero. The example below makes use of this to build a list step by step.

```
b.list <- list()
b.list[["x"]] <- 1:3
b.list[["y"]] <- "ab"
b.list[["z"]] <- c(TRUE, FALSE)
```


Compare `b.list` to `a.list`, used for the examples above.

```
b.list[["y"]] <- b.list[["x"]]
```

Compare them again, and try to understand why `b.list` has changed as it did. Pay also attention to possible changes to the members' names.

 Surprisingly, `a.list[[c(1, 3)]]` returns the value at position 3 in the first member of the list, an operation that normally would be written as `a.list[[1]][3]` using two extractions, one after another. In most cases statements like the one below will be entered by mistake rather than intentionally, but being valid in R, they will not trigger an error message.

```
a.list[[c(1, 3)]]
## [1] 3
```

 *Lists*, as usually defined in languages like C, are based on pointers to memory locations, with pointers stored at each node. These pointers chain or link the different member nodes (this allows, for example, sorting of lists in place by modifying the pointers). In such implementations, indexing by position is not possible, or at least requires “walking” down the list, node by node. In R, `list` members can be accessed through positional indexes, similarly to vectors. Of course, insertions and deletions in the middle of a list, shift the position of members and change which member is pointed at by indexes for positions past the modified location. The names, in contrast remain valid.

```
list(a = 1, b = 2, c = 3)[-2]
## $a
## [1] 1
##
## $c
## [1] 3
```

Two frequent simple operations on lists are insertions and deletions. In R, function `append()` can be used both to append elements at the end of a list and insert elements into the head or any position in the middle of a list.

```
another.list <- append(a.list, list(yy = 1:10, zz = letters[5:1]), 2L)
another.list
## $x
## [1] 1 2 3
##
## $y
## [1] "ab"
##
## $yy
## [1] 1 2 3 4 5 6 7 8 9 10
##
## $zz
## [1] "e" "d" "c" "b" "a"
##
## $z
## [1] TRUE FALSE
```

To delete a member from a list we assign `NULL` to it.

```
a.list$y <- NULL
a.list
## $x
## [1] 1 2 3
##
## $z
## [1] TRUE FALSE
```

To investigate the members contained in a list, function `str()` (*structure*), used above, is convenient, especially when lists have many members. The `print()` method for the structure formats lists more compactly than function `print()` applied directly to a list.

```
print(a.list)
## $x
## [1] 1 2 3
##
## $z
## [1] TRUE FALSE
```

2.3.2 Nested lists

Lists can be nested, i.e., lists of lists can be constructed to an arbitrary depth.

```
a.list <- list("a", "aa", 10)
b.list <- list("b", TRUE)
nested.list <- list(A = a.list, B = b.list)
str(nested.list)
## List of 2
## $ A:List of 3
## ..$ : chr "a"
## ..$ : chr "aa"
## ..$ : num 10
## $ B:List of 2
## ..$ : chr "b"
## ..$ : logi TRUE
```


A nested list can alternatively be constructed within a single statement in which several member lists are created. Here we combine the first three statements in the earlier chunk into a single one.

```
nested.list <- list(A = list("a", "aa", 10), B = list("b", TRUE))
str(nested.list)
## List of 2
## $ A:List of 3
## ..$ : chr "a"
## ..$ : chr "aa"
## ..$ : num 10
## $ B:List of 2
## ..$ : chr "b"
## ..$ : logi TRUE
```


A list can contain a combination of list and vector members.

```
nested.list <- list(A = list("a", "aa", 10),
                  B = list("b", TRUE),
                  C = c(1, 3, 9),
                  D = 4321)


str(nested.list)
## List of 4
## $ A:List of 3
## ..$ : chr "a"
## ..$ : chr "aa"
## ..$ : num 10
## $ B:List of 2
## ..$ : chr "b"
## ..$ : logi TRUE
## $ C: num [1:3] 1 3 9
## $ D: num 4321
```

 The logic behind extraction of members of nested lists using indexing is the same as for simple lists, but applied recursively—e.g., `nested.list[[2]]` extracts the second member of the outermost list, which is another list. As, this is a list, its members can be extracted using again the extraction operator: `nested.list[[2]][[1]]`. It is important to remember that these concatenated extraction operations are written so that the leftmost operator is applied to the outermost list.

The example above uses the `[[]]` operator, but the left to right precedence also applies to concatenated calls to `[]`.

 What do you expect each of the statements below to return? *Before running the code*, predict what value and of which mode each statement will return. You may use implicit or explicit calls to `print()`, or calls to `str()` to visualize the structure of the different objects.

```
nested.list <- list(A = list("a", "aa", "aaa"), B = list("b", "bb"))
str(nested.list)
nested.list[2:1]
nested.list[1]
nested.list[[1]][2]
nested.list[[1]][[2]]
nested.list[2]
nested.list[2][[1]]
```

 When dealing with deep lists, it is sometimes useful to limit the number of levels of nesting returned by `str()` by means of a numeric argument passed to parameter `max.level`s.

```
str(nested.list, max.level = 1)
## List of 4
## $ A:List of 3
## $ B:List of 2
## $ C: num [1:3] 1 3 9
## $ D: num 4321
```


Sometimes we need to flatten a list, or a nested structure of lists within lists. Function `unlist()` is what should be normally used in such cases.

The list `nested.list` is a nested system of lists, but all the “terminal” members are character strings. In other words, terminal nodes are all of the same mode, allowing the list to be “flattened” into a character vector.

```
nested.list <- list(A = list("a", "aa", "aaa"), B = list("b", "bb"))
c.vec <- unlist(nested.list)
c.vec
##      A1      A2      A3      B1      B2
##      "a"     "aa"    "aaa"     "b"     "bb"

is.list(nested.list)
## [1] TRUE

is.list(c.vec)
## [1] FALSE

mode(nested.list)
## [1] "list"

mode(c.vec)
## [1] "character"

names(nested.list)
## [1] "A" "B"

names(c.vec)
## [1] "A1" "A2" "A3" "B1" "B2"
```

The returned value is a vector with named member elements. We use function `str()` to figure out how this vector relates to the original list. The names, always of mode character, are based on the names of list elements when available, while characters depicting positions as numbers are used for anonymous nodes. We can access the members of the vector either through numeric indexes or names.

```
str(c.vec)
## Named chr [1:5] "a" "aa" "aaa" "b" "bb"
## - attr(*, "names")= chr [1:5] "A1" "A2" "A3" "B1" ...

c.vec[2]
##      A2
##      "aa"

c.vec["A2"]
##      A2
##      "aa"
```



Function `unlist()` has two additional parameters, with default argument values, which we did not modify in the example above. These parameters are `recursive` and `use.names`, both of them expecting a `logical` value as an argument. Modify the statement `c.vec <- unlist(c.list)`, by passing `FALSE` as an argument to these two parameters, in turn, and in each case, study the value returned and how it differs with respect to the one obtained above.

