

# **The Practice R Tutorials**

Edgar J. Treischl

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# Preface

This website gives access to all tutorials of [Practice R](#) (Treischl 2023). Practice R is a text book for the social sciences which provides several tutorials supporting students to learn R. Feel free to inspect the tutorials even if you are not familiar with the book, but keep in mind the tutorials are supposed to complement the Practice R book.

## The book

Many students learn to analyze data using commercial packages, even though there is an open-source software with cutting-edge possibilities: R, a programming language with countless cool features for applied empirical research.

Practice R introduces R to social science students, inspiring them to consider R as an excellent choice. In a non-technical pragmatic way, this book covers all typical steps of applied empirical research.

Learn how to prepare, analyze, and visualize data in R. Discover how to collect data, generate reports, or automate error-prone tasks.

The book is accompanied by an R package. This provides further learning materials that include interactive tutorials, challenging you with typical problems of applied research. This way, you can immediately practice the knowledge you have learned. The package also includes the source code of each chapter and templates that help to create reports.

Practice R has social science students in mind, nonetheless a broader audience may use Practice R to become a proficient R user.

- Introduces R in a non-technical fashion
- Covers typical steps of applied empirical research
- Complemented by interactive tutorials
- With access to all materials via the Practice R Package

# 1 Base R

Welcome to the **base** R tutorial (Chapter 2) of the [Practice R](#) book (Treischl 2023). Practice R is a text book for the social sciences which provides several tutorials supporting students to learn R. Feel free to inspect the tutorials even if you are not familiar with the book, but keep in mind these tutorials are supposed to complement the Practice R book.

In Chapter 2, I introduced R and we learned the basics about **base** R. Of course, **base** R has more to offer than I could possibly outline, but also much more than is necessary for your first steps with R. Consider how a `while()` loop works. A while loop repeats code until a certain condition is fulfilled. The next console shows the principle. The loop prints `i` and adds one to `i` until `i` is, for example, smaller than four. This example is extremely boring, but it illustrates the concept.

```
# Boring base R example
i <- 1

# while loop
while (i < 4) {
  print(i)
  i <- i + 1
}

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

I will introduce further **base** R features when we need them and I will not ask you to assign objects, create simple functions, or other probably boring **base** R examples in this tutorial. Such tasks are important but abstract in the beginning. Instead, we focus on typical errors that may occur while we start to work with R. Why do we not practice the discussed content of **base** R, but concentrate on errors in this tutorial?

To learn a new programming language is a demanding task. It does not even matter which programming language we talk about, there is an abundance of mistakes and errors (new) users face. For this reason we will get in touch with typical errors messages. For example, sometimes an error occurs only because of a spelling mistake. Can you find the typo in the next console?

```
# Find the typo
print("Hello World")
```

```
#> Error in print("Hello World"): could not find function "print"
```

```
# Solution:
# Ah c'mon, read my friend ;)
```

RStudio has an auto-completion function which helps us to avoid such syntax errors, but learning R implies that you will come across many and sometimes cryptic errors messages (and warnings). Errors and debugging is hard work as the artwork from Allison Horst clearly shows. Thus, as a new user you will run into many errors and the question is how we can manage the process of debugging.

To support you in this process, we will reproduce errors in this tutorial. We try to understand what they mean and I ask you to fix them. We focus on typical errors that all new users face, explore cryptic errors you will soon come across, and further sources of errors. Finally, I summarize the introduced base R functions and I show you where to find more help in case you run into an error.

## 1.1 Typical error messages

What kind of errors do we need to talk about? Sometimes we introduce errors when we are not cautious enough about the code. Spelling mistakes (e.g., typos, missing and wrong characters, etc.) are easy to fix yet hard to find. For example, I tried to use the assignment operator, but something went wrong. Do you know what might be the problem?

```
#Assigning the values the wrong way
```

```
a -< 5
```

```
b -< 3
```

```
a + b
```

```
#> Error: <text>:2:4: unexpected '<'
```

```
#> 1: #Assigning the values the wrong way
```

```
#> 2: a -<
```

```
#>      ^
```

```
# Keep the short cut for the assignment operator in mind:  
#<Alt/Option> + <->
```

```
# Solution:
```

```
a <- 5
```

```
b <- 3
```

```
a + b
```

```
#> [1] 8
```

Finding spelling mistakes in your own code can be hard. There are certainly several reasons, but our human nature to complete text certainly is part of it. This ability gives us the possibility to read fast, but it makes it difficult to see our own mistakes. Don't get frustrated, it happens even if you have a lot of experience working with R. Thus, check if there are no simple orthographically mistakes - such as typos, missing (extra) parentheses, and commas - which prevents the code from running.

I highlighted in Chapter 2 that RStudio inserts opening and closing parentheses, which reduces the chance that missing (or wrong) characters create an error, but there is no guarantee that we insert or delete one by chance. Suppose you try to estimate a mean in combination with the `round()` function. I put a parenthesis at a wrong place, which is why R throws an error. Can you see which parenthesis is causing the problem?

```
#Check parenthesis
```

```
round(mean(c(1, 4, 6))), digits = 2)
```

```
#> Error: <text>:2:24: unexpected ','
```

```
#> 1: #Check parenthesis
```

```
#> 2: round(mean(c(1, 4, 6))),
```

```
#> ^
```

```
# Solution:
```

```
round(mean(c(1, 4, 6)), digits = 2)
```

```
#> [1] 3.67
```

This error is hard to spot, but it illustrates that we need to be careful not to introduce mistakes. Moreover, RStudio gives parentheses that belong together the same color which help us to keep

overview. Go to the RStudio menu (via the <Code> tab) and select *rainbow parentheses* if they are not displayed in color in the Code pane.

Unfortunately, RStudio cannot help us all the time because some R errors messages (and warnings) are cryptic. There are even typical errors messages that are quite obscure for beginners. For example, R tells me all the time that it can't find an object, functions, and data. There are several explanations why R throws such an error. If R cannot find an object, check if the object is listed in the environment. If so, you know for sure that the object exists and that other reasons cause the error. R cannot find an object even in the case of a simple typo.

```
# R cannot find an object due to typos
mean_a <- mean(1, 2, 3)
maen_a
```

```
#> Error in eval(expr, envir, enclos): object 'maen_a' not found
```

```
# Solution:
mean_a <- mean(1, 2, 3)
mean_a
```

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

R tells us that a function (an object) cannot be found if different notations are used. Keep in mind that R is case-sensitive (`r` vs. `R`) and cannot apply a function (or find an object) that does not exist, as the next console illustrates. Of course, the same applies if you forgot to execute the function before using it or if the function itself includes an error and cannot be executed. In all these examples R cannot find the function (or object).

```
# R is case-sensitive
return_fun <- function(x) {
  return(x)
}
```

```
Return_fun(c(1, 2, 3))
```

```
#> Error in Return_fun(c(1, 2, 3)): could not find function "Return_fun"
```

```
# Solution:
return_fun(c(1, 2, 3))
```



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

What is the typical reason why a function from an R package cannot be found? I started to introduce the `dplyr` package in Chapter 2 (Wickham, François, et al. 2022). Suppose we want to use the `select` function from the package. To use anything from an R package, we need to load the package with the `library()` function each time we start (over). Otherwise, R cannot find the function.

```
# Load the package to use a function from a package
library(palmerpenguins)
select(penguins, species)
```

```
#> Error in select(penguins, species): could not find function "select"
```

```
# Solution:
dplyr::select(penguins, species)
```

```
#> # A tibble: 344 x 1
#>   species
#>   <fct>
#> 1 Adelie
#> 2 Adelie
#> 3 Adelie
#> 4 Adelie
#> 5 Adelie
#> 6 Adelie
#> 7 Adelie
#> 8 Adelie
#> 9 Adelie
#> 10 Adelie
#> # i 334 more rows
```

The same applies to objects from a package (e.g., data). The `.packages()` function returns all loaded (attached) packages, but there is no need to keep that in mind. Go to the packages pane and check if a package is installed and loaded. R tells us only that the function cannot be found if we forget to load it first.

```
# Inspect the loaded packages via the Packages pane
loaded_packages <- .packages()
loaded_packages
```

```
#> [1] "palmerpenguins" "stats"          "graphics"      "grDevices"
#> [5] "utils"           "datasets"       "methods"       "base"
```

Ultimately, suppose we try to import data. Never mind about the code, we focus on this step in Chapter 5 in detail, but R tells us that it *cannot open the connection* if the file cannot be found in the current working directory.

```
# Load my mydata
read.csv("mydata.csv")
```

```
#> Warning in file(file, "rt"): cannot open file 'mydata.csv': No such file or
#> directory
```

```
#> Error in file(file, "rt"): cannot open the connection
```

R tells that data, or other files cannot be found because we provided the wrong path to the file. We will learn how to import data later, but keep in mind that R cannot open a file if we search in the wrong place. In Chapter 2, I outlined many possibilities to change the work directory for which RStudio supplies convenient ways. In addition, the `getwd()` function returns the current work directory in case of any doubts.

```
# Do we search for files in the right place
getwd()
#> [1] "C:/Users/Edgar/R/Practice_R/Tutorial/02"
```

```
#> [1] "C:/Users/Edgar/R/Practice_R/Tutorial/02"
```

Loading the right packages and searching in the right place does not imply that we cannot inadvertently introduce mistakes. Suppose you want to apply the `filter` function from the `dplyr` package. You copy and adjust the code from an old script, but R returns an error. Can you see where I made the mistake? I tried to create a subset with `Adelie` penguins only, but `dplyr` seems to know what the problem might be.

```
# Mistakes happen all the time ...
library(dplyr)
filter(penguins, species = "Adelie")
```

```
#> Error in `filter()`:
#> ! We detected a named input.
#> i This usually means that you've used `=` instead of `==`.
#> i Did you mean `species == "Adelie"`?
```

```
# Solution:
library(dplyr)
filter(penguins, species == "Adelie")

#> # A tibble: 152 x 8
#>   species island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
#>   <fct>   <fct>         <dbl>         <dbl>             <int>      <int>
#> 1 Adelie  Torgersen         39.1          18.7             181       3750
#> 2 Adelie  Torgersen         39.5          17.4             186       3800
#> 3 Adelie  Torgersen         40.3           18             195       3250
#> 4 Adelie  Torgersen          NA           NA              NA         NA
#> 5 Adelie  Torgersen         36.7          19.3             193       3450
#> 6 Adelie  Torgersen         39.3          20.6             190       3650
#> 7 Adelie  Torgersen         38.9          17.8             181       3625
#> 8 Adelie  Torgersen         39.2          19.6             195       4675
#> 9 Adelie  Torgersen         34.1          18.1             193       3475
#> 10 Adelie Torgersen         42           20.2             190       4250
#> # i 142 more rows
#> # i 2 more variables: sex <fct>, year <int>
```

Typos, missing functions (objects), and confusion about operators are typical mistakes and some packages return suggestions to fix the problem. Unfortunately, R can also return cryptic error messages, which are often harder to understand.

## 1.2 Cryptic errors

Not all error R messages and warnings are cryptic. Suppose you wanted to estimate a mean of an `income` variable. The variable is not measured numerically which implies that the mean cannot be estimated. Consequently, R warns us about wrong and inconsistent data types.

```
# Warning: argument is not numeric or logical
income <- c("More than 10000", "0 - 999", "2000 - 2999")
mean(income)

#> Warning in mean.default(income): argument is not numeric or logical: returning
#> NA
```

Unfortunately, some errors and warnings seem more like an enigma than useful feedback. Imagine, R tells you that a *non-numeric argument* has been applied to a *binary operator*. The

next console reproduces the error with two example vectors. The last value of the vector `y` is a character (e.g., a missing value indicator: `NA`) and for obvious reasons we cannot multiply `x` with `y` as long as we do clean the latter.

```
# Cryptic error: A non-numeric argument to binary operator
x <- c(3, 5, 3)
y <- c(1, 4, "NA")

result <- x * y
```

```
#> Error in x * y: non-numeric argument to binary operator
```

```
result
```

```
#> Error in eval(expr, envir, enclos): object 'result' not found
```

We will learn how to fix such problem in a systematic manner later, for now just keep in mind that such an error message might be due to messy, not yet prepared data. Or suppose you tried to estimate the sum but R tells you that the code includes an *unexpected numeric constant*. Any idea what that means and how to fix the example code of the next console?

```
#Cryptic error: Unexpected numeric constant
sum(c(3, 2 1))
```

```
#> Error: <text>:2:12: unexpected numeric constant
#> 1: #Cryptic error: Unexpected numeric constant
#> 2: sum(c(3, 2 1
#>      ^
```

```
# Solution:
sum(c(3, 2, 1))
```

```
#> [1] 6
```

R finds an unexpected numeric constant (here 1) because I forgot the last comma inside the `c()` function. The same applies to strings and characters. R tells us that there is an unexpected *string constant*. Can you see where?

```

#Cryptic error: Unexpected string constant
names <- c("Tom", "Diana"___"Pete")
names

#> Error: <text>:2:26: unexpected input
#> 1: #Cryptic error: Unexpected string constant
#> 2: names <- c("Tom", "Diana" _
#>                                     ^

# Solution:
names <- c("Tom", "Diana", "Pete")
names

#> [1] "Tom"    "Diana" "Pete"

```

Or consider *unexpected symbols*. Can you find the problem of the next console. I used to `round` function but something went wrong with the `digits` option.

```

#Cryptic error: Unexpected symbol
x <- mean(c(1:3))
round(x digits = 2)

#> Error: <text>:3:9: unexpected symbol
#> 2: x <- mean(c(1:3))
#> 3: round(x digits
#>                                     ^

# Solution:
x <- mean(c(1:3))
round(x, digits = 2)

#> [1] 2

```

Thus, we introduce a mistake with a function argument because the comma is missing. A similar mistake happens if we forget to provide a necessary argument or provide a wrong one. For example, there is no `numbers` option of the `round` function as the next console (and the help files `?round`) outline.

```
# Cryptic error: Unused argument
x <- mean(c(1:3))
round(x, numbers = 2)

#> Error in round(x, numbers = 2): unused argument (numbers = 2)

# Solution:
x <- mean(c(1:3))
round(x, digits = 2)

#> [1] 2
```

Try to be patient and be kind to yourself should you run into such an error. You will become better to solve errors, but they will happen all the time. Let me give you one more for the road. Consider the error message: *object of type 'closure' is not subsettable*. R returns this error message if we try to slice a variable that does not exist or if we try to slice a function instead of providing a column vector. Can you fix the next console and provide a column vectors instead of slicing the `mean()` function?

```
# Cryptic error: Object of type 'closure' is not subsettable
mean[1:5]

#> Error in mean[1:5]: object of type 'closure' is not subsettable

# Solution:
mean(1:5)

#> [1] 3
```

## 1.3 Further sources of errors

There are further errors and mistakes and this tutorial cannot capture them all. As a minimum, I try to give you a heads-up that it takes time and experience to overcome such problems. For example, consider one more time the small data that we used to slice data in Practice R.

```
# Save data as df
df <- tibble::tribble(
  ~names, ~year, ~sex,
  "Bruno", 1985, "male",
  "Justin", 1994, "male",
  "Miley", 1992, "female",
  "Ariana", 1993, "female"
)
```

Do you still remember how to slice the data? Give it a try with the following examples:

```
# Slice the first column (variable)
df[1]
```

```
#> # A tibble: 4 x 1
#>   names
#>   <chr>
#> 1 Bruno
#> 2 Justin
#> 3 Miley
#> 4 Ariana
```

```
# First row
df[1, ]
```

```
#> # A tibble: 1 x 3
#>   names  year sex
#>   <chr> <dbl> <chr>
#> 1 Bruno  1985 male
```

Suppose that you have not worked with R for a few weeks, would you still be able to remember how slicing works? We all face the same problems when we start to learn something new: you need several attempts before you understand how to get the desired information. Later, after slicing data many times, you will no longer think about how it works. Thus, be patient and kind to yourself, because some concepts need time and experience to internalize them.

Moreover, there are often several approaches to reach the same goal and - depending on your preferred style - some are harder or easier to apply. Say you need the **names** of the stars as a column vector. Can you slice the data or use the **\$** operator to get the **names** variable from the data frame?

```
# Slice or use the $ operator
names <- df$names
names <- df[1]
names
```

```
#> # A tibble: 4 x 1
#>   names
#>   <chr>
#> 1 Bruno
#> 2 Justin
#> 3 Miley
#> 4 Ariana
```

Unfortunately, some mistakes are logical in nature and pure practice cannot help us to overcome such problems. Consider the next console. I created a slice function (`slice_function`) which is supposed to return an element of a vector `x`, but so far it only returns non-sense. Why does it not return the second element of the input data?

```
# A pretty messed up slice_function
data <- c(3, 9, 1, 5, 8, "999", 1)

slice_function <- function(data, x) {
  data[x]
}

slice_function(2)
```

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

```
# Solution:
data <- c(3, 9, 1, 5, 8, 1)

slice_function <- function(data, x) {
  data[x]
}

slice_function(data, x = 2)
```

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



Soon, your code will encompass several steps, try to break it into its separate elements and then examine each step carefully. For example, inspect the vector `x` to see if error was introduced in the first step. Use the `class()` function to examine if the input of a variable is as expected (e.g. numerical). If we are sure about the input, we would go on to the next step and so on. Certainly, the last example is not complicated but the complexity of code (and the tasks) will increase from the chapter to chapter. By breaking down all steps into elements, you may realize where the error occurs and how you can fix it.

## 1.4 Summary

All tutorials of Practice R will end with a short code summary of the corresponding book chapter. The summary only contains the function name from the R help file and code example of the most important functions and packages. In connection with Chapter 2, keep the following functions in mind:

- Install packages from repositories or local files (`install.packages`)
- Loading/attaching and listing of packages (`library`)
- Inspect the help file (`?function`)
- Combine Values into a vector or list (`c`)
- Compare objects (`<=`, `>=`, `==`, `!=`)
- Replicate elements of vectors and lists (`rep`)
- Sequence generation (`seq`)
- Sum of vector elements (`sum`)
- Length of an object (`length`)
- Object classes (`class`)
- Data frames (`data.frame`)
- Build a data frame (`tibble::tibble`, Müller and Wickham 2022b)
- Row-wise tibble creation (`tibble::tribble`)
- The number of rows/columns of an array (`nrow/ncol`)

Base R and many R packages have cheat sheets that summarize the most important features. You can inspect them directly from RStudio (via the `<help>` tab) and I included the link to the base R cheat sheet in the `PracticeR` package.

```
# Cheat sheets summarize the most important features
# The base R cheat sheet
PracticeR::show_link("base_r")
```

## 2 Data Exploration

Welcome to the data exploration tutorial of the [Practice R](#) book (Treischl 2023). Practice R is a text book for the social sciences which provides several tutorials supporting students to learn R. Feel free to inspect the tutorials even if you are not familiar with the book, but keep in mind these tutorials are supposed to complement the Practice R book.

In this tutorial we recapture the most important functions to explore data, but this time you will explore the `palmerpenguins` package and the `penguins` data (Horst, Hill, and Gorman 2022). The latter contains information about three different penguins species (Adélie, Chinstrap, and Gentoo) and [Allison Horst](#) has made some wonderful illustrations of them. Click on the hex sticker to inspect the package website.

```
# Tutorial 03: Explore data
library(dplyr)
library(GGally)
library(summarytools)
library(skimr)
library(palmerpenguins)
library(visdat)
```

The tutorial has the same structure as Chapter 3: We explore categorical variables, continuous variables, and effects. Before we start with variables, it is always a good idea to explore the data in general terms. First, I assigned the data as `df`, which makes it possible for us to recycle a lot of code from Chapter 3. Next, explore which variables does the `penguins` data contain. Use the `glimpse()` or the `str()` function for a first look of the `penguins` data. The `glimpse()` function is loaded via the `dplyr` package, but comes from the `pillar` package (Müller and Wickham 2022a).

