Data analysis using R for Psychology and Social Science

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Contents

Introduction

This book will (try to) teach you how to perform typical data analysis tasks: reading data, transforming and cleaning it up so you can visualize it and perform a statistical analysis of your choice. It covers most topics that you need to get you started but it cannot cover them all. One advantage of R is a sheer size of its ecosystem with new incredible libraries appearing very much on a daily basis. Covering them all is beyond the scope of any book, so instead I will concentrate on (trying to) building a solid understanding of things that you need to extend your R knowledge. Because of that some early chapters (e.g., on vectors, tables, or functions) might feel boring and too technical making you wonder why didn't we start with some exciting and useful analysis, working our way down to finer details. I have tried that[1] but, unfortunately, philosophy of R is about having many almost identical ways of achieving the same end. If you do not learn these finer details, you waste time wondering why seemingly the same code works in one case but fails in mysterious ways in the other one[2]. Therefore, please bear with me and struggle through vectors (which are everywhere), oddities and inconsistencies of subsetting, and learning how to write a function before you even started to use them properly. I can only promise that, from my personal experience, this is definitely worth the effort.

An important note: this book will *not* teach you statistics or machine learning beyond several examples at the very end. The reason for this is that it teaches data preparation and both statistics and machine learning are 90% about data preparation. This is most obvious in machine learning where data acquisition, cleaning, feature engineering, etc. to make it suitable for analysis take most of your time. The actual machine learning part boils down to trying various (all!) standard machine learning methods on it and picking one that gives best out-of-sample performance. That last part is so automated by now that it requires little knowledge beyond details of a specific package. Knowing how methods work is obviously beneficial but, and I hate to write this, not *that* critical for machine learning (not so for statistics or deep learning!). Same is true for statistical methods, although where time is split between preparing data for statistical analysis and interpreting and comparing models. As with machine learning,

[1] As a matter of fact, this was my approach when learning R.

[2] Talking from a personal experience here.

running statistical models itself is easy and automatic. If you know (enough of) statistics, you will have little trouble understanding how to work with these packages and functions. If you do not, no amount of reading of manuals will make it clearer.

Why R?

There are many software tools that allow you preprocess, plot, and analyze your data. Some cost money (SPSS, Matlab), some are free just like R (Python, Julia). Moreover, you can replicate all analyses that we will perform using Python in combination with Jupyter notebooks (for reproducible analysis), Pandas (for Excel-style table), and statmodels (for statistical analysis). R is hardly perfect. For example, its subsetting system is confusing and appears to follow "convenience over safety" approach that does not sit particularly well with me. However, R in combination with piping and Tidyverse family of packages makes it incredibly easy to write simple, powerful and expressive code, which is very easy to understand (a huge plus, as you will discover). I will run circles around myself trying to replicate the same analysis in Python or Matlab. In addition, R is loved by mathematicians and statisticians, so it tends to have implementations for all cutting edge statistical methods (but Python is your go to for machine and deep learning).

Why Tidyverse

The material is heavily skewed towards using Tidyverse family of packages. It looks different enough from base R to the point that one might call it a "dialect" of R[3]. Learning Tidyverse means that you have twice as many things to learn: I will always introduce both base R and Tidyverse version. Tidyverse is the main reason I use R (rather than Python or Julia) as it makes data analysis a breeze and makes your life so much easier. This is why I want you to learn its ways. At the same time, there is plenty of useful code that uses base R, so you need to know and understand it as well.

As a matter of fact, R is so rich and flexible that there many dialects and, therefore, plenty of opinion differences [4]. For example, data.table package reimplements the same functionality as base R and Tidyverse in very compact way. I does not fit my style but it might be something that feels natural to you, so I encourage you to take a look. There are also other packages to handle things like layout out your figures or working with summary tables that might suit you better. Point is, these material barely scratches the surfaces in terms of tools and approaches that you can use. View it as a starting point for your exploration not the complete map.

[3] R is extremely flexible, making it possible to redefine its own syntax.

[4] Just ask about "base R vs. Tidyverse" on Twitter and see the thread set itself on fire

Another thing to keep in mind is that Tidyverse is under very active development. This means that parts of this material could be outdated by the time you read it. E.g., *dplyr* do() verb was superseded by a group_modify() function, a warning generated by readr package was adapted for humans but now require an extra step to be used for column specification, we are now on the *third* set of pivoting functions, etc. None of the changes are breaking and deprecation process is deliberately slow (e.g., do() still works), so even when outdated the code in the book should still work for quite some time. However, you should keep in mind that things *might* have changed, so it is a good idea to check an official manual from time to time.

About the seminar itself

This is a material for *Applied data analysis for psychology using the open-source software R* seminar as taught at Institute of Psychology at University of Bamberg. Each chapter covers a single seminar, introducing necessary ideas and is accompanied by a notebook with exercises, which you need to complete and submit. To pass the seminar, you will need to complete all assignments. You do not need to complete or provide correct solutions for *all* the exercises to pass the course and information on how the points for exercises will be converted to an actual grade (if you need one) or "pass" will be available during the seminar.

The material assumes no foreknowledge of R or programming in general from a reader. Its purpose is to gradually build up your knowledge and introduce to a typical analysis pipeline. It is based on a data that is typical for the field (repeated measures, appearance, accuracy and response time measurements, Likert scale reports, etc.) and you are welcome to suggest your own data set for analysis. Even if you already performed the analysis using some other program, it would still be insightful to compare the different ways and, perhaps, you might gain a new insight. Plus, it is more engaging to work on your data.

Remember that throughout the seminar you can and should(!) always ask me whenever something is unclear, you do not understand a concept or logic behind certain code, or you simply got stuck. Do not hesitate to write me in the team or (better) directly to me in the chat (in the latter case, the notifications are harder miss and we don't spam others with our conversation).

Thinking like a computer

In some exercises your will not be writing code but reading and understanding it. Your job in this case is "to think like a computer". Your advantage is that computers are very dumb, so instructions for them must be written in a very simple, clear, and unambiguous way. This means that, with practice, reading code is easy for a human (well, reading a well-written code is easy, you will eventually encounter "spaghetti-code" which is easier to rewrite from scratch

than to understand). In each case, you simply go through the code line-by-line, doing all computations by hand and writing down values stored in the variables (if there are too many to keep track of). Once you go through the code in this manner, it should be completely transparent for you. No mysteries should remain, you should have no doubts or uncertainty about any(!) line. Moreover, you then can run the code and check that the values you are getting from computer match yours. Any difference means you made a mistake and code is working differently from how you think it does. In any case, **if you not 100% sure about any line of code, ask me, so we can go through it together!**

In a sense, this is the most important programming skill. It is impossible to learn how to write, if you cannot read the code first! Moreover, when programming you will probably spend more time reading the code and making sure that it works correctly than writing the new code. Thus, use this opportunity to practice and never use the code that you do not understand completely. Thus, there is nothing wrong in using stackoverflow but **never** use the code you do not understand (do not blindly copy-paste)!

About the material

Software

Installing R

Go to r-project.org and download a current stable version of R for your platform. Run the installer, accepting all defaults.

Installing R-Studio

Go to rstudio.com and download *RStudio Desktop Free* edition for your platform. Install it using defaults. The *R-Studio* is an integrated development environment for R but you need to install R separately first! The R-Studio will automatically detect latest R that you have and, in case you have several versions of R installed, you will be able to alter that choice via *Tools / Global Options…* menu.

I will explain the necessary details on using R-Studio throughout the seminar but the official cheatsheet is an excellent, compact, and up-to-date source of information. In fact, R Studio has numerous cheatsheets that describe individual packages in a compact form.

Installing RTools

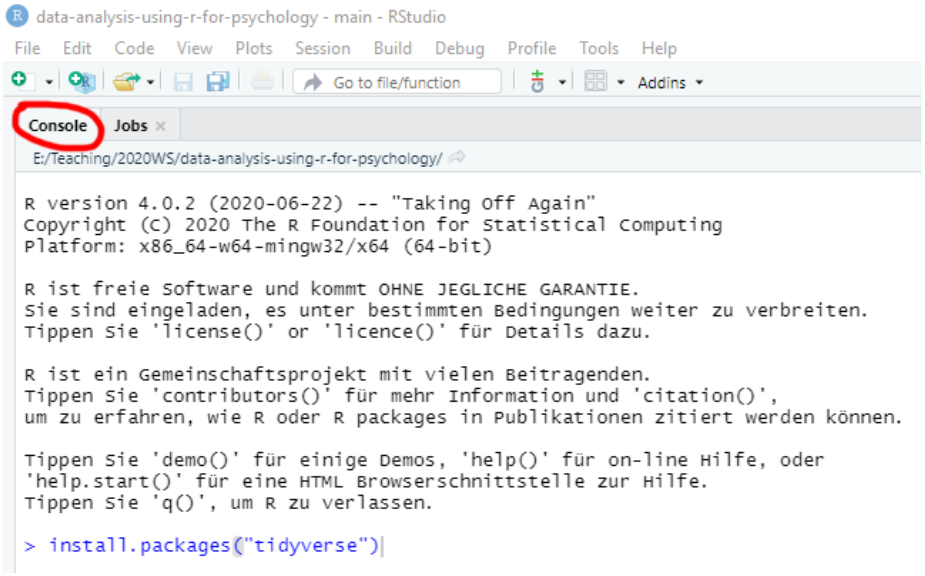
If you are using Windows, you might need Rtools for building and running some packages. You do not need to install it at the beginning, but when we will need it later, just following the link above, download the latest *Rtools* version, run the installer using the defaults and follow the instructions on that page to put Rtools on the PATH!

Installing packages

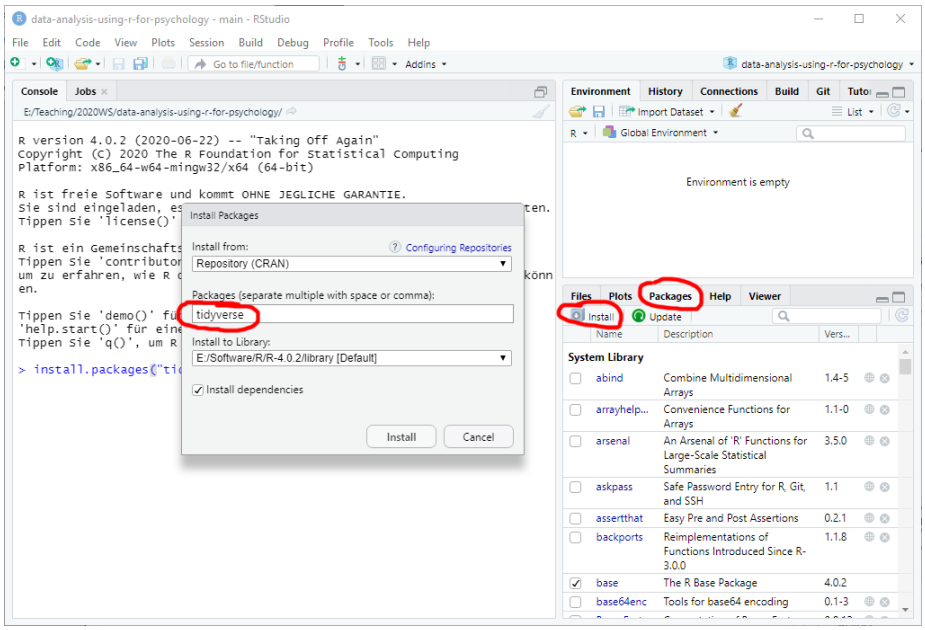
The real power of R lies in a vast community-driven family of packages suitable for any occasion. The default repository used by R and R-Studio is The Comprehensive R Archive Network (a.k.a. *CRAN*). It has very strict requirements

for submitted packages, which makes it very annoying for the authors but ensures high quality for you. We will use CRAN as a sole source of packages, but there are alternatives, such as Bioconductor that might have a package that is missing on CRAN. The Bioconductor relies on its own package manager, so you will need to consult the latest manual on their website.