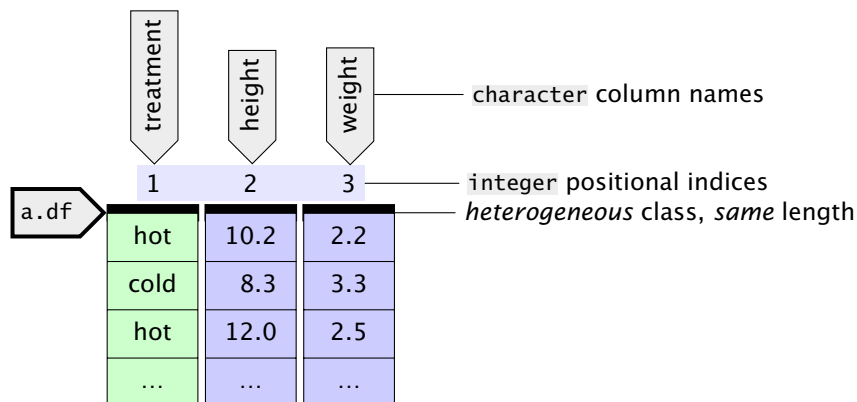
Function `unname()` can be used to remove names safely—i.e., without risk of altering the mode or class of the object.

```
unname(c.vec)
## [1] "a" "aa" "aaa" "b" "bb"

unname(nested.list)
## [[1]]
## [[1]][[1]]
## [1] "a"
##
## [[1]][[2]]
## [1] "aa"
##
## [[1]][[3]]
## [1] "aaa"
##
##
## [[2]]
## [[2]][[1]]
## [1] "b"
##
## [[2]][[2]]
## [1] "bb"
```

2.4 Data frames

Data frames are a special type of list, in which each element is a vector or a factor of the same length (or rarely a matrix with the same number of rows as the enclosing data frame). They are central to most data manipulation and analysis procedures in R. They are commonly used to store observations, so that some columns (or member variables) are numeric vectors containing values from measurements and others are factors describing membership into a category, such as a treatment or genotype. Columns can also be date-, time-, character-, or logical vectors. In the diagram below column `t` is a factor encoding two conditions, and `x` and `y` are numeric vectors containing measurements.



Data frames are created with constructor function `data.frame()` with a syntax similar to that used for lists—in object-oriented programming we say that data frames are derived from class `list`. As the expectation is equal length, if vectors of different lengths are supplied as arguments, the shorter vector(s) is/are recycled, possibly several times, until the required full length is reached.

```
a.df <- data.frame(treatment = factor(rep(c("hot", "cold"), 3)),
                  height = c(10.2, 8.3, 12.0, 9.0, 11.2, 8.7),
                  weight = c(2.2, 3.3, 2.5, 2.8, 2.4, 3.0))

a.df
##   treatment height weight
## 1      hot   10.2    2.2
## 2     cold    8.3    3.3
## 3      hot   12.0    2.5
## 4     cold    9.0    2.8
## 5      hot   11.2    2.4
## 6     cold    8.7    3.0

colnames(a.df)
## [1] "treatment" "height"    "weight"

rownames(a.df)
## [1] "1" "2" "3" "4" "5" "6"

str(a.df)
## 'data.frame': 6 obs. of  3 variables:
## $ treatment: Factor w/ 2 levels "cold","hot": 2 1 2 1 2 1
## $ height   : num  10.2 8.3 12.9 11.2 8.7
## $ weight   : num  2.2 3.3 2.5 2.8 2.4 3

class(a.df)
## [1] "data.frame"

mode(a.df)
## [1] "list"

is.data.frame(a.df)
## [1] TRUE

is.list(a.df)
## [1] TRUE
```

With function `class()` we can query the class of an R object (see section 1.8 on page 26). As we saw in the previous chunk, `list` and `data.frame` objects belong to two different classes. However, their relationship is based on a hierarchy of classes. We say that class `data.frame` is derived from class `list`. Consequently, data frames inherit the methods and characteristics of lists, as long as they have not been hidden by new ones defined for data frames.

Extraction of individual member variables or “columns” can be done like in a list with operators `[[]]` and `$`.

```
a.df$height
## [1] 10.2  8.3 12.0  9.0 11.2  8.7

a.df[["height"]]
## [1] 10.2  8.3 12.0  9.0 11.2  8.7
```

```
a.df[[2]]
## [1] 10.2  8.3 12.0  9.0 11.2  8.7

class(a.df[["height"]])
## [1] "numeric"
```

In the same way as with lists, we can add members to data frames.

```
a.df$x2 <- 6:1
a.df[["x3"]] <- "b"
str(a.df)
## 'data.frame': 6 obs. of  5 variables:
##  $ treatment: Factor w/ 2 levels "cold","hot": 2 1 2 1 2 1
##  $ height   : num  10.2 8.3 12 9 11.2 8.7
##  $ weight   : num  2.2 3.3 2.5 2.8 2.4 3
##  $ x2       : int   6 5 4 3 2 1
##  $ x3       : chr   "b" "b" "b" "b" ...
```

We have added two columns to the data frame, and in the case of column `x3` recycling took place. This is where lists and data frames differ substantially in their behavior. In a data frame, although class and mode can be different for different member variables (columns), they are required to be vectors or factors of the same length (or a matrix with the same number of rows, or a list with the same number of members). In the case of lists, there is no such requirement, and recycling never takes place when adding a member. Compare the values returned below for `a.ls`, to those in the example above for `a.df`.

```
a.ls <- list(x = 1:6, y = "a", z = c(TRUE, FALSE))
str(a.ls)
## List of 3
##  $ x: int [1:6] 1 2 3 4 5 6
##  $ y: chr  "a"
##  $ z: logi [1:2] TRUE FALSE

a.ls$x2 <- 6:1
a.ls$x3 <- "b"
str(a.ls)
## List of 5
##  $ x : int [1:6] 1 2 3 4 5 6
##  $ y : chr  "a"
##  $ z : logi [1:2] TRUE FALSE
##  $ x2: int [1:6] 6 5 4 3 2 1
##  $ x3: chr  "b"
```

Being two dimensional and rectangular in shape, data frames, in relation to indexing and dimensions behave similarly to a matrix. They have rows and columns, and two indices identify the location of a member “cell”. We provide some examples here, but please consult section 1.10 on page 31 and section 1.11 on page 38 for additional details.

Matrix-like notation allows simultaneous extraction from multiple columns, which is not possible with lists. The value returned is in most cases a “smaller” data frame as in this example.

```

a.df[2:3, 1:2]
##   treatment height
## 2      cold    8.3
## 3       hot   12.0

# first column, a.df[[1]] preferred
a.df[, 1]
## [1] hot  cold hot  cold hot  cold
## Levels: cold hot

# first column, a.df[["x"]] or a.df$x preferred
a.df[, "treatment"]
## [1] hot  cold hot  cold hot  cold
## Levels: cold hot

# first row
a.df[1, ]
##   treatment height weight x2 x3
## 1       hot   10.2    2.2 6  b

# first two rows of the third and fourth columns
a.df[1:2, c(FALSE, FALSE, TRUE, TRUE, FALSE)]
##   weight x2
## 1    2.2 6
## 2    3.3 5

# the rows for which comparison is true
a.df[a.df$treatment == "hot", ]
##   treatment height weight x2 x3
## 1       hot   10.2    2.2 6  b
## 3       hot   12.0    2.5 4  b
## 5       hot   11.2    2.4 2  b

# the heights > 8
a.df[a.df$height > 8, "height"]
## [1] 10.2  8.3 12.0  9.0 11.2  8.7

```

As explained earlier for vectors (see section 1.10 on page 31), indexing can be present both on the right-hand side and left-hand side of an assignment, allowing the replacement individual values as well as rectangular chunks.

