

An Introductory R Session

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1 Introduction

The following section is intended to give you a first feeling what **R** (R Core Team 2021) is and how it works. It assumes that the following software is installed:

1. The R system for statistical computing: <https://www.r-project.org>
2. R Studio, a program that makes working with R more convenient: <https://www.rstudio.org>

Note: please install **R** first before installing **RStudio**.

You may also consider to watch a Youtube video about **R**, a good example for the very beginning is the short video “R tutorial - The True Basics of R” from DataCamp, see <https://youtu.be/SWxoJqTqo08>.

2 First Steps

2.1 Program start and help system

The easiest way to learn **R** is the creative understanding and modification of given examples, the usage of **R** for solving practical problems and the diagnosis of the frequently occurring problems and error messages. Don't worry: error messages are a normal phenomenon in scientific computing and not an indication of a dysfunction of the computer or the human brain. The opposite is true, a certain amount of stress hormones helps to acquire permanent learning effects. Then, after a certain level of experience reading the official **R**-Documentation “An Introduction to R” (Venables, Smith, and Team 2021). or any good **R**-book is strongly recommended.

The first sections of this “crash course” are intended to give an overview over some of the most important elements of **R** and an insight into a typical work flow, that may be useful for the first statistical analyses and as a starting point for self-education.

We begin our first session by starting **RStudio**, a platform independent interface that makes working with R easier. RStudio divides the screen into 3 (resp. 4) windows (called panes), where some of them have additional tabs to switch between different views.

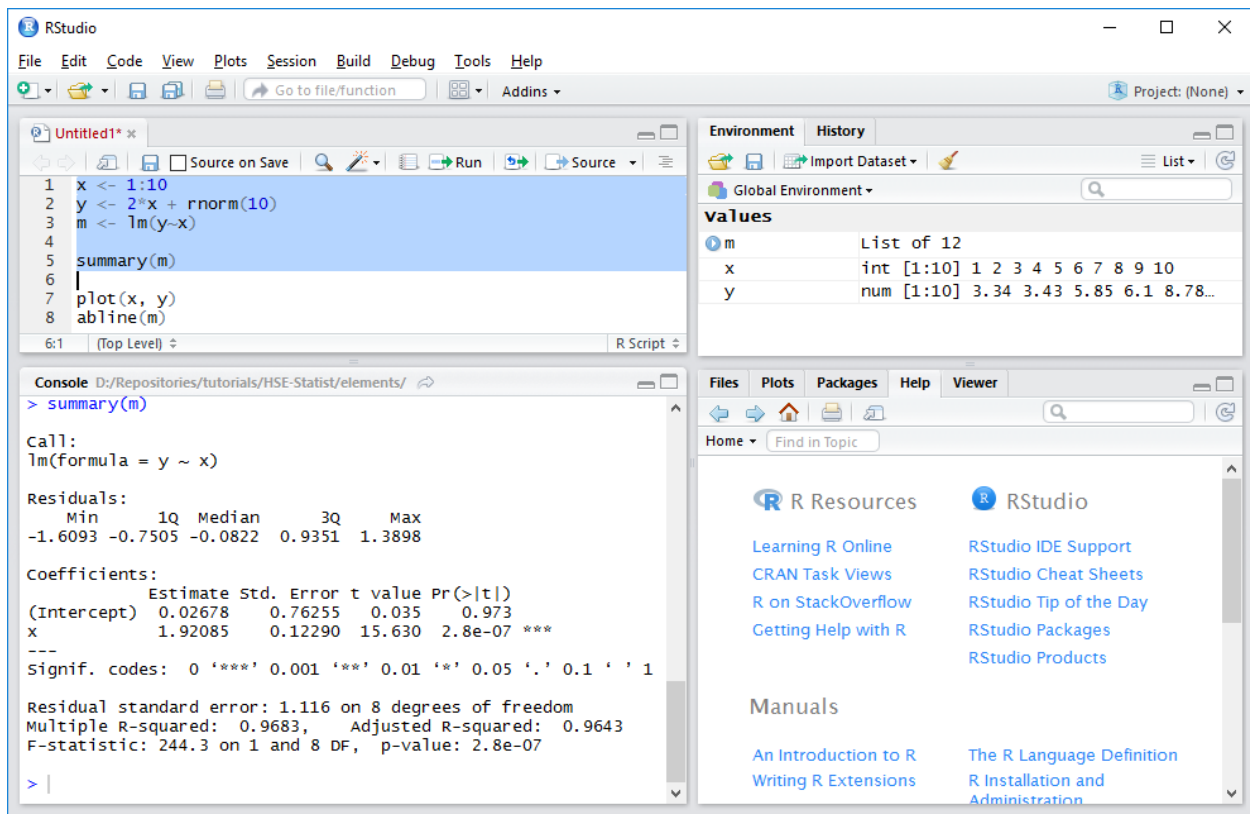


Figure 1: R Studio with 4 panes. Use **File – New R Script** to open the the source code pane (shown top left). Then enter some code and don't forget to explore the help files.

In a fresh RStudio session, one “Pane” should be the main help page of **R**. It is a good idea to browse a little bit around to get an impression about the amount and the typical style of the available help topics. The most important sections are “An Introduction to R,” “Search Engine & Keywords,” “Packages,” the “Frequently Asked Questions” and possibly “**R** Data Import/Export.”

We start now to explore the **R**-System itself.