To install a CRAN package you have two alternatives: via command line function or via R-Studio package manager interface (which will call the function for you). In the former case, go to *Console* tab and type `install.packages("package-name")`, for example `install.packages("tidyverse")`, and press **Enter**.



Alternatively, go to *Packages* tab, click on *Install* button, enter a package name in the window (it has autocomplete to help you), and press *Install*.



Sometimes, R will ask whether you want to install packages from source. In this case, it will grab the source code and compile the package, which takes time and requires RTools. In most cases, you can say "No" to install a pre-build binary version. The binary version will be slightly outdated but the emphasis is on *slightly*.

On other occasions, R-Studio will suggest restarting R Session as packages that need to be updated in use. You can do that but, in my experience, this could become a repetitive experience if one of the packages is used R Studio itself (so it starts it in a new session, realizes that it is in use, suggests to restart the session, etc.) My solution is to close *all* R Studio windows and use R directly. For Windows, you can find it the Start Menu, just make sure that you are using the correct version. Then, I use `install.packages()` to install and update everything I need.

Minimal set of packages

Please install the following packages:

- `tidyverse` : includes packages from data creation (`tibble`), reading (`readr`), wrangling (`dplyr`, `tidyr`), plotting (`ggplot2`). Plus type specific packages (`stringr` for strings, `forcats` for factors) and functional programming (`purrr`).
- `rmarkdown` : package for working with RMarkdown notebooks, which will we use to create reproducible analysis.
- `fs` : file system utilities.

Keeping R and packages up-to-date

R and packages are getting constantly improved, so it is a good idea to regularly update them. For packages, you can use *Tools / Check for Packages Updates…* menu in R-Studio. To update R and, optionally, packages, you can use installr package that can install newest R (but it keeps old version!) optionally copying your entire library of packages, updating packages, etc. It is easy to use even in R itself, as it creates an extra menu to make your life easier. For R-Studio itself, use *Help / Check for Updates* menu and install a newer version, if it is available (it is generally a good idea to keep your R-Studio in the newest state).

Chapter 1

Reproducable Research: Projects and Markdown Notebooks

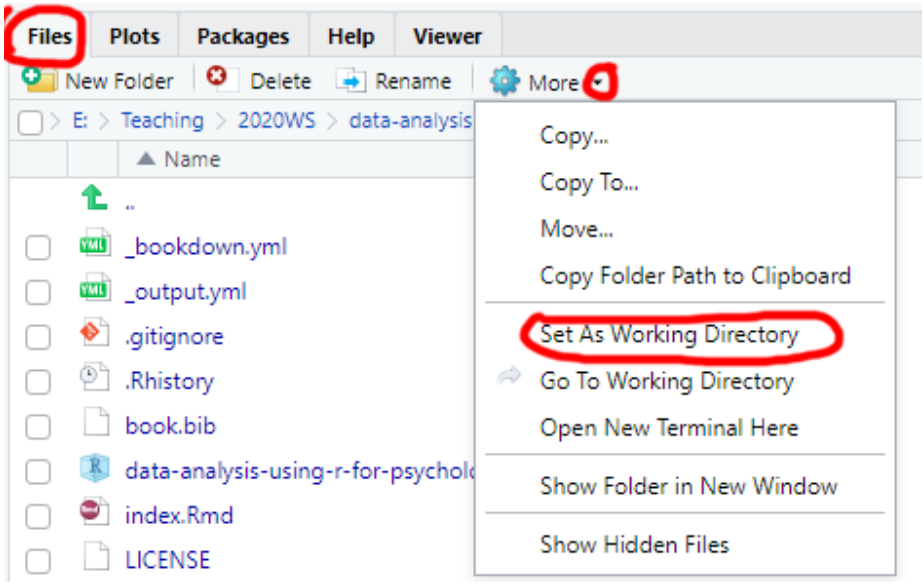
Our aim is to create reproducible research and analysis. It is a crucial component of the open science movement but is even more important for your own research or study projects. You want to create a self-contained well-documented easy-to-understand reproducible analysis. A complete self-sufficient code that others and, most importantly, future-you can easily understand saves you time and gives you a deeper insight into the results (less mystery is better in cases like these). It also makes it easier to communicate your results to other researchers or fellow students.

You should also *always* consider posting your results and analysis online at public repositories such as OSF, Science Data Bank, or GitHub. This not only help others but forces you into making such data + analysis archive more thoroughly. That, in turns, makes it easier for future-you to return to the data and the analysis. Using a GitHub (private) repository is a good idea even if you are not planning to collaborate with others as it gives you a version-controlled code in a cloud and makes synchronizing it between different machines easy.

1.1 Projects

One of the most annoying features of R is that it looks for files and folders only relative to its "working directory", which is set via setwd(dir) function. What makes it particularly confusing is that your currently open file may be in some *other* folder. If you simply use *File / Open*, navigate to that file and open it, it does not change your working directory. Similarly, in R-Studio you can navigate

through file system using *Files* tab and open some folder you are interested in but that **does not make it a working directory**. You need to click on *More* and *Set As Working Directory* to make this work (that trick won't work for an opened file).



In short, it may *look* that you are working in a particular folder but R will have its own opinion about this. Whenever this happens, it is really confusing and involves a lot of cursing as R cannot find files that you can clearly see with your own eyes. To avoid this, you should organize any program, project or seminar as an *R Project*, which assumes that all necessary files are in the project folder, which is also the working directory. R Studio has some nice project-based touches as well, like keeping tracking of which files you have open, providing version control, etc. Bottom line, **always** create a new R-project to organize yourself, even if it involves just a single file to try something out. Remember, "Nothing is more permanent than a temporary solution!" Which is why you should **always** write your code, as if it is for a long term project (good style, comprehensible variable names, comments, etc.), otherwise your temporary solution grows into permanent incomprehensible spaghetti code.

Let us create a new project for this seminar. Use *File / New Project...*, which will give you options of creating it in a new directory (you get to come up with a name), using an existing directory (project will be named after that directory), or check it out from remote repository (if you know git, this is very convenient). You can do it either way. This will be a project folder for this seminar and you will need to put all notebooks and external data files into that folder. Next time you need to open it, you can use *File / Recent Projects* menu, *File / Open Project...*_ `menu, or simply open the`.Rproj' file in that folder.

1.2 Quattro and RMarkdown notebooks

There are two very similar notebook formats in R: an older R Markdown and a new Quatro. On the one hand, the latter is the future, so it would make sense to use Quatro notebooks. On the other hand, there is little practical difference for you, as from a R-only end-user point of view, they differ mostly in how they specify chunk options (more on that later).

Both RMarkdown and Quattro rely on a markdown language to combine formatted text, figures, references (via bibtex) and cross-references with code[1]. When a notebook is knitted, all the code is ran and its output, such as tables and figures, is inserted into the final document. This allows you to combine the narrative (the background, the methodology, comments, discussion, conclusions, etc.) with the actual code that implements what you described. And, you can be sure that the figures and numbers are the latest correct version.

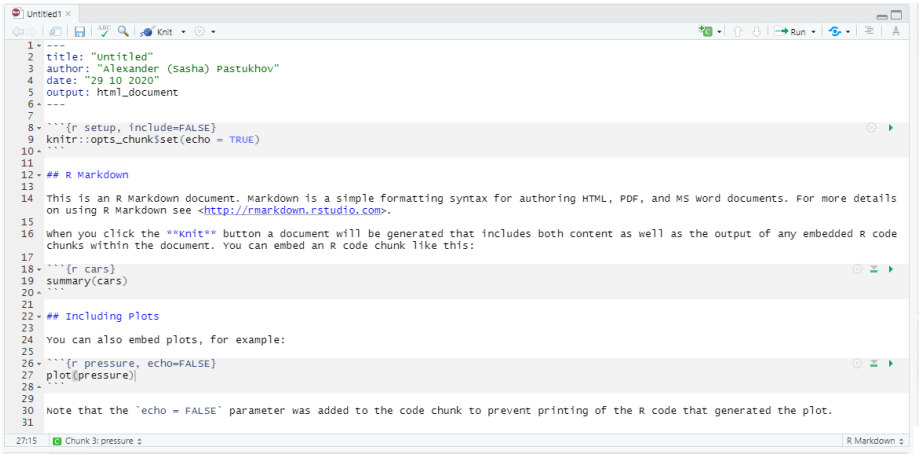
Notebooks can be knitted into a variety of formats including HTML, PDF, Word document, EPUB book, etc. Thus, instead of creating plots and tables to save them into separate files so you can copy-paste them into your Word file (and then redoing this, if something changed, and trying to find the correct code that you used the last time, and wondering why it does not run anymore…), you simply "knit" the notebook and get the current and complete research report, semester work, presentation, etc. Even more importantly, same goes for others, as they also can knit your notebook and generate its latest version in format they need. All exercises will involve using RMarkdown notebooks, so you need to familiarize yourself with them.

We will start by learning the markdown, which is a family of human-oriented markup languages. Markup is a plain text that includes formatting syntax and can be translated into visually formatted text. For example, HTML and LaTeX are markup languages. The advantage of markup is that you do not need a special program to edit it, any plain text editor will suffice. However, you do need a special program to turn this plain text into the document. For example, you need Latex to compile a PDF or a browser to view HTML properly. However, anyone can read your original file even if they do not have Latex, PDF reader, or a browser installed (you do need Word to read a Word file!). **Markdown** markup language was designed to make formatting simple and unobtrusive, so the plain document is easier to read (you can read HTML but it is hardly fun!). It is not as feature-rich as HTML or LaTeX but covers most of your usual needs and is very easy to learn!

Create a new markdown file via *File / New File / Quatro Document…* or *File / New File / R Markdown…* menu. Use `Seminar 1` for its title and HTML as default output format. Then you need to save the file (press **Ctrl + S** or use *File/Save* menu) and call the file `seminar-01` (R Studio will add `.qmd` or `.Rmd` extension automatically). The file you created is not empty, as R Studio is kind

[1] This material was prepared using RMarkdown, knitr, and bookdown

enough to provide an example for you. Knit the notebook by clicking on *Knit* button or pressing **Ctrl+Shift+K** to see how the properly typeset text will look (it will appear in a *Viewer* tab).



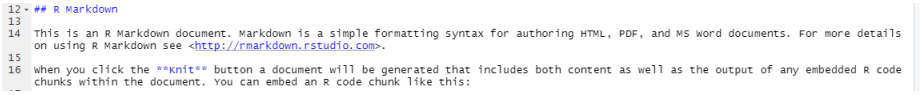
Let us go through the default RMarkdown notebook that R Studio created for us (it has more content than a default Quatro document).

```
---
title: "Untitled"
author: "Alexander (Sasha) Pastukhov"
date: "29 10 2020"
output: html_document
---
```

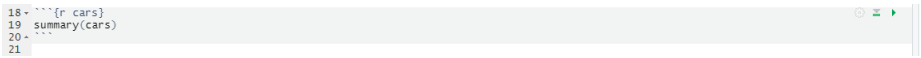
The top part between two sets of `---` is a notebook header with various configuration options written in YAML (yes, we have two different languages in one file). `title`, `author`, and `date` should be self-explanatory. `output` defines what kind of output document knitr will generate. You can specify it by hand (e.g., `word_document`) or just click on drop down next to `Knit` button and pick the option you like (we will use the default HTML most of the time). These are sufficient for us but there are numerous other options that you can specify, for example, to enable indexing of headers. You can read about this at yihui.org/knitr.

```
```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
```
```

The next section is the "setup code chunk" that specifies default options for how the code chunks are treated by default (whether they are executed, whether the output, warnings, or messages are shown, etc.). By default code in chunks is run and its output is shown (`echo = TRUE`) but you can change this behavior on per-chunk basis by pressing the gear button at the top-right. The setup chunk is also a good place to import your libraries (we will talk about this later) as it is always run before any other chunks (so, even if you forgot to run it to load libraries, R Studio will do this for you).