The next few examples do assignments to “cells” of `a.df`, either to one whole column, or individual values. The last statement in the chunk below copies a number from one location to another by using indexing of the same data frame both on the right side and left side of the assignment.

```

a.df[1, 2] <- 99
a.df
##   treatment height weight x2 x3
## 1       hot   99.0    2.2 6  b
## 2      cold    8.3    3.3 5  b
## 3       hot   12.0    2.5 4  b
## 4      cold    9.0    2.8 3  b
## 5       hot   11.2    2.4 2  b
## 6      cold    8.7    3.0 1  b

a.df[, 2] <- -99
a.df


```

```
## treatment height weight x2 x3
## 1 hot -99 2.2 6 b
## 2 cold -99 3.3 5 b
## 3 hot -99 2.5 4 b
## 4 cold -99 2.8 3 b
## 5 hot -99 2.4 2 b
## 6 cold -99 3.0 1 b

a.df[["height"]] <- c(10, 12)
a.df
## treatment height weight x2 x3
## 1 hot 10 2.2 6 b
## 2 cold 12 3.3 5 b
## 3 hot 10 2.5 4 b
## 4 cold 12 2.8 3 b
## 5 hot 10 2.4 2 b
## 6 cold 12 3.0 1 b

a.df[1, 2] <- a.df[6, 3]
a.df
## treatment height weight x2 x3
## 1 hot 3 2.2 6 b
## 2 cold 12 3.3 5 b
## 3 hot 10 2.5 4 b
## 4 cold 12 2.8 3 b
## 5 hot 10 2.4 2 b
## 6 cold 12 3.0 1 b

a.df[3:6, 2] <- a.df[6, 3]
a.df
## treatment height weight x2 x3
## 1 hot 3 2.2 6 b
## 2 cold 12 3.3 5 b
## 3 hot 3 2.5 4 b
## 4 cold 3 2.8 3 b
## 5 hot 3 2.4 2 b
## 6 cold 3 3.0 1 b
```

 We mentioned above that indexing by name can be done either with double square brackets, `[[]]`, or with `$`. In the first case the name of the variable or column is given as a character string, enclosed in quotation marks, or as a variable with mode `character`. When using `$`, the name is entered as a constant, without quotation marks, and cannot be a variable.

```
x.list <- list(abcd = 123, xyzw = 789)
x.list[["abcd"]]
## [1] 123

a.var <- "abcd"
x.list[a.var]
## [1] 123
```

```
x.list$abcd
## [1] 123

x.list$ab
## [1] 123

x.list$a
## [1] 123
```

Both in the case of lists and data frames, when using double square brackets, by default an exact match is required between the name in the object and the name used for indexing. In contrast, with `$`, an unambiguous partial match is silently accepted. For interactive use, partial matching is helpful in reducing typing. However, in scripts, and especially R code in packages, it is best to avoid the use of `$` as partial matching to a wrong variable present at a later time, e.g., when someone else revises the script, can lead to very difficult-to-diagnose errors.

In addition, as `$` is implemented by first attempting a match to the name and then calling `[[]]`, using `$` for indexing can result in slightly slower performance compared to using `[[]]`. It is possible to set R option `warnPartialMatchDollar` so that partial matching triggers a warning when using `$` to extract a member, which can be very useful when debugging.

Similarly as with matrices, if we extract a single column from a data frame using matrix-like indexing, it is by default simplified into a vector or factor, i.e., the column-dimension is dropped. By passing `drop = FALSE`, we can prevent this. Contrary to matrices, rows are not simplified.

```
is.data.frame(a.df[1, ])
## [1] TRUE

is.data.frame(a.df[ , 2])
## [1] FALSE

is.data.frame(a.df[ , "treatment"])
## [1] FALSE

is.data.frame(a.df[1:2, 2:3])
## [1] TRUE

is.vector(a.df[1, ])
## [1] FALSE


is.vector(a.df[ , 2])
## [1] TRUE


is.factor(a.df[ , "treatment"])
## [1] TRUE

is.vector(a.df[1:2, 2:3])
## [1] FALSE

is.data.frame(a.df[ , 1, drop = FALSE])
## [1] TRUE

is.data.frame(a.df[ , "treatment", drop = FALSE])
## [1] TRUE
```

 In contrast to matrices and data frames, the extraction operator `[]` of tibbles—defined in package ‘tibble’— never simplifies returned one-column tibbles into vectors (see section ?? on page ?? for details on the differences between data frames and tibbles).

 Usually data frames are created from lists or by passing individual vectors and factors to the constructors. It is also possible to construct data frames starting from matrices, other data frames and named vectors and combinations of them. In these cases additional nuances become important. We give only some examples here, as the details are well described in `help(data.frame)`.

We use a named numeric vector, and a factor. The names are moved from the vector to the rows of the data frame! Consult `help(data.frame)` for an explanation.

```
my.vector <- c(one = 1, two = 2, three = 3, four = 4)
my.factor <- as.factor(c(1, 2, 3, 2))
df1 <- data.frame(my.factor, my.vector)
df1
##           my.factor my.vector
## one             1          1
## two             2          2
## three           3          3
## four            2          4

df1$my.vector
## [1] 1 2 3 4
```

If we protect the vector with R’s identity function `I()` the names are not removed from the vector as can be seen by extracting the column from the data frame.

```
df2 <- data.frame(my.factor, I(my.vector))
df2
##           my.factor my.vector
## one             1          1
## two             2          2
## three           3          3
## four            2          4

df2$my.vector
##   one  two three four
##    1    2    3    4
```

If we start with a matrix instead of a vector, the matrix is by default split into separate columns in the data frame. If the matrix has no column names, new ones are created.

```
my.matrix <- matrix(1:12, ncol = 3)
df4 <- data.frame(my.factor, my.matrix)
df4
##   my.factor x1 x2 x3
## 1           1 1 5 9
## 2           2 2 6 10
## 3           3 3 7 11
## 4           2 4 8 12
```


If we protect the matrix with function `I()`, it is not split, and the whole matrix becomes a column in the data frame.

```
df5 <- data.frame(my.factor, I(my.matrix))
df5
##   my.factor my.matrix.1 my.matrix.2 my.matrix.3
## 1         1           1           5           9
## 2         2           2           6          10
## 3         3           3           7          11
## 4         2           4           8          12

df5$my.matrix
##      [,1] [,2] [,3]
## [1,]    1    5    9
## [2,]    2    6   10
## [3,]    3    7   11
## [4,]    4    8   12
```