2.2 R as a pocket calculator

Entering an arithmetic expression like this:

```
2 + 4
```

shows that **R** can be used as a pocket calculator, that immediately outputs the result:

```
[1] 6
```

Instead of printing the result to the screen, it is also possible to save the result into a named **variable** using the assignment operator “`<-`.”

```
a <- 2 + 4
```

It seems that nothing happens, but the result is now saved in the variable **a** that can be recalled at any time by entering the variable name alone:

```
a
```

Variable names in **R** start always with a character (or for special purposes a dot), followed by further characters, numerals, dots or underscores, where a distinction is made between small and capital letters,

i.e. the variables `value`, `Value` and `VALUE` can contain different data. A few character combinations are **reserved words** and cannot be used as variables:

`break`, `for`, `function`, `if`, `in`, `next`, `repeat`, `while` and “`\dots`” (three dots).

Other identifiers like `plot` can be re-defined, but this should be done with care to avoid unwanted confusion and side effects.

2.3 Vectors

You may have noticed, that the output of the example above had a leading `[1]`, which means that the line begins with the first element of `a`. This brings us to a very important feature of **R** that variables can contain more than single values: vectors, matrices, lists, data frames (tables) and so on.

The most basic data type is the vector, that can be filled with data using the `c` (combine) function:

```
values <- c(2, 3, 5, 7, 8.3, 10)
values
```

```
[1] 2.0 3.0 5.0 7.0 8.3 10.0
```

To create a sequence of values, one can use the `:` (colon):

```
x <- 1:10
x
```

or, even more flexibly the `seq` function:

```
x <- seq(2, 4, 0.25)
x
```

Sequences of repeated equal values can be obtained with `rep`:

```
x <- rep(2, 4)
x
```

2.4 Exercise

There are many ways to use these functions, try for example:

```
seq(0, 10)
seq(0, 10, by = 2)
seq(0, pi, length = 12)
rep(c(0, 1, 2, 4, 9), times = 5)
rep(c(0, 1, 2, 4, 9), each = 2)
rep(c(0, 1, 2, 4, 9), each = 2, times = 5)
```

2.5 Access to vector elements

Instead of accessing vectors as a whole, it is also possible to extract single elements, where the index of the requested data is itself a vector:

```
values[5]
values[2:4]
values[c(1, 3, 5)]
```

Sometimes, elements of a vector may have individual names, which makes it easy to access them:

```
named <- c(a = 1, b = 2.3, c = 4.5)
named
named["a"]
```

In **R** (and in contrast to other languages like **C/C++**) vector indices start with 1. Negative indices are also possible, but they have the special purpose to delete one or several elements:

```
values[-3]
```

It is also possible to extend a given vector by preceding or appending values with the combine function (**c**):

```
c(1, 1, values, 0, 0)
```

The length of a vector can be determined with:

```
length(values)
```

and it is also possible to have empty vectors, i.e. vectors that exist, but do not contain any values. Here the keyword **NULL** means “nothing” in contrast to “0” (zero) that has length 1:

```
values <- NULL
values
length(values)
```

Such empty vectors are sometimes used as “containers” for appending data step by step:

```
values <- NULL
values
length(values)
values <- c(values, 1)
values
values <- c(values, 1.34)
values
```

If a data element should be removed completely, this can be done using the **remove** function:

```
rm(values)
values
Error: Object "values" not found
```

The complete workspace can be deleted from the menu of **R** or **RStudio** (Session – Clear workspace) or from the command line with **rm** (remove):

```
rm(list = ls(all = TRUE))
```

The **R** session can be closed by using the menu as usual or by entering:

```
q()
```

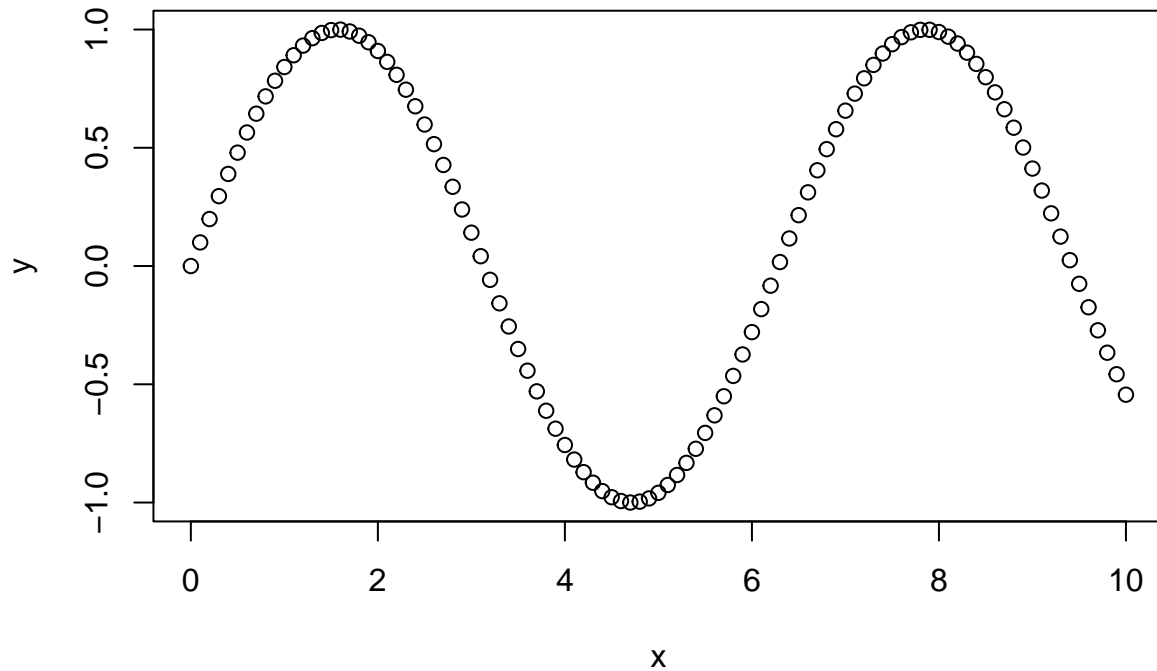
Sometimes and depending of the configuration, **R** asks whether the “**R** workspace” should be saved to the hard disk. This may be useful for continuing work at a later time, but has the risk to clutter the workspace and to get irreproducible results at a later session, so it is recommended to say “No” for now, except if you exactly know why.