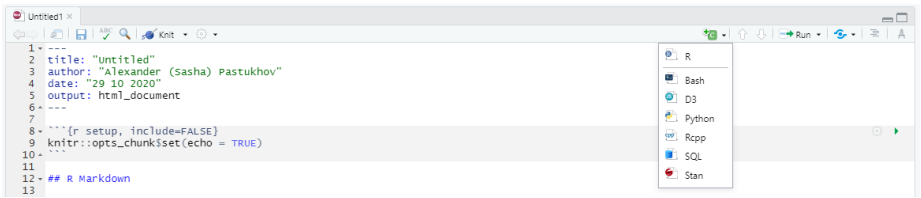


Next, we have plain text with rmarkdown, which gets translated into formatted text when you click on *Knit* button. You can write like this anywhere outside of code chunks to explain the logic of your analysis. You should write why and how the analysis is performed but leave technical details on programming to the chunk itself, where you can comment the code.



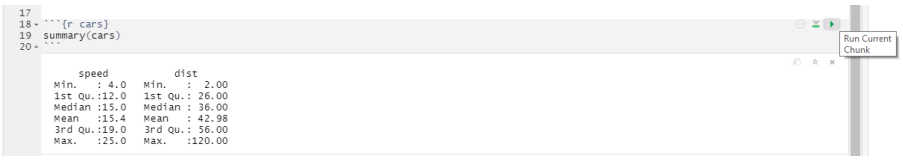
Finally, we have our first "proper" chunk of code (the "setup" chunk above is a special case). A code chunk is simply the code embedded between `` ```{r <name of the chunk>} `` and the seconds set of ticks `` ``` ``. Here `r` specifies that the code inside is written in R language but you can use other languages such as Python (via reticulate package), Stan, or SQL. The `name of the chunk` is optional but I would recommend to specify it, as it reminds you what this code is about and it makes it easier to navigate in large notebooks. In the bottom-left corner, you can see which chunk or section you are currently at and, if you click on it, you can quickly navigate to a different chunk. If chunks are not explicitly named, they will get labels `Chunk 1`, `Chunk 2`, etc. making it hard to distinguish them.

There are additional options that you can specify per chunk (whether to run the code, to show the output, what size the figures should be, etc.). Generally we won't need these options but you can get an idea about them by looking at the official manual. You can create a chunk by hand or click on "Create chunk" drop-down list (in this case, it will create the chunk at the position of the cursor)



Finally, you run **all** the code in the chunk by clicking on *Run current chunk button* at the top-right corner of the chunk or by pressing **Ctrl+Shift+Enter** when the you are inside the chunk. However, you can also run just a *single line* or only *selected lines* by pressing **Ctrl+Enter**. The cool thing about RMarkdown

in RStudio is that you will see the output of that chunk right below it. This means that you can write you code chunk-by-chunk, ensure that each works as intended and only when knit the entire document. Run the chunks in your notebook to see what I mean.



Working with Quatro notebook is very similar but certain YAML header options are different (e.g., `format: html` instead of `output: html_document`) and chunk settings are inside the chunk instead of being inside curly brackets. These become important when you go in deeper and want to build a website or write a book using Quatro but won't matter much for this seminar.

1.3 Exercise

For the today's exercise, I want you to familiarize yourself with markdown. Create a RMarkdown (not Quatro!) notebook for this. Go to markdownguide.org and look at basic and extended syntax (their cheat sheet is also very good). Write any text you want that uses all the formatting and submit the `.Rmd` file to MS Teams. Please note that if you use an external image, you must submit it (zip everything into a single file) and the path that you use must be *relative*. Remember, if your file path is "c:/Documents/R-seminar/funny.png" chances are I do not have that file and that set of folders on my computer and your markdown won't render for me.

Chapter 2

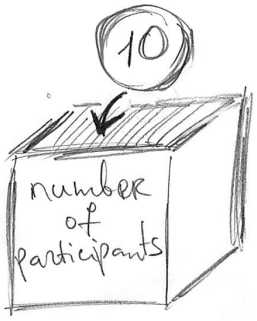
Vectors! Vectors everywhere!

Before reading the chapter, please download the exercise notebook (**Alt+Click** to download it or right-click as *Save link as...*), put it into your seminar project folder, and open the project. You need both the text and the notebook with exercises to be open, as you will be switching between them.

Before we can start using R for analysis, you need to learn about vectors. This is a key concept in R, so your understanding of it will determine how easy it will be for you to use R in general. Do all of the exercises and do not hesitate to ask me whenever something is unclear. Remember, you need to master vectors before you can master R!

2.1 Variables as boxes

In programming, a concept of a variable is often described as a box you can put something in. A box has a name tag on it, which is the *name* of the variable. Whatever you put in is the *value* that you store.



This "putting in" concepts is reflected in R syntax

```
number_of_participants <- 10
```

Here, `number_of_participants` is the name of the variable (name tag for the box that we will be using), `10` is the value you store, and `<-` means *"put `10` into variable `number_of_participants`"*. If you know other programming languages, you probably expected the usual assignment operator `=`. Confusingly, you can use it in R as well, but there are some subtle, yet important, differences in how they operate behind the scenes. We will meet `=` again when we will be talking about functions and, in particular, Tidyverse way of doing things but for now **only use `<-` operator**!

2.2 Assignment statement in detail

One *very important* thing to remember about the assignment statement `<variable> <- <value>`: The *right side* is evaluated first until the final value is established and then, and only then, it is stored in a `<variable>` specified on the left side. This means that you can use the same variable on *both* sides. Take a look at the example

```
x <- 2
print(x)
```

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

```
x <- x + 5
print(x)
```

```
## [1] 7
```

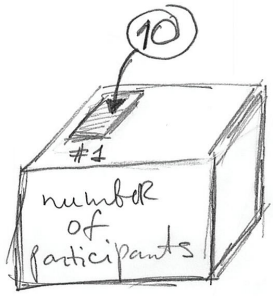
We are storing value `2` in a variable `x`. In the next line, the *right side* is evaluated first. This means that the current value of `x` is substituted in its place on the right side: `x + 5` becomes `2 + 5`. This expression computed and we get `7`. Now, that the *right side* is fully evaluated, the value can be stored in `x` replacing (overwriting) the original value it had.

R's use of `<-` makes it easier to memorize this *right side is fully evaluated first* rule. However, as noted above, we will meet `=` operator and this one makes it look like a mathematical equation. However, assignments (storing values in a variable) have nothing in common with mathematical equations (finding values of variables to ensure equality)!

Do exercise 1.

2.3 Vectors and singluar values (scalars, which are also vectors)

The box metaphor you've just learned, doesn't quite work for R. Historically, R was developed as a language for statistical computing, so it was based on concepts of linear algebra instead of being a "normal" programming language like Python or C. This means that there is no conceptual divide between single values and containers (arrays, lists, dictionaries, etc.) that hold many single values. Instead, the primary data unit in R is a *vector*, which you may remember from geometry or, hopefully, from linear algebra, as an arrow that goes from 0 to a specific point in space. From computer science point of view, a vector is just a list of numbers (or some other values, as you will learn later). This means that there are no "single values" in R, there are only vectors of variable length. Special cases are vectors of length one, which are called *scalars* [1] (but they are still vectors) and zero length vectors that are, sort of, a Platonic idea of a vector without actual values. With respect to the "box metaphor", this means that we always have a box with indexed (numbered) slots in it. A simple assignment makes sure that "the box" has as many slots as values you want to put in and stores these values one after another starting with slot #1[2]. Therefore, the example above `number_of_participants <- 10` creates a *vector* variable with one (1) slot and stores the value in it.



But, as noted above, a single value (vector with length of one) is a special case. More generally you write:

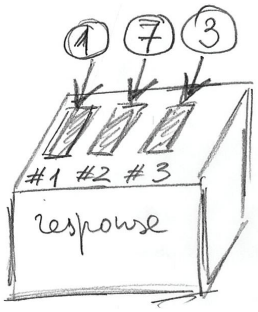
```
response <- c(1, 7, 3)
```

Here, you create a variable (box) named `response` that has three slots in it because you want to store three values. You put values `1`, `7`, `3` into the slots #1, #2, and #3. The `c(1, 7, 3)` notation is how you create a vector in R by **c**oncatenating (or **c**ombining) values[3]. The figure below illustrates the idea:

[1] Multiplication of a vector by another vector *transforms* it but for a single element vector the only transformation you can get is "scaling", hence, the name.

[2] If you have experience with programming languages like Python, C, or Java: indexes in R start with 1, not with 0.

[3] I find this to be a very poor choice of name but we are stuck with it, so your only option is to get used to it.



Building on the box metaphor: If you can store something in a box, you can take it out! In the world of computers it works even better, because rather than taking something out, you just make a copy of that and store this copy somewhere else or to use it to compute things. Minimally, we would like to see what is inside of the box. For this, you can use print function:

```
response <- c(1, 7, 3)
print(response)
```

```
## [1] 1 7 3
```

Or, we can make a copy of values in one variable and store them in another:

```
x <- c(3, 6, 9)
y <- x

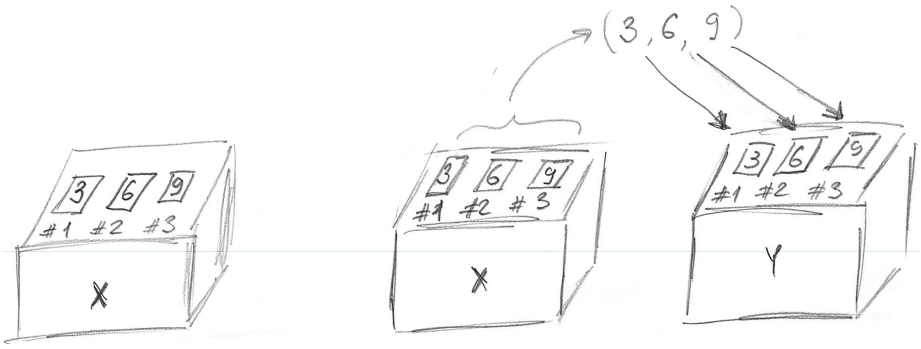
print(x)
```

```
## [1] 3 6 9
```

```
print(y)
```

```
## [1] 3 6 9
```

Here, we create a 3-slot variable `x` so that we can put in a vector of length 3 created via concatenation `c(3, 6, 9)`. Next, we make a copy of these three values and store them in a different variable `y`. Importantly, the values in variable `x` stayed as they were. Take a look at the figure below, which graphically illustrate this:



Do exercise 2.

Remember, everything is a vector! This means that `c(3, 6, 9)` does not concatenate numbers, it concatenates three length one vectors (scalars) `3`, `6`, `9`. Thus, concatenation works on longer vectors in exactly the same way:

```
x <- c(1, 2, 3)
y <- c(4, 5)
print(c(x, y))
```

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

Do exercise 3.

2.4 Vector indexes (subsetting)

A vector is an ordered list of values (box with some slots) and, sometimes, you need only one of the values. Each value (slot in the box) has its own index from 1 till N, where N is the length of the vector. To access that slot you use square brackets `some_vector[index]`. You can both get and set the value for the individual slots the same way you do it for the whole vector.

```
x <- c(1, 2, 3)
# set SECOND element to 4
x[2] <- 4

# print the entire vector
print(x)
```

```
## [1] 1 4 3
```

```
# print only the third element
print(x[3])
```

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

Do exercise 4.