If we start with a list, each member with a suitable number of elements, each member becomes a column in the data frame. In the case of a too short one, recycling is applied.

```
my.list <- list(a = 4:1, b = letters[4:1], c = "n", d = "z")
df6 <- data.frame(my.factor, my.list)
df6
##   my.factor a b c d
## 1         1 4 d n z
## 2         2 3 c n z
## 3         3 2 b n z
## 4         2 1 a n z
```

The behaviour is quite different if we protect the list with `I()`: then the list is added in whole as a variable or column in the data frame. In this case the length or number of members in the list itself must match the number of rows in the data frame, while the length of the individual members of the list can vary. This is similar to the default behaviour of tibbles with use of `I()` (see chapter ?? starting on page ?? for details about the 'tibble').

```
df7<- data.frame(my.factor, I(my.list))
df7
##   my.factor    my.list
## a         1 4, 3, 2, 1
## b         2 d, c, b, a
## c         3          n
## d         2          z

df7$my.list
## $a
## [1] 4 3 2 1
##
## $b
## [1] "d" "c" "b" "a"
##
## $c
## [1] "n"
##
## $d
## [1] "z"
```

What is this exercise about? Do check the documentation carefully and think of uses where the flexibility gained by use of function `I()` to protect arguments passed to the `data.frame()` constructor can be useful. In addition, write code to extract individual members of embedded matrices and lists using indexing in a single R statement in each case.

2.4.1 Sub-setting data frames

When the names of data frames are long, complex conditions become awkward to write using indexing—i.e., subscripts. In such cases `subset()` is handy because evaluation is done in the “environment” of the data frame, i.e., the names of the columns are recognized if entered directly when writing the condition. Function `subset()` “filters” rows, usually corresponding to observations or experimental units. The condition is computed for each row, and if it returns `TRUE`, the row is included in the returned data frame, and excluded if `FALSE`.

```
a.df <- data.frame(x = 1:6, y = "a", z = c(TRUE, FALSE))
subset(a.df, x > 3)
##   x y    z
## 4 4 a FALSE
## 5 5 a  TRUE
## 6 6 a FALSE
```



What is the behavior of `subset()` when the condition is `NA`? Find the answer by writing code to test this, for a case where tests for different rows return `NA`, `TRUE` and `FALSE`.

When calling functions that return a vector, data frame, or other structure, the extraction operators `[]`, `[[]]`, or `$` can be appended to the rightmost parenthesis of the function call, in the same way as to the name of a variable holding the same data.

```
subset(a.df, x > 3)[ , -3]
##   x y
## 4 4 a
## 5 5 a
## 6 6 a

subset(a.df, x > 3)[ , "x", drop = FALSE]
##   x
## 4 4
## 5 5
## 6 6

subset(a.df, x > 3)[ , "x"]
## [1] 4 5 6
```



When do extraction operators applied to data frames return a vector or factor, and when do they return a data frame?



In the case of `subset()` we can select columns directly as shown below, while for most other functions, extraction using operators `[]`, `[[]]` or `$` is needed.

```
subset(a.df, x > 3, select = 2)
##   y
## 4 a
## 5 a
## 6 a

subset(a.df, x > 3, select = x)
##   x
## 4 4
## 5 5
## 6 6

subset(a.df, x > 3, select = "x")
##   x
## 4 4
## 5 5
## 6 6
```

None of the examples in the last four code chunks alters the original data frame `a.df`. We can store the returned value using a new name if we want to preserve `a.df` unchanged, or we can assign the result to `a.df`, deleting in the process, the previously stored value.



In the examples above, the names in the expression passed as the second argument to `subset()` were searched within `a.df` and found. However, if not found in the data frame objects with matching names are searched for in the environment. There being no variable `A` in the data frame `a.df`, vector `A` from the environment is silently used in the chunk below resulting in a returned data frame with no rows as `A > 3` returns `FALSE`.

```
A <- 1
subset(a.df, A > 3)
## [1] x y z
## <0 rows> (or 0-length row.names)
```

This also applies to the expression passed as argument to parameter `select`, here shown as a way of selecting columns based on names stored in a character vector.


```
columns <- c("x", "z")
subset(a.df, select = columns)
##   x     z
## 1 1  TRUE
## 2 2 FALSE
## 3 3  TRUE
## 4 4 FALSE
## 5 5  TRUE
## 6 6 FALSE
```

The use of `subset()` is convenient, but more prone to bugs compared to directly using the extraction operator `[]`. This same “cost” to achieving convenience applies to functions like `attach()` and `with()` described below. The longer time that a script is expected to be used, adapted and reused, the more careful we should be when using any of these functions. An alternative way of avoiding excessive verbosity is to keep the names of data frames short.

A frequently used way of deleting a column by name from a data frame is to assign `NULL` to it—i.e., in the same way as members are deleted from `lists`. This approach modifies `a.df` in place.

```
aa.df <- a.df
colnames(aa.df)
## [1] "x" "y" "z"

aa.df[["y"]] <- NULL
colnames(aa.df)
## [1] "x" "z"
```

 Alternatively, we can use negative indexing to remove columns from a copy of a data frame. In this example we remove a single column. As base R does not support negative indexing by name with the extraction operator, we need to find the numerical index of the column to delete. (See the examples above using `subset()` with bare names to delete columns.)

```
a.df[, -which(colnames(a.df) == "y")]
##   x     z
## 1 1  TRUE
## 2 2 FALSE
## 3 3  TRUE
## 4 4 FALSE
## 5 5  TRUE
## 6 6 FALSE
```

Instead of using the equality test, we can use the operator `%in%` or function `grep()` to create a `logical` vector useful to delete or select multiple columns in a single statement.



In the previous code chunk we deleted the last column of the data frame `a.df`. Here is an esoteric trick for you to first untangle how it changes the positions of columns and rows, and then for you to think how and why it can be useful to use indexing with the extraction operator `[]` on both sides of the assignment operator `<-`.

```
a.df[1:6, c(1,3)] <- a.df[6:1, c(3,1)]
a.df
```



Although in this last example we used numeric indexes to make it more interesting, in practice, especially in scripts or other code that will be reused, do use column or member names instead of positional indexes whenever possible. This makes code much more reliable, as changes elsewhere in the script could alter the order of columns and *invalidate* numerical indexes. In addition, using meaningful names makes programmers' intentions easier to understand.

2.4.2 Splitting and summarizing data frames

R function `split()` makes it possible to split a data frame into a list of data frames, based on the levels of a factor.

```
a.df <- data.frame(x1 = 1:6, x2 = c(1, 5, 4, 2, 6, 3), z = c("a", "b"))
```

```
split(a.df, a.df$z)
## $a
##   x1 x2 z
## 1  1  1 a
## 3  3  4 a
## 5  5  6 a
##
## $b
##   x1 x2 z
## 2  2  5 b
## 4  4  2 b
## 6  6  3 b
```

Or using formula notation,

```
split(a.df, ~ z)
## $a
##   x1 x2 z
## 1  1  1 a
## 3  3  4 a
## 5  5  6 a
##
## $b
##   x1 x2 z
```

```
## 2 2 5 b
## 4 4 2 b
## 6 6 3 b
```

Function `unsplit()` can be used to reverse splitting by `split()`.