Later we will learn how to save only the data (and commands) that are needed.

3 Graphics

Now, we will see how to use **R** as a function plotter by drawing sine or cosine functions within an interval between 0 to 10. First, we create a table of values for **x** and **y** and in order to get a smooth curve, it is reasonable to choose a small step size. As a rule of thumb I always recommend to use about 100...400 small steps as a good compromise between smoothness and memory requirements, so let’s set the step size to 0.1:

```
x <- seq(0, 10, 0.1)
y <- sin(x)
plot(x, y)
```



Instead of plotting points, it is of course also possible to draw continuous lines. This is indicated by supplying an optional argument `type="l"`. **Please note**, that the symbol used here for `type` is the **small letter “L”** for “line” and not the – in printing very similar – numeral “1” (one)!

We see also, that optional arguments like `type` can be given as “keyword = value” pair. This has the advantage that the order of arguments does not matter, because arguments are referenced by their name:

```
plot(x, y, type = "l")
```

Now we want to add a cosine function with another color. This can be done with one of the functions `lines` or `points`, for adding lines or points to an existing figure:

```
y1 <- cos(x)
lines(x, y1, col = "red")
```

With the help of `text` it is also possible to add arbitrary text, by specifying first the x and y coordinates and then the text:

```
x1 <- 1:10
text(x1, sin(x1), x1, col = "green")
```

Many options exist to modify the behavior of most graphics functions so the following specifies user-defined coordinate limits (`xlim`, `ylim`), axis labels and a heading (`xlab`, `ylab`, `main`).

```
plot(x, y, xlim = c(-10, 10), ylim = c(-2, 2),
     xlab = "x-Values", ylab = "y-Values", main = "Example Graphics")
```

3.1 Code formatting and line breaks

The above example is a rather long command and may not fit on a single line. In such cases, **R** displays a + (plus sign) to indicate that a command must be continued, e.g. because a closing parenthesis or a closing quote is still missing. Such a + at the beginning of a line is an automatic “prompt” similar to the ordinary > prompt and must never be typed in manually. If, however, the + continuation prompt occurs by accident, press “ESC” to cancel this mode.

In contrast to the long line continuation prompt, it is also possible to write several commands on one line, separated by a semi-colon “;” This is useful in some cases, but as a general rule it is better to

- write each command to a separate line
- avoid long lines with more than about 60 characters
- use proper indentation, e.g. 2 characters per indentation level

Finally, a number (or hash) symbol # means that a complete line or the part of the line that follows # is a comment and should be ignored by **R**.

3.2 Additional plotting options

In order to explore the wealth of graphical functions, you may now have a more extensive look into the online help, especially regarding ?plot or ?plot.default, and you should experiment a little bit with different plotting parameters, like lty, pch, lwd, type, log etc. **R** contains uncountable possibilities to get full control over the style and content of your graphics, e.g. with user-specified axes (axis), legends (legend) or user-defined lines and areas (abline, rect, polygon). The general style of figures like (font size, margins, line width) can be influenced with the par function.