Unfortunately, vector indexing in R behaves in a way that may[4] catch you by surprise. Or, even worse, you will not even notice that your indexing does not work and screwes up your analysis. If your vector contains five values, you would expect that an index of `0` (negative indexes are special and will be discussed below) or above `5` generates an error. Not in R! Index of `0` is a special case and produces an *empty vector* (vector of zero length).

```
x <- c(1, 2, 3)
x[0]
```

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

If you try to get vector element using index that is larger than vector length (so `6` and above for a 5 element vector), R will return `NA` ("Not Available" / Missing Value).

```
x <- c(1, 2, 3)
x[5]
```

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

In both cases, it won't generate an error or even warn you!

When *setting* a value by index, using `0` will produce no effect, because you are trying to put a value into a vector with no "slots". Oddly enough, this will also generate neither an error nor a warning, so beware!

```
x <- c(1, 2, 3)
x[0] <- 5
print(x)
```

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

If you set an element with index **larger** than vector length, the vector will be automatically expanded to that length and all the elements between the old values and the new one will be `NA` ("Not Available" / Missing Value).

```
x <- c(1, 2, 3)
x[10] <- 5
print(x)
```

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

This may sound too technical but I want you to learn about this because R conventions are so different from other programming languages and, also, from what you would intuitively expect. If you are not aware of these highly peculiar rules, you may never realize that your code is not working properly because, remember, you will never see an error or even a warning! It should also make you more cautious and careful when programming in R. It is a very powerful language that allows you to be very flexible and expressive. Unfortunately, that

[4] Who am I kidding? Will!

flexibility means that base R won't stop you from shooting yourself in a foot. Even worse, sometimes you won't even notice that your foot is shot and bleeding because R won't generate either errors or warnings, as in examples above. Good news is that things are far more restricted and consistent in Tidyverse.

Do exercise 5.

You can also use *negative* indexes. In that case, you *exclude* the value with that index and return or modify the rest[5].

```
x <- c(1, 2, 3, 4, 5)
# this will return all elements but #3
x[-3]
```

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

```
x <- c(1, 2, 3, 4, 5)
# this will assign new value (by repeating length one vector) to all elements but #2
x[-2] <- 10
x
```

```
## [1] 10  2 10 10 10
```

Given that negative indexing returns everything **but** the indexed value, what do you think will happen here?

```
x <- c(10, 20, 30, 40, 50)
x[-10]
```

Do exercise 6.

Finally, somewhat counterintuitively, the entire vector is returned if you do not specify an index in the square brackets. Here, lack of index means "everything".

```
x <- c(10, 20, 30, 40, 50)
x[]
```

```
## [1] 10 20 30 40 50
```

2.5 Names as an Index

As you've just learned, every slot in vector has its numeric (integer) index. However, this number only indicates an index (position) of a slot but tells you nothing on how it is conceptually different from a slot with a different index. For example, if we are storing width and height in a vector, remembering their order may be tricky: was it `box_size <- c(<width>, <depth>, <height>)` or `box_size <- c(<height>, <width>, <depth>)`? Similarly, looking at

[5] People who use Python, please be aware that negatives indexes in R and in Python behave completely differently!

`box_size[1]` tells that you are definitely using the *first* dimension but is it `height` or `width` (or `depth`)?

In R, you can use names to supplement numeric indexes. It allows you to add meaning to a particular vector index, something that becomes extremely important when we use it for tables. There are two ways to assign names to indexes, either when you are creating the index via c() function or, afterwards, via names() function.

To create named vector via c() you specify a name before each value as `c(<name1> = <value1>, <name2> = <value2>, ...)`:

```
box_size <- c("width"=2, "height"=4, "depth"=1)
print(box_size)
```

```
##  width height  depth
##      2      4      1
```

Note the names appearing above each value. You can now use either numeric index or name to access the value.

```
box_size <- c("width"=2, "height"=4, "depth"=1)
print(box_size[1])
```

```
## width
##     2
```

```
print(box_size["depth"])
```

```
## depth
##     1
```

Alternatively, you can use names() function to both get and set the names. The latter works via a *very counterintuitive* syntax `names(<vector>) <- <vector-with-names>`

```
# without names
box_size <- c(2, 4, 1)
print(box_size)
```

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

```
# with names
names(box_size) <- c("width", "height", "depth")
print(box_size)
```

```
##  width height  depth
##      2      4      1
```

```
# getting all the names
print(names(box_size))
```

```
## [1] "width"  "height" "depth"
```

Because everything is a vector, `names(<vector>)` is also a vector, meaning that you can get or set just one element of it.

```
box_size <- c("width"=2, "height"=4, "depth"=1)

# modify SECOND name
names(box_size)[2] <- "HEIGHT"
print(box_size)
```

```
##  width HEIGHT  depth
##      2      4      1
```

Finally, if you use a name that is not in the index, this is like using numeric index larger than the vector length. Just as for out-of-range numeric index, there will be neither error not warning and you will get an `NA` back.

```
box_size <- c("width"=2, "height"=4, "depth"=1)
print(box_size["radius"])
```

```
## <NA>
##   NA
```

Do exercise 7.

2.6 Slicing

So far we were reading or modifying either the whole vector or just one of its elements. However, the index you pass in square brackets (you've guessed it) is also a vector! Which means that you can construct a vector of indexes the same way you construct a vector of any values (the only restriction is that index values must integers and that you cannot mix negative and positive indexes).

```
x <- c(10, 20, 30, 40, 50)
x[c(2, 3, 5)]
```

```
## [1] 20 30 50
```

When constructing a vector index, you can put index values in the order you require (normal ascending order, starting from the end of it, random order, etc.) or use the same index more than once.

```
x <- c(10, 20, 30, 40, 50)
x[c(3, 5, 1, 1, 4)]
```

```
## [1] 30 50 10 10 40
```

You can also use several negative indexes to exclude multiple values and return the rest. Here, neither order nor duplicate indexes matter. Regardless of which

value you exclude first or how many times you exclude it, you still get *the rest* of the vector in its default order.

```
x <- c(10, 20, 30, 40, 50)
x[c(-4, -2, -2)]
```

```
## [1] 10 30 50
```

Note that you cannot mix positive and negative indexes as R will generate an error (at last!).

```
x <- c(10, 20, 30, 40, 50)

# THIS WILL GENERATE AN ERROR:
# "Error in x[c(-4, 2, -2)] : only 0's may be mixed with negative subscripts"
x[c(-4, 2, -2)]
```

Finally, including zero index makes no difference but generates neither an error nor a warning.

```
x <- c(10, 20, 30, 40, 50)
x[c(1, 0, 5, 0, 0, 2, 2)]
```

```
## [1] 10 50 20 20
```

You can also use names instead of numeric indexes.

```
box_size <- c("width"=2, "height"=4, "depth"=1)
print(box_size[c("height", "width")])
```

```
## height  width
##      4      2
```

However, you cannot mix numeric indexes and names. The reason is that a vector can hold only values of one type (more on that next time), so all numeric values will be converted to text (`1` will become `"1"`) and treated as names rather than indexes.

2.7 Colon Operator and Sequence Generation

To simplify vector indexing, R provides you with a shortcut to create a range of values. An expression `A:B` (a.k.a.Colon Operator) builds a sequence of integers starting with `A` and ending with **and including(!)** `B`[6].

```
3:7
```

```
## [1] 3 4 5 6 7
```

Thus, you can use it to easily create an index and, because everything is a vector!, combine it with other values.

[6]The latter is not so obvious, if you come from Python

```
x <- c(10, 20, 30, 40, 50)
x[c(1, 3:5)]
```

```
## [1] 10 30 40 50
```

The sequence above is increasing but you can also use the colon operator to construct a decreasing one.

```
x <- c(10, 20, 30, 40, 50)
x[c(5:2)]
```

```
## [1] 50 40 30 20
```

The colon operator is limited to sequences with steps of `1` (if end value is larger than the start value) or `-1` (if end value is smaller than the start value). For more flexibility you can use Sequence Generation function: `seq(from, to, by, length.out)`. The `from` and `to` are starting and ending values (just like in the colon operator) and you can specify either a step via `by` parameter (as, in "from A to B by C") or via `length.out` parameter (how many values you want to generate, effectively `by = ((to - from)/(length.out - 1))`. Using `by` version:

```
seq(1, 5, by=2)
```

```
## [1] 1 3 5
```

Same sequence but using `length.out` version:

```
seq(1, 5, length.out=3)
```

```
## [1] 1 3 5
```

You have probably spotted the `=` symbol. Here, it is not an assignment but is used to specify values of parameters when you call a function. Thus, we are still sticking with `<-` **outside** of the function *calls* but are using `=` **inside** the function calls.

Do exercise 8.

2.8 Working with two vectors of *equal* length

You can also use mathematical operations on several vectors. Here, vectors are matched element-wise. Thus, if you add two vectors of *equal* length, the *first* element of the first vector is added to the *first* element of the second vector, *second* element to *second*, etc.

```
x <- c(1, 4, 5)
y <- c(2, 7, -3)
z <- x + y
print(z)
```

```
## [1]  3 11  2
```

Do exercise 9.

2.9 Working with two vectors of *different* length

What if vectors are of *different* length? If the length of the longer vector is a *multiple* of the shorter vector length, the shorter vector is "recycled" , i.e., repeated N-times (where $N = length(longer\ vector)/length(shorter\ vector)$) and this length-matched vector is then used for the mathematical operation. Please note that this generate neither an error, nor a warning! This is another example of "convenience over safety" approach in R, so you should be very careful and *always* double-check length of your vectors. Otherwise, your code will work incorrectly and, *if you are lucky*, you might notice this.

To see how recycling works, take a look at the results of the following computation

```
x <- 1:6
y <- c(2, 3)
print(x + y)
```

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

Here, the values of `y` were repeated three times to match the length of `x`, so the actual computation was `c(1, 2, 3, 4, 5, 6) + c(2, 3, 2, 3, 2, 3)`. A vector of length 1 (scalar) is a special case because any integer is a multiple of 1, so that single value is repeated `length(longer_vector)` times before the operation is performed.

```
x <- 1:6
y <- 2
print(x + y)
```

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

Again, the actual computation is `c(1, 2, 3, 4, 5, 6) + c(2, 2, 2, 2, 2, 2)`.

If the length of the longer vector **is not** a multiple of the shorter vector length, R will repeat the shorter vector N times, so that $N = ceiling(length(longer\ vector)/length(shorter\ vector))$ (where ceiling() rounds a number up) and truncates (throws away) extra elements it does not need. Although R will do it, it will also issue a warning (yay!) about mismatching objects' (vectors') lengths.

```
x <- c(2, 3)
y <- c(1, 1, 1, 1, 1)
print(x + y)
```

```
## Warning in x + y: longer object length is not a multiple of shorter object
## length
```

```
## [1] 3 4 3 4 3
```

Finally, combining any vector with null length vector produces a null length vector[7].

```
x <- c(2, 3)
y <- c(1, 1, 1, 1, 1)
print(x + y[0])
```

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

One thing to keep in mind: R does this length-matching-via-vector-repetition automatically and shows a warning only if two lengths are not multiples of each other. This means that vectors will be matched by length even if that was not your plan. Imagine that your vector, which contains experimental condition (e.g. contrast of the stimulus), is about all ten blocks that participants performed but your vector with responses is, accidentally, only for block #1. R will **silently(!)** replicate the responses 10 times to match their length without ever telling you about this. Thus, do make sure that your vectors are matched in their length, so that you are not caught surprised by this behavior (you can use function length() for this). Good news, it is much more strict in Tidyverse, which is designed to make shooting yourself in a foot much harder.