```
# Use glimpse, head, or the str function for a first look
df <- penguins
glimpse(df)
```

```
#> Rows: 344
#> Columns: 8
#> $ species      <fct> Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, Adel~
```

```
#> $ island          <fct> Torgersen, Torgersen, Torgersen, Torgersen, Torgerse~
#> $ bill_length_mm  <dbl> 39.1, 39.5, 40.3, NA, 36.7, 39.3, 38.9, 39.2, 34.1, ~
#> $ bill_depth_mm   <dbl> 18.7, 17.4, 18.0, NA, 19.3, 20.6, 17.8, 19.6, 18.1, ~
#> $ flipper_length_mm <int> 181, 186, 195, NA, 193, 190, 181, 195, 193, 190, 186~
#> $ body_mass_g      <int> 3750, 3800, 3250, NA, 3450, 3650, 3625, 4675, 3475, ~
#> $ sex              <fct> male, female, female, NA, female, male, female, male~
#> $ year             <int> 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007~
```

Thus, there are several factor variables such as penguin's `species` or `island`; numerical variables such as `bill` (`bill_length_mm`) and `flipper` length (`flipper_length_mm`); and integers such as the `year` variable. Keep in mind that R packages come with help files that show us how functions work and they provide more information about data. Use the help function (`?penguins`) if you feel insecure about the content of the data.

## 2.1 Categorical variables

We started to explore categorical variables in Chapter 3 and I outlined a few basics about factor variables. Suppose we want to explore the factor variable `island`, which indicates where the penguins live. How can you examine unique group levels?

```
# Inspect the levels() of the penguin's home island
levels(df$island)
```

```
#> [1] "Biscoe"      "Dream"       "Torgersen"
```

We will deepen our knowledge about factor variables in Chapter 5, but keep in mind that we can (re-) create and adjust `factor()` variables. For example, suppose the data looks like a messy character vector for penguin's `sex` that I have created in the next console. In such a case it is good to remember that we can give the variable proper text labels (e.g., `female` for `f`) and examine the results.

```
# Example of a messy factor variable
sex <- c("m", "f", "f")

# Give clearer labels
sex <- factor(sex,
  levels = c("f", "m"),
  labels = c("female", "male"),
)
head(sex)
```

```
#> [1] male    female female
#> Levels: female male
```

Tables help us to explore data and we used the `summarytools` package to make frequency and cross tables (Comtois 2022). Keep in mind that we will learn how to create text documents with tables and graphs in Chapter 8. For the moment it is enough to remember that we can create different sort of tables with the `summarytools` package. For example, create a frequency (`freq`) table to find out on which `island` most of the penguins live.

```
# Create a frequency table
freq(df$island)
```

```
#> Frequencies
#> df$island
#> Type: Factor
#>
#>          Freq  % Valid  % Valid Cum.  % Total  % Total Cum.
#> -----
#>      Biscoe   168    48.84      48.84    48.84    48.84
#>      Dream   124    36.05      84.88    36.05    84.88
#>  Torgersen    52    15.12     100.00    15.12   100.00
#>      <NA>      0      0.00     100.00     0.00   100.00
#>      Total   344   100.00     100.00   100.00   100.00
```

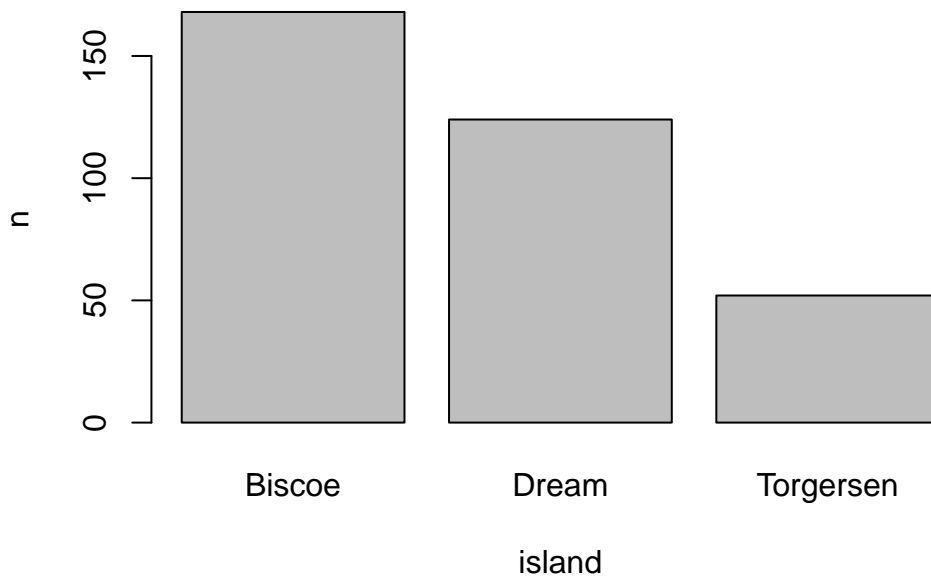
As outlined in the book, we can use the `table()` function to count categorical variables and plot the result as a bar graph. I introduced the latter approach because it is very easy to apply, but our code becomes clearer if we make the necessary steps visible. First, we need to count the levels before we can plot the results. The `count()` function from the `dplyr` package does this job (Wickham, François, et al. 2022). It needs only the data frame and the factor variable.

```
# Count islands with dplyr
count_island <- dplyr::count(df, island)
count_island
```

```
#> # A tibble: 3 x 2
#>   island     n
#>   <fct>   <int>
#> 1 Biscoe   168
#> 2 Dream    124
#> 3 Torgersen  52
```

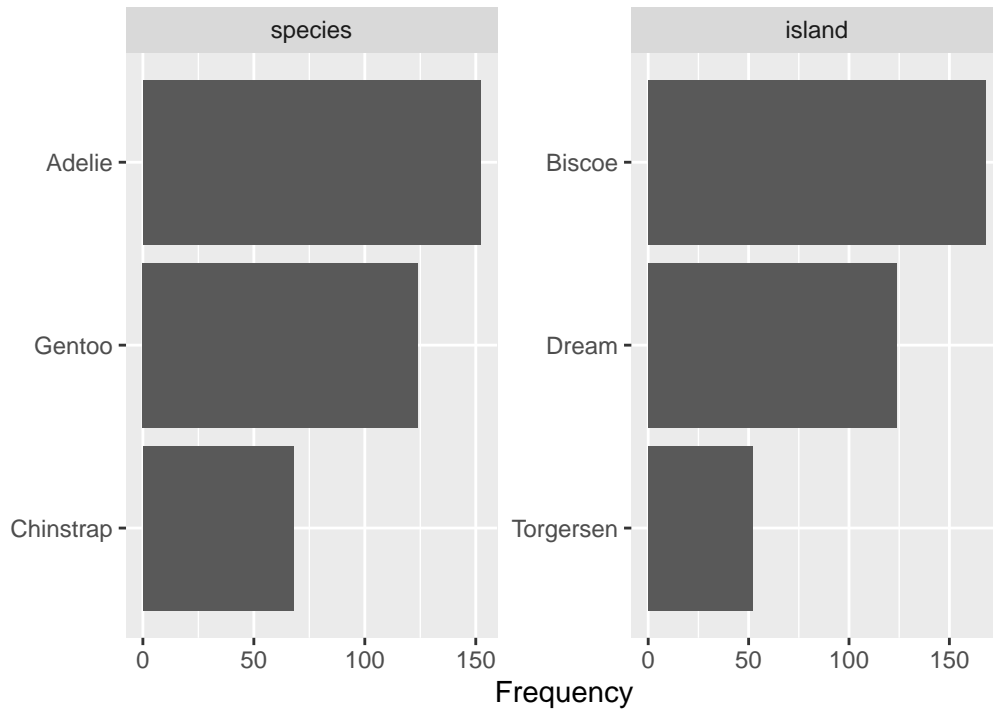
Next, use the assigned results (`count_island`) and insert the variables into the `barplot()` function (with the formula `y ~ x`).

```
# Create a barplot
barplot(n ~ island, data = count_island)
```



In a similar vein, I introduced functions from the `DataExplorer` package that help us to get a quick overview (Cui 2020). For example, use the `plot_bar()` function to depict several or all discrete variables of a data frame.

```
# Inspect all or several plots at once
DataExplorer::plot_bar(df[1:2])
```



## 2.2 Continuous variables

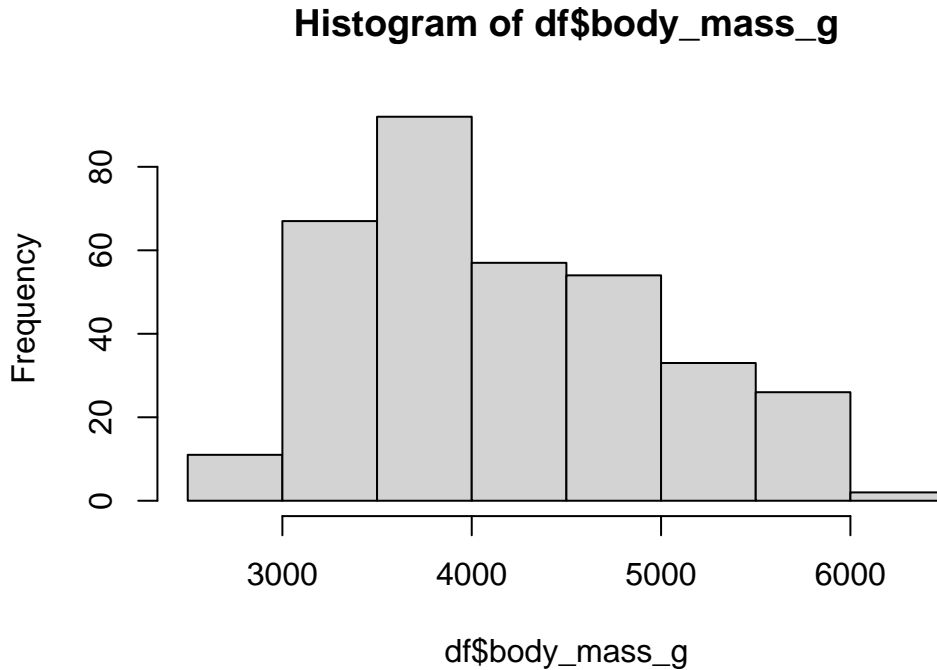
To explore continuous variables, estimate the summary statistics with the `summary()` function. Pick one variable such as penguin's body mass in gram (`body_mass_g`) or use the entire data frame.

```
# Get a summary
summary(df[1:4])
```

```
#>      species      island  bill_length_mm  bill_depth_mm
#> Adelie   :152  Biscoe   :168    Min.    :32.10    Min.    :13.10
#> Chinstrap: 68  Dream    :124   1st Qu.:39.23   1st Qu.:15.60
#> Gentoo   :124  Torgersen: 52   Median :44.45   Median :17.30
#>                                     Mean   :43.92   Mean   :17.15
#>                                     3rd Qu.:48.50   3rd Qu.:18.70
#>                                     Max.   :59.60   Max.   :21.50
#>                                     NA's   :2      NA's    :2
```

The classic approach to visualize the distribution of a continuous variable is a histogram. Use the `hist()` function to display the distribution of the penguins body mass.

```
# Create a histogram  
hist(df$body_mass_g)
```



Keep in mind that we only explored the data for the first time. We did not clean the data nor did we prepare the variables. We have to be explicit about missing values when we want to apply functions such as the `mean`. The function returns `NA`, but only because of a missing values problem. Can you remember how to fix this problem and estimate, for example, the mean?

```
# Calculate the mean, but what about missing values (na.rm)?  
mean(df$body_mass_g, na.rm = TRUE)
```

```
#> [1] 4201.754
```

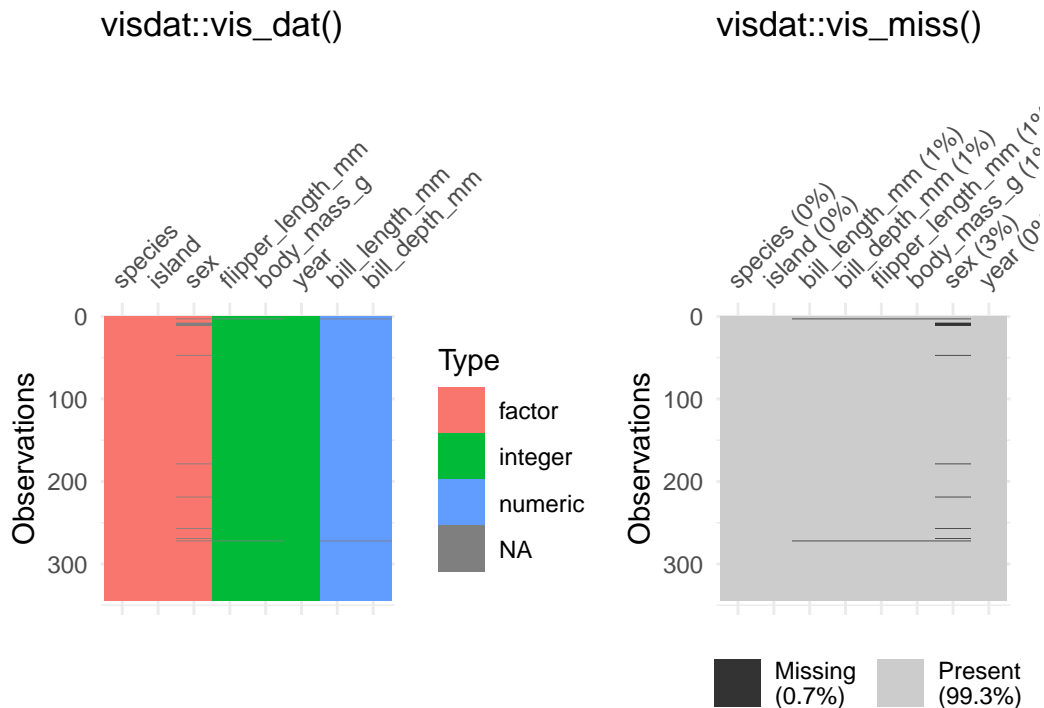
I picked data that was more or less prepared to be explored, because data preparation needs more time and effort especially in the beginning. For this reason we will learn how to manipulate data in Chapter 4; and Chapter 5 tries to prepare you for own journey. For example,

we use packages such as `visdat` and `naniar` to identify missing values, as the next console illustrates with two examples (Tierney et al. 2021). The `vis_dat()` function from the corresponding packages shows us which type of data we have with missing values in gray; while `vis_miss()` visualizes missing values in general terms. Keep in mind that Chapter 3 did not introduce data preparation steps which are often necessary to explore data and effects between variables.

```
library(visdat)

# Left plot: vis_dat()
vis_dat(df)

# Right plot: vis_miss()
vis_miss(df)
```



## 2.3 Explore effects

Let's start with an *effect between two categorical variables*. There are different packages that provides functions to create (cross) tables, but we used the `summarytools` package. It even



provides a simulated data set which we will use the repeat the steps to create a cross table. The package comes with the `tobacco` data, which illustrates that smoking is harmful. As the next console shows, it indicates if a person is a `smoker` and if the person is `diseased`.

```
head(tobacco)[1:8]
```

```
#>  gender age age.gr      BMI smoker cigs.per.day diseased      disease
#> 1      M  75   71 + 29.50225     No           0       No       <NA>
#> 2      F  35  35-50 26.14989     No           0      Yes Neurological
#> 3      F  70  51-70 27.53183     No           0       No       <NA>
#> 4      F  40  35-50 24.05832     No           0       No       <NA>
#> 5      F  75   71 + 22.77486     No           0      Yes    Hearing
#> 6      M  38  35-50 21.46412     No           0       No       <NA>
```

Use the `ctable` function from the `summarytools` package to make a cross table for these variables. See also what happens if you adjust the `prop` option. Insert `c` or `t`. Furthermore, explore what happens if you set the `chisq`, `OR`, or `RR` option to `TRUE`.

```
# Create a cross table with summarytools
summarytools::ctable(
  x = tobacco$smoker,
  y = tobacco$diseased,
  prop = "r",
  chisq = TRUE,
  OR = TRUE
)
```

```
#> Cross-Tabulation, Row Proportions
```

```
#> smoker * diseased
```

```
#> Data Frame: tobacco
```

```
#>
```

```
#>
```

```
#> -----
#>      diseased      Yes      No      Total
#>  smoker
#>    Yes      125 (41.9%)    173 (58.1%)    298 (100.0%)
#>    No       99 (14.1%)    603 (85.9%)    702 (100.0%)
#>    Total     224 (22.4%)    776 (77.6%)   1000 (100.0%)
#> -----
#>
#> -----
```

```

#>  Chi.squared    df    p.value
#>  -----
#>    91.7088      1      0
#>  -----
#>
#>  -----
#> Odds Ratio    Lo - 95%    Hi - 95%
#>  -----
#>    4.40        3.22        6.02
#>  -----

```

The **prop** option lets you determine the proportions: rows (**r**), columns (**c**), total (**t**), or none (**n**). Furthermore, the function even adds the chi-square statistic (**chisq**); the odds ratio (**OR**) or the relative risk (**RR**) if we set them to **TRUE**. Never mind if you are not familiar with the latter, the discussed options only illustrated how the **summarytools** package helps us to explore data and effects.

In the social sciences we are often interested in comparing *numerical outcomes between categorical variables* (groups). For example, one of the penguin's species has a higher body mass and we can examine which penguins **species** differ in terms of their body mass (**body\_mass\_g**). With **base R**, the **aggregate()** function lets us split the data and we are able to estimate the mean for each species.

```

# Aggregate splits the data into subsets and computes summary statistics
aggregate(df$body_mass_g, list(df$species), FUN = mean, na.rm = TRUE)

```

```

#>      Group.1      x
#> 1    Adelie 3700.662
#> 2 Chinstrap 3733.088
#> 3   Gentoo 5076.016

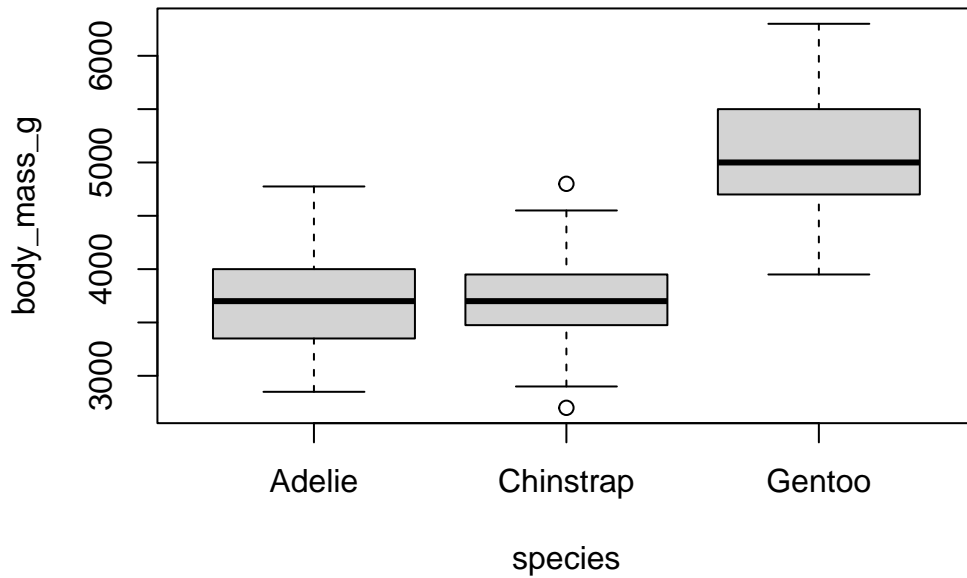
```

To calculate a group-mean looks quite complicated and I did not introduce the latter since we will systematically work on our skills to manipulate data in the next Chapter. Instead, we used a box plot to explore a continuous outcome between groups. As outlined in the book, box plots can be very helpful to compare groups even though they have graphical limitations since they do not display the data. Keep the **boxplot()** function in mind and practice one more time how it works. Inspect how penguin's body mass differs between the species.