 `split()` is sometimes used in combination with apply functions (see section ?? on page ??) to compute group or treatment summaries. However, in most cases it is simpler to use `aggregate()` for computing such summaries.

When using `aggregate()`, the *lhs* of the formula indicates the variable to summarize and the *rhs* the factor used to split the data before summarizing them.

```
aggregate(x1 ~ z, FUN = mean, data = a.df)
##    z x1
## 1 a  3
## 2 b  4
```

We can summarize more than one column at a time.

```
aggregate(cbind(x1, x2) ~ z, FUN = mean, data = a.df)
##    z x1      x2
## 1 a  3 3.666667
## 2 b  4 3.333333
```


If all the columns not used for grouping are valid input to the function passed as argument to `FUN` the formula can be simplified into.

```
aggregate(. ~ z, FUN = mean, data = a.df)
##    z x1      x2
## 1 a  3 3.666667
## 2 b  4 3.333333
```

 Function `aggregate()` can be also used to aggregate time series data based on time intervals.

2.4.3 Re-arranging columns and rows

The most direct way of changing the order of columns and/or rows in data frames (and matrices and arrays) is to use subscripting as described above. Once we know the original position and target position we can use numerical indexes on both right-hand side and left-hand side of an assignment.

 When using the extraction operator `[]` on both the left-hand-side and right-hand-side to swap columns, the vectors or factors are swapped, while the names of the columns are not! The same applies to row names, which makes storing important information in them inconvenient and error prone.

To retain the correspondence between column naming and column contents after swapping or rearranging the columns, we need to separately move the names of the columns. This seems counter intuitive, unless we think in terms of positions being named rather than the contents of the columns being linked to the names.

```

my_data_frame.df <- data.frame(A = 1:10, B = 3)
head(my_data_frame.df, 2)
##   A B
##  1 1 3
##  2 2 3

my_data_frame.df[, 1:2] <- my_data_frame.df[, 2:1]
head(my_data_frame.df, 2)
##   A B
##  1 3 1
##  2 3 2

colnames(my_data_frame.df)[1:2] <- colnames(my_data_frame.df)[2:1]
head(my_data_frame.df, 2)
##   B A
##  1 3 1
##  2 3 2

```

Taking into account that `order()` returns the indexes needed to sort a vector (see page 36), we can use `order()` to generate the indexes needed to sort rows of a data frame. In this case, the argument to `order()` is usually a column of the data frame being arranged. However, any vector of suitable length, including the result of applying a function to one or more columns, can be passed as an argument to `order()`. Function `order()` is very rarely useful for sorting columns of data frames as it requires a vector across columns as input, which is possible only when all columns are of the same class. In the case of `matrix` and `array` this approach can be applied to any of their dimensions as all their elements homogeneously belong to one class.



The first task to be completed is to sort a data frame based on the values in one column, using indexing and `order()`. Create a new data frame and with three numeric columns with three different haphazard sequences of values. Call these columns `A`, `B` and `C`. 1) Sort the rows of the data frame so that the values in `A` are in decreasing order. 2) Sort the rows of the data frame according to increasing values of the sum of `A` and `B` without adding a new column to the data frame or storing the vector of sums in a variable. In other words, do the sorting based on sums calculated on the fly.



Repeat the tasks in the playground immediately above but using factors instead of numeric vectors as columns in the data frame. Hint: revisit the exercise on page 51 where the use of `order()` on factors is described.

2.4.4 Re-encoding or adding variables

It is common that some variables need to be added to an existing data frame based on existing variables, either as a computed value or based on mapping for example treatments to sample codes already in a data frame. In the second case, named vectors can be used to replace values in a variable or to add a variable to a data frame.

Mapping is possible because the length of the value returned by the extraction

operator `[]` is given by the length of the indexing vector (see section 1.10 on page 31). Although we show toy-like examples, this approach is most useful with data frames containing many rows.

If the existing variable is a character vector or factor, we need to create a named vector with the new values as data and the existing values as names.

```
my.df <-
  data.frame(genotype = rep(c("WT", "mutant1", "mutant2"), 2),
             value = c(1.5, 3.2, 4.5, 8.2, 7.4, 6.2))
mutant <- c(WT = FALSE, mutant1 = TRUE, mutant2 = TRUE)
my.df$mutant <- mutant[my.df$genotype]
my.df
##   genotype value mutant
## 1      WT    1.5  FALSE
## 2  mutant1    3.2   TRUE
## 3  mutant2    4.5   TRUE
## 4      WT    8.2  FALSE
## 5  mutant1    7.4   TRUE
## 6  mutant2    6.2   TRUE
```

If the existing variable is an **integer** vector, we can use a vector without names, being careful that the positions in the *mapping* vector match the values of the existing variable

```
my.df <- data.frame(individual = rep(1:3, 2),
                   value = c(1.5, 3.2, 4.5, 8.2, 7.4, 6.2))
genotype <- c("WT", "mutant1", "mutant2")
my.df$genotype <- genotype[my.df$individual]
my.df
##   individual value genotype
## 1          1    1.5      WT
## 2          2    3.2  mutant1
## 3          3    4.5  mutant2
## 4          1    8.2      WT
## 5          2    7.4  mutant1
## 6          3    6.2  mutant2
```



Add a variable named **genotype** to the data frame below so that for individual 4 its value is "WT", for individual 1 its value is "mutant1", and for individual 2 its value is "mutant2".

```
my.df <- data.frame(individual = rep(c(2, 4, 1), 2),
                   value = c(1.5, 3.2, 4.5, 8.2, 7.4, 6.2))
```

2.4.5 Operating within data frames

In the case of computing new values from existing variables named vectors are of limited use. Instead, variables in a data frame can be added or modified with R functions `transform()`, `with()` and `within()`. These functions can be thought as convenience functions as the same computations can be done using the extraction operators to access individual variables, in either the lhs, rhs or both lhs and rhs (see section 1.10 on page 31).

In the case of `with()` only one, possibly compound code statement is affected and this statement is passed as an argument. As before, we need to fully specify the left-hand side of the assignment. The value returned is the one returned by the statement passed as an argument, in the case of compound statements, the value returned by the last contained simple code statement to be executed. Consequently, if the intent is to modify the container, assignment to an individual member variable (column in this case) is required.