Do exercise 10.

2.10 Applying functions to a vector

Did I mention that everything is a vector? This means that when you are using a function, you are always applying it to a vector. This, in turn, means that you apply the function to **all values** in one go. For example, you can compute a cosine of all values in the vector.

```
cos(c(0, pi/4, pi/2, pi, -pi))
```

```
## [1]  1.000000e+00  7.071068e-01  6.123032e-17 -1.000000e+00 -1.000000e+00
```

In contrast, in Python or C you would need to loop over values and compute cosine for one value at a time (matrix-based NumPy library is a different story). Or think about Excel, where you need to extend formula over the rows but each row is computed independently (so you can deliberately or accidentally miss some rows). In R, because everything is the vector, the function is applied to every value automatically. Similarly, if you are using aggregating functions, such as mean() or max(), you can pass a vector and it will return a length-one vector with the value.

[7] No idea!

```
mean(c(1, 2, 6, 9))
```

```
## [1] 4.5
```

2.11 Wrap up

By now you have learned more about vectors, vector indexing, and vector operations in R than you probably bargained for. Admittedly, not the most exciting topic. On top of that, there was not a single word on psychology or data analysis! However, R is obsessed with vectors (everything is a vector!) and understanding them will make it easier to understand lists (a polyamorous cousin of a vector), tables (special kind of lists made of vectors), and functional programming (on which R is built on). Finish this seminar by doing remaining exercises. Let's see whether R can still surprise you!

Do exercises 11-18.

Chapter 3

Tables and Tibbles (and Tribbles)

Please download the exercise notebook (**Alt+Click** to download it or right-click as *Save link as…*), put it into your seminar project folder and open the project. You need both the text and the notebook with exercises to be open, as you will be switching between them.

3.1 Primary data types

Last time we talked about the fact that everything[1] is a vector in R. All examples used numeric vectors which are two of the four primary types in R.

- Real numbers (double precision floating point numbers) that can be written in decimal notation with or without a decimal point (`123.4` or `42`) or in a scientific notation (`3.14e10`). There are two special values specific to the real numbers: `Inf` (infinity) and `NaN` (not a number). The latter looks similar to `NA` (Not Available / Missing Value) but is a different special case (see R documentation for details.
- Integer numbers that can be specified by adding `L` to the end of an integer number `5L`. Without that `L` a *real* value will be created (`5` would be stored as `5.0`).
- Logical or Boolean values of `TRUE` and `FALSE`. They can also be written as `T` and `F` but this practice is discouraged by the Tidyverse style guide.
- Character values (strings) that hold text between a pair of matching `"` or `'` characters. The two options mean that you can surround your text by `'` if you need to put a quote inside: `'"I have never let my schooling interfere with my education." Mark Twain'` or by `"` if you need an

[1] Terms and conditions apply.

apostrophe `"participant's response"`. Note that a string **is not** a vector of characters. This would make a lot of sense but it is not. This is why indexing or slicing will not work and you need to use special functions.

You can convert from one type to another and check whether a particular vector is of specific type. Note that if a vector cannot be converted to a specified type, it is "converted" to `NA` instead.

- to integer via as.integer(), use is.integer() to check a value. When converting
  - from a real number the fractional part is *discarded*, so `as.integer(1.8)` → `1` and `as.integer(-2.1)` → `2`
  - from logical value `as.integer(TRUE)` → 1 and `as.integer(FALSE)` → 0
  - from string only if it is a properly formed number, e.g., `as.integer("12")` → `12` but `as.integer("_12_")` is `NA`. Note that a real number string is converted first to a real number and then to an integer so `as.integer("12.8")` → `12`.
  - from `NA` → `NA`
- to real number via as.numeric() / as.double(), check a value via is.double() (avoid is.numeric() as Hadley Wickham writes that it is not doing what you would think it should).
  - from logical value `as.double(TRUE)` → 1.0 and `as.double(FALSE)` → 0.0
  - from string only it is a properly formed number, e.g. `as.double("12.2")` → `12.2` but `as.double("12punkt5")` is `NA`
  - from `NA` → `NA`
- to logical `TRUE`/`FALSE` via as.logical and check a value via is.logical().
  - from integer or real, zero (`0` or `0.0`) is `FALSE`, any other non-zero value is `TRUE`
  - from a string, it is `TRUE` for `"TRUE"`, "`True`", `"true"`, or `"T"` but `NA` if `"t"` `"TRue"`, `"truE`, etc. Same goes for `FALSE`.
  - from `NA` → `NA`
- to a character string via as.character() and check via is.character()[2]
  - numeric values are converted to a string representation with scientific notation being used for large numbers.
  - logical `TRUE`/`T` and `FALSE`/`T` are converted to `"TRUE"` and `"FALSE"`.
  - `NA` → `NA`

Do exercise 1.

[2]Be aware that str() function has nothing to do with strings but displays a structure of an object. A very unfortunate choice of name but we are stuck with it.

3.2 All vector values must be of the same type

All values in a vector must be of the same type - all integer, all double, all logical, or all strings, which is why they are also called *atomic* vectors. This ensures that you can apply the same function or operation to the entire vector without worrying about type compatibility. However, this means that you cannot mix different value types in a vector. If you do try to concatenate vectors of different types, all values will be converted to a more general / flexible type. Thus, if you mix numbers and logical values, you will end up with a vector of numbers. Mixing anything with strings will convert the entire vector to string. Mixing in `NA` does not change the vector type.

Do exercise 2.

3.3 Lists

(Atomic) vectors are homogeneous lists of primary types items, whereas lists are lists that can contain *any* item including vectors of different primary type data, other lists, or other objects[3]. Otherwise, (well, almost, see below) you work with them the same way is with vectors. You create a list via `list()` function and then you can concatenate lists via the same c() function, access individual elements via numeric index or names, use slicing, etc.

3.4 Subsetting, a fuller version

Unfortunately, this is the point where we need to talk about subsetting (accessing individual elements of a vector or of a list via indexes or names) yet again. This is because R has several different ways of doing this that look similar and, to make things worse, *sometimes* produce identical results. I do not expect you to memorize or even fully appreciate all the intricate details (I am not even sure I know them all). But I do need you to understand the fundamental difference between the two ways of doing subsetting and to be aware of potential issues that can easily cause confusion. If the latter is the case, return to this section, read the official manual, or read the subsetting section in "Advanced R" book by Hadley Wickham.

You already know subsetting via *single* square brackets: `x[1]`. This is called *preserving* subsetting because it returns a *part of an object* (vector or list) that your requested *as is*. I.e., if you used them to access part of a a vector, you get a vector. If you used them to access a list or a table, you get a list or a table.

In addition, you can use *double* square brackets: `x[[1]]`. These are called *simplifying* subsetting because they extract *content* at that location. If you have a list of vectors `l` then `l[2]` (preserving) would return a single item list

[3] If you are familiar with Python, you can think of R lists as Python lists and dictionaries mixed together.

but `l[[2]]` would return a vector stored at that location. A metaphor based on @RLangTip: "If list `x` is a train carrying objects, then `x[[5]]` is the object in car 5; `x[5]` is a train consisting only of car 5."

Note that the simplifying notation allows you to extract content of only *one* item. Therefore, you cannot use it with slicing (extracting content of many items), negative indexes (even if you will end up with just one index), or zero index. The good news is that R will actually generate an error message instead of failing silently, although error messages will be both mysterious and *different* depending on exact circumstances. To deepen your feeling of arbitrariness of R design: using a non-existent *name* index will generate an error for vectors but not for lists (you get `NULL`)[4].

Confusing? Let us go through some examples, so you can see the difference these two kinds of brackets make for vectors and lists.

3.4.1 Subsetting for (atomics) vectors

First, we create a named vector

```
x <- c("a"=1, "b"=2, "c"=3)
```

Preserving subsetting via `[]` returns a part of original vector, notice that the *name* associated with an index is retained.

```
x[2]
```

```
## b
## 2
```

Simplifying subsetting via `[[]]` extracts value at the location. Because the *name* is associated with an *index*, not with the content, it gets stripped off.

```
x[[2]]
```

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

Trying to extract multiple items will fail for *simplifying* subsetting.

```
x[[1:2]]
```

```
## Error in x[[1:2]]: attempt to select more than one element in vectorIndex
```

Same is true for negative indexes, even though we are excluding two out of three indexes, so end up with content from just one item.

```
x[[-(1:2)]]
```

```
## Error in x[[-(1:2)]]: attempt to select more than one element in vectorIndex
```

And the zero index generates an error as well but the error message is different.

[4] Insert a hair-pulling picture of your preference here.

```
x[[0]]
```

```
## Error in x[[0]]: attempt to select less than one element in get1index <real>
```

Using of a non-existent name will generate an error for *simplifying* but not for *preserving* subsetting.

```
x["a"]
```

```
## a
## 1
```

This also works but strips the name off.

```
x[["a"]]
```

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

This fails silently by returning `NA`.

```
x["d"]
```

```
## <NA>
##   NA
```

But this will generate an error.

```
x[["d"]]
```

```
## Error in x[["d"]]: subscript out of bounds
```

General rule: when using vectors, always use `[]`. The only potential usage-case I can see is wanting to strip a name off a single item (not sure I ever needed to do this). If, for some reason, this is what you need, you should write a comment explaining that. Otherwise, everyone including future-you will be confused and think that this is a typo.

3.4.2 Subsetting for lists

First, we create a named list

```
l <- list("a"=1, "b"=2, "c"=list(3, 4, 5))
```

Preserving subsetting via `[]` returns a list that is a part of original list, again the *name* associated with an index so it is retained in the returned list.

```
l[2]
```

```
## $b
## [1] 2
```

Simplifying subsetting via `[[]]` extracts value at the location. This is why you get a *vector* (of length 1).

```
l[[2]]
```

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

What about our list inside of the list at position 3? Using preserving subsetting give us a list inside of the list (car of the train).

```
l["c"]
```

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

Using simplifying subsetting return a list that was inside the list at that location (object inside that car). Note that, as with the vector before, the name gets stripped off, as it belongs to the index (car of the train) and not the content (object inside the car).

```
l[["c"]]
```

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

Again, using multiple indexes will fail.

```
l[[1:2]]
```

```
## Error in l[[1:2]]: subscript out of bounds
```

Same for negative indexe.

```
l[[-(1:2)]]
```

```
## Error in l[[-(1:2)]]: attempt to select more than one element in integerOneIndex
```

And for the zero index (but notice a *different* error message).

```
l[[0]]
```

```
## Error in l[[0]]: attempt to select less than one element in get1index <real>
```

Using a non-existent name index for lists with preserving subsetting (`[]`) will return a single item list with `NULL` as a content[5] but just `NULL` for simplifying one (`[[]]`). And none of them will generate an error.

```
l["d"]
```

```
## $<NA>
## NULL
```

```
l[["d"]]
```

```
## NULL
```

General rule: use `[[]]` if you are interested in list or table content, e.g., you need a column from the table. Use `[]` if you interested in using a smaller (part of the original) list or table.

If this is the point when you want to start running around screaming or bang your head against the screen, please tell me, cause I would definitely join you. Let us do some exercises that might help to build some intuition. However, as you probably noticed already, subsetting in R is fairly haphazard, so you probably will still end up being confused or have a code that does not work for seemingly mysterious reasons.

Do exercise 3.