```

# Inspect group differences with a box plot
boxplot(body_mass_g ~ species, data = df)

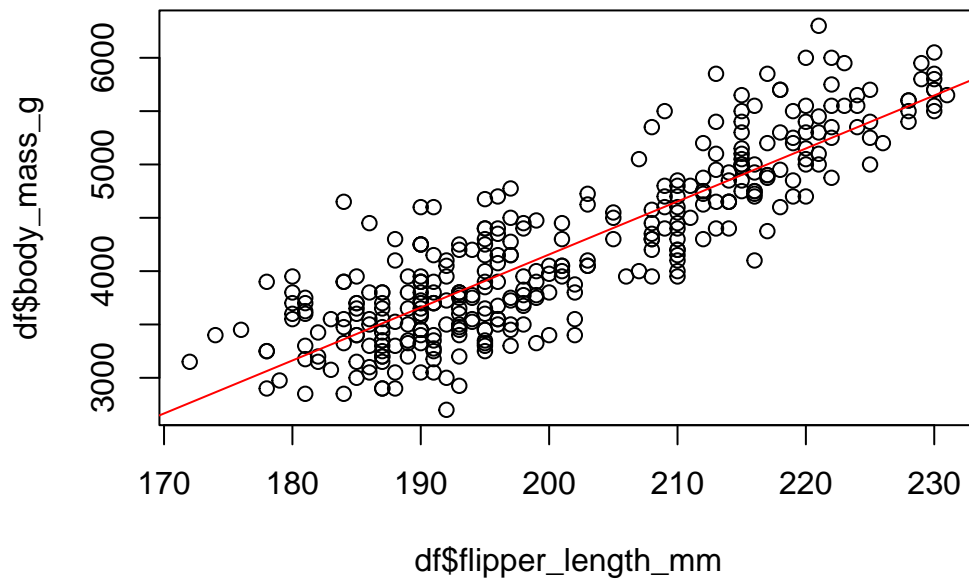
```



If we examine an *effect between two continuous outcomes*, we have to keep in mind that the `plot` function returns a scatter plot and we may insert a regression line with the `abline` and the `lm` function. Do you still know how it works? Create a scatter plot to examine the association between the body mass (`body_mass_g`) and the flipper length (`flipper_length_mm`) of the penguins.

```
# Create a scatter plot
plot(y = df$body_mass_g, x = df$flipper_length_mm)

# And a red regression line
abline(lm(body_mass_g ~ flipper_length_mm, data = df),
       col = "red"
)
```



Furthermore, we learned how to calculate the correlation coefficient. The code of the next console does not work if I apply the `cor()` with the penguins data. Do you have any idea how to fix the problem?

```
# Calculate the correlation between x and y
cor_penguins <- cor(df$body_mass_g, df$flipper_length_mm,
  use = "complete"
)
cor_penguins
```

```
#> [1] 0.8712018
```

By the way, the `cor()` also returns Kendall's or Spearman's if you adjust the `method` option:

```
# estimate a rank-based measure of association
cor(x,
  y = NULL, use = "complete",
  method = c("pearson", "kendall", "spearman")
)
```

Finally, the `effectsize` package helped us with the interpretation of Pearson's  $r$  (and other stats, see Chapter 6). I copied the code from the book; can you adjust it to interpret the effect of the examined variables with the `effectsize` package (Ben-Shachar et al. 2022)?

```
#> [1] 0.8712018

# Use effectsize to interpret R
effectsize::interpret_r(cor_penguins, rules = "cohen1988")

#> [1] "large"
#> (Rules: cohen1988)
```

There are more R packages to explore data than I could possibly outline. For example, consider the `skimr` package (Waring et al. 2022). It skims a data set and returns, for example, a short summary, summary statistics, and missing values. Inspect the vignette and `skim()` the data frame.

```
# Inspect skimr package (and vignette)
# vignette("skimr")
skimr::skim(df)
```

```
--- Data Summary -----

```

	Values
Name	penguins
Number of rows	344
Number of columns	8
-----	
Column type frequency:	
factor	3
numeric	5
-----	
Group variables	None

```
--- Variable type: factor
-----

```

	skim_variable	n_missing	complete_rate	ordered	n_unique
1	species	0	1	FALSE	3
2	island	0	1	FALSE	3
3	sex	11	0.968	FALSE	2

```

top_counts
```

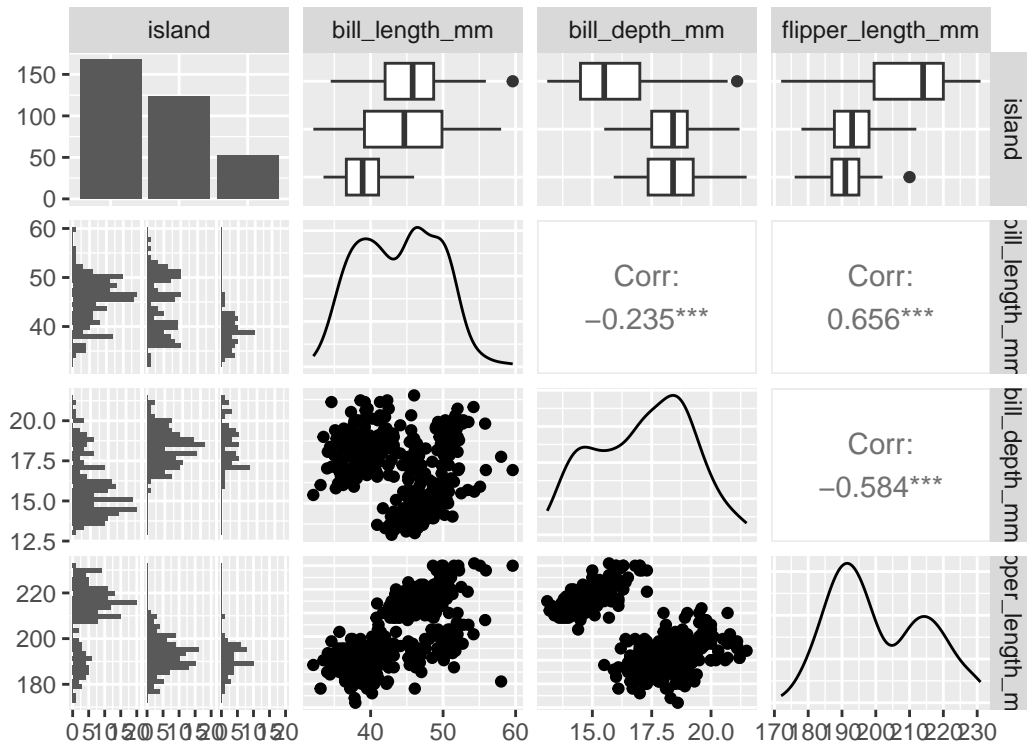
```
1 Ade: 152, Gen: 124, Chi: 68
2 Bis: 168, Dre: 124, Tor: 52
3 mal: 168, fem: 165
```

```
--- Variable type: numeric
```

```
-----
      skim_variable      n_missing complete_rate   mean      sd      p0      p25      p50
1 bill_length_mm          2          0.994   43.9    5.46    32.1    39.2    44.4
2 bill_depth_mm          2          0.994   17.2    1.97    13.1    15.6    17.3
3 flipper_length_mm       2          0.994  201.    14.1    172     190     197
4 body_mass_g             2          0.994 4202.   802.    2700    3550    4050
5 year                    0           1    2008.    0.818  2007    2007    2008
      p75      p100
1   48.5    59.6
2   18.7    21.5
3   213     231
4  4750    6300
5  2009    2009
```

Or examine the `ggpairs()` function from the `GGally` package (Schloerke et al. 2021). It provides many extensions to create graphs (with `ggplot2` see Chapter 7); and it also has functions to explore data and effects. The `ggpairs()` function returns a graph for a pairwise comparison of all variables. Depending on the data type, it returns bar plots, density plot, or the correlation between variables and combines all plots in one graph.

```
# GGally: https://ggobi.github.io/ggally/
GGally::ggpairs(df[2:5])
```



## 2.4 Summary

Data exploration can be exciting since we explore something new. Unfortunately, it can be painful if the data is complex or messy. For this reason we used a simple and clean data, but we will start to manipulate complex(er) data and prepare messy data soon. Keep the following functions from Chapter 3 in mind:

- Get a glimpse of your data (`dplyr::glimpse`); display the structure of an object (`str`); and inspect the first or last parts of an object (`head/tail`)
- Create a factor variable (`factor`); levels attributes (`levels`); object labels (`labels`)
- Simple cross table (`table`)
- Get a summary (`summary`)
- Summary statistics (`min`, `mean`, `max`, `sd`)
- Correlation, variance and covariance (matrices) via (`cor`); or with the `correlation` package (Makowski et al. 2022)

- Graphs: Bar plots (`barplot`); histograms (`hist`), spine plot (`spineplot`), box plot (`boxplot`), scatter plot (`plot`), correlation matrix (`corrplot::corrplot`)
- Packages:
  - The `summarytools` package provides many tables: (e.g., `freq`, `ctable`)
  - The `DataExplorer` to visualize several variable at once: (e.g., `plot_bar`)
  - The `effectsize` package to interpret results: (e.g., `interpret_r`)



## 3 Data manipulation with dplyr

Welcome to tutorial of the [Practice R](#) book (Treischl 2023). Practice R is a text book for the social sciences which provides several tutorials supporting students to learn R. Feel free to inspect the tutorials even if you are not familiar with the book, but keep in mind these tutorials are supposed to complement the Practice R book.

In Chapter 4 we used the `dplyr` package to manipulate data (Wickham, François, et al. 2022). In addition, we will learn how to systemically manipulate categorical variables with the `forcats` package (Wickham 2022) in Chapter 5. Both packages help you to handle many common steps to manipulate data. This tutorial gives a `dplyr` recap and asks you to apply the introduced functions.

As the next output shows, we use the `gss2016` again to select variables, create a filter, generate new variables, and summarize the data. Ask R to provide a description of the data (`?data`) if you are not familiar with the `gss2016` data yet.

```
# The setup of tutorial 4
library(dplyr)
library(PracticeR)
head(gss2016)[1:9]

#> # A tibble: 6 x 9
#>   year   id ballot   age childs sibs degree race  sex
#>   <dbl> <dbl> <labell> <dbl>  <dbl> <lab> <fct>  <fct> <fct>
#> 1  2016     1 1      47     3 2   Bache~ White Male
#> 2  2016     2 2      61     0 3   High ~ White Male
#> 3  2016     3 3      72     2 3   Bache~ White Male
#> 4  2016     4 1      43     4 3   High ~ White Fema~
#> 5  2016     5 3      55     2 2   Gradu~ White Fema~
#> # i 1 more row
```

### 3.1 Select

Especially in case of large and cluttered data, we use `select()` to specify which variables we work with. For example, pick only one variable such as school `degree` from the `gss2016` data.

```
# Select a variable
select(gss2016, degree)
```

```
#> # A tibble: 2,867 x 1
#>   degree
#>   <fct>
#> 1 Bachelor
#> 2 High School
#> 3 Bachelor
#> 4 High School
#> 5 Graduate
#> # i 2,862 more rows
```

Select comes with handy functions and applies the same logic as **base R**. For example, select several columns by providing a start (e.g., `id`) and endpoint (e.g., `degree`).

```
# Select all variables from x to y
select(gss2016, id:degree) |> head()
```

```
#> # A tibble: 6 x 6
#>       id ballot      age childs sibs      degree
#>   <dbl> <labelled> <dbl>  <dbl> <labelled> <fct>
#> 1     1 1         47      3 2      Bachelor
#> 2     2 2         61      0 3      High School
#> 3     3 3         72      2 3      Bachelor
#> 4     4 1         43      4 3      High School
#> 5     5 3         55      2 2      Graduate
#> # i 1 more row
```

Maybe we need all columns except the variables shown in the last output. Ask for the opposite and insert parentheses and a minus signs to turn the selection around.

```
# Turn around the selection
select(gss2016, -(id:degree)) |> head()
```

```
#> # A tibble: 6 x 27
#>   year race sex    region    income16 relig marital padeg
#>   <dbl> <fct> <fct>  <fct>      <fct>    <fct> <fct>  <fct>
#> 1  2016 White Male  New Engla~ $170000~ None  Married Grad~
#> 2  2016 White Male  New Engla~ $50000 ~ None  Never ~ Lt H~
```

```
#> 3 2016 White Male New Engla~ $75000 ~ Cath~ Married High~
#> 4 2016 White Female New Engla~ $170000~ Cath~ Married <NA>
#> 5 2016 White Female New Engla~ $170000~ None Married Bach~
#> # i 1 more row
#> # i 19 more variables: madeg <fct>, partyid <fct>,
#> # polviews <fct>, happy <fct>, partners <fct>,
#> # grass <fct>, zodiac <fct>, pres12 <labelled>,
#> # wtssall <dbl>, income_rc <fct>, agegrp <fct>,
#> # ageq <fct>, siblings <fct>, kids <fct>, religion <fct>,
#> # bigregion <fct>, partners_rc <fct>, obama <dbl>, ...
```

The `gss2016` data does not contain variables with a running number nor other systematic variable names. However, `dplyr` helps to select such variables without much effort. Consider toy data with several measurements and running numbers to illustrate how we can select such variables efficiently.

```
# A new df to illustrate
df <- tibble(
  measurement_1 = 1:3,
  x1 = 1:3,
  measurement_2 = 1:3,
  x2 = 1:3,
  x3 = 1:3,
  other_variables = 1
)
```

Suppose we measured a variables several times and all start with an identical name (e.g., `measurement_`). Select all variables which start (or end) with a certain string. Thus, insert the `starts_with()` function and select all `measurement` variables.

```
# Select variables that start with a string
select(df, starts_with("measurement"))
```

```
#> # A tibble: 3 x 2
#>   measurement_1 measurement_2
#>   <int>         <int>
#> 1         1         1
#> 2         2         2
#> 3         3         3
```

Or pick variables with the running number. The `num_range` functions needs the name (`x`) and the running number.

```
# Select based on a running number
select(df, num_range("x", 1:3))
```

```
#> # A tibble: 3 x 3
#>       x1     x2     x3
#>   <int> <int> <int>
#> 1     1     1     1
#> 2     2     2     2
#> 3     3     3     3
```

The package offers more helpers to select variables than I can possibly outline. For example, `contains()` checks if a variable includes a certain word; `matches()` let us specify search patterns (regular expression, see Chapter 10); and we can also include other functions to select variables. For example, the `is.numeric` function checks if an input is numeric and we can combine it with `where()` to select columns only *where* the content is numeric.

```
# Insert a function to select variables
gss2016 |> select(where(is.numeric))
```

```
#> # A tibble: 2,867 x 10
#>   year   id ballot  age childs sibs  pres12 wtssall obama
#>   <dbl> <dbl> <labe> <dbl>  <dbl> <lab> <labe>   <dbl> <dbl>
#> 1  2016     1 1      47     3 2     3     0.957     0
#> 2  2016     2 2      61     0 3     1     0.478     1
#> 3  2016     3 3      72     2 3     2     0.957     0
#> 4  2016     4 1      43     4 3     2     1.91     0
#> 5  2016     5 3      55     2 2     1     1.44     1
#> # i 2,862 more rows
#> # i 1 more variable: income <dbl>
```

Next, we filter data but since all R outputs are large due to the `gss2016` data, let us first create a smaller subset to reduce the size of the output and the length of this document.

```
# Select a smaller subset for the rest of this tutorial
gss2016 <- select(PracticeR::gss2016, year:sex, income)
```

## 3.2 Filter

Use `filter()` to subset the data. The `dplyr` filters the data and returns a new data frame depending on the specified conditions. Use one or several relational or logical operators to select observations. For example, suppose you want to analyze persons who have a bachelor's degree only.

```
# Apply a filter
gss2016 |>
  filter(degree == "Bachelor") |>
  head()

#> # A tibble: 6 x 10
#>   year   id ballot   age childs sibs degree race  sex
#>   <dbl> <dbl> <labell> <dbl>   <dbl> <lab> <fct>  <fct> <fct>
#> 1  2016     1 1      47     3 2   Bache~ White Male
#> 2  2016     3 3      72     2 3   Bache~ White Male
#> 3  2016    37 2      59     2 2   Bache~ White Male
#> 4  2016    38 1      43     2 6   Bache~ White Fema~
#> 5  2016    39 3      58     0 1   Bache~ White Fema~
#> # i 1 more row
#> # i 1 more variable: income <dbl>
```

Can you adjust the code so that two conditions have to be fulfilled simultaneously. For example, keep only observations from adults (18 years and older) with a bachelor's degree.

```
# Combine several conditions
gss2016 |>
  filter(degree == "Bachelor" & age > 17) |>
  head()

#> # A tibble: 6 x 10
#>   year   id ballot   age childs sibs degree race  sex
#>   <dbl> <dbl> <labell> <dbl>   <dbl> <lab> <fct>  <fct> <fct>
#> 1  2016     1 1      47     3 2   Bache~ White Male
#> 2  2016     3 3      72     2 3   Bache~ White Male
#> 3  2016    37 2      59     2 2   Bache~ White Male
#> 4  2016    38 1      43     2 6   Bache~ White Fema~
#> 5  2016    39 3      58     0 1   Bache~ White Fema~
#> # i 1 more row
#> # i 1 more variable: income <dbl>
```

As outlined, keep your **base R** skills in mind when selecting or filtering data. For example, keep all degrees but exclude persons who have a **Bachelor**.

```
# All degrees, but not! Bachelors
gss2016 |>
  filter(degree != "Bachelor") |>
  head()

#> # A tibble: 6 x 10
#>   year   id ballot   age childs sibs degree race sex
#>   <dbl> <dbl> <labell> <dbl>  <dbl> <lab> <fct>  <fct> <fct>
#> 1  2016     2 2      61     0 3    High ~ White Male
#> 2  2016     4 1      43     4 3    High ~ White Fema~
#> 3  2016     5 3      55     2 2    Gradu~ White Fema~
#> 4  2016     6 2      53     2 2    Junio~ White Fema~
#> 5  2016     7 1      50     2 2    High ~ White Male
#> # i 1 more row
#> # i 1 more variable: income <dbl>
```

Use the `operators()` function from the `PracticeR` package when you have trouble to remember how **logical** and **relational** operators are implemented. The function inserts and runs examples via the console.

```
PracticeR::operators("logical")
# Logical Operators
# > x <- TRUE
# > y <- FALSE
# > #Elementwise logical AND
# > x & y == TRUE
# [1] FALSE
# > #Elementwise logical OR
# > x | y == TRUE
# [1] TRUE
# > #Elementwise OR
# > xor(x, y)
# [1] TRUE
# > #Logical NOT
# > !x
# [1] FALSE
# > #In operator
# > 1:3 %in% rep(1:2)
# [1] TRUE TRUE FALSE
```

### 3.3 Mutate

In Chapter 4 I outline several ways to generate new variables based on observed ones. For example, raw data often contains a person's year of birth but not their age. With `mutate()` we can extend the data frame and estimate such a variable. Unfortunately, the `gss2016` has an `age` variable, but the variable does only reveal their age when the survey was conducted. To recap how `mutate()` works, recreate their birth year and a recent age variable, say for the year 2023.

```
# Create birth_year and a recent (year: 2023) age variable
gss2016 |>
  select(id, year, age) |>
  mutate(
    birth_year = year - age,
    age_2023 = 2023 - birth_year
  ) |>
  head()
```

```
#> # A tibble: 6 x 5
#>       id  year  age birth_year age_2023
#>   <dbl> <dbl> <dbl>      <dbl>      <dbl>
#> 1     1   2016   47       1969        54
#> 2     2   2016   61       1955        68
#> 3     3   2016   72       1944        79
#> 4     4   2016   43       1973        50
#> 5     5   2016   55       1961        62
#> # i 1 more row
```

Keep in mind that you can use relational and logical operators, as well other functions (e.g., `log`, `rankings`, etc.) to generate new variables. For example, generate a logical variable that indicates whether a person was an adult (older than 17) in the year 2016. The `if_else()` function helps you with this job.