In this example, column A of `my_data_frame.df` takes precedence, and the returned value is the expected one.


```
my_data_frame.df$C <- NULL
my_data_frame.df$C <- with(my_data_frame.df, (A + B) / A)
head(my_data_frame.df, 2)
##   B A   C
## 1 3 1 4.0
## 2 3 2 2.5
```

In the case of `within()`, assignments in the argument to its second parameter affect the object returned, which is a copy of the container (In this case, a whole data frame), which still needs to be saved through assignment. Here the intention is to modify it, so we assign it back to the same name, but it could have been assigned to a different name so as not to overwrite the original data frame.

```
my_data_frame.df$C <- NULL
my_data_frame.df <- within(my_data_frame.df, C <- (A + B) / A)
head(my_data_frame.df, 2)
##   B A   C
## 1 3 1 4.0
## 2 3 2 2.5
```

In the example above, using `within()` makes little difference compared to using `with()` with respect to the amount of typing or clarity, but with multiple member variables being operated upon, as shown below, `within()` has an advantage resulting in more concise and easier to understand code.

```
my_data_frame.df$C <- NULL
my_data_frame.df <- within(my_data_frame.df,
  {C <- (A + B) / A
    D <- A * B
    E <- A / B + 1}
)
head(my_data_frame.df, 2)
##   B A     E D   C
## 1 3 1 1.333333 3 4.0
## 2 3 2 1.666667 6 2.5
```

 Repeatedly pre-pending the name of a *container* such as a list or data frame to the name of each member variable being accessed can make R code verbose and difficult to understand. Functions `attach()` and its matching `detach()` allow us to change where R looks for the names of objects we include in a code statement. When using a long name for a data frame, entering a simple calculation can easily result in a difficult to read statement. (Method `head()` is used here to limit the

displayed value to the first two rows—`head()` is described in section 2.7 on page 82.)

```
my_data_frame.df <- data.frame(A = 1:10, B = 3)
my_data_frame.df$C <-
  (my_data_frame.df$A + my_data_frame.df$B) / my_data_frame.df$A
head(my_data_frame.df, 2)
##   A B   C
## 1 1 3 4.0
## 2 2 3 2.5
```

Using `attach()` we can alter how R looks up names and consequently simplify the statement. With `detach()` we can restore the original state. It is important to remember that here we can only simplify the right-hand side of the assignment, while the “destination” of the result of the computation still needs to be fully specified on the left-hand side of the assignment operator. We include below only one statement between `attach()` and `detach()` but multiple statements are allowed. Furthermore, if variables with the same name as the columns exist in the search path, these will take precedence, something that can result in bugs or crashes, or as seen below, a message warns that variable `A` from the global environment will be used instead of column `A` of the attached `my_data_frame.df`. The returned value is, of course, not the desired one.

```
my_data_frame.df$C <- NULL
attach(my_data_frame.df)

## The following object is masked _by_ .GlobalEnv:
##
##      A

my_data_frame.df$C <- (A + B) / A
detach(my_data_frame.df)
head(my_data_frame.df, 2)
##   A B   C
## 1 1 3   4
## 2 2 3   4
```

Use of `attach()` and `detach()`, which function as a pair of ON and OFF switches, can result in an undesired after-effect on name lookup if the script terminates after `attach()` is executed but before `detach()` is called, as cleanup is not automatic. In contrast, `with()` and `within()`, being self-contained, guarantee that cleanup takes place. Consequently, the usual recommendation is to give preference to the use of `with()` and `within()` over `attach()` and `detach()`. Use of these functions not only saves typing but also makes code more readable.

2.5 Attributes of R objects

R objects can have attributes. Attributes are named slots normally used to store ancillary data such as object properties. There are no restrictions on the class

of what is assigned to an attribute. They are used by R itself to store things like column names in data frames and labels of factor levels. All these attributes are visible to user code, and user code can read and write objects' attributes. However, they are rarely displayed explicitly when an object is printed. They can be also used to store metadata accompanying the data stored in an object, which is important for reproducible research and data sharing.

Attribute `"comment"` is meant to be set by users to store a character string—e.g., to store metadata as text together with data. As comments are frequently used, R has functions for accessing and setting comments.

```
a.df <- data.frame(x = 1:6, y = "a", z = c(TRUE, FALSE))
comment(a.df)
## NULL

comment(a.df) <- "this is stored as a comment"
comment(a.df)
## [1] "this is stored as a comment"
```

Methods like `names()`, `dim()` or `levels()` return values retrieved from attributes stored in R objects, and methods like `names()<-`, `dim()<-` or `levels()<-` set (or unset with `NULL`) the value of the respective attributes. Specific query and set methods do not exist for all attributes. Methods `attr()`, `attr()<-` and `attributes()` can be used with any attribute. With `attr()` we access, and with `attr()<-` we set individual attributes by name. With `attributes()` we retrieve all attributes of an object as a named list. In addition, method `str()` displays all components and structure of R objects including their attributes.

Continuing with the previous example, we can retrieve and set the comment using these functions. In the second statement we delete the value stored in the `"comment"` attribute by assigning `NULL` to it.

```
attr(a.df, "comment")
## [1] "this is stored as a comment"

attr(a.df, "comment") <- NULL
attr(a.df, "comment")
## NULL

comment(a.df) # same as previous line
## NULL
```

The `"names"` attribute of `a.df` was set by the `data.frame()` constructor when it was created above. In the next example, in the first statement we retrieve the names, and implicitly print them. In the second statement, read from right to left, we retrieve the names, convert them to upper case and save them back to the same attribute.

```
names(a.df)
## [1] "x" "y" "z"

names(a.df) <- toupper(names(a.df))
names(a.df)
## [1] "X" "Y" "Z"

attr(a.df, "names") # same as previous line
## [1] "X" "Y" "Z"
```

We can add a new attribute, under our own control, as long as its name does not clash with that of existing attributes.

```
attr(a.df, "my.attribute") <- "this is stored in my attribute"
attributes(a.df)
## $names
## [1] "x" "y" "z"
##
## $class
## [1] "data.frame"
##
## $row.names
## [1] 1 2 3 4 5 6
##
## $my.attribute
## [1] "this is stored in my attribute"
```



The attributes used internally by R can be directly modified by user code. In most cases this is unnecessary as R provides pairs of functions to query and set the relevant attributes. This is true for the attributes `dim`, `names` and `levels`. In the example below we read the attributes from a vector.

```
M <- matrix(1:10, ncol = 2)
M
##      [,1] [,2]
## [1,]    1    6
## [2,]    2    7
## [3,]    3    8
## [4,]    4    9
## [5,]    5   10

attr(M, "dim")
## [1] 5 2

attr(M, "dim") <- c(2, 5)
M
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    3    5    7    9
## [2,]    2    4    6    8   10
```

In this case we could have used `dim()` instead of `attr()`.



There is no restriction to the creation, setting, resetting and reading of attributes, but not all methods and operators that can be used to modify objects will preserve non-standard attributes. This can be a problem when using some R packages, such as the ‘tidyverse’. So, using private attributes is a double-edged sword that usually is worthwhile considering only when designing a new class together with the corresponding methods for it. A good example of extensive use of class-specific attributes are the values returned by model fitting functions like `lm()` (see section ?? on page ??).