3.5 Yet another subsetting via $

I am terribly sorry but I need to deepen your confusion and despair but telling you that R has yet another way of subsetting via a `$` sign. In fact, this is the most common way of subsetting for lists and tables that you will encounter almost everywhere. It is a shortcut version for *partial matching* of simplifying subsetting: `l$c` is the same as writing `l[["c", exact = FALSE]]`. The last new part `exact = FALSE` means that you can use an *incomplete* name after the `$` and R will guess what you mean. So, if you made a typo while meaning some completely different column name, R will second-guess your intentions and give you a variable that has the same beginning (no error, don't even hope).

```
l <- list("aa" = 1, "bb" = 2, "bc" = 3)
l$a
```

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

The good news is that it won't autocomplete ambiguous cases. The bad news that it won't generate an error and will return a `NULL` (just like `[[]]` would).

```
l$b
```

```
## NULL
```

[5] And `NA` as a name. Don't ask.

```
l[['b']]
```

```
## NULL
```

My advice would be to stick to `[[]]` notation despite the ubiquitous use of `$` out where. `[[]]` is slightly more strict and more universal: You can hard code a column/item name or put it into a variable for indexing. Only hard-coding works for `$`.

```
l[["bb"]]
```

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

```
column_of_interest <- "bb"
l[[column_of_interest]]
```

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

3.6 Tables, a.k.a. data frames

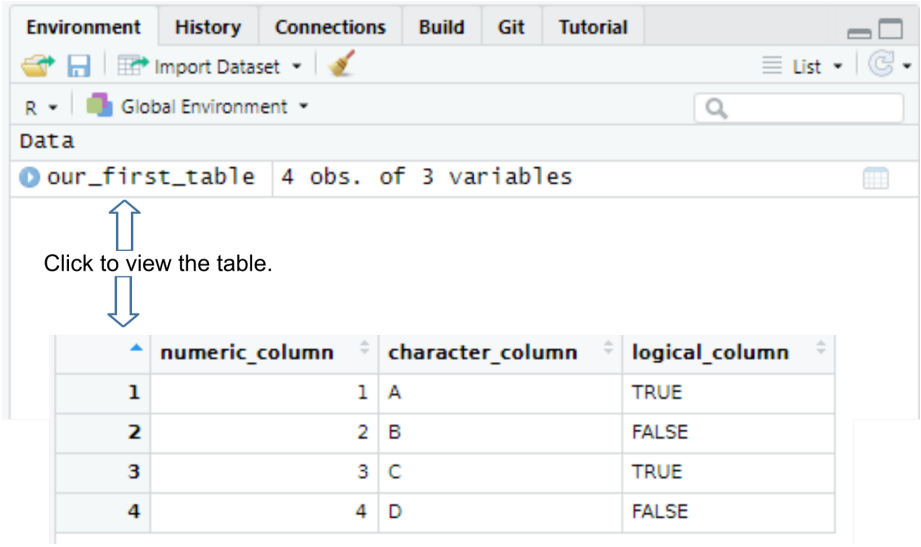
R tables are a mix between lists and matrices. You can think about it as a list of vectors (columns) of *identical* length. The default way to construct a table, which are called *data frames* in R, is via data.frame() function.

```
our_first_table <- data.frame(numeric_column = c(1, 2, 3, 4),
                              character_column = c("A", "B", "C", "D"),
                              logical_column = c(TRUE, F, T, FALSE))

our_first_table
```

```
##   numeric_column character_column logical_column
## 1              1                A           TRUE
## 2              2                B          FALSE
## 3              3                C           TRUE
## 4              4                D          FALSE
```

Once you create a table, it will appear in your environment, so you can see it in the *Environment* tab and view it by clicking on it or typing `View(table_name)` in the console (note the capital V in the `View()`).



	numeric_column	character_column	logical_column
1	1	A	TRUE
2	2	B	FALSE
3	3	C	TRUE
4	4	D	FALSE

Do exercise 4.

All columns in a table **must** have the same number of items (rows). This is similar to the process of matching vectors' length that you have learned the last time. However, it works automatically only if length of *all* vectors is a multiple of the longest length. Thus, the example below will work, as the longest vector (`numeric_column`) is 6, `character_column` length is 3, so it will be repeated twice, and `logical_column` length is 2 so it will be repeated thrice.

```
the_table <- data.frame(numeric_column = 1:6,                  # length 6
                        character_column = c("A", "B", "C"),   # length 3
                        logical_column = c(TRUE, FALSE))       # length 2
the_table
```

```
##   numeric_column character_column logical_column
## 1              1                A           TRUE
## 2              2                B          FALSE
## 3              3                C           TRUE
## 4              4                A          FALSE
## 5              5                B           TRUE
## 6              6                C          FALSE
```

If the simple *multple-of-length* rule does not work, R generates an error (finally!).

```
# this will generate an error: arguments imply differing number of rows
the_table <- data.frame(numeric_column = 1:7,                  # length 7
                        character_column = c("A", "B", "C"))   # length 3, cannot be multiplied by
```

```
## Error in data.frame(numeric_column = 1:7, character_column = c("A", "B", : arguments imply dif
```

Do exercise 5.

3.7 Subsetting tables

One way to think about a table as a list of columns (vectors). Hence, both preserving (`[]`) and simplifying (`[[]]`) subsetting will work as you would expect returning either a `data.frame` (`[]`) or a *vector* that was a column your were interested in (`[[]]`).

The preserving returns a *table* with *one* column.

```
our_first_table <- data.frame(numeric_column = c(1, 2, 3),
                              character_column = c("A", "B", "C"),
                              logical_column = c(TRUE, F, T))

# via index
our_first_table[1]
```

```
##   numeric_column
## 1              1
## 2              2
## 3              3
```

```
# via name
our_first_table['numeric_column']
```

```
##   numeric_column
## 1              1
## 2              2
## 3              3
```

```
# via slicing
our_first_table[1:2]
```

```
##   numeric_column character_column
## 1              1                A
## 2              2                B
## 3              3                C
```

the_table

	N	C	L
1	1	A	TRUE
2	2	B	FALSE
3	3	C	FALSE
4	4	D	TRUE
5	5	E	TRUE

the_table[1] ⟶
the_table["N"] ⟶

	N
1	1
2	2
3	3
4	4
5	5

The simplifying returns a *vector*.

```
# via $ notation
our_first_table$numeric_column
```

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

```
# via name and double square brackets
our_first_table[['numeric_column']]
```

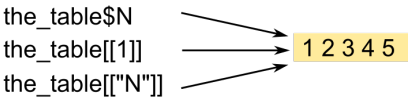
```
## [1] 1 2 3
```

```
# via index and double square brackets
our_first_table[[1]]
```

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

the_table

	N	C	L
1	1	A	TRUE
2	2	B	FALSE
3	3	C	FALSE
4	4	D	TRUE
5	5	E	TRUE



The only new thing is that, because tables are two-dimensionsional, you can use preserving subsetting to extract or access a rectangular region within a table. To select a subset rows and columns you write `table[rows, columns]`. If you omit either rows or columns this implies that you want *all* rows or columns.

```
# getting ALL rows for the FIRST column -> confusingly this gives you a VECTOR,
# so even though you used [] they work as simplifying subsetting
our_first_table[, 1]
```

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

```
# getting FIRST row for ALL columns -> this gives you DATA.FRAME
our_first_table[1, ]
```

```
##   numeric_column character_column logical_column
## 1              1                A           TRUE
```

```
# ALL rows and ALL columns, equivalent to just writing `our_first_table` or `our_first_table[]`
our_first_table[,]
```

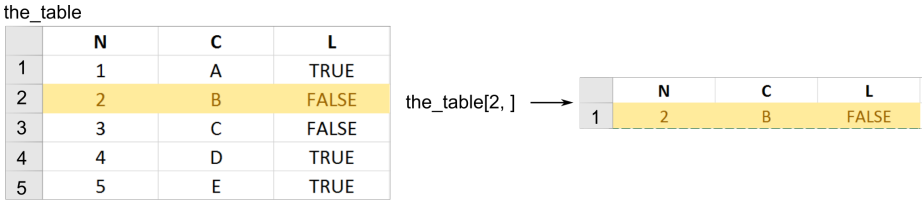
```
##   numeric_column character_column logical_column
## 1              1                A           TRUE
## 2              2                B          FALSE
## 3              3                C           TRUE
```

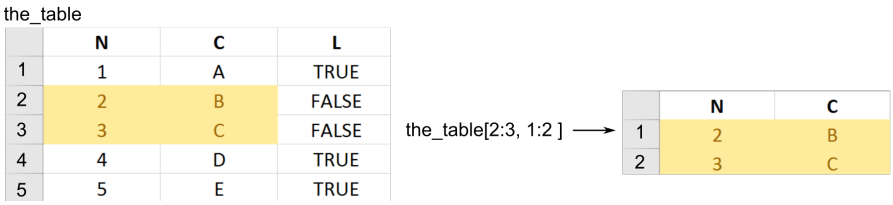
```
# getting SECOND element of the THIRD column
our_first_table[2, 3]
```

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

```
# getting first two elements of the logical_column
our_first_table[1:2, "logical_column"]
```

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





Do exercise 6.

3.8 Using libraries

There is a better way to construct a table but to use it, we need to first import a library that implements it. As with most modern programming languages, the real power of R is not in what comes bundled with it (very little, as a matter of fact) but in community developed libraries that extend it. We already discussed how you install libraries.To use a library in your code, you use library() function[6]. So, to use *tidyverse* library that you already installed, you simply write

```
library(tidyverse)
# or
library("tidyverse")
```

One thing to keep in mind is that if you import two libraries that have a function with same name, the function from the *latter* package will overwrite (mask) the function from the former. You will get a warning but if you miss it, it

[6]It has a sister function `require()` but it should be used inside functions and packages not in scripts or notebooks

may be very confusing. My favorite stumbling block are functions `filter()` from `dplyr` package (we will use it extensively, as it filters a table by row) and `filter()` function from `signal` package (applies a filter to a time-series)[7]. This overwriting of one function by another can lead to very odd looking mistakes. In my case I think that I am using `dplyr::filter()` and get confused by error messages that I get (they are not really informative). The first time I did this, it took me an hour to figure it out. Here are the warnings I should have paid attention to.

```
library(signal)
```

```
##
## Attaching package: 'signal'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, poly
```

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following object is masked from 'package:signal':
##
##     filter
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

Thus, keep that in mind or, better still, explicitly mention which package the function is coming from via `library::function()` notation. In this case, you will use the function that you are interested in and need not to worry about other functions with the same name that may conflict with it. In general, it is a good idea to *always* disambiguate function via library but in practice it may make your code hard to read by cluttering it with `library::` prefixes. Thus, you will need to find a balance between disambiguation and readability.

```
library(tibble)

# imported from the library into the global environment
print(tribble(~a, 1))
```

```
## # A tibble: 1 x 1
```

[7] There is also a filter function is stats library.

```
##       a
##   <dbl>
## 1     1
```

```
# used directly from the package
tibble::tribble(~a, 1)
```

```
## # A tibble: 1 x 1
##       a
##   <dbl>
## 1     1
```

When using a notebook (so, in our case, always) put the libraries into the first chunk of the notebook. In case of Rmarkdown notebooks, this is a *setup* chunk and this ensures that your libraries are always initialized, even if you first run some other chunk. Word of advice, keep you library list in alphabetical order. Libraries are very specialized, so you will need quite a few of them for a typical analysis. Keeping them alphabetically organized makes it easier to see whether you imported the required library and whether you need to install a new one.