```
# In theory: if_else(condition, true, false, missing = NULL)
gss2016 |>
  select(id, year, age) |>
  mutate(adult = if_else(age > 17, TRUE, FALSE)) |>
  head()
```

```
#> # A tibble: 6 x 4
#>       id  year  age adult
#>   <dbl> <dbl> <dbl> <lgl>
```

```
#>   <dbl> <dbl> <dbl> <lgl>
#> 1     1   2016    47 TRUE
#> 2     2   2016    61 TRUE
#> 3     3   2016    72 TRUE
#> 4     4   2016    43 TRUE
#> 5     5   2016    55 TRUE
#> # i 1 more row
```

In terms of generating new variables, also keep the `case_when()` function in mind, which provides a very flexible approach. Suppose we need to identify parents with a academic background. Parents educational background has many levels or attributes in the `gss2016` data, which makes a first attempt harder to apply (and we learn more about factor variables in Chapter 5). For this reason I created a smaller toy data set and I started to prepare the code. Can you complete it? The variable `academic_parents` is supposed to identify persons with a high educational background (`education`) with one or more kids. All other conditions are set to `FALSE`.

```
# Data to illustrate
df <- data.frame(
  kids = c(0, 1, 3, 0, NA),
  educ = c("high", "low", "high", "low", NA)
)

# In theory: case_when(condition ~ value)
df |>
  mutate(academic_parents = case_when(
    kids >= 1 & educ == "high" ~ "TRUE",
    TRUE ~ "FALSE"
  ))

#>   kids educ academic_parents
#> 1     0 high             FALSE
#> 2     1 low              FALSE
#> 3     3 high              TRUE
#> 4     0 low              FALSE
#> 5    NA <NA>             FALSE
```

### 3.4 Summarize

The `summarize()` function collapses several columns into a single row. By the way, the `dplyr` package understands both, British (e.g., `summarise`) and American English (e.g. `summarize`)



and it's up to you to decide which one you prefer.

Let's calculate the mean age of the survey participants. As outlined in Practice R, the variable has missing values which is why we need to drop them first. In Chapter 5 we will focus on this problem and we learn more about the consequences of such decisions. I already excluded missing values, can you `summarize()` the age?

```
# Exclude missing values but consider the consequences (see Chapter 5)
gss2016 <- gss2016 |>
  tidyr::drop_na(age, sex)
```

```
# Summarize age
gss2016 |> summarize(mean_age = mean(age))
```

```
#> # A tibble: 1 x 1
#>   mean_age
#>   <dbl>
#> 1     49.2
```

The `dplyr` package comes with several help functions to summarize data. For example, to count the number of observation per group (e.g., for `sex`), split the data by groups (`group_by`) and apply the `n()` function.

```
# County by (sex)
gss2016 |>
  group_by(sex) %>%
  summarize(count = n())
```

```
#> # A tibble: 2 x 2
#>   sex      count
#>   <fct>   <int>
#> 1 Male    1272
#> 2 Female  1585
```

Moreover, compare the groups by calculating the `median` age instead of the mean; add the standard deviation (`sd`); and count the number of distinct values (`n_distinct`) of the `degree` variable.

```
# Dplyr has more summary functions
gss2016 |>
  group_by(sex) |>
  summarise(
    median_age = median(age),
    sd_age = sd(age),
    distinct_degree = n_distinct(degree)
  )

#> # A tibble: 2 x 4
#>   sex    median_age sd_age distinct_degree
#>   <fct>      <dbl>  <dbl>          <int>
#> 1 Male         48    17.4              6
#> 2 Female       50    17.9              6
```

In the last examples we grouped the data and then collapsed it. The counterpart to `group` is `ungroup()` which we may add as a last step to disperse the data again. For example, we can estimate how old men or women are on average and add this information to the original data frame. Use `mutate()` instead of `summarise()` to see the logic behind `ungroup`.

```
# Mutate ungroups the data again
gss2016 |>
  select(id, sex, age) |>
  group_by(sex) |>
  mutate(count = round(mean(age), 2))

#> # A tibble: 2,857 x 4
#> # Groups:   sex [2]
#>    id sex    age count
#>   <dbl> <fct>  <dbl> <dbl>
#> 1     1 Male    47  48.3
#> 2     2 Male    61  48.3
#> 3     3 Male    72  48.3
#> 4     4 Female  43  49.8
#> 5     5 Female  55  49.8
#> # i 2,852 more rows
```

### 3.5 Arrange

Last but not least, keep the `arrange()` function in mind. It is easy to apply and I don't believe there is much to practice. However, it gives us the chance to repeat how `transmute()`

and the `between()` function works.

Consider the steps to build a restricted age sample to examine adults only. Use `mutate` to create a logical variable (`age_filter`) that indicates if a person is between 18 and 65. Furthermore, explore the difference between `mutate()` and `transmute()` if you can't remember it.

```
# Create a restricted analysis sample
# between: x >= left & x <= right
gss2016 |>
  transmute(age,
    age_filter = between(age, 18, 65)
  )
```

```
#> # A tibble: 2,857 x 2
#>   age age_filter
#>   <dbl> <lgl>
#> 1    47 TRUE
#> 2    61 TRUE
#> 3    72 FALSE
#> 4    43 TRUE
#> 5    55 TRUE
#> # i 2,852 more rows
```

Next, we need a `filter()` to restrict the sample, but how can we know that code worked? We can inspect the entire data frame with `View`, but we can also use `arrange()` to inspect if the filter was correctly applied. Sort in ascending and descending (`desc`) order.

```
# Filter and arrange the data
gss2016 |>
  transmute(age,
    age_filter = between(age, 18, 65)
  ) |>
  filter(age_filter == "TRUE") |>
  arrange(desc(age)) |>
  head()
```

```
#> # A tibble: 6 x 2
#>   age age_filter
#>   <dbl> <lgl>
#> 1    65 TRUE
#> 2    65 TRUE
#> 3    65 TRUE
```

```
#> 4    65 TRUE
#> 5    65 TRUE
#> # i 1 more row
```

The `dplyr` package offers many functions to manipulate data and this tutorial only summarizes the main functions. Consider the cheat sheet and the package website for more information.

```
# The dplyr website
PracticeR::show_link("dplyr", browse = FALSE)
#> [1] "https://dplyr.tidyverse.org/"
```

Keep in mind that data preparation steps may appear simple, but only as long as we are not supposed to prepare data on our own. In the latter case we will often need several attempts to come up with a solution that works. Thus, be patient with yourself when your first attempts will not work. Most of the time we all need more than one shot to come up with a workable solution. In addition, we will use the package one more time to combine data in Chapter 5 and other `dplyr` functions will appear through the Practice R book. Thus, there will be plenty of opportunities to apply and develop your `dplyr` skills.

There are often different approaches that lead to the same result. As the artwork by Jake Clark illustrates and the Practice R info box about *data manipulation approaches* underlines, the `subset()` function from base R does essentially the same as `dplyr::filter`. Base R provides the most stable solution, while `dplyr` is more verbose and often easier to learn. Don't perceive them as two different dialects that forces us to stick to one approach. Instead, embrace them both because you will come across different approaches if you use Google to solve a problem. Fortunately, many roads lead to Rome.

## 3.6 Summary

Keep the main `dplyr` functions in mind, among them:

- Keep rows that match a condition (`filter`)
- Order rows using column values (`arrange`)
- Keep or drop columns using their names and types (`select`)
- Create, modify, and delete columns (`mutate`, `transmute`)
- Summarize each group down to one row (`summarize`)
- Change column order (`relocate`)
- Vectorized if-else (`if_else`)
- A general vectorized if-else (`case_when`)
- Apply a function (or functions) across multiple columns (`across`)
- Select all variables or the last variable (e.g., `everything`)

And the following **base** functions:

- The names of an object (**names**)
- Sub-setting vectors, matrices and data frames (**subset**)
- Apply a function over a list or vector (**lapply**, **sapply**)
- Read R code from a file, a connection or expressions (**source**)

## 4 Prepare categorical variables

Welcome to the data preparation tutorial of the [Practice R](#) book (Treischl 2023). Practice R is a text book for the social sciences which provides several tutorials supporting students to learn R. Feel free to inspect the tutorials even if you are not familiar with the book, but keep in mind these tutorials are supposed to complement the Practice R book.

Chapter 5 was dedicated to support you to prepare data. We learned how to import, clean, and combine data. In addition, we got in touch with the `naniar` package which offers many functions to inspect missing values (Tierney et al. 2021); and I introduced the `forcats` package to prepare categorical variables for the analysis (Wickham 2022).

What preparation steps you need to apply is dependent on the data at hand and the analysis intended, which is why Chapter 5 provided a detailed overview of what happens under the hood when we import data. Keep in mind that RStudio has many cool features (e.g., data preview) to import data and packages such as `readr` helps us with this task:

```
# Import a csv file
library(readr)
my_data <- read_csv("path_to_the_file/data.csv")
```

Since I have no idea what your data looks, this tutorial will not focus on how to import and clean data. Instead, let's focus systematically on the `forcats` package. Suppose we started to analyze whether participant's income has an effect on their happiness, but we need to control for participant's educational background, religious beliefs, and if other categorical variables affect our estimation results. I already introduced several functions of the `forcats` package, but this tutorial systematically focuses on the main tasks of the package, as is outlined in its cheat sheet (click on the hex sticker to download the cheat sheet from the website).

Thus, we repeat and systematize our `forcats` skills: (1) We inspect factors; (2) change the order of levels; (3) change the value of levels; (4) and we add or drop levels. For this purpose, we use the `gss2016` data and I assigned a smaller subset as `df` with several categorical variables.

```
# Packages for Tutorial Nr. 5
library(naniar)
library(dplyr)
library(tidyr)
library(forcats)
```

```
library(PracticeR)

# The gss2016 data
df <- PracticeR::gss2016 |>
  select(id, degree, relig, income16, happy, marital)
head(df)

#> # A tibble: 6 x 6
#>   id degree      relig income16      happy      marital
#>   <dbl> <fct>      <fct>   <fct>      <fct>      <fct>
#> 1     1 Bachelor    None   $170000 or over Pretty Happy Married
#> 2     2 High School  None   $50000 to 59999 Pretty Happy Never Married
#> 3     3 Bachelor    Catholic $75000 to $89999 Very Happy Married
#> 4     4 High School  Catholic $170000 or over Pretty Happy Married
#> 5     5 Graduate    None   $170000 or over Very Happy Married
#> 6     6 Junior College None   $60000 to 74999 Very Happy Married
```

Finally, we transform and combine data once more given that such steps are often necessary before we can start to prepare data. However, this time we examine how built-in data sets from the `tidyr` and the `dplyr` package make the first move a bit easier.

## 4.1 Inspect factors

Suppose we need to prepare several categorical variables, such as religion (`relig`) or marital status (`marital`), for an analysis. To inspect factors, count them with `fct_count()`.

```
# Count factor variable
fct_count(df$marital)

#> # A tibble: 6 x 2
#>   f           n
#>   <fct>     <int>
#> 1 Married    1212
#> 2 Widowed     251
#> 3 Divorced     495
#> 4 Separated    102
#> 5 Never Married 806
#> 6 <NA>         1
```

Or examine the unique levels of a variable with the `fct_unique()` function:

```
# How many unique levels do we observe
fct_unique(df$marital)

#> [1] Married      Widowed      Divorced      Separated      Never Married
#> [6] <NA>
#> Levels: Married Widowed Divorced Separated Never Married
```

## 4.2 Change the order of levels

The variable religion (`relig`) has 13 different levels. Let's assume we want to control for the largest religious groups only in the analysis. Use the `fct_infreq()` function to identify how often each level appears.

```
# fct_infreq: Reorder factor levels by frequency
f <- fct_infreq(df$relig)
fct_count(f)
```

```
#> # A tibble: 14 x 2
#>   f              n
#>   <fct>         <int>
#> 1 Protestant    1371
#> 2 Catholic      649
#> 3 None          619
#> 4 Jewish        51
#> 5 Other         44
#> 6 Christian     40
#> 7 Buddhism      21
#> 8 Moslem/Islam   19
#> 9 Hinduism      13
#> 10 Orthodox-Christian 7
#> 11 Inter-Nondenominational 7
#> 12 Other Eastern    4
#> 13 Native American  4
#> 14 <NA>            18
```

The `fct_infreq()` sorts them in order of their frequency, but note we can also order the levels by first appearance (`fct_inorder`) or in a numeric order (`fct_inseq`). As the next console illustrates, R sorts levels alphabetically, which is clearly not always a desirable default behavior. Use the `fct_inorder()` to sort them by appearance.



```
# Example factor
f <- factor(c("b", "a", "c"))
levels(f)
```

```
#> [1] "a" "b" "c"
```

```
# fct_inorder: Reorder factor levels by first appearance
fct_inorder(f)
```

```
#> [1] b a c
#> Levels: b a c
```

Can you still remember how to manually relevel? Use the `fct_relevel()` and sort the level `Never Married` at the second position. You can provide a vector with level names or use the `after` option to change the position of the level.

```
# Relevel manually
# f <- fct_relevel(df$marital, c("Married", "Never Married"))
f <- fct_relevel(df$marital, "Never Married", after = 1)
fct_count(f)
```

```
#> # A tibble: 6 x 2
#>   f           n
#>   <fct>     <int>
#> 1 Married    1212
#> 2 Never Married 806
#> 3 Widowed     251
#> 4 Divorced    495
#> 5 Separated   102
#> 6 <NA>         1
```

Sometimes we need to turn the order around. Reverse the order of the levels with `fct_rev()`.

```
# fct_rev: Reverse order of factor levels
f <- fct_rev(df$marital)
fct_count(f)
```

```

#> # A tibble: 6 x 2
#>   f           n
#>   <fct>       <int>
#> 1 Never Married   806
#> 2 Separated      102
#> 3 Divorced       495
#> 4 Widowed        251
#> 5 Married      1212
#> 6 <NA>           1

```

### 4.3 Change the value of levels

The `relig` variable has many levels and even has a category named `other`, since there are so many religious groups. The same logic applies the `fct_other()` function which collapses all levels but the one we actually need. Create a variable that includes the five largest groups only. Use the `fct_other()` function and tell R which variables to `keep`.

```

# Create a variable with the five largest, rest are others
df$relig5 <- fct_other(df$relig,
  keep = c("Protestant", "Catholic", "None", "Jewish")
)

```

```

fct_count(df$relig5)

```

```

#> # A tibble: 6 x 2
#>   f           n
#>   <fct>       <int>
#> 1 Protestant  1371
#> 2 Catholic    649
#> 3 Jewish      51
#> 4 None        619
#> 5 Other       159
#> 6 <NA>        18

```

The `fct_other()` function includes in the code the used levels. If we are unconcerned about this information, you can use one of the `fct_lump()` functions. The function picks between different methods to lump together factor levels. Nowadays the authors recommend to use one of the specific `fct_lump_*` functions (`fct_lump_min`, `fct_lump_prop`, `fct_lump_lowfreq`) as outlined in the help file. In our case, use the `fct_lump_n()` function to lump together the most frequent (`n`) ones.

```
# Lump uncommon factor together levels into "other"
f <- fct_lump_n(df$relig, n = 5, other_level = "Further groups")
fct_count(f)
```

```
#> # A tibble: 7 x 2
#>   f           n
#>   <fct>       <int>
#> 1 Protestant 1371
#> 2 Catholic   649
#> 3 Jewish      51
#> 4 None       619
#> 5 Other       44
#> 6 Further groups 115
#> 7 <NA>        18
```

Next, we are going to prepare the educational background. The variable `degree` includes several levels, as the console shows.

```
# Count degrees
fct_count(df$degree)
```

```
#> # A tibble: 6 x 2
#>   f           n
#>   <fct>       <int>
#> 1 Lt High School 328
#> 2 High School   1461
#> 3 Junior College 216
#> 4 Bachelor      536
#> 5 Graduate      318
#> 6 <NA>           8
```

We already used the `fct_recode()` function to change factor levels by hand. The lowest category of `degree` is called *less than high school* but the text label is confusing. Recode the variable, insert the new label in back ticks to replace the old label (Lt High School).

```
# fct_recode: Change factor levels by hand
f <- fct_recode(df$degree, `Less than high school` = "Lt High School")
fct_count(f)
```

```

#> # A tibble: 6 x 2
#>   f           n
#>   <fct>     <int>
#> 1 Less than high school 328
#> 2 High School          1461
#> 3 Junior College        216
#> 4 Bachelor             536
#> 5 Graduate             318
#> 6 <NA>                 8

```

Suppose we want to control only if participants have a high educational background. Use the `fct_collapse()` function to create a binary dummy variable. The variable should indicate if a person's educational background is low (Lt High School; High School, and Junior College) or high (Bachelor and Graduate).

```

# Collapse factor variable
df$edu_dummy <- fct_collapse(df$degree,
  low = c(
    "Lt High School",
    "High School",
    "Junior College"
  ),
  high = c("Bachelor", "Graduate")
)

fct_count(df$edu_dummy)

```

```

#> # A tibble: 3 x 2
#>   f           n
#>   <fct> <int>
#> 1 low    2005
#> 2 high    854
#> 3 <NA>      8

```

## 4.4 Add or drop levels

As always, the `forcats` package has more to offer than I can outline. For example, suppose we observed the following `religion` variable.

```
# New religion variable
religion <- factor(
  x = c("Protestant", "Jewish", NA, NA),
  levels = c("Protestant", "Jewish", "Catholic")
)
```

```
religion
```

```
#> [1] Protestant Jewish      <NA>      <NA>
#> Levels: Protestant Jewish Catholic
```

Did you notice that the variable has a level for `Catholic` even though we do not observe it. The `fct_expand()` can be used to expand levels, while the `fct_drop()` function helps us to get rid of unused levels.

```
# Drop unused levels
fct_drop(religion)
```

```
#> [1] Protestant Jewish      <NA>      <NA>
#> Levels: Protestant Jewish
```

Furthermore, I included missing values on purpose and the latter may have an impact on our analysis. We can make them explicit and include them as a level with `fct_na_value_to_level()`.

```
# Make NAs explicit
fct_na_value_to_level(religion, level = "Missing")
```

```
#> [1] Protestant Jewish      Missing    Missing
#> Levels: Protestant Jewish Catholic Missing
```

## 4.5 Further steps

Chapter 5 discussed many steps to prepare data, but of course this was not an all-encompassing list. I introduced data formats and we learned how to combine data given that many official data sets are split into several files. Unfortunately, transforming and combining data can be tricky and we may introduce mistakes if we neglected to prepare and clean the data properly. Thus, it is up to you to assure that the data can be transformed (combined) and further cleaning steps might be necessary.

Instead of re-running these steps with the `gss2016` data, let us explore how the `tidyr` package can help with the task (Wickham and Girlich 2022). As other packages, `tidyr` has a cheat sheet and provides a tiny data set that lets us repeat how the functions work. For example, the `table4a` data is a wide data set with observations of three countries and two years.

```
# Example wide table
head(table4a)

#> # A tibble: 3 x 3
#>   country    `1999` `2000`
#>   <chr>      <dbl> <dbl>
#> 1 Afghanistan    745   2666
#> 2 Brazil        37737  80488
#> 3 China         212258 213766
```

Use the `pivot_longer()` function to transform the data. The long data should have a new variable for the year (via `names_to`) and you can give the values (`values_to`) to a variable named `cases`.

```
# Make em longer
pivot_longer(table4a,
  cols = 2:3, names_to = "year",
  values_to = "cases"
)
```

```
#> # A tibble: 6 x 3
#>   country    year    cases
#>   <chr>      <chr> <dbl>
#> 1 Afghanistan 1999     745
#> 2 Afghanistan 2000    2666
#> 3 Brazil      1999   37737
#> 4 Brazil      2000   80488
#> 5 China       1999  212258
#> 6 China       2000  213766
```

Or consider the `table2` data, the variable `type` has two outcome types (`cases` and `population`) which underline why we should transform the data into the wide format.

```
# Example long table
head(table2)
```

```
#> # A tibble: 6 x 4
#>   country      year type      count
#>   <chr>      <dbl> <chr>      <dbl>
#> 1 Afghanistan 1999 cases        745
#> 2 Afghanistan 1999 population 19987071
#> 3 Afghanistan 2000 cases        2666
#> 4 Afghanistan 2000 population 20595360
#> 5 Brazil      1999 cases        37737
#> 6 Brazil      1999 population 172006362
```

Keep in mind that we need to provide *where* the names (`names_from`) and the values (`values_from`) are coming from to transform the data.