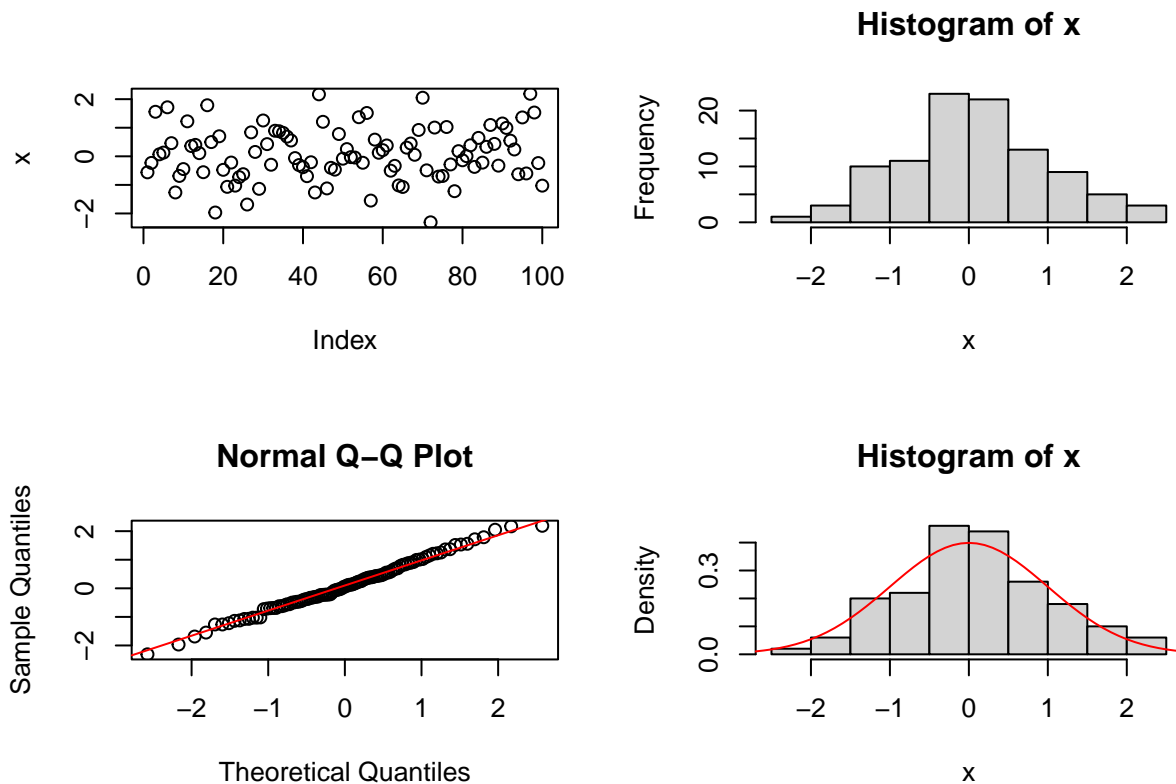
3.3 High level plotting functions

In addition, **R** and its packages contain numerous “high level”-graphics functions for specific purposes. To demonstrate a few, we first generate a data set with normally distributed random numbers (mean = 0, standard deviation sd = 1), then we plot them and create a histogram. Here, the function par(mfrow = c(2, 2)) divides the plotting area into 2 rows and 2 columns to show 4 separate figures:

```
par(mfrow = c(2, 2))
x <- rnorm(100)
plot(x)
hist(x)
```

Now, we add a so-called *normal probability plot* and a second histogram with relative frequencies together with the bell-shaped density curve of the standard normal distribution. The optional argument probability = TRUE makes sure that the histogram has the same scaling as the density function, so that both can be overlaid:

```
qqnorm(x)
qqline(x, col = "red")
hist(x, probability = TRUE)
xx <- seq(-3, 3, 0.1)
lines(xx, dnorm(xx, 0, 1), col = "red")
```



Here it may also be a good chance to do a little bit summary statistics like: z.B. `mean(x)`, `var(x)`, `sd(x)`, `range(x)`, `summary(x)`, `min(x)`, `max(x)`, ...

Or we may consider to test if the generated random numbers `x` are approximately normal distributed using the Shapiro-Wilks-W-Test:

```
x <- rnorm(100)
shapiro.test(x)
```

A p-value bigger than 0.05 tells us that the test has no objections against normal distribution of the data. The concrete results may differ, because `x` contains random numbers, so it makes sense to repeat this several times. It can be also useful compare these normally distributed random numbers generated with `rnorm` with uniformly distributed random numbers generated with `runif`:

```
par(mfrow=c(2,2))
y <- runif(100)
plot(y)
hist(y)
qqnorm(y)
qqline(y, col="red")
mean(y)
var(y)
min(y)
max(y)
hist(y, probability=TRUE)
yy <- seq(min(y), max(y), length = 50)
lines(yy, dnorm(yy, mean(y), sd(y)), col = "red")
shapiro.test(y)
```

At the end, we compare the pattern of both data sets with box-and-whisker plots:

```
par(mfrow=c(1, 1))  
boxplot(x, y)
```

3.4 Exercise

Repeat this example with new random numbers and vary sample size (**n**), mean value (**mean**) and standard deviation (**sd**) for random numbers created with **rnorm**, and use different **min** and **max** for **runif**. Consult the help pages for an explanation of the functions and its arguments, and create boxplots with different data sets.

4 Basic Data Structures of R

In addition to vectors, **R** contains several other classes of objects for saving data, e.g. `matrix`, `array`, `list` or `data.frame`. Both, “base **R**” and contributed packages contain many more classes. It is also possible to define user-defined classes.

All objects have the two built-in attributes `mode` (data type) and `length` (number of data in the object). Under specific circumstances some of these data types can be converted into each other, e.g. by using functions like `as.matrix`, `as.data.frame` etc.

Modes can be “numeric” for calculations or “character” for text elements. A special kind of mode is `factor`. This is, statistically speaking, a nominal variable that appears like characters (e.g. “control,” “treatment A,” “treatment B” ...), but its **levels** are internally encoded as integer. Conversion of such factors into other data types should be done with care, because a character “123” may be encoded with another value (e.g. 1) and not 123, see the following demonstration of a correct and wrong factor conversions:

```
x <- c(2, 4, 6, 5, 8)
f <- as.factor(x)
as.numeric(f)           # wrong !!!
as.numeric(as.character(f)) # correct
as.numeric(levels(f))[f] # even better
```

This type of factor coding is not specific to R and appears also in other statistics packages. Attributes of objects can be accessed and changed with functions `attributes` and `attr`, classes with `class`:

```
attributes(f)
attr(f, "class")
class(f)
```

The different classes allow specific operations, e.g. set operations with lists, matrix algebra with numeric matrices or text operations with character data. In the following we focus on tables (in **R** called `data.frame`), the typical input format for statistical analyses.