2.6 Saving and loading data

2.6.1 Data sets in R and packages

To be able to present more meaningful examples, we need some real data. Here we use `cars`, one of the many data sets included in base R. Function `data()` is used to load data objects that are included in R or contained in packages. It is also possible to import data saved in files with *foreign* formats, defined by other software or commonly used for data exchange. Package ‘foreign’, included in the R distribution, as well as contributed packages make available functions capable of reading and decoding various foreign formats. How to read or import “foreign” data is discussed in R documentation in *R Data Import/Export*, and in this book, in chapter ?? starting on page ?. It is also good to keep in mind that in R, URLs (Uniform Resource Locators) are accepted as arguments to the `file` or `path` parameter of many functions (see section ?? starting on page ?).

In the next example we load data included in R as R objects by calling function `data()`. The loaded R object `cars` is a data frame.

```
data(cars)
```

Once we have a data set available, the first step is usually to explore it, and we will do this with `cars` in section 2.7 on page 82.

2.6.2 .rda files

By default, at the end of a session, the current workspace containing the results of your work is saved into a file called `.RData`. In addition to saving the whole workspace, it is possible to save one or more R objects present in the workspace to disk using the same file format (with file name tag `.rda` or `.Rda`). One or more objects, belonging to any mode or class can be saved into a single file using function `save()`. Reading the file restores all the saved objects into the current workspace with their original names. These files are portable across most R versions—i.e., old formats can be read and written by newer versions of R, although the newer, default format may be not readable with earlier R versions. Whether compression is used, and whether the “binary” data is encoded into ASCII characters, allowing maximum portability at the expense of increased size can be controlled by passing suitable arguments to `save()`.

We create a data frame object and then save it to a file.

```
my.df <- data.frame(x = 1:5, y = 5:1)
my.df
##   x y
## 1 1 5
## 2 2 4
## 3 3 3
## 4 4 2
## 5 5 1

save(my.df, file = "my-df.rda")
```

We delete the data frame object and confirm that it is no longer present in the workspace.

```
rm(my.df)
ls(pattern = "my.df")
## character(0)
```

We read the file we earlier saved to restore the object.

```
load(file = "my-df.rda")
ls(pattern = "my.df")
## [1] "my.df"

my.df
##   x y
## 1 1 5
## 2 2 4
## 3 3 3
## 4 4 2
## 5 5 1
```

The default format used is binary and compressed, which results in smaller files.



In the example above, only one object was saved, but one can simply give the names of additional objects as arguments. Just try saving more than one data frame to the same file. Then the data frames plus a few vectors. After creating each file, clear the workspace and then restore from the file the objects you saved.

Sometimes it is easier to supply the names of the objects to be saved as a vector of character strings passed as an argument to parameter `list`. One case is when wanting to save a group of objects based on their names. We can use `ls()` to list the names of objects matching a simple `pattern` or a complex regular expression. The example below does this in two steps, first saving a character vector with the names of the objects matching a pattern, and then using this saved vector as an argument to `save`'s `list` parameter.

```
objects <- ls(pattern = "*.df")
save(list = objects, file = "my-df1.rda")
```

The two statements above can be combined into a single statement by nesting the function calls.

```
save(list = ls(pattern = "*.df"), file = "my-df1.rda")
```



Practice using different patterns with `ls()`. You do not need to save the objects to a file. Just have a look at the list of object names returned.

As a coda, we show how to clean up by deleting the two files we created. Function `unlink()` can be used to delete any files for which the user has enough rights.

```
unlink(c("my-df.rda", "my-df1.rda"))
```

2.6.3 .rds files

The RDS format can be used to save individual objects instead of multiple objects (usually using file name tag `.rds`). They are read and saved with functions `readRDS()` and `saveRDS()`, respectively. When RDS files are read, different from when RDA files are loaded, we need to assign the object read to a possibly different name for it to be added to the search path. Of course, it is also possible to use the returned object as an argument to a function or in an expression without saving it to a variable.

```
saveRDS(my.df, "my-df.rds")
```

If we read the file, by default the read R object will be printed at the console.

```
readRDS("my-df.rds")
##      x y
## 1 1 5
## 2 2 4
## 3 3 3
## 4 4 2
## 5 5 1
```

In the next example we assign the read object to a different name, and check that the object read is identical to the one saved.

```
my_read.df <- readRDS("my-df.rds")
identical(my.df, my_read.df)
## [1] TRUE
```

As above, we clean up by deleting the file.

```
unlink("my-df.rds")
```

2.7 Looking at data

There are several functions in R that let us obtain different views into objects. Function `print()` is useful for small data sets, or objects. Especially in the case of large data frames, we need to explore them step by step. In the case of named components, we can obtain their names with `colnames()`, `rownames()`, and `names()`. If a data frame contains many rows of observations, `head()` and `tail()` allow us to easily restrict the number of rows printed. Functions `nrow()` and `ncol()` return the number of rows and columns in the data frame (also applicable to matrices but not to lists or vectors where we use `length()`). As mentioned earlier, function `str()` concisely displays the structure of R objects.

```

class(cars)
## [1] "data.frame"

head(cars)
##   speed dist
## 1     4    2
## 2     4   10
## 3     7    4
## 4     7   22
## 5     8   16
## 6     9   10

tail(cars)
##   speed dist
## 45    23   54
## 46    24   70
## 47    24   92
## 48    24   93
## 49    24  120
## 50    25   85

nrow(cars)
## [1] 50

ncol(cars)
## [1] 2


names(cars)
## [1] "speed" "dist"

colnames(cars)
## [1] "speed" "dist"

head(rownames(cars))
## [1] "1" "2" "3" "4" "5" "6"

str(cars)
## 'data.frame': 50 obs. of  2 variables:
##  $ speed: num  4 4 7 7 8 9 10 10 10 11 ...
##  $ dist : num  2 10 4 22 16 10 18 26 34 17 ...

```

 Look up the help pages for `head()` and `tail()`, and edit the code above to print only the first two lines, or only the last three lines of `cars`, respectively.

The different columns of a data frame can be factors, or vectors of various modes (e.g., numeric, logical, character, etc.) (see section 2.4 on page 61). To explore the mode of the columns of `cars`, we can use an *apply* function. In the present case, we want to apply function `class()` to each column of the data frame `cars`. (Apply functions are described in section ?? on page ??.)


```


sapply(X = cars, FUN = class)
##   speed    dist
## "numeric" "numeric"

```

The statement above returns a vector of character strings, with the mode of

each column. Each element of the vector is named according to the name of the corresponding "column" in the data frame. For this same statement to be used with any other data frame or list, we need only to substitute the name of the object, the argument to the first parameter called `x`, to the one of current interest.


 Data set `airquality` contains data from air quality measurements in New York, and, being included in the R distribution, can be loaded with `data(airquality)`. Load it, and repeat the steps above, to learn what variables (columns) it contains, their classes, the number of rows, etc.

 Although the R language allows data frame columns of class `matrix`, their use is infrequent. On the other hand, columns belonging to class `list` are disallowed in data frames. The reverse is true for tibbles (described in section ?? on page ??).