```
# Make it wider
pivot_wider(table2,
  names_from = type,
  values_from = count
)
```

```
#> # A tibble: 6 x 4
#>   country      year cases population
#>   <chr>      <dbl> <dbl>      <dbl>
#> 1 Afghanistan 1999     745    19987071
#> 2 Afghanistan 2000    2666    20595360
#> 3 Brazil      1999   37737    172006362
#> 4 Brazil      2000   80488    174504898
#> 5 China       1999  212258   1272915272
#> 6 China       2000  213766   1280428583
```

I introduced these data sets because `tidyr` offers such simple examples in the cheat sheet that demonstrates how we can transform data. In addition, the `copycat` package has the code snippets from the `tidyverse` cheat sheets included. As the animation shows, it only takes a few seconds to insert these examples via the add-in. Start with such a simple example if you do not transform and combine data on a regular basis. After you made sure that the code works, adjust it for your purpose, but be careful how the data is transformed.

The same applies if you need to combine data. The `dplyr` also offers a small data set to practice mutating joins (Wickham, François, et al. 2022). The `band_members` data includes `names` from members of two different music bands; and the `band_instruments` data includes their instruments.

```
# Small data to recapture the join_* functions
band_members
```

```
#> # A tibble: 3 x 2
#>   name band
#>   <chr> <chr>
#> 1 Mick  Stones
#> 2 John  Beatles
#> 3 Paul  Beatles
```

```
band_instruments
```

```
#> # A tibble: 3 x 2
#>   name plays
#>   <chr> <chr>
#> 1 John  guitar
#> 2 Paul  bass
#> 3 Keith guitar
```

Use one of the join function (e.g., `inner_join`, `full_join`) to combine the data.

```
# Mutating joins
```

```
band_members |> inner_join(band_instruments, by = "name")
```

```
#> # A tibble: 2 x 3
#>   name band plays
#>   <chr> <chr> <chr>
#> 1 John  Beatles guitar
#> 2 Paul  Beatles bass
```

```
band_members |> full_join(band_instruments, by = "name")
```

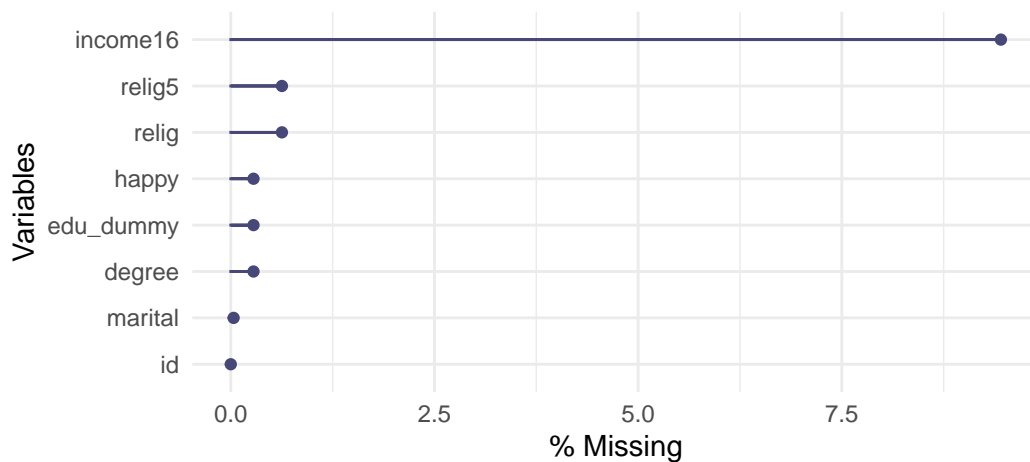
```
#> # A tibble: 4 x 3
#>   name band plays
#>   <chr> <chr> <chr>
#> 1 Mick  Stones <NA>
#> 2 John  Beatles guitar
#> 3 Paul  Beatles bass
#> 4 Keith <NA> guitar
```



```
# Further joins:
# band_members |> left_join(band_instruments)
# band_members |> right_join(band_instruments)
```

Finally, one last word about missing values: make sure you explore the data before you run an analysis, but don't neglect to inspect missing and implausible values as well. The **naniar** package has a lot to offer for this task and of course I did not introduce everything it is capable of in Chapter 5. For example, we used the `vis_miss()` function to visualize missing values, but not the amount of missing values. Give the `gg_miss_var()` function a try. It returns a lollipop chart to visualize the amount of missing values. To display percentages, set the `show_pct` option to `TRUE`.

```
# Visualize the amount of missing values
library(naniar)
gg_miss_var(df, show_pct = TRUE)
```



## 4.6 Summary

In addition to the discussed content, keep the following R functions and packages in mind:

- Import data with different packages. For example:
  - CSV with the **readr** package (Wickham, Hester, and Bryan 2022)
  - Excel with the **readxl** package (Wickham and Bryan 2022)
  - SPSS or Stata with the **haven** package (Wickham, Miller, and Smith 2022)

- Convert objects into numeric (character) vectors (`as.numeric`, `as.character`)
- Rename columns (`dplyr::rename`)
- Cleans names of an object (`janitor::clean_names`: Firke 2021)
- Combine data:
  - Pivot data from long to wide (`tidyr::pivot_wider`)
  - Pivot data from wide to long (`tidyr::pivot_longer`)
  - Mutating joins (`dplyr::inner_join`, `left_join`, `right_join`, `full_join`)
  - Filtering joins (`dplyr::semi_join`, `anti_join`)
  - Set operations (`base::union`, `intersect`, `setdiff`, `setequal`)
- Missing (and implausible) values:
  - The `naniar` package and its function to explore missing values (e.g., `n_miss`, `n_complete`, `vis_miss`)
  - Check if something is not available (e.g., `base::is.na`)
  - Convert values to NA (`dplyr::na_if`)
  - Drop rows containing missing values (`tidyr::drop_na`)
  - Replace NAs with specified values (`tidyr::replace_na`)

## 5 Analyze data

Welcome to the tutorial six of the [Practice R](#) book (Treischl 2023). Practice R is a text book for the social sciences which provides several tutorials supporting students to learn R. Feel free to inspect the tutorials even if you are not familiar with the book, but keep in mind these tutorials are supposed to complement the Practice R book.

We explored how a linear regression analysis works in Chapter 6. I introduced the corresponding `lm()` function and many packages that help us to develop a linear regression model. This tutorial summarizes the discussed steps and asks you to apply them by running an example analysis. We examine whether life satisfaction, participant's sex, or age has an effect on people's income.

In order to focus on data analysis steps, I have already prepared the `gss2016` data. Keep its limitations in mind. It is a cross-sectional survey and some of the variables such as `income` and `happy` are not measured on a numerical scale, as the raw data shows. The same applies to `degree`, the educational background is measured as a categorical variable, which is why I transformed it (`degree_num`). We will nonetheless use the `gss2016` data to summarize how a linear regression analysis is implemented in R and which packages help us to develop a model.

```
# Select variables
library(dplyr)
library(PracticeR)
varlist <- c("income", "age", "sex", "happy", "degree")

# And mutate to create a numerical variable for degree
df <- PracticeR::gss2016 |>
  select(all_of(varlist)) |>
  mutate(degree_num = case_when(
    degree == "Lt High School" ~ 8,
    degree == "High School" ~ 9,
    degree == "Junior College" ~ 12,
    degree == "Bachelor" ~ 15,
    degree == "Graduate" ~ 17,
    degree == NA ~ NA
  ))
```

Furthermore, we implicitly assume that an independent variable  $x$  influences a dependent variable  $y$ , although the research design and the data may not allow such a wide-ranging assumptions. For this reason, Chapter 6 introduced the main idea of causality and elaborated which variables we need to control in a linear regression analysis. The *correlation vs. causation* comic strip underlines this point once more.

This tutorial focus on the coding skills to run a linear regression and not on the underlying causal structure between the examined variables. First, we repeat the basics to estimate a linear regression analysis. Next, I ask you to develop your model by examining non-linear effects, interaction effects, and by comparing the performance of such adjustment steps. Finally, I briefly summarize several package that help us with the model specification and assumptions.

```
# Setup of tutorial 6
library(effectsize)
library(estimatr)
library(dotwhisker)
library(huxtable)
library(interactions)
library(jtools)
library(lmtest)
library(performance)
```

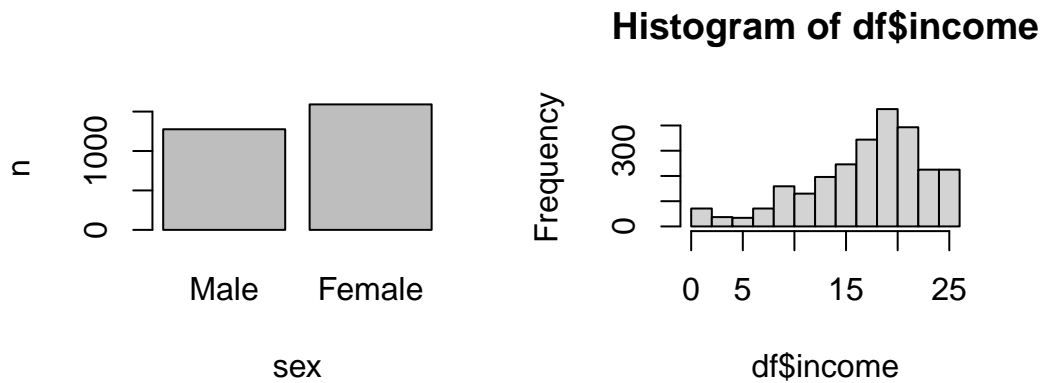
## 5.1 Estimate a linear regression analysis

I used data for teaching purposes to introduce a linear regression analysis in Practice R. This made it possible to focus on the code and its implementation; we did not explore the data, there was no need to clean the data, prepare variables, or deal with missing values. Such steps are necessary to analyze data and the process is not linear: We start to explore the data, we prepare variables, and run a first analysis. However, often we need to circle back to improve the model due to different reasons (e.g. to include control variables, check on implausible values, etc.). Thus, the first estimation results are preliminary and may substantially change during the course of the model development.

So, we need to explore the variable first. Suppose we examine the gender wage gap: how large is the effect of `sex` on `income`? Explore the distribution of each variable. This gives us an overview how many men and women we observe and whether we may transform the outcome variable in a later step. I already adjusted the graphical parameters (`par`) to put the two graphs next to each other (`mfrow` creates one row and two columns). Create a bar plot and a histogram to examine the variables.

```
# Count sex
count_sex <- dplyr::count(df, sex)

# Plot two graphs
par(mfrow = c(1, 2))
barplot(n ~ sex, data = count_sex)
hist(df$income)
```



We may run a first analysis after we have explored the data, cleaned, and prepared the variables. Use the `lm()` function to estimate a linear regression analysis. The function needs the data and a formula ( $y \sim x_1$ ) to estimate the effect of sex on income.

```
# The lm function
lm(income ~ sex, data = df)

#>
#> Call:
#> lm(formula = income ~ sex, data = df)
#>
#> Coefficients:
#> (Intercept)    sexFemale
#>    17.7642      -0.7323
```

Since income is not measured on a numeric scale, this coefficient is hard to interpret, but in accordance with theoretical expectations, females have a lower income. The `summary()` function helps us with the interpretation of the model. It returns the estimated coefficients,

$R^2$ , and further information about the model. In addition, add a second variable with a plus sign (+) and examine whether the educational background (`degree_num`) mediates the effect.

```
# The summary function
summary(lm(income ~ sex + degree_num, data = df))

#>
#> Call:
#> lm(formula = income ~ sex + degree_num, data = df)
#>
#> Residuals:
#>      Min       1Q   Median       3Q      Max
#> -20.8416  -2.7738   0.9904   3.7014  11.2262
#>
#> Coefficients:
#>              Estimate Std. Error t value Pr(>|t|)
#> (Intercept)  10.06283    0.39773   25.300 < 2e-16 ***
#> sexFemale    -0.83192    0.21199   -3.924 8.92e-05 ***
#> degree_num    0.69287    0.03285   21.090 < 2e-16 ***
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Residual standard error: 5.375 on 2590 degrees of freedom
#> (274 observations deleted due to missingness)
#> Multiple R-squared:  0.15, Adjusted R-squared:  0.1493
#> F-statistic: 228.5 on 2 and 2590 DF, p-value: < 2.2e-16
```

Apparently, the wage gap can't be explained by the educational background of the participants since sex has a significant effect. Use the `predict()` function to apply the model. I have already saved the `model` and I created a new data frame with example values. Apply the model and predict how income changes if `degree_num` increases; or examine how predicted values differ between male and female participants. Predicting values give you a better intuition about the model.

```
# The model
model <- lm(income ~ sex + degree_num, data = df)

# Generate example data
new_data <- data.frame(
  sex = c("Female", "Male"),
  degree_num = c(10, 10)
)
```

```
# Apply the model with predict(model, data)
predict(model, new_data)
```

```
#>           1           2
#> 16.15957 16.99149
```

Finally, keep in mind that the `effectsize` package helps us to interpret model parameters such as  $R^2$  (Ben-Shachar et al. 2022). I have saved the summary as `sum_model`. Can you extract  $R^2$  (`r.squared`) from the latter and interpret it with `interpret_r2()` function. As default, it uses the Cohen's rules to interpret the effect size.

```
# Assign summary of the model
sum_model <- summary(model)

# Interpret R2
effectsize::interpret_r2(sum_model$r.squared, rules = "cohen1988")

#> [1] "moderate"
#> (Rules: cohen1988)
```

## 5.2 Develop the model

As outlined in Chapter 6, we develop models step by step. We start simple with a bivariate model. We include control variables to inspect how our estimation results change; we examine whether interaction effects mediate the effect; and to which extent an effect is linear. This is not an all-encompassing list, but developing a model step by step implies that we need to compare models to see how the estimation results change between steps. For this purpose we need tables and visualization to compare the estimated models.

We already started to develop a model as we included a second independent variable, but our approach made it hard to comprehend how the estimations results change if we add (drop) a variable. Use the `huxreg()` function from the `huxtable` package to compare models (Hugh-Jones 2022).

```
# Models
m1 <- lm(income ~ sex, data = df)
m2 <- lm(income ~ sex + degree_num, data = df)

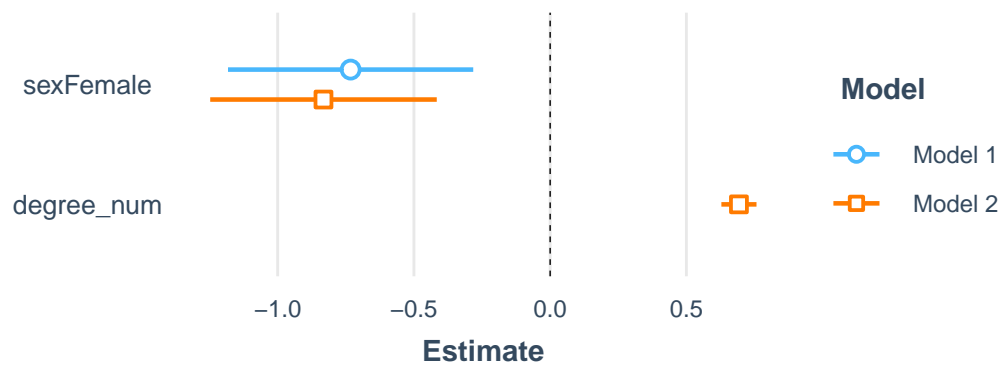
# Develop models step by step
huxtable::huxreg(m1, m2)
```

	(1)	(2)
(Intercept)	17.764 ***	10.063 ***
	(0.169)	(0.398)
sexFemale	-0.732 **	-0.832 ***
	(0.230)	(0.212)
degree_num		0.693 ***
		(0.033)
N	2596	2593
R2	0.004	0.150
logLik	-8256.549	-8038.689
AIC	16519.099	16085.377

\*\*\* p < 0.001; \*\* p < 0.01; \* p < 0.05.

In addition, use dot-and-whisker plots to compare model graphically. The `plot_summs()` function from the `jtools` package only needs the model names (Long 2022).

```
# jtools returns a dot-and-whisker plot
jtools::plot_summs(m1, m2)
```

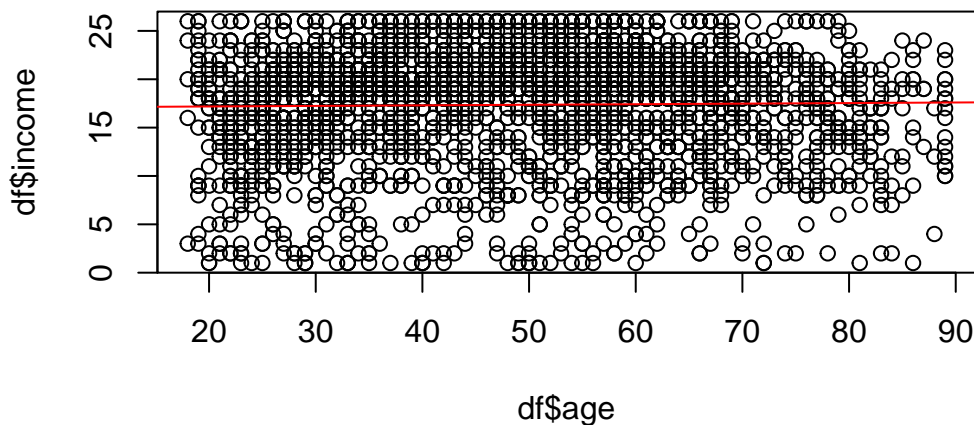


Now that we have established the framework to develop models, let us inspect how we can examine non-linear effects, transform variables, and include interaction effects. Finally we need to check how model changes affect the performance of the model.



We have already applied to `lm()` function when we first created a scatter plot. Since we assume a linear relationship, we should start to examine the effect with a scatter plot in the case of a numerical independent variable. As outlined in Chapter 3, we may insert a regression line with `abline` and the `lm()` function. For example, consider the scatter plot for the effect of age on income.

```
# Create a scatter plot
plot(y = df$income, x = df$age)
abline(lm(income ~ age, data = df), col = "red")
```



It seems though that both variables are not or only weakly related. Does this mean that we are supposed to stop here since there is no (large) effect? A linear regression assumes a linear effect, but the effect of age on income might not be linear. For example, create a squared age variable and including it in second model to examine if age has a non-linear effect. By including a squared variable for age, we can estimate if the effect increases (decreases) for older people.