5 Entering Data

Several different methods exist to input data into **R**. The most important are extensively explained in a special manual **R** Data Import/Export and we want to show only a selection here:

1. direct input in the **R** code,
2. input from the clipboard,
3. input from a text file.

Other methods are direct data base access, import of data from other statistics packages like SPSS, SAS or Stata (`library(foreign)`), reading of GIS-Shapefiles (`library(shapefiles)`), and even sound files or pictures.

5.1 Direct input

We used this method already when creating vectors with the `c` (combine)-Function:

```
x <- c(1, 2, 5, 7, 3, 4, 5, 8)
x
```

In the same way it is possible to create other data types like data frames:

```
dat <- data.frame(f = c("a", "a", "a", "b", "b", "b"),
                  x = c(1, 4, 3, 3, 5, 7)
)
dat
```

or matrices:

```
A <- matrix(c(1:9), nrow=3)
A
```

We see that a matrix is not much different from a vector, formatted into rows and columns.

5.2 Copy and Paste from the Clipboard

R is able to read data directly from the clipboard that were pasted from an editor or a spreadsheet program like Excel or LibreOffice. Let's for example create a spreadsheet table from the following example that contains some data from a lake area in north-eastern Germany (Table 1).

Table 1: Morphometrical and chemical properties of selected lakes (S=Stechlinsee, NN=Nehmitzsee Nord, NS=Nehmitzsee Süd, BL=Breiter Luzin, SL = Schmaler Luzin, DA = Dagowsee, HS = Feldberger Haussee; z=mean depth (m), t=theoretical retention time (a), P=phosphorus concentration (μgL^{-1}), N=nitrogen concentration (mgL^{-1}), Chl=chlorophyll concentration (μgL^{-1}), PP=annual primary production ($\text{gCm}^{-2}\text{a}^{-1}$), SD = secchi depth (m)). The data are an adapted and simplified “toy version” taken from Casper (1985) and Koschel and Scheffler (1985).

Lake	z	t	P	N	Chl	PP	SD
S	23.7	40	2.5	0.20	0.7	95	8.4
NN	5.9	10	2.0	0.20	1.1	140	7.4
NS	7.1	10	2.5	0.10	0.9	145	6.5
BL	25.2	17	50.0	0.10	6.1	210	3.8
SL	7.8	2	30.0	0.10	4.7	200	3.7
DA	5.0	4	100.0	0.50	14.9	250	1.9
HS	6.3	4	1150.0	0.75	17.5	420	1.6

We now select the data and copy them to the clipboard (right mouse, copy), then we change to **R** and retrieve the content of the clipboard with the following command line:

```
dat <- read.table("clipboard", header = TRUE)
```

The character argument "clipboard" is the file name for the data source, **header=TRUE** tells us that the first line contains the variable names. In some countries that have the comma and not the dot as a decimal separator, an additional argument **dec = ","** may be required.

Now, the data are saved in the data frame **dat** and it is possible to access them as usual:

```
dat
summary(dat)
boxplot(dat[-1])
```

Here **summary** shows a quick overview and **boxplot** creates a boxplot for all columns except the first, that contains no numbers.

5.3 Read from a textfile

Reading from the clipboard sounds attractive, but it has a big disadvantage because it needs several manual steps and cannot be automated. Therefore, it is much better to first save the data to a text file on the hard disk before using read table. In the same way it is also possible to read text files directly from the internet.

5.4 Set working directory

Sometimes, it is necessary to know the full path to the data set, but it preferred to set the **working directory** of **R** to the data directory. This can be done in **RStudio** like follows:

1. Locate the folder in the “Files” pane
2. Select “More”
3. Select “Set As Working Directory”

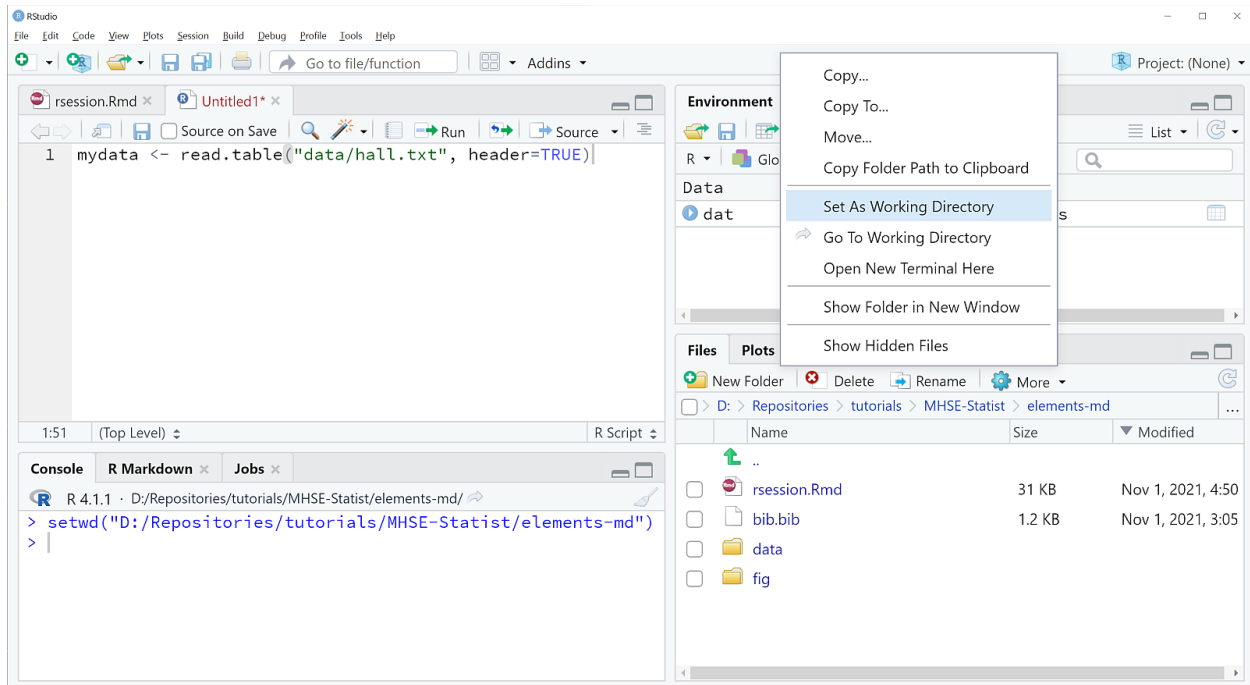


Figure2: Setting the working directory in **RStudio**

After this, data can be retrieved directly from the **working directory** (e.g. `read.csv("hall.csv")`) or from a sub-folder relative to it:

```
mydata <- read.table("data/hall.txt", header=TRUE)
```

Note also that we use always the ordinary slash “/” and not the backslash “\,” even on Windows. It is also possible to use a file browser dialog box to locate and select a data file:

```
mydata <- read.csv(file.choose(), header=TRUE)
```

However, this has, again, the disadvantage that it cannot be automated.

If the data are available on an internet server, it can be read directly from there:

```
mydata <- read.csv("https://raw.githubusercontent.com/tpetzoldt/datasets/main/data/hall.csv",
                  header=TRUE)
```

Now, we are ready to inspect the content of this new variable `mydata`:

```
View(mydata)
```

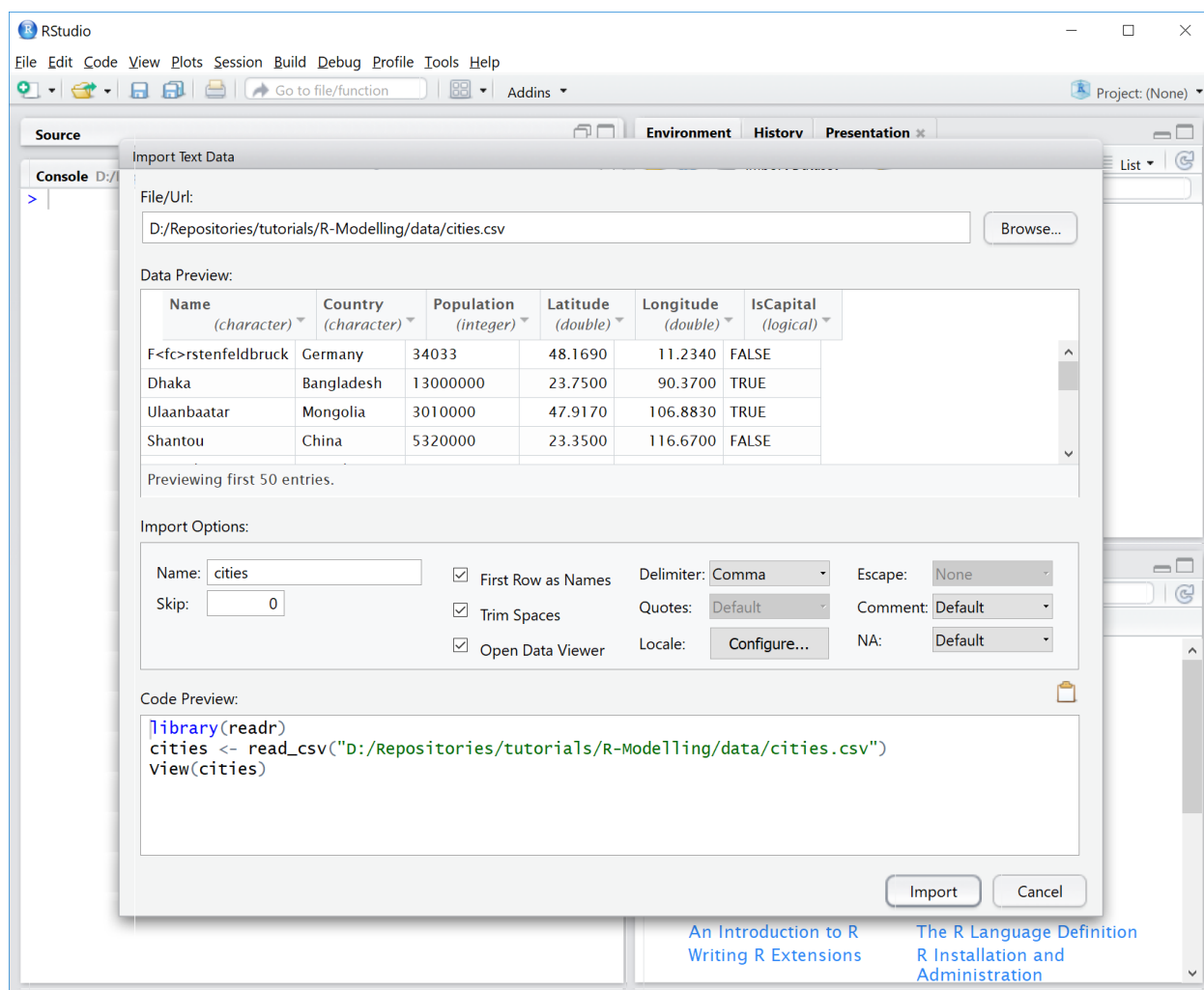
In **RStudio View** can also be invoked by clicking to `mydata` in the environment window.