3.9 Tibble, a better data.frame

Although the `data.frame()` function is the default way of creating a table, it is a legacy implementation with numerous shortcomings. Tidyverse implemented its own version of the table called tibble() that provides a more rigorous control and more consistent behavior. For example, it allows you to use any symbol in columns names (including spaces), prints out only the beginning of the table rather than entire table, etc. It also gives more warnings. If you try to access a non-existing column both `data.frame()` and `tibble()` will return `NULL` but the former will do it silently, whereas the latter will give you a warning but only if you use the `$` notation[8].

```
library(tibble)

# data.frame will return NULL silently
df <- data.frame(b = 1)
print(df[["A"]])
```

```
## NULL
```

```
# data.frame will return NULL for a variable that does not exist

tbl <- tibble(b = 1)
print(tbl[["A"]])
```

```
## NULL
```

[8] Arbitrariness strikes again! But this also means that `$` is safer to use with tibbles but not with data.frames.

```
tbl$A
```

```
## Warning: Unknown or uninitialised column: `A`.
```

```
## NULL
```

In short, `tibble()` provides a more robust version of a `data.frame` but otherwise behaves (mostly) identically to it. Thus, it should be your default choice for a table.

3.10 Tribble, table from text

The tibble package also provides an easier way of constructing tables via the tribble() function. Here, you use tilde to specify column names, and then write its content row-by-row.

```
tribble(
    ~x, ~y,
    1,  "a",
    2,  "b"
)
```

```
## # A tibble: 2 x 2
##       x y
##   <dbl> <chr>
## 1     1 a
## 2     2 b
```

Do exercise 7.

3.11 Reading example tables

One of the great things about R is that most packages come with an example data set that illustrates their function. You can see the list of some of them here. In case of an example data set, you need to import the library that it is part of and then load them by writing `data(tablename)`. For example, to use use `mpg` data on fuel economy from `ggplot2` package, you need to import the library first, and then call `data(mpg)`.

```
library(ggplot2)
data(mpg) # this create a "promise" of the data
print(mpg) # any action on the promise leads to data appearing in the environment
```

```
## # A tibble: 234 x 11
##    manufacturer model      displ  year   cyl trans drv     cty   hwy fl    class
##    <chr>        <chr>      <dbl> <int> <int> <chr> <chr> <int> <int> <chr> <chr>
##  1 audi         a4           1.8  1999     4 auto~ f        18    29 p     comp~
```

```
##  2 audi         a4           1.8  1999     4 manu~ f        21    29 p     comp~
##  3 audi         a4           2    2008     4 manu~ f        20    31 p     comp~
##  4 audi         a4           2    2008     4 auto~ f        21    30 p     comp~
##  5 audi         a4           2.8  1999     6 auto~ f        16    26 p     comp~
##  6 audi         a4           2.8  1999     6 manu~ f        18    26 p     comp~
##  7 audi         a4           3.1  2008     6 auto~ f        18    27 p     comp~
##  8 audi         a4 quattro   1.8  1999     4 manu~ 4        18    26 p     comp~
##  9 audi         a4 quattro   1.8  1999     4 auto~ 4        16    25 p     comp~
## 10 audi         a4 quattro   2    2008     4 manu~ 4        20    28 p     comp~
## # ... with 224 more rows
```

3.12 Reading csv files

So far we covered creating a table by hand via `data.frame()`, `tibble()`, or `tribble()` functions and loading an example table from a package via `data()` function. More commonly, you will need to read a table from an external file. These files can come in many formats because they are generated by different experimental software. Below, you will see how to handle those but my recommendation is to always store your data in a csv (Comma-separated values) files. These are simple plain text files, which means you can open them in any text editor, with each line representing a single row (typically, top row contains column names) with individual columns separated by some symbol or symbols. Typical separators are a comma (hence, the name), a semicolon (this is frequently used in Germany, with comma serving as a decimal point), a tabulator, or even a space symbol. Here is an example of such file

```
Participant,Block,Trial,Contrast,Correct
A1,1,1,0.5,TRUE
A1,1,2,1.0,TRUE
A1,1,2,0.05,FALSE
...
```

that is turned into a table when loaded

	Participant	Block	Trial	Contrast	Correct
1	A1	1	1	0.50	TRUE
2	A1	1	2	1.00	TRUE
3	A1	1	2	0.05	FALSE

There are several ways of reading CSV files in R. The default way by using read.csv() function that has different versions optimized for different combinations of the decimal point and separator symbols, e.g. `read.csv2()` assumes a comma for the decimal point and semicolon as a separator. However, a better way is to use readr library that re-implements same functions. Names of the functions are slightly different with underscore replacing the dot, so `readr::read_csv()` is a replacement for `read.csv()`. These are faster (although it will be noticeable only on large data sets), do not convert text to

factor variables (we will talk about factors later but this default conversion by `read.csv()` can be very confusing), etc.

However, most important difference between `read.csv()` and `read_csv()` is they constraint the content of a CSV file. `read.csv()` has not assumptions about which columns are in the file and what their value types are. It simply reads them as is, *silently* guessing their type.

```
results <- read.csv("data/example.csv")
results
```

```
##   Participant Block Trial Contrast Correct
## 1          A1     1     1     0.50    TRUE
## 2          A1     1     2     1.00    TRUE
## 3          A1     1     2     0.05   FALSE
```

You can use `read_csv()` the same way and it will work the same way but will inform (warn) you about the table structure it deduced.

```
results <- readr::read_csv("data/example.csv")
```

```
## Rows: 3 Columns: 5
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (1): Participant
## dbl (3): Block, Trial, Contrast
## lgl (1): Correct
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
results
```

```
## # A tibble: 3 x 5
##   Participant Block Trial Contrast Correct
##   <chr>       <dbl> <dbl>    <dbl> <lgl>
## 1 A1              1     1     0.5  TRUE
## 2 A1              1     2     1    TRUE
## 3 A1              1     2     0.05 FALSE
```

This annoying *Column specification* print out, which gets even more annoying if you need to read many CSV files, is there for a reason: it wants to annoy you! You can turn it off via `show_col_types = FALSE` but I strongly recommend against this. Instead, you should specify the column structure yourself via `col_types` parameter. The simplest way to do this is via `spec()` function, as suggested by the printout.

```
readr::spec(results)
```

```
## cols(
```

```
##   Participant = col_character(),
##   Block = col_double(),
##   Trial = col_double(),
##   Contrast = col_double(),
##   Correct = col_logical()
## )
```

This is a specification that the reader prepared for you. So you can take a look at it, adjust it, if necessary, and copy-paste to the `read_csv` call. By default, it suggested `double` values for `Block` and `Trial` but we know they are integers, so we can copy-paste the suggested structure, replace `col_double()` with `col_integer()` and read the table without a warning.

```
library(readr)
results <- read_csv("data/example.csv",
                    col_types = cols(Participant = col_character(),
                                     Block = col_integer(), # read_csv suggested col_d
                                     Trial = col_integer(), # read_csv suggested col_d
                                     Contrast = col_double(),
                                     Correct = col_logical()))
results
```

```
## # A tibble: 3 x 5
##   Participant Block Trial Contrast Correct
##   <chr>       <int> <int>    <dbl> <lgl>
## 1 A1              1     1     0.5  TRUE
## 2 A1              1     2     1    TRUE
## 3 A1              1     2     0.05 FALSE
```

You may feel that this a lot of extra work just to suppress an annoying but, ultimately, harmless warning. Your code will work with or without it, right? Well, *hopefully* it will but you probably want to *know* that it will work not just *hope* for it. Imagine that you accidentally overwrote your experimental data file with data from a different experiment (that happens more often than one would want). You still have `results.csv` file in your project folder and so the `read.csv()` will read it as is (it does not know what should be in that file) and your analysis code will fail in some mysterious ways at a much later point (because, remember, if you try to access a column/variable that does not exist in the table, you just get `NULL` rather than an error). You will eventually trace it back to the wrong data file but that will cost time and nerves. However, if you specify the column structure in `read_csv()` it will show a warning, if the file does not match the description. It would warn about wrong column names (`TheBlock` in the example below) and about wrong type (it does not like `TRUE`/`FALSE` in a column it expected to find integers in).

```
library(readr)
results <- read_csv("data/example.csv",
                    col_types = cols(Participant = col_character(),
```

```
                                        TheBlock = col_integer(), # read_csv suggested col_double()
                                        Trial = col_integer(), # read_csv suggested col_double() bu
                                        Contrast = col_double(),
                                        Correct = col_integer()))
```

```
## Warning: The following named parsers don't match the column names: TheBlock
```

```
## Warning: One or more parsing issues, call `problems()` on your data frame for details,
## e.g.:
##   dat <- vroom(...)
##   problems(dat)
```

Personally, I would prefer for `read_csv()` to loudly fail with an error in cases like these but having a nice red warning is already very helpful to quickly detect the problem with your data (and if your data is wrong, your whole analysis is meaningless). Thus, *always* use `read_` rather than `read.` functions and *always* specify the table structure. The lazy, and my preferred, way to do it, is to first read the file without specifying the structure and copy-paste-edit the warning column-specification message into the code adjusting as necessary.

Do exercise 8, you need face_rank.csv file for it. Download it and place it in the project folder. *Warning*, if you use Chrome or any Chromium-based browsers like MS Edge, Opera, etc. they might, for some odd reason, automatically *rename it* into *face_rank.xls* during the download. Just rename it back to *face_rank.csv*, because the file itself is not converted to an Excel, it is only the extension that gets changed (why? No idea, ask Google!).

3.13 Reading Excel files

There are several libraries that allow you to read Excel files directly. My personal preference is readxl package, which is part of the Tidyverse. Warning, it will be installed as part of the Tidyverse (i.e., when you typed `install.packages(tidyverse)`) but you still need to import it explicitly via `library(readxl)`. Because an Excel file has many sheets, by default the `read_excel()` function reads the *first* sheet but you can specify it via a `sheet` parameter using its index `read_excel("my_excel_file.xls", sheet=2)` or name `read_excel("my_excel_file.xls", sheet="addendum")`.

Do exercise 9, you need face_rank.xlsx file for it.

You can read about further options at the package's website but I would generally discourage you from using Excel for your work and, definitely, for your data analysis. Because, you see, Excel is very smart and it can figure out the *true* meaning and type of columns by itself. The fact that you might disagree is your problem. Excel knows what is best for you. The easiest way to screw a CSV file up (at least in Germany) is to open it in Excel and immediately save it. The file name will remain the same but Excel will "adjust" the content as it

feels is better for you (you don't need to be consulted with). If you think I am exaggerating, read this article at The Verge on how Excel messed up thousands of human genome data tables by turning some values into dates because why not[9]? So now the entire community is *renaming* some genes because it is easier to waste literally thousands of man-hours on that than to fix Excel. In short, friends don't let friends use Excel.

3.14 Reading files from other programs

World is a very diverse place, so you are likely to encounter a wide range of data files generated by Matlab, SPSS, SAS, etc. There are two ways to import the data. First, that I would recommend, use the original program (Matlab, SPSS, SAS, etc.) to export data as a CSV file. Every program can read and write CSV, so it a good common ground. Moreover, this is a simple format with no embedded formulas (as in Excel), service structures, etc. Finally, if you store your data in CSV, you do not need a special program to work with it. In short, unless you have a good reason, store your data in CSV files.

However, sometimes you have a file but you do not have the program (Matlab, SPSS, SAS, etc.). The second way is to use various R libaries, starting with foreign, which can handle most typical cases, e.g., SPSS, SAS, State, or Minitab. The problem here is that all programs differ in the internal file formats and what exactly is included. For example, when importing from an SPSS sav-file via read.spss you will get a list with various components rather than a table (`data.frame`). You can force the function to convert everything to a single table via `to.data.frame=TRUE` option but you may lose some information. Bottom line, you need to be extra careful when importing from other formats and the safest way is to ensure complete and full export of the data to a CSV from the original program.