```
# Make a squared age variable
df$age_sqr <- df$age^2

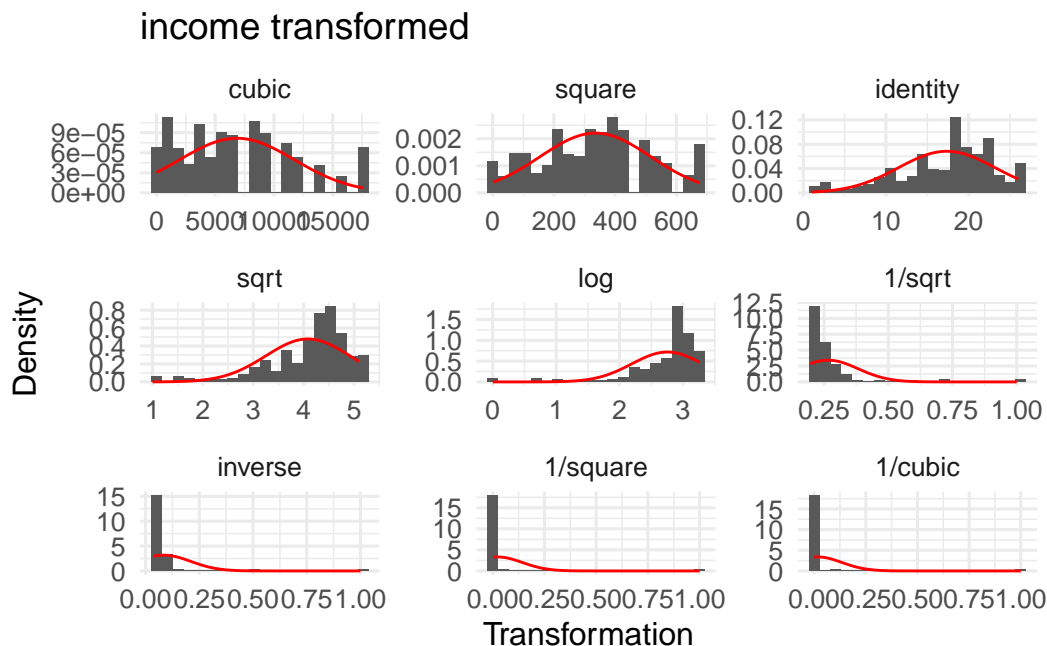
# Compare models
m1 <- lm(income ~ age, data = df)
m2 <- lm(income ~ age + age_sqr, data = df)
huxtable::huxreg(m1, m2)
```

	(1)	(2)
(Intercept)	17.066 *** (0.343)	10.421 *** (0.880)
age	0.006 (0.007)	0.305 *** (0.037)
age_sqr		-0.003 *** (0.000)
N	2589	2589
R2	0.000	0.026
logLik	-8238.575	-8205.475
AIC	16483.151	16418.951

\*\*\* p < 0.001; \*\* p < 0.01; \* p < 0.05.

We may transform the outcome variable to increase the model fit as well. In the case of income, we often observe many people with little or average income while the amount of people with of a very high income is low. In such a case a logarithm of the income may help to increase the model fit. Keep in mind that the interpretation of the coefficient will change if we transform the variables. Regardless of the interpretation, the `transformer()` function shows what the distribution of a numerical variable would look like (e.g. `log`) if you transform it.

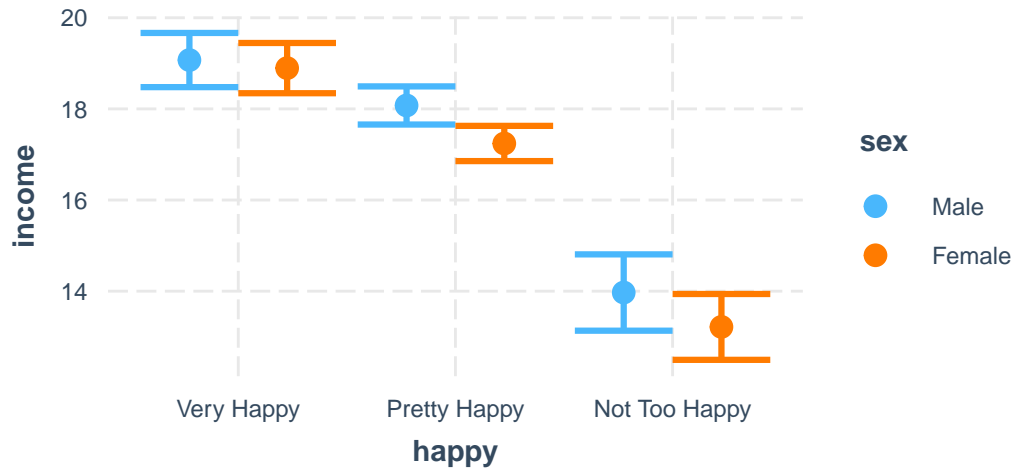
```
# Transform a numerical variable
PracticeR::transformer(df$income)
```



Next, we examine interaction effects: I estimated a model with an interaction effect between **happy** and **sex**. Certainly, I only included it to repeat how this works, but it implies that the effect of happiness on income is moderated by sex. Regardless of my ad-hoc hypothesis, visualize the effect with `cat_plot()` function from the `interactions` package (Long 2021); it needs the model, the name of the predictor (`pred`) and the moderator variable (`modx`). As the plots shows, there is no significant interaction effect.

```
# Interaction of two categorical variables
library(interactions)
m3 <- lm(income ~ happy * sex, data = df)

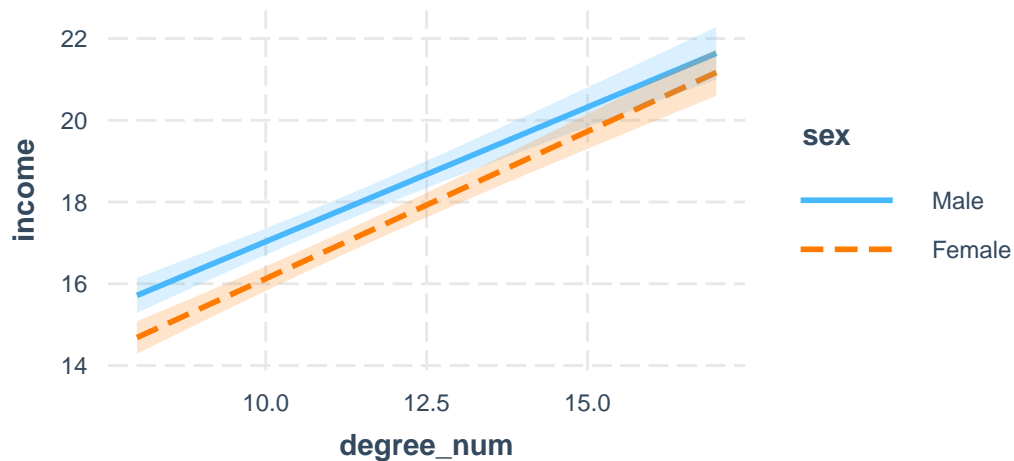
# cat_plot for categorical predictors
cat_plot(m3, pred = happy, modx = sex)
```



Suppose we believe there is an interaction between sex and education. We may expect that male participants gain much more advantages from education than female participants. Use the `interact_plot()` function with the predictor variable (`pred`) and the moderator (`modx`) variable. The `interval` option shows the confidence interval and we can see the overlap.

```
# Interaction model
m3 <- lm(income ~ sex * degree_num, data = df)

# Interaction between sex*degree_num
interact_plot(m3,
  pred = degree_num, modx = sex,
  interval = TRUE, plot.points = FALSE
)
```



Finally, keep the `performance` package in mind when developing models (Lüdtke, Makowski, Ben-Shachar, et al. 2022). Check how the performance changes if you insert a non-linear parameter, include interaction terms or if you compare different model specifications. The `compare_performance()` function returns several performance indicators and it even creates a radar plot if we assign and plot the results.

```
# Compare performance
library(performance)
performance_models <- compare_performance(m1, m2,
  metrics = c("AIC", "BIC", "R2_adj")
)

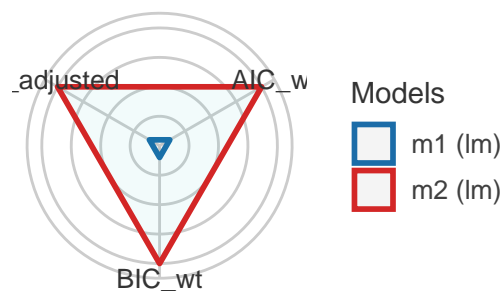
# Compare performance
performance_models

#> Comparison of Model Performance Indices

#>Name | Model |   AIC (weights) |   BIC (weights) |  R2 (adj.)
#>-----
#>m1   |    lm | 16483.2 (<.001) | 16500.7 (<.001) | -8.117e-05
#>m2   |    lm | 16419.0 (>.999) | 16442.4 (>.999) |      0.025

# Plot results
plot(performance_models)
```

### Comparison of Model Indices



## 5.3 Improve the model

There are more steps to develop and improve the model. Up to this point we developed the model from a theoretical point of view: we checked if variables interact with each other or in case of a non-linear effect. There is still much room for improvement after we worked off theoretical points. At least we should be aware about the assumptions of a linear regression analysis and the packages that can help us to address such concerns. So, what shall we do if we finalized the first model(s)?

```
# Final model(s)
m_all <- lm(income ~ sex + degree_num, data = df)
```

I introduce the performance package because it gives you a quick overview about potential violations. First, the `check_model()` returns an overview with several plots to check the model assumptions.

```
# Get a quick overview
check_model(m_all)
```

Second, the package has several `check_*` functions to examine assumptions individually. For example, what about multicollinearity and heteroscedasticity?

```
# multicollinearity
check_collinearity(m_all)
```

```
#> Check for Multicollinearity
```

```
#> Low Correlation
```

```
#>      Term  VIF  VIF 95% CI Increased SE Tolerance
#>      sex 1.00 [1.00, Inf]          1.00      1.00
#> degree_num 1.00 [1.00, Inf]          1.00      1.00
#>
#> Tolerance 95% CI
#>      [0.00, 1.00]
#>      [0.00, 1.00]
```

```
# check_heteroscedasticity
check_heteroscedasticity(m_all)
```

```
#> Warning: Heteroscedasticity (non-constant error variance) detected (p < .001).
```

The last function runs a statistical test to check on the assumptions; in the case of heteroscedasticity we can apply the Breusch & Pagan (1979) test (`bptest`), which runs in the background. The `lmtest` package gives you access to such statistical tests (Hothorn et al. 2022).

```
# Breusch & Pagan test (1979)
lmtest::bptest(m1)

#>
#> studentized Breusch-Pagan test
#>
#> data: m1
#> BP = 3.2195, df = 1, p-value = 0.07277
```

The error of our model is heteroscedastic and the `estimatr` package runs a regression with (cluster) robust standard errors to address this point (Blair et al. 2022). Run a regression with the `lm_robust()` function and adjust the type of standard errors with the `se_type` option.

```
# Robust standard errors
library(estimatr)
robust_model <- lm_robust(income ~ age,
  data = df,
  se_type = "stata"
)

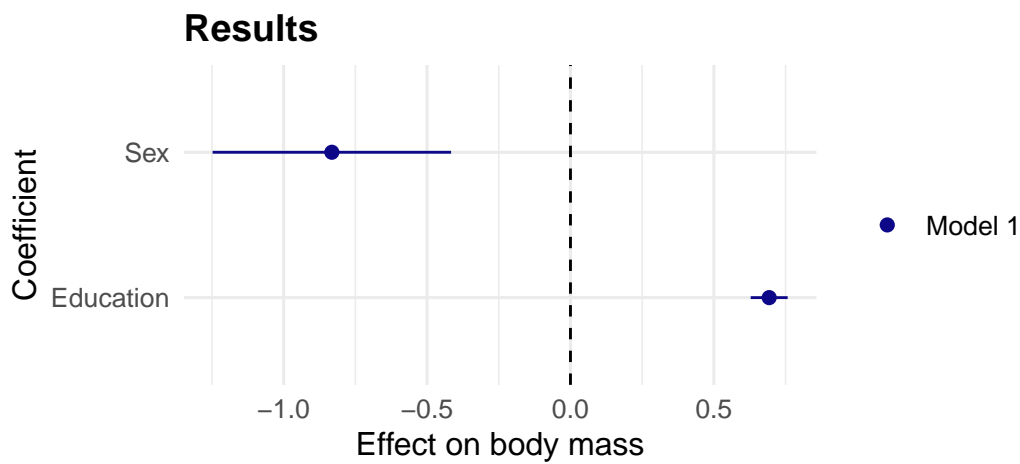
summary(robust_model)

#>
#> Call:
#> lm_robust(formula = income ~ age, data = df, se_type = "stata")
#>
#> Standard error type: HC1
#>
#> Coefficients:
#>           Estimate Std. Error t value Pr(>|t|)  CI Lower CI Upper  DF
#> (Intercept) 17.066368   0.348788 48.9305   0.0000 16.382436 17.75030 2587
#> age          0.005891   0.006638  0.8875   0.3749 -0.007125  0.01891 2587
#>
#> Multiple R-squared:  0.0003053 , Adjusted R-squared:  -8.117e-05
#> F-statistic: 0.7876 on 1 and 2587 DF,  p-value: 0.3749
```

Finally, one last word about the visualization of regression results. The `jtools` package provides convenient solutions to create dot-and-whisker plots; and the `dotwhisker` package lets us customize the graph (Solt and Hu 2021). For this purpose I introduce the package, but this does not mean that we have to build a long and complicated code from the ground up each time we need an individual dot-and-whisker plot. In the next chapter we learn more about `ggplot2` which will boost your visualization skills and in a later step we will create functions to create plots efficiently (Wickham, Chang, et al. 2022).

The same applies to the `dotwhisker` package. Once you have built a graph, you can build your own function to create such plots. Don't let complicated code scare you off, we'll soon work on strategies how to create plots without the trouble of memorizing complex code. For example, I created a function called `visualize_model()` which rebuilds the complicated code to create a dot-and-whisker plot from Chapter 6. However, it only needs the models and the names for each predictor to create the plot.

```
# visualize_model() runs dotwhisker in the background
visualize_model(m_all, p1 = "Sex", p2 = "Education")
```



## 5.4 Summary

Keep the following R functions and packages in mind:

- Fitting linear models (`lm`)
- Model predictions (`predict`)
- Interpret coefficient of determination (`effectsize::interpret_r2`)



- Reorder levels of factor (`relevel`)
- Create a huxtable to display model output (`huxtable::huxreg`)
- Plot regression summaries (`jtools::plot_summs`)
- Plot interaction effects in regression models (e.g., `interactions::interact_plot`)
- The **performance** package and its functions to examine the performance of a model.
  - Compute the model's R2 ( `r2`)
  - Compare performance of different models (`compare_performance`)
  - Visual check of model assumptions (e.g.,`check_model`, `check_outliers`, `check_heteroscedasticity`)
- Transform a numerical input (`PracticeR::transformer`)
- Export regression summaries to tables (`jtools::export_summs`)
- OLS with robust standard errors (`estimatr::lm_robust`)
- Create fine tuned dot-and-whisker plots API with the `dotwhisker` package

## 6 Visualize data

Welcome to tutorial of the [Practice R](#) book (Treischl 2023). Practice R is a text book for the social sciences which provides several tutorials supporting students to learn R. Feel free to inspect the tutorials even if you are not familiar with the book, but keep in mind these tutorials are supposed to complement the Practice R book.

Chapter 7 introduced `ggplot2` which gives us plenty of opportunities to visualize data (Wickham, Chang, et al. 2022). We got in touch with the `ggplot()` function, we applied themes, add color, changed fonts, and we learned many more details about the package. Against this background there are at least two options for a `ggplot2` tutorial: I could ask you to apply steps to create a similar plot. It is my personal believe that it needs a lot of time and experience to get fluent in `ggplot2`, which is why we do not pursue such a heroic aim. Some people document the long process to generate a graph as the artwork by Cédric Scherer underlines. It is an animation that shows the steps to create a graph. Thus, it needs a lot of time and effort to develop a customized plot.

Besides the technical skills, the *guiding principles of visualization* will help you to create insightful visualizations. Cairo (2016) summarizes five qualities of a graph as:

1. *It is truthful*, as it's based thorough and honest research.
2. *It's functional*, as it constitutes an accurate depiction of the data, and it's build in a way that lets do people meaningful operations based on it (seeing change in time).
3. *It's beautiful*, in the sense of being attractive, intriguing, and even aesthetically pleasing for its intended audience – scientists, in the first place, but the general public, too.
4. *It is insightful*, as it reveals evidence that we would have a hard time seeing otherwise.
5. *It is enlightening* because if we grasp and accept the evidence it depicts, it will change our minds for the better.” (Cairo 2016: 45).

These principles give us a guidance, but some of them seem complex and depend on the creator and viewer. For example, we probably all agree on the first quality of being truthful, but who says that a graph is (not) beautiful? And what does that even mean? Or a graph might be less insightful if the topic is not novel for the audience. We may argue for a long time whether a principle is fulfilled, but hopefully we agree in the case of obvious flaws that could be improved.

For this reason, this tutorial is dedicated providing first insights about well-known visualization pitfalls and we increase our `ggplot2` skills by learning how to fix them. First, we learn why it is important *to order data*. Then, we inspect why a lot of people perceive *box plots* with

suspicion. Next, we get in touch with a *spaghetti plot*. Finally, we will see what it means *to cut the clutter*.

```
# Tutorial 7 needs the following packages in addition:
library(babynames)
library(forcats)
library(patchwork)
library(dplyr)
library(viridis)
library(ggthemes)
library(ggplot2)
library(showtext)
```

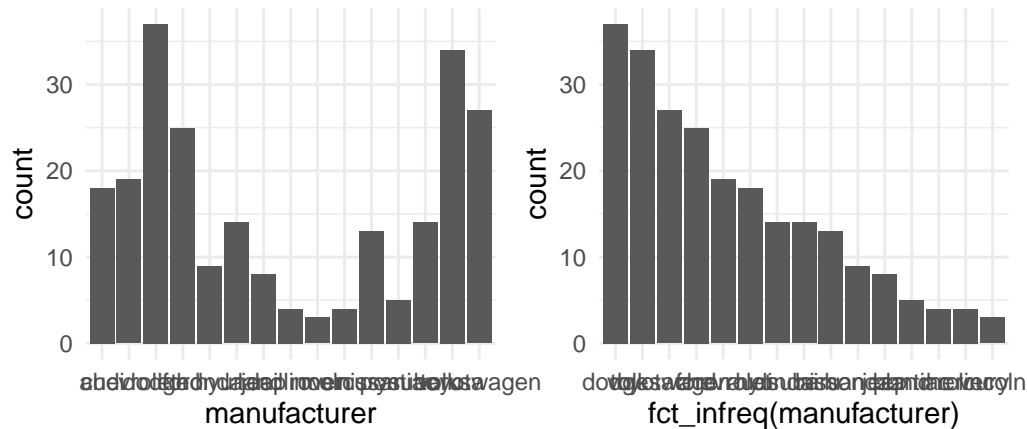
## 6.1 Order the data

Suppose you created a bar graph to examine cars and their manufacturer (`mpg$manufacturer`). The data is not important, but we need to learn how to order the levels of a categorical variable. As the next console illustrates, the displayed information is difficult to perceive because the bars are all mixed up. Adjust the levels of a factor variable manually or use the `fct_infreq()` function from the `forcats` package to order the data by frequency (Wickham 2022).

```
#Simple bar graph
p1 <- ggplot(data=mpg, aes(x=manufacturer)) +
  geom_bar()

#Order the data
p2 <- ggplot(data=mpg, aes(x=fct_infreq(manufacturer))) +
  geom_bar()

p1 + p2
```



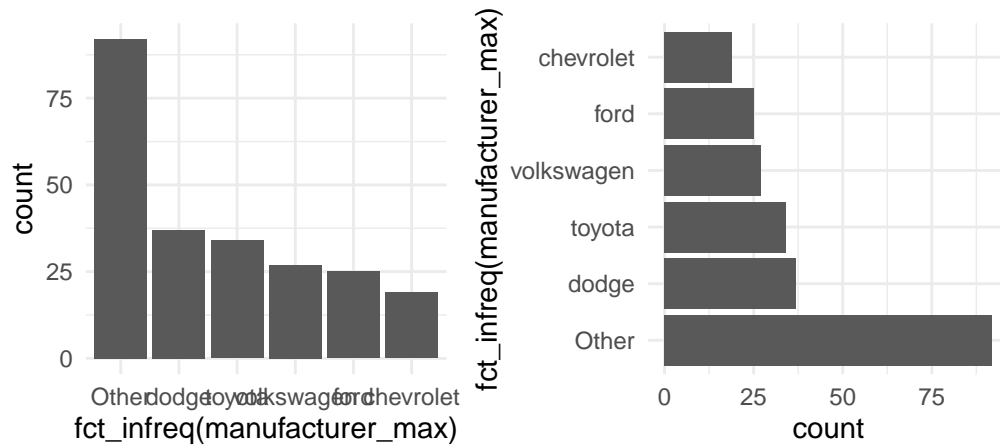
It is our job is to make the graph and its insights accessible. The example underlines that we need to structure and present the data in a way that leverages the message. The last graph also illustrates that there are many group levels making it difficult to depict them all in one graph even if we ordered the data. Moreover, look at the labels, they are not vertically aligned which makes it hard to read. Remember, the `forcats` package offers many functions to manipulate factor variables. For example, display only the five largest groups with the `fct_lump` function and use the `coord_flip()` function to turn around the axes to align the labels vertically.