Function `View` opens a table view, because `mydata` is a data frame. The data set `hall.txt` contains growth curves from an experiment with *Daphnia* (water flea) that were taken from a figure of a publication Hall (1964), where body length was measured in dependence on time (`day`), temperature (`temp`) and food concentration (`food`), that was measured in a historical turbidity unit “Klett”, but this does not matter for our example.

5.5 “Import Dataset” in RStudio

RStudio contains a handy feature that makes importing of data more convenient. Essentially, this “Import Dataset” wizard helps us to construct the correct `read.table`, `read.csv` or `read_delim` function interactively. It is possible to try different options until a satisfying result is obtained. Current versions of **RStudio** contain several different ways to import data. Here we demonstrate the “Import Dataset From Text (readr)” assistant:

1. From the menu select: File – Import Data Set – From CSV.
2. Select the requested file and select suitable options like the name of the variable the data are to be assigned to, the delimiter character (comma or Tab) and whether the first row of the file contains variable names.
3. Hint: The Code Preview contains the commands that the wizard created. If you copy these commands to the script pane, you can re-read the data several times without going back to the menu system.



Import Dataset From Text (readr) assistant of **RStudio**.

Hint: Do not forget to set a **Name** for the resulting data frame (e.g. `dat`), otherwise **R** uses the file name.

6 Working with Dataframes

For large tables it is often not very useful to display the full content, so it is much better to use the function `str` (structure) or the “Environment” explorer of **RStudio** that gives a compact overview over type, size

and content of a variable:

```
str(mydata)
```

This function is universal and also suitable for complicated object types like lists. Of course, there are many more possibilities for inspecting the content of a variable:

```
names(mydata)
mode(mydata)
length(mydata)
```

and sometimes even:

```
plot(mydata)
```

6.1 Access single columns with \$

Single columns of a data frame can be accessed by using indices (with `[]`) similar to a vector or a matrix or by using the column name and the `$` operator:

```
mean(mydata[,4])
mean(mydata$leng)
mean(mydata[, "leng"])
mean(mydata[["leng"]])
plot(mydata$day, mydata$leng)
```

Note the difference of the output of the `[]` and the `[[]]`- version. The difference is as follows: single brackets return a data frame with one column, but double square brackets return the content of the column, i.e. a vector.

The `$`-style can be abbreviated using the `attach` and `detach`-functions, but this “prehistoric relict” is strongly discouraged, as it can lead to data inconsistency and strange errors. If you find it somewhere where it is still used, then it is a good idea to use `detach` repeatedly until an error message confirms us that there is nothing else that can be detached. Finally: never use `attach/detach` in a package.

Instead, it is much better to use another function `width`, that opens the data frame only temporarily:

```
with(mydata, plot(day, leng))
```

Here we can also use curly brackets to combine a series of statements:

```
with(mydata, {
  print(mean(leng))
  print(sd(leng))
})
```

6.2 Subsets and logical indices

A very powerful feature of **R** is the use of logical vectors as “indices,” with similar results like data base queries. A prerequisite for this is that all vectors have the same length.

```
par(mfrow=c(1, 2))
with(mydata, {
  plot(day[temp == 20], leng[temp == 20])
  plot(day[temp == 20 & food == 16], leng[temp == 20 & food == 16])
})
```

A logical comparison requires always a double “`==`” Logical operations like `&` (and) and `|` (or) are also possible. Note that “and” has always precedence before “or,” except this is changed with parenthesis.

A subset of a data frame can also be extracted with the `subset` function:

```
twentydegrees <- subset(mydata, mydata$temp == 20)
View(twentydegrees)
```

Like in the example before, the condition argument allows also logical expressions with `&` (and) and `|` (or).

At the end of this section we show how to convert a data frame into a matrix and how to access single elements in matrix-like manner:

```
mydata <- read.csv("data/hall.csv")
mymatrix <- as.matrix(mydata)
```

The element from the 2nd row and the 4th column can be selected with:

```
mymatrix[2, 4]
```

the complete 5th row with:

```
mymatrix[5, ]
```

and rows 5:10 of the 4th column (`leng`) with:

```
mymatrix[5:10, 4]
```

Additional methods for working with matrices, data frames and lists can be found in **R** textbooks or in the official **R** documentation.

6.3 Mean values of factor combinations

The last examples are intended to demonstrate how powerful a single line can be in **R**. Function `aggregate` can be used to compute statistics (e.g. mean values) depending on given criteria. The first argument of the function is a data frame containing numeric data, the second argument a list (or data frame) of criteria (as factors) and the third argument a function that will be applied to all possible factor combinations, e.g., `mean`, `median`, `sd`, `max` etc.

```
aggregate(mydata, list(food = mydata$food, temp = mydata$temp), mean)
```

or, because it is not meaningful here to calculate mean values for temperature, food concentration and time:

```
aggregate(list(leng = mydata$leng),
           list(food = mydata$food, temp = mydata$temp), mean)
```