Function `summary()` can be used to obtain a summary from objects of most R classes, including data frames. We can also use `sapply()`, `lapply()` or `vapply()` to apply any suitable function to individual columns.

```
summary(cars)
##      speed      dist
##  Min.   : 4.0    Min.   : 2.00
##  1st Qu.:12.0    1st Qu.: 26.00
##  Median :15.0    Median : 36.00
##  Mean   :15.4    Mean   : 42.98
##  3rd Qu.:19.0    3rd Qu.: 56.00
##  Max.   :25.0    Max.   :120.00

sapply(cars, range)
##      speed dist
## [1,]     4    2
## [2,]    25 120
```

 Obtain the summary of `airquality` with function `summary()`, but in addition, write code with an `apply` function to count the number of non-missing values in each column. Hint: using `sum()` on a `logical` vector returns the count of `TRUE` values as `TRUE`, and `FALSE` are transparently converted into `numeric` 1 and 0, respectively, when `logical` values are used in arithmetic expressions.

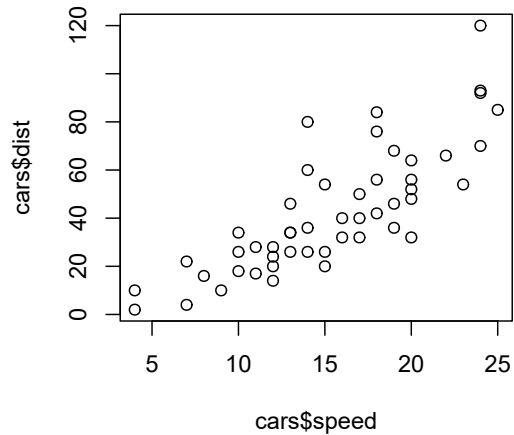
2.8 Plotting

The base-R generic method `plot()` can be used to plot different data. It is a generic method that has specializations suitable for different kinds of objects (see section ?? on page ?? for a brief introduction to objects, classes and methods). In this section we only very briefly demonstrate the use of the most common base-R graphics functions. They are well described in the book *R Graphics* (Murrell 2019). We will not describe the Lattice (based on S's Trellis) approach to plotting (Sarkar 2008).

Instead we describe in detail the use of the *grammar of graphics* and plotting with package ‘ggplot2’ in chapter ?? starting on page ??.

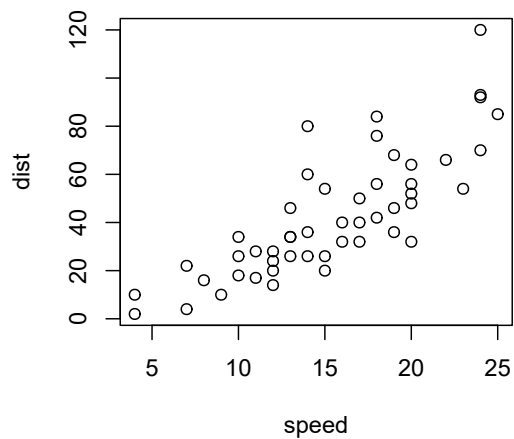
It is possible to pass two variables (here columns from a data frame) directly as arguments to the `x` and `y` parameters of `plot()`.

```
plot(x = cars$speed, y = cars$dist)
```



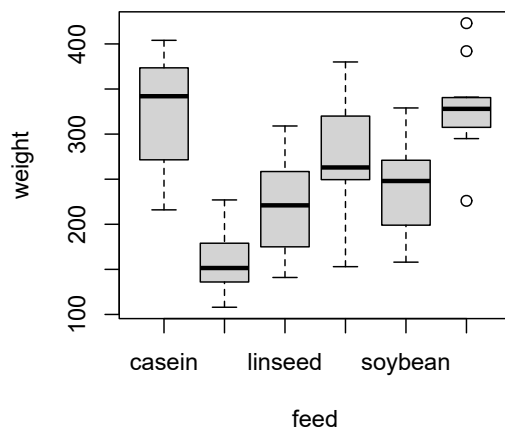
It is also possible, and usually more convenient, to use a *formula* to specify the variables to be plotted on the x and y axes, passing additionally as an argument to parameter `data` the name of the data frame containing these variables. The formula `dist ~ speed`, is read as `dist` explained by `speed`—i.e., `dist` is mapped to the y -axis as the dependent variable and `speed` to the x -axis as the independent variable.

```
plot(dist ~ speed, data = cars)
```



Within R there exist different specializations, or “flavors,” of method `plot()` that become active depending on the class of the variables passed as arguments: passing two numerical variables results in a scatter plot as seen above. In contrast passing one factor and one numeric variable to `plot()` results in a box-and-whiskers plot being produced. To exemplify this we need to use a different data set, here `chickwts` as `cars` does not contain any factors. Use `help("chickwts")` to learn more about this data set, also included in R.

```
plot(weight ~ feed, data = chickwts)
```



Method `plot()` and variants defined in R, when used for plotting return their graphical output to a *graphical output device*.

When R is used interactively, a software device is opened automatically to output the graphical output to a physical device, usually the computer screen. The name of the R software device used may depend on the operating system (e.g., MS-Windows or Linux), or on the IDE (e.g., RStudio).

In R, software graphical devices not necessarily generate output on a physical device like a printer, as several of these devices translate the plotting commands into a file format and save it to disk. Several different graphical devices are available in R and they differ in the kind of output they produce: raster files (e.g., TIFF, PNG and JPEG formats), vector graphics files (e.g., SVG, EPS and PDF), or output to a physical device like the screen of a computer. Additional devices are available through contributed R packages.

Devices follow the paradigm of ON and OFF switches, opening and closing a destination for `print()`, `plot()` and related functions. Some devices producing a file as output, can save their output one plot at a time to single-page graphic files or only when the device is closed, possibly as a multi-page file.

When opening a device the user supplies additional information. For the PDF device that produces output in a vector-graphics format, width and height of the output are specified in *inches*. A default file name is used unless we pass a character string as an argument to parameter `file`.

```
pdf(file = "output/my-file.pdf", width = 6, height = 5, onefile = TRUE)
plot(dist ~ speed, data = cars)
plot(weight ~ feed, data = chickwts)
dev.off()
## cairo_pdf
##      2
```

Raster devices return bitmaps and `width` and `height` are specified in *pixels*.

```
png(file = "output/my-file.png", width = 600, height = 500)
plot(weight ~ feed, data = chickwts)
dev.off()
## cairo_pdf
##      2
```

The approach of direct output to a software device is used in base R, and the addition of plot components, as shown below, is done directly to the output device.

```
png(file = "output/my-file.png", width = 600, height = 500)
plot(dist ~ speed, data = cars)
text(x = 10, y = 110, labels = "some texts to be added")
dev.off()
## cairo_pdf
##      2
```

i This is not the only approach available. As we will see in chapter ?? starting on page ??, an alternative approach is to build a *plot object* as a list of member components that is later rendered as a whole on a graphical device by calling `print()` once.

2.9 Further reading

For further reading on the aspects of R discussed in the current chapter, I suggest the books *R Programming for Data Science* (Peng) and *The Art of R Programming: A Tour of Statistical Software Design* (Matloff).



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