```
# Lump levels with fct_lump
mpg$manufacturer_max <- fct_lump(mpg$manufacturer, n = 5)

# Left: Plot less levels
p1 <- ggplot(data = mpg, aes(x = fct_infreq(manufacturer_max))) +
  geom_bar()

# Right: Flip axes
p2 <- ggplot(data = mpg, aes(x = fct_infreq(manufacturer_max))) +
  geom_bar() +
  coord_flip()

p1 + p2
```

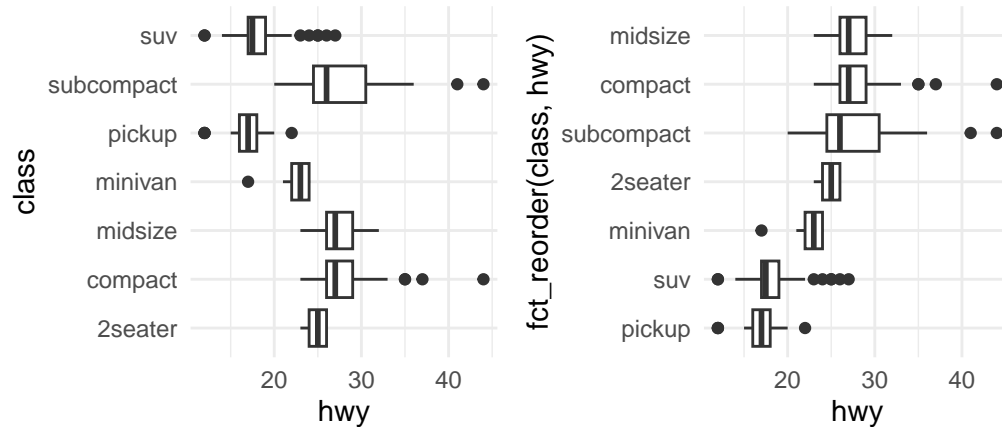


To order the data is important, regardless of the graph created. For example, suppose you examine car consumption (`mpg$hwy`) for different classes of cars (`mpg$class`) with a box plot. Look at the unsorted plot, can you tell me which level has the highest mean? It is complicated to compare groups without a useful order. Try to apply the `fct_reorder()` function, because it lets us reorder the `class` variable by its consumption (`hwy`).

```
# A basic plot
p1 <- ggplot(mpg, aes(hwy, class)) +
  geom_boxplot()

# Use fct_reorder to sort class by their consumption
p2 <- ggplot(mpg, aes(hwy, fct_reorder(class, hwy))) +
  geom_boxplot()

p1 + p2
```



We therefore are supposed to order the data and communicate in a coherent way, otherwise the audience may get confused. There are however additional pitfalls when it comes to box plots.

## 6.2 Boxplot pitfalls

I generated fake data with a `group` and an `outcome` variable to illustrate the main concerns against box plots.

```
# Some fake data
glimpse(data)

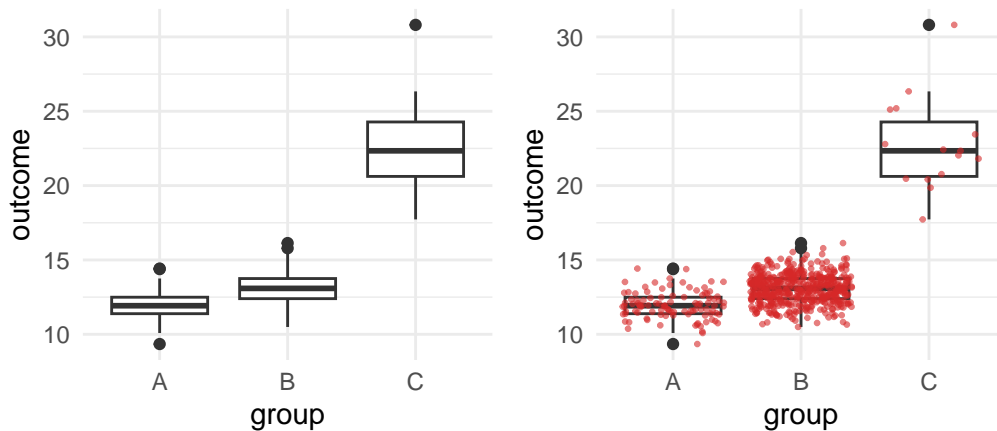
#> Rows: 615
#> Columns: 2
#> $ group   <chr> "A", "A", "A", "A", "A", "A", "A", "A", "A", "A", "A", "A", "A~
#> $ outcome <dbl> 12.58454, 12.05603, 11.34906, 11.82956, 10.18393, 12.25932, 10~
```

Say you estimated a box plot to examine the differences between the groups. At first glance there seems to be a large differences between groups as the first box plot reveals, but are we comparing on fair grounds? See what happens if you add a `geom_jitter()`. It displays observations with points, but compared to a `geom_point` it adds a small amount of random variation to reduce over plotting.

```
#A Basic geom_boxplot
p1 <- ggplot(data, aes(x = group, y = outcome)) +
  geom_boxplot()

#Add a geom_jitter(color, size, alpha)
p2 <- ggplot(data, aes(x = group, y = outcome)) +
  geom_boxplot() +
  geom_jitter(color = "#d62828",
             size = 0.5,
             alpha = 0.6)

p1 + p2
```



We are comparing three different groups, but the amount of observations are unevenly distributed between the groups and we hardly observe any from group C. This becomes visible when using `geom_jitter()` to add observations, compared to `geom_boxplot()` which does not display the data. A box plot disguises such problems which is obviously a serious concern.

The `geom_jitter` already improved the graph, what else can we do to fulfill the guiding principles of visualization. For example, include the sample size in the graph to make our reader conscious about the problem. The next steps are a bit trickier to apply: Estimate the sample size per group and assign the results. Use the `dplyr::n()` function to count observations, but you will need to group the data first (Wickham, François, et al. 2022).

```
# Estimate sample_size (n) per group
sample_size <- data |>
  dplyr::group_by(group) |>
```

```
dplyr::summarize(num = dplyr::n())

sample_size
```

```
#> # A tibble: 3 x 2
#>   group  num
#>   <chr> <int>
#> 1 A      100
#> 2 B      500
#> 3 C       15
```

To include the sample size in the graph, we need to combine the `group` label and the sample size. We can paste text strings together with the `paste` (and `paste0`) function, as the next console illustrates. It returns text strings which we can include in the graph.

```
# Concatenate Strings with paste (and paste0)
paste(sample_size$group, "has N =", sample_size$num, " observations.")

#> [1] "A has N = 100 observations." "B has N = 500 observations."
#> [3] "C has N = 15 observations."
```

First, combine both data sets with a `left_join()`. Second, create a new variable to add the text label. Use the `paste` function to paste the text label, but also add a new line (`\n`) to separate the group name and the text to display the sample size (`num`).

```
# Join data and mutate with text labels for group_N
data <- data |>
  dplyr::left_join(sample_size) |>
  dplyr::mutate(group_N = paste0(group, "\n", "N=", num))

head(data)
```

```
#>   group outcome num group_N
#> 1     A 12.58454 100 A\nN=100
#> 2     A 12.05603 100 A\nN=100
#> 3     A 11.34906 100 A\nN=100
#> 4     A 11.82956 100 A\nN=100
#> 5     A 10.18393 100 A\nN=100
#> 6     A 12.25932 100 A\nN=100
```

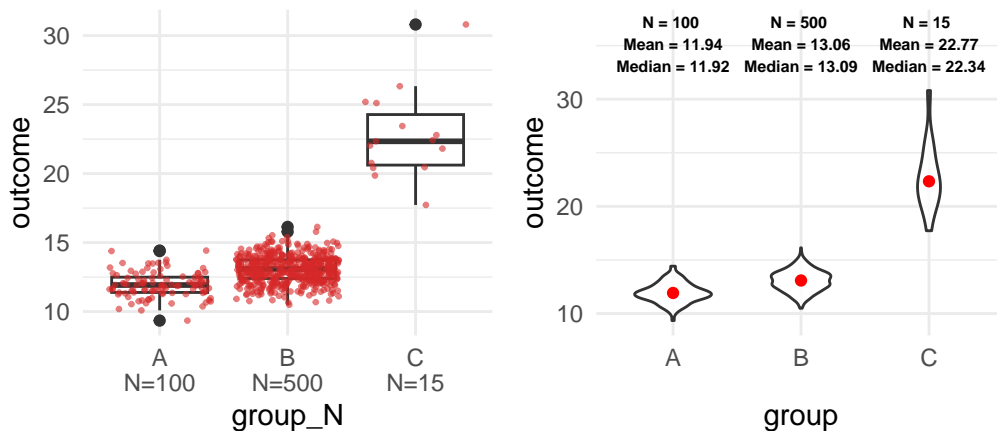


Now we can use the new variable (`group_N`) as `x` and include the sample size. It goes without saying that there are more ways to improve a box plot (and to include text). For example, we can use a `geom_violin()` to examine the distribution, as the second plot on the right side shows.

```
#Use the new variable group_N as x
p1 <- ggplot(data, aes(x = group_N, y = outcome)) +
  geom_boxplot()+
  geom_jitter(color = "#d62828",
             size = 0.5,
             alpha = 0.6)

#A violin plot and stat_summary
p2 <- ggplot(data, aes(x = group, y = outcome)) +
  geom_violin(width=0.6, alpha=0.8)+
  stat_summary(fun = "median", color = "red",
             size = 1.5, geom = "point")+
  stat_summary(fun.data = return_stats,
             geom = "text",
             size = 2, fontface = "bold",
             hjust = 0.5, vjust = 0.9)
```

`p1 + p2`



As the right plot shows, I used the `stat_summary()` function twice to include further statistics. First, I used the function to display the median of each group. Second, I used a function (`return_stats`) that returns the statistics and finally the `stat_summary()` function which includes them as text in the plot. The latter approach is more flexible but also more complicated

than the first approach. The next console shows how the function works and we will learn more about the `geom_text` at the end of this tutorial.

```
# The return_stats function
return_stats <- function(y) {
  return(data.frame(
    value = max(y) * 1.2,
    label = paste(
      "N =", length(y), "\n",
      "Mean =", round(mean(y), 2), "\n",
      "Median =", round(median(y), 2), "\n"
    )
  ))
}

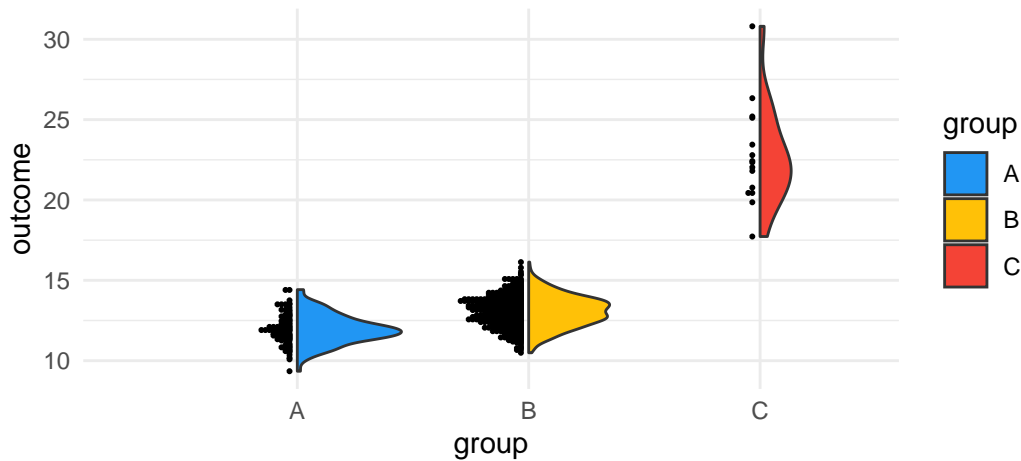
return_stats(data$outcome)

#>      value      label
#> 1 36.96905 N = 615 \n Mean = 13.11 \n Median = 12.89 \n
```

Regardless of the approach, keep in mind that a box plot does not show the data nor does it display the distribution. Compared to that, the `geom_jitter()` displays the data and the violin plot reveals the underlying distribution.

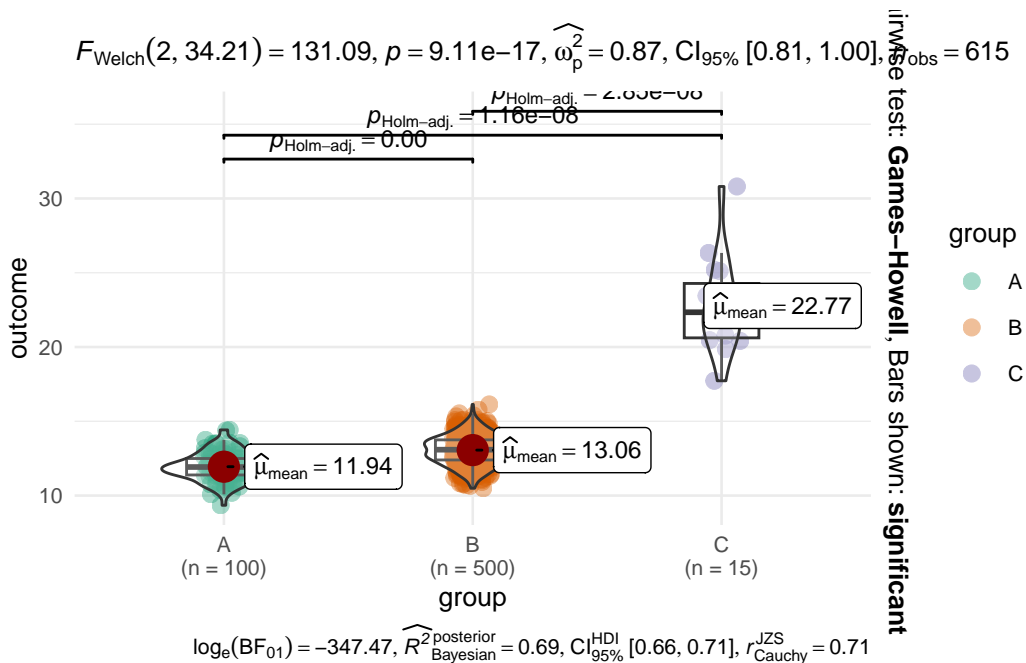
To calculate the sample size or other statistics seems a bit awkward if you are not used to customized plots. Fortunately, there are further `ggplot2` extension package that help us with this task. For example, the `see` package has a `geom_violindot()` function, which combines a violin with a dot plot. The latter makes it convenient to inspect the sample size and the distribution (Lüdecke, Makowski, Patil, et al. 2022). Add the geom, fill the dots black (via `fill_dots`); and find a reasonable size for the dots via `size_dots` option.

```
# The see package adds a geom_violindot
library(see)
ggplot(data, aes(x = group, y = outcome, fill = group)) +
  geom_violindot(fill_dots = "black", size_dots = 5) +
  scale_fill_material_d(palette = "contrast")
```



Or consider the `ggstatsplot` package: As the result from the `ggbetweenstats()` function shows, the package automatically adds statistical details to the graph. In our case, it combines box and violin plots to compare the outcome *between* the subjects (Patil 2023).

```
# The ggstatsplot package
library(ggstatsplot)
ggbetweenstats(data, group, outcome) +
  theme_minimal(base_size = 10)
```



## 6.3 The spaghetti plot

Another classic visualization pitfall is the spaghetti plot. Essentially it is a line graph with too many lines and colors which is why we cannot see what is going on. We can create a spaghetti plot with the **babynames** package and the corresponding data (Wickham 2021). The package contains names of newborn babies in the US and includes proportion for a long period (1880-2017). Suppose we examine how the most popular male names have been developed over time. I have already prepared the data to identify the most popular male names (Top 10: `name_pop`).

```
# The Top 10 male names
name_pop
```

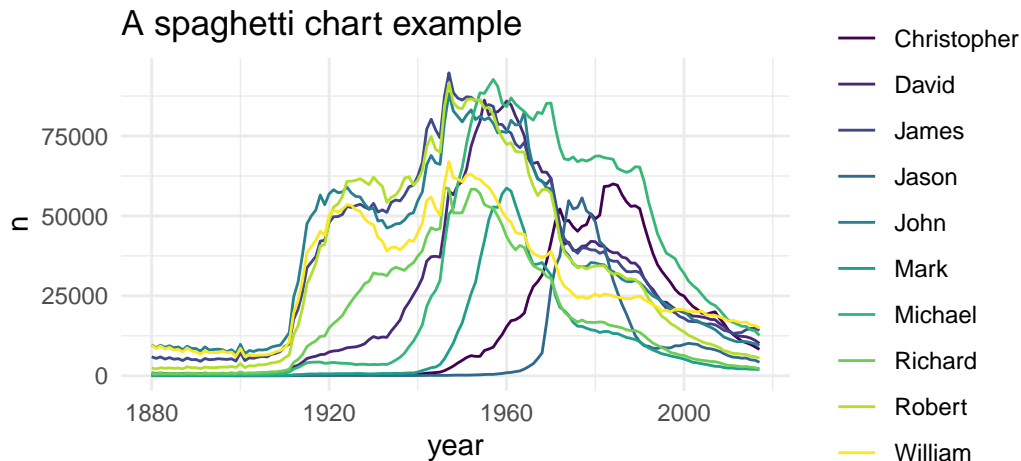
```
#> [1] "James"      "Michael"    "Robert"     "John"       "David"
#> [6] "William"    "Christopher" "Richard"    "Mark"       "Jason"
```

To visualize how often these names appear, we need to apply a filter to get only male **babynames** and to filter the data for the Top 10 names.

```
# Get male baby names for the Top 10 names
babynames_df <- babynames %>%
  filter(sex == "M" & name %in% name_pop)
```

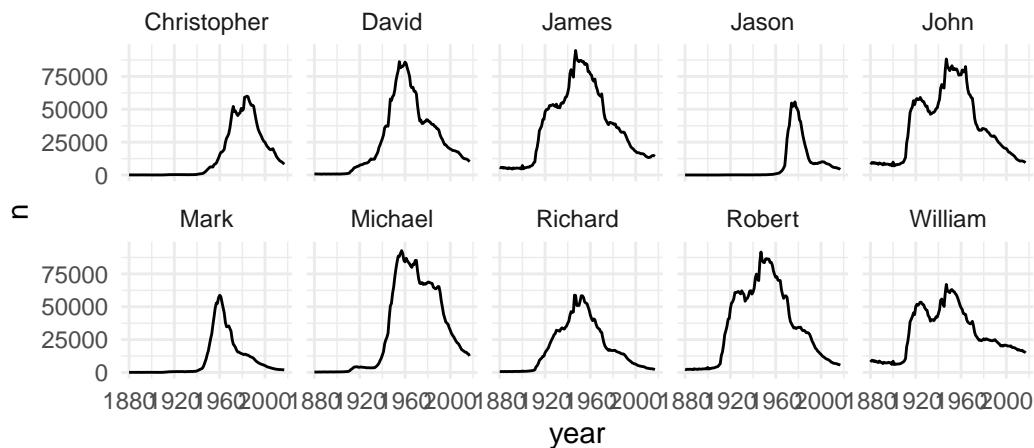
Next, visualize the data with a line plot (`geom_line`). Use `year` as `x`, `n` as `y`, and `name` as group and color aesthetic.

```
# Plot
babynames_df %>%
  ggplot(aes(x = year, y = n, group = name, color = name)) +
  geom_line() +
  scale_color_viridis(discrete = TRUE) +
  ggtitle("A spaghetti chart example")
```



What a confusing graph: single lines look like spaghetti and we can't see how often each name was used over the time. How can we improve the spaghetti plot? You are already familiar with a simple, but powerful solution. Apply a `facet_wrap()` and split the graph in subplots.