6.4 Categorical plots

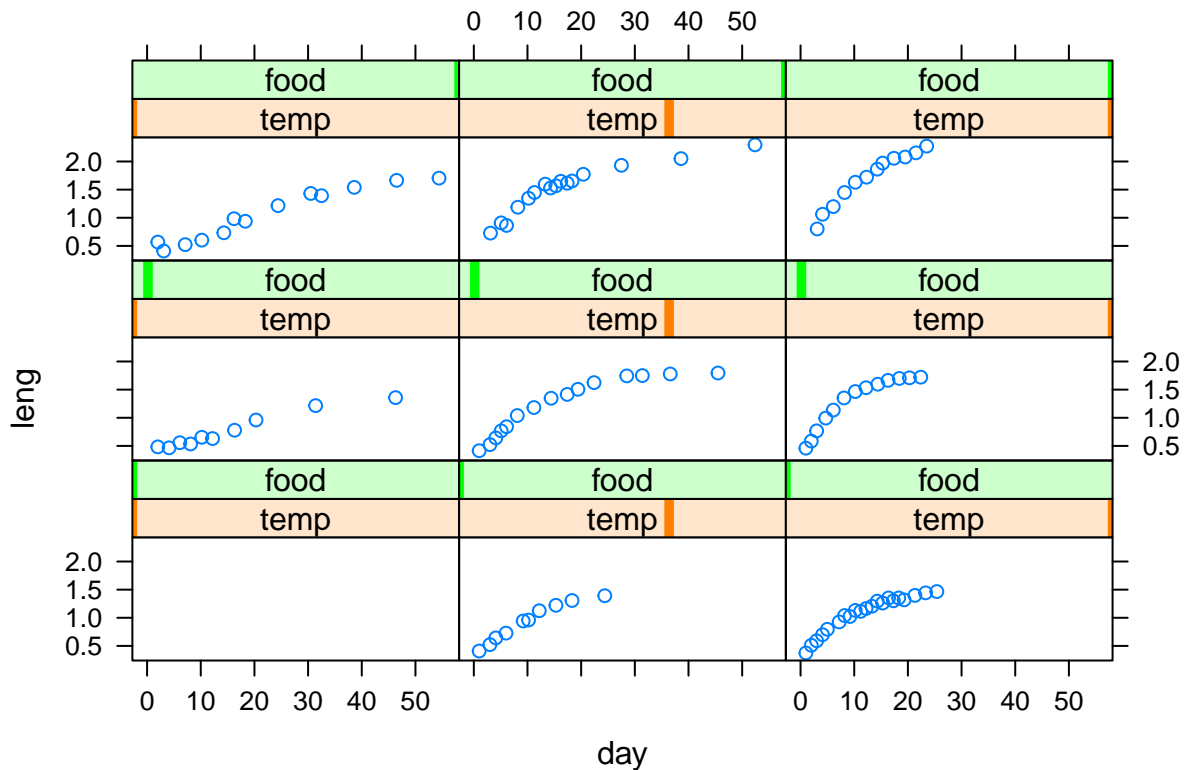
Categorical boxplots can be obtained by using the so-called “formula-interface.” The variable at the left hand side is the dependent variable, while independent factors used for classification are written at the right hand side. The formula is then read “leng as a function of food and temp”:

```
boxplot(leng ~ food + temp, data = mydata)
```

Many, but not all **R** -Functions support this formula interface, details are found in the documentation.

For categorical xy-plots, the formula syntax is also used in the the **lattice**-package (Sarkar 2008):

```
library(lattice)
xyplot(leng ~ day|temp * food, data = mydata)
```



Though the **lattice** package has a rather complex syntax, it is also very flexible and powerful, so the time to learn it is worth the effort. Instead of **lattice**, categorical plots can also be obtained with the **ggplot2** package. This will be explained later.

6.5 Output of Results

The most simple method to save outputs from **R** is to copy it directly from the **R** console to any other program (e.g. LibreOffice, Microsoft Word or Powerpoint) via the Clipboard. This is convenient, but cannot be automated. Therefore, it is better to use a programmatic approach.

Data frames can be saved as text files with `write.table` or `write.csv`:

```
write.csv(mydata, file="output-data.csv", row.names = FALSE)
```

In addition to these basic functions **R** has a wealth of possibilities to save output and data for later use in reports and presentations. All of them are of course documented in the online help, e.g. `print`, `print.table`, `cat` for text files, and `pdf`, `png` for figures. The add-on packages **xtable** contains functions for creating **LaTeX** or HTML-tables while full HTML output is supported by the **R2HTML** or **knitr** packages.

6.6 Exercises

1. Explore different possibilities to plot the Hall-Data set. Draw one figure for each temperature level and distinguish food concentration by using different colors, plot symbols or line types. Make use of the annotation options for adding axis labels and main titles.
2. **R** contains lots of data sets for exploring its graphical and statistical functions and that can be activated by using the data function, e.g. `data(iris)`. Use this data set and find appropriate ways for visualization. A description of the data set can be found as usual in the help file `?iris`.

7 Quitting an R-Session

The **R**-window can be closed as usual with the menu or by entering `q()` (quit):

```
q()
```

Depending on the configuration, we may now be asked whether we want to “Save workspace image” and answering “Yes” would force to save all data from the **R**-Workspace into a file `.Rdata`, so that all data will be automatically and immediately available in the next session, given that **R** is started in the same working directory. Alternatively it is also possible to save or restore an **R**-Workspace manually into a file (Save Workspace, Load Workspace).

8 Acknowledgments

This document was written in **RStudio** (RStudio Team 2021) with **RMarkdown** and the **knitr** package (Xie 2015).

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