```
# Split with facet_wrap
ggplot(babynames_df, aes(x = year, y = n, group = name)) +
  geom_line() +
  facet_wrap(name ~ ., nrow = 2)
```



There is still room for further improvement: We could - for example - to draw all lines in gray and highlight for each facet the corresponding line in a different color. First, we need to create a copy of the `name` variable (`facet_names`), which we will use to facet the graph.

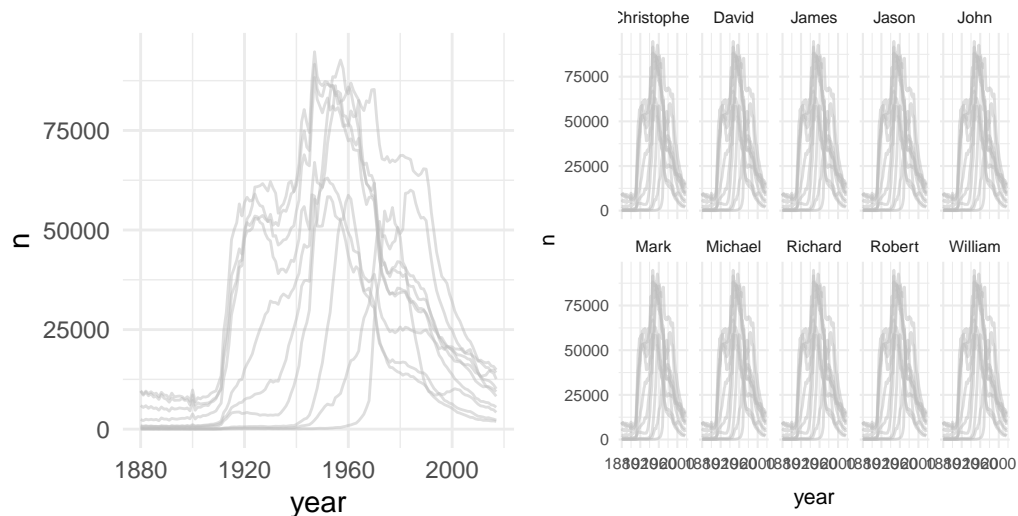
```
# Copy the names column
babynames_df$facet_names <- babynames_df$name
```

Next, I prepared the `geom_line()` to create a spaghetti plot one more time with gray lines only, as the first plot on the left side shows. However, see what happens if you add the `facet_wrap()` function and the `facet_names` variable to split the graph.

```
p1 <- ggplot(babynames_df, aes(x=year, y=n)) +
  geom_line(data = babynames_df %>% select(-facet_names),
            aes(group=name),
            color="grey",
            linewidth=0.5,
            alpha=0.5)
```

```
p2 <- ggplot(babynames_df, aes(x=year, y=n)) +
  geom_line(data = babynames_df %>% select(-facet_names),
            aes(group=name),
            color="grey",
            linewidth=0.5,
            alpha=0.5)+
  theme_minimal(base_size = 8)+
  facet_wrap(facet_names ~ ., nrow = 2)
```

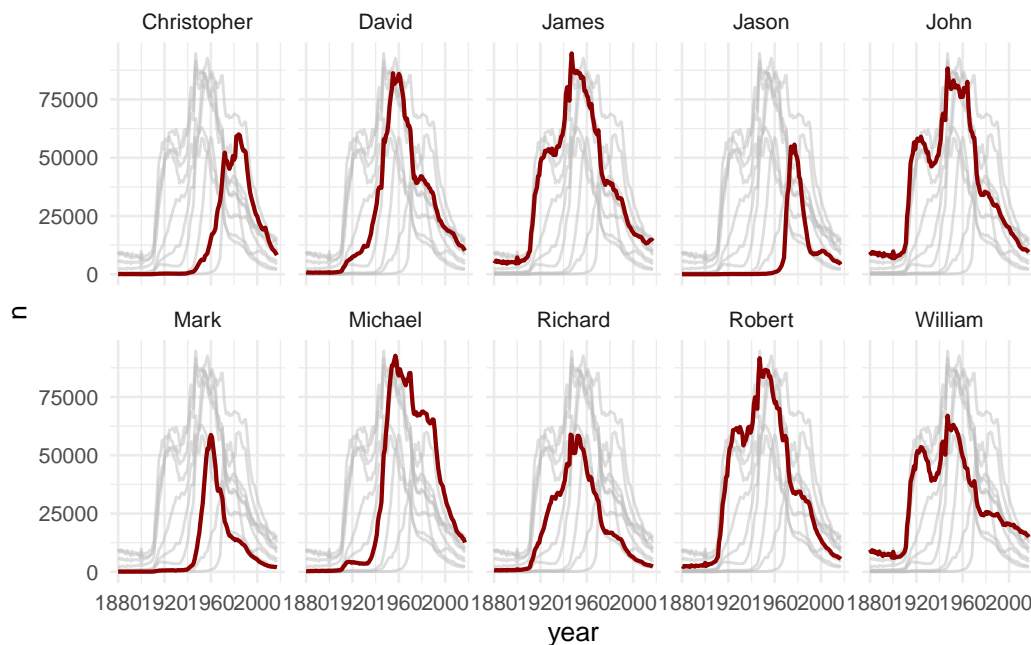
```
p1 + p2
```



As the second plot show, the new variable gives us the chance to create subplot for each name, but all lines are still included if we use the copy. Next, use a second `geom_line()` for the overlay. Insert the `name` as a color aesthetic, which will make a comparison easier. Moreover, give the overlaying line a distinct color and adjust its size with `linewidth`.

```
#add another geom_line as overlay
final_plot <- ggplot(babynames_df, aes(x=year, y=n)) +
  geom_line(data = babynames_df %>% select(-facet_names),
            aes(group=name),
            color="grey",
            linewidth=0.5,
            alpha=0.5) +
  theme_minimal(base_size = 10)+
  facet_wrap(facet_names ~ ., nrow = 2)+
  geom_line(aes(color=name), color="darkred", linewidth=0.75)
```

final\_plot



We focused on `ggplot2`, because we need a print version to visualize data in applied empirical research. However, we could also make the last plot interactive to untangle the spaghetti plot. For example, *Highcharts* is a JavaScript software library to create interactive charts and I used the `highcharter` package to create a responsive HTML version of the spaghetti plot

(Kunst 2022). The next console shows the code for an improved version of the graph with the `highcharter` package.

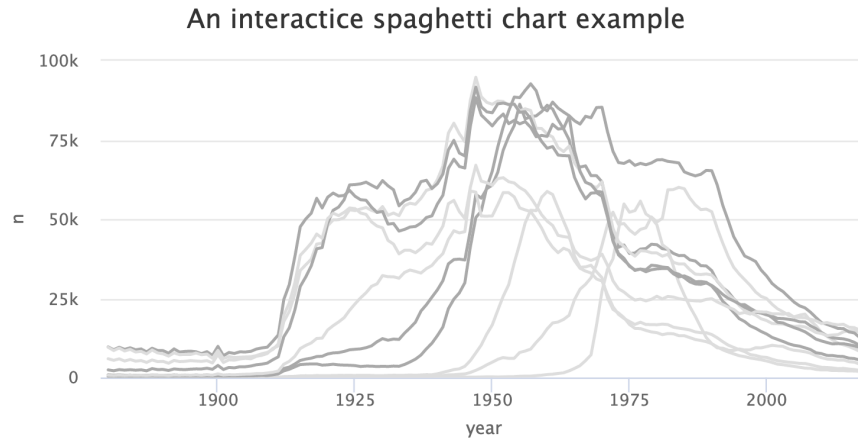


Figure 6.1: The `highcharter` package

Learning a new package and creating interactive graphs might be too far reaching in the beginning, just keep in mind that such possibilities exists. And in this case it is not even necessary to learn a new package to make the graph interactive, because the `plotly` package can create an interactive version for many standard graphs that are made with `ggplot2` (Sievert et al. 2022). Plotly is a JavaScript library to visualize data and can convert a `ggplot2` object into a plotly chart.

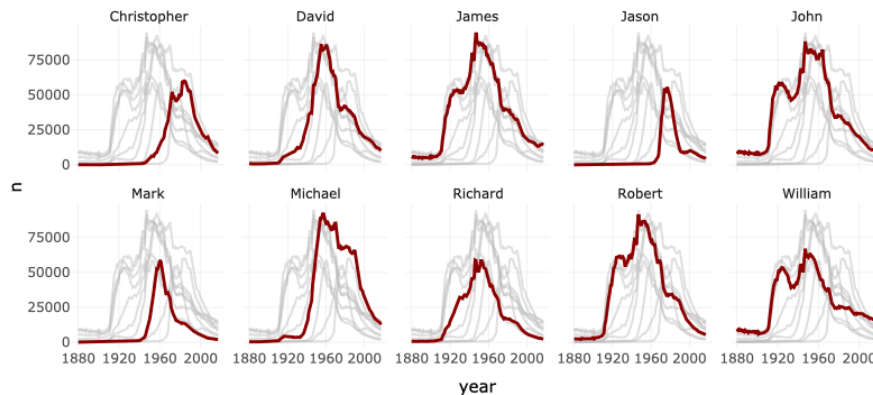


Figure 6.2: The `plotly` package

Consider reading *Interactive web-based data visualization with R, plotly, and shiny* by Carson Sievert if you want to improve your interactive visualization skills



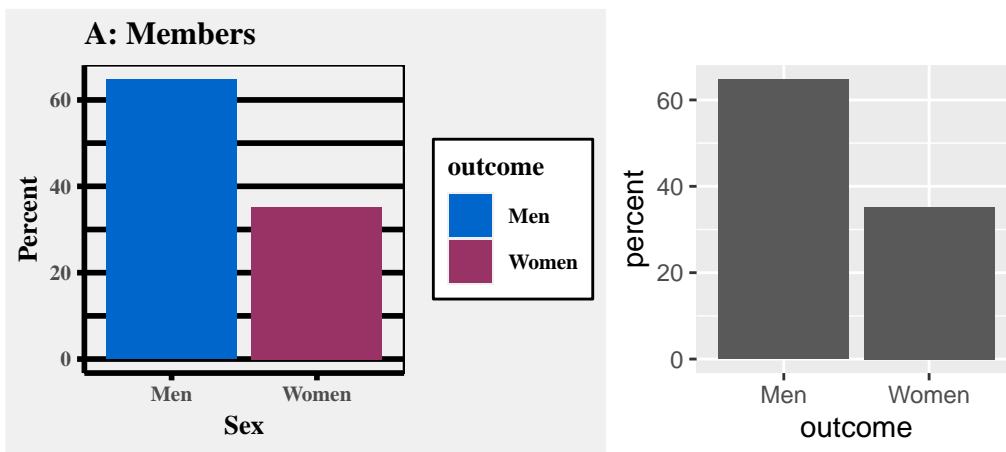
```
# Interactive web-based data visualization with R, plotly, and shiny
PracticeR::show_link("plotly")
```

Instead of learning more about interactive visualization techniques, the last pitfall is not a flaw, it is a principle and an important advice.

## 6.4 Clutter

Edward Tufte underlines: “Clutter and confusion are failures of design, not attributes of information”. He highlights that we are supposed to cut the clutter and get rid of everything that is not necessary to visualize the data.

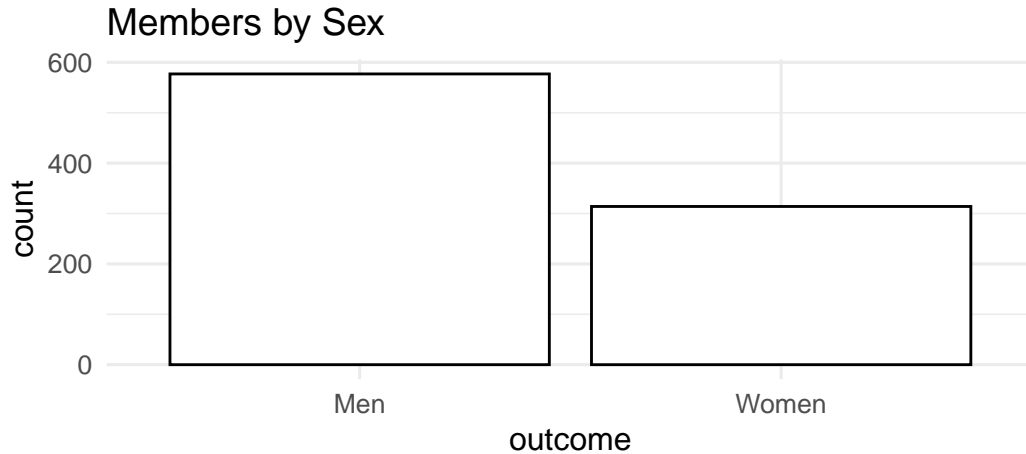
Consider the next two graphs. I made two bar graphs with a toy data frame and a binary outcome to keep it as simple as possible. I took my quite some time to create a graph that outlines the idea. As the plot on the left side shows, I created a theme that is supposed to look like the old Excel theme with a lot of clutter: The background is gray, I colored the bars even though the color and the legend do not transport any information, and I picked thick, black grid lines for a finishing touch. To compare this ugly beast, the right side shows the `ggplot2` default version. Unfold the code if you want to create a ugly, cluttered graph on your own.



The reinvention of the old Excel theme seems a bit drastic, but even the default `ggplot2` theme has some clutter that we could get rid of. This might not be necessary, but it highlights that there is always room to improve a graph, especially when it comes to clutter. For example, we could use a different `theme` to get rid of the gray background, there is no need to color each bar since they do not represent information, and we could integrate a label for each bar to communicate clearly.

So, fill the bars white and make the border of the bars black. In addition, use a theme without background colors and provide a descriptive title.

```
# De-color de bars
ggplot(df_clutter, aes(x = outcome, y = count)) +
  geom_col(color = "black", fill = "white") +
  theme_minimal(base_size = 12) +
  labs(title = "Members by Sex")
```



Next, the `geom_text()` helps us to integrate text labels. Essentially, the function displays texts as a geometrical object which is why the main logic is not different compared to other geoms. I added a simple data frame (`df_text`) to illustrate how the geom works. It contains coordinates for `x` and `y` and an example `text` to visualize.

```
df_text <- tibble::tribble(
  ~x, ~y, ~text, ~group,
  -1, -1, "bottom left", "B",
  -1, 1, "top right", "A",
  1, 1, "top left", "A",
  1, -1, "bottom right", "B",
  0, 0, "center", "C"
)
```

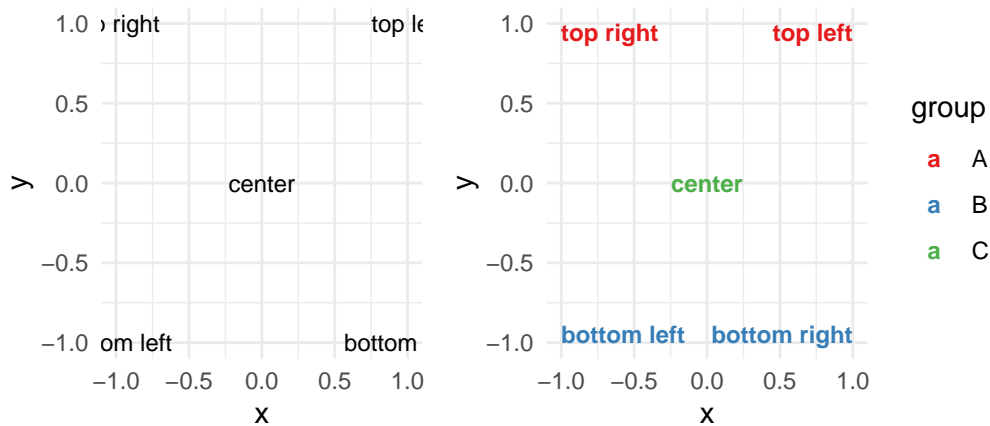
As the next console highlights, the function depicts the `text` in accordance with the `x` and `y` coordinate, as the plot on the right side shows. The geom understands supplementary aesthetics and options (e.g., `size`, `fontface`) to display text. To give you an idea how it works, add the color aesthetics for each `group` and adjust the alignment of the text with the

`vjust` (vertical adjustment) and the `hjust` (horizontal adjustment) option. If you set them to `inward`, the text will be aligned towards the center, but there are more alignment options available (e.g., `left`, `right`, `center`) should you prefer those.

```
# geom_text example
p1 <- ggplot(df_text, aes(x, y)) +
  geom_text(aes(label = text),
    size = 3
  )

# insert color aesthetic and adjust options (e.g., size, fontface)
p2 <- ggplot(df_text, aes(x, y, color = group)) +
  geom_text(aes(label = text),
    vjust = "inward",
    hjust = "inward",
    size = 3,
    fontface = "bold"
  ) +
  scale_color_brewer(palette = "Set1")

p1 + p2
```



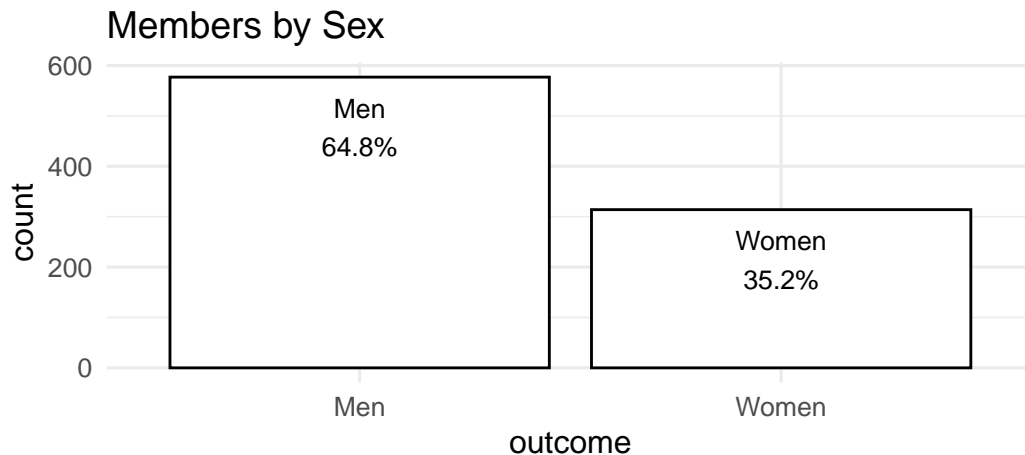
Since the data does not contain text to improve the bar graph, we may use the `paste()` function to create a `label`. It contains the group level, a new line (`\n`), and the percentages.

```
# Paste a label
paste0(df_clutter$outcome, "\n", df_clutter$percent, "%")
```

```
#> [1] "Men\n64.8%" "Women\n35.2%"
```

Include the latter as a label and adjust the position via the `y` parameter. Use the `count` and adjust it by increasing (decreasing) it manually. In addition, pick a text `color` and a reasonable text `size`.

```
#Include text labels inside the bars
ggplot(df_clutter, aes(x=outcome, y=count)) +
  geom_col(color = "black", fill = "white")+
  geom_text(aes(label = paste0(outcome, "\n", percent, "%"),
    y = count - 100),
    color="black",
    size = 3.5)+
  theme_minimal(base_size = 12)+
  labs(title= "Members by Sex")
```



## 6.5 Summary

I highlighted several books to improve your `ggplot2` and data visualizations skills, but at the end of the day your skills will improve faster, if you start to visualize data on your own and accept that trial and error are not necessarily a wrong approach. To this end, the `ggplot2` cheat sheet (from the package website) will support you as well.

In addition, keep the following functions and packages from Chapter 7 in mind:

- Create a new `ggplot` (`ggplot`), aesthetic mappings (`aes`), and add a `geom_*` (e.g., `geom_bar`, `geom_point`, `geom_smooth`)

- Add a layer with `+`, start each new function on a new line, don't forget to delete the plus sign if you delete the last line of code
- There are several predefined theme functions (e.g., `theme_bw`, `theme_light`).
- Modify axis, legend, and plot labels (e.g., with `labs`)
- Lay out panels in a grid (e.g., `facet_grid`)
- Discard (or adjust) the legend (e.g., `theme(legend.position = "none")`)
- Adjust the coordinate system (e.g., `coord_cartesian`)
- Further packages:
  - Themes: `ggthemes` (Arnold 2021)
  - Font types: `showtext` (Qiu 2022)
  - Color: The `RColorBrewer` (Neuwirth 2022) and the `viridis` package (Garnier 2021)
  - Many color palettes: `paletteer` (Hvitfeldt 2021)
  - Combine graphs: `patchwork` (Pedersen 2022b)
  - Zoom in: `ggforce` (Pedersen 2022a)

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