3.15 Writing and reading a single object

There is another option for saving and reading data in R via saveRDS() and readRDS functions[10]. saveRDS() saves an arbitrary object (vector, list, table, model fit, etc.), whereas readRDS reads it back. This is useful, if your table is very large, so using CSV is inefficient, or if you want to save something that is not a table, again, something like a model fit for later use. You probably will not use this frequently but it is a good option to keep in mind.

[9] Best joke on that that I've heard so far is: Optimist thinks that the glass is half full, pessimist thinks it is half empty, Excel thinks is it second of February.

[10] This is another example of odd inconsistencies in R. Why `readRDS()` instead of `loadRDS()`? Or `writeRDS()` if you read it.

3.16 Wrap up

We have started with vectors and now extended them to tables. Next time, we will look at how to visualize the data using The Grammar of Graphics approach.

Chapter 4

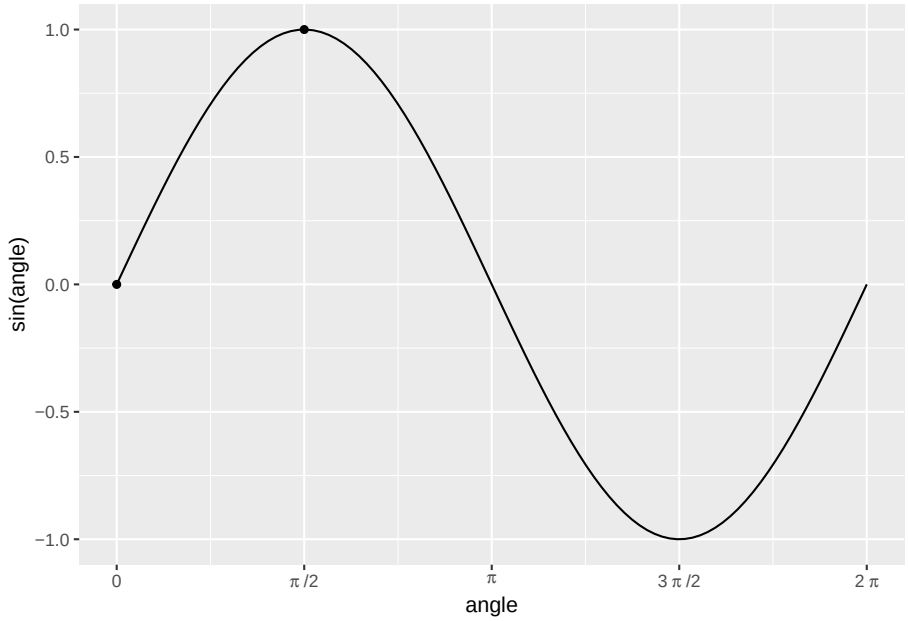
Functions! Functions everywhere!

In this chapter you will learn about *functions* in R, as they are the second most important concept in R and are everywhere (just like vectors and lists). You will also learn how to *pipe* your computation through series of functions without creating a mess of temporary variables or nested calls. Don't forget to download the notebook.

4.1 Functions

In the previous chapters, you have learned that you can store information in variables — "boxes with slots" — as vectors or as tables (bundles of vectors of equal length). To use these stored values for computation you need functions. In programming, function is an *isolated* code that receives some input, performs some action on it, and, optionally, returns a value[1]. The concept of functions comes from mathematics, so it might be easier to understand them using R implementation of mathematical functions. For example, you may remember a sinus function from trigonometry. It is typically abbreviated as `sin`, it takes a numeric value of angle (in radians) as its *input* and returns (this is its *output*) a corresponding value between -1 and 1: $sin(0) = 0$, $sin(\pi/2) = 1$, etc.

[1] Function that does not return a value, probably, generates its output to a console, external file, etc. There is little point in running a function that does not affect the world.



In R, you write a function using the following template

```
name_of_the_function <- function(parameter1, parameter2, parameter3, ...){
  ...some code that computes the value...
  return(value)
}
```

A `sin` function with a single parameter `angle` would look something like this

```
sin <- function(angle){
  ...some math that actually computes sinus of angle using value of angle parameter ..
  return(sin_of_angle)
}
```

Once we have the function, we can use it by *calling* it. You simply write `sin(0)`[2] and get the answer!

```
sin(0)
```

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

As you hopefully remember, all simple values are vectors, so instead of using a scalar `0` (merely a vector of length of one) you can write and apply this function to (compute sinus for) every element in the vector.

```
sin(seq(0, 3.141593, length.out = 5))
```

[2] I've cheated here by using R implementation of sin().

```
## [1]  0.000000e+00  7.071068e-01  1.000000e+00  7.071066e-01 -3.464102e-07
```

You can think of functions parameters as local function variables those values are set before the function is called. A function can have any number of parameters, including zero[3], one, or many parameters. For example, an arctangent atan2 function takes 2D coordinates (`y` and `x`, in that order!) and returns a corresponding angle in *radians*.

```
atan2(c(0, 1), c(1, 1))
```

```
## [1] 0.0000000 0.7853982
```

A definition of this function would look something like this

```
atan2 <- function(y, x){
  ...magic that uses values of y and x parameters...
  ...to compute the angle_in_rad value...
  return(angle_in_rad);
}
```

Do exercise 1.

4.2 Writing a function

Let us start practicing computing things in R and writing functions at the same time. We will begin by implementing a very simple function that doubles a given number. We will write this function in steps. First, think about how you would name[4] this function (meaningful names are your path to readable and reusable code!) and how many parameters it will have. Write the definition of the function without any code inside of wiggly brackets (so, no actual computation or a return statement at the end of it).

Do exercise 2.1

Next, think about the code that would *double-the-value* based on the parameter. This is the code that will eventually go inside the wiggly brackets. Write that code (just the code, without the bits from exercise 2.1) in exercise 2.2 and test it by creating a variable with the same name as your parameter inside the function. E.g., if my parameter name is `the_number`, I would test it as

```
the_number <- 1
...my code to double the value usign the_number variable...
```

Do exercise 2.2

By now you have your formal function definition (exercise 2.1) and the actual code that should go inside (exercise 2.2). Now, we just need to combine them

[3] This, probably, means that the function always does the same thing or a random thing and you cannot influence this.

[4] `double_or_nothing`?

by putting the code inside the function and *returning* the value. You can do this two ways:

1) you can store the results of the computation in a separate local variable and then return that variable,
2) return the results of the computation directly

```
# 1) first store in a local variable, then return it
  result <- ...some computation you perform...
  return(result)

# 2) returning results of computation directly
  return(...some computation you perform...)
```

Do it *both* ways in exercises 2.3 and 2.4. Call the function using different inputs to test that it works.

Do exercise 2.3 and 2.4

More practice is always good, so write a function that converts an angle in *degrees* to *radians*. The formula[5] is

$$rad = \frac{deg \cdot \pi}{180}$$

Decide whether you want to a have an intermediate local variable inside the function or to return the results of the computation directly.

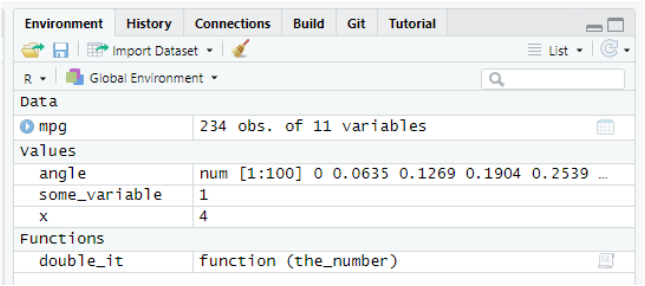
Do exercise 3

4.3 Scopes: Global versus Local variables

I suggested that you use a variable to store the results of double-it-up computation before returning it. But why did I call it *local?* This is because each function has it own *scope* (environment with variables and functions) that is (mostly) independent from the scope of the global script. Unfortunately, environment scopes in R are different and more complicated than those in other programming languages, such as Python, C/C++, or Java, so always pay attention and be careful in the future.

The *global* scope/environment is the environment for the code *outside* of functions. All *global* variables and functions, the ones that you define in the code *outside* of functions (typing in the console, running scripts, running chunks of code in notebooks, etc.), live where. You can see what you have in the global scope at any time by looking at *Environment* tab (note the *Global Environment* tag).

[5] Hint: Constants



In my case, it has one table (`mpg`, all tables go under *Data*), three vectors (`angle`, `some_variable`, and `x`, all vectors go under `Values`), and an example function from exercise #2 that I created (`double_it`, all functions go under *Functions*, makes sense). However, it has no access to parameters of the functions and variables that you define inside these function. When you run a function, it has it own scope/environment that includes *parameters* of the function (e.g., `the_number` for my `double_it` function and the value it was assigned during the call), any *local* variables you create inside that function (e.g., `result <- ...some computation you perform...` creates such local variable), and a **copy(!)** of all *global* variables[6]. In the code below, take a look at the comments that specify the accessibility of variables between global script and functions (ignore glue for a moment, it *glues* a variable's value into the text, so I use it to make printouts easier to trace)[7]

```
# this is a GLOBAL variable
global_variable <- 1

i_am_test_function <- function(parameter){
  # parameter live is a local function scope
  # its values are set when you call a function
  print(glue("  parameter inside the function: {parameter}"))

  # local variable created inside the function
  # it is invisible from outside
  local_variable <- 2
  print(glue("  local_variable inside the function: {local_variable}"))
```

[6]You can write to a parent (e.g., global) environment from inside the function via «- operator. However, this should be your last resort, as it makes the code brittle and harder to understand and debug, because if depends not only on local things but on global variables that may or may not be where at any given moment.

[7]These rules — a **copy** of a global scope is accessible inside a function but function scope is inaccessible from outside — should be how *you* write your code. However, R's motto is "anything is possible", so be aware that *other people* may not respect these rules. This should not be an issue most of the time but if you are curious how R can let you break all rules of good responsible programming and do totally crazy things, read Advanced R book by Hadley Wickham. However, it is really **advanced**, aimed primarily at programmers who develop R and packages, not at scientists who use them.

```
  # here, a_global_variable is a LOCAL COPY of the the global variable
  # of the same name. You can use this COPY
  print(glue("  COPY of global_variable inside the function: {global_variable}"))

  # you can modify the LOCAL COPY but that won't affect the original!
  global_variable <- 3
  print(glue("  CHANGED COPY of global_variable inside the function: {global_variable}"
}

print(glue("global_variable before the function call: {global_variable}"))
```

```
## global_variable before the function call: 1
```

```
i_am_test_function(5)
```

```
##   parameter inside the function: 5
##   local_variable inside the function: 2
##   COPY of global_variable inside the function: 1
##   CHANGED COPY of global_variable inside the function: 3
```

```
# the variable outside is unchanged because we modify its COPY, not the variable itsel
print(glue("UNCHANGED global_variable after the function call: {global_variable}"))
```

```
## UNCHANGED global_variable after the function call: 1
```

Do exercise 4 to build understanding of scopes.

4.4 Function with two parameters

Let us write a function that takes *two* parameters — `x` and `y` — and computes *radius* (distance from `(0,0)` to `(x, y)`)[8]. The formula is

$$R = \sqrt{x^2 + y^2}$$

This is very similar to exercises 2 and 3, with number of parameters being the only difference.

Do exercise 5.

4.5 Table as a parameter

So far, we only passed vectors (a.k.a. values) to functions but you can pass any object including tables[9]. Let us use mpg table from the *ggplot2* package. Write

[8] This function is complementary to `atan2()`, as two of them allow transformation of coordinates from Cartesian to polar coordinate system

[9] And even functions themselves, not just what they computed! This is part of *functional programming* you will learn about later.

a function that takes a table as a *parameter*. This mean that the function should not assume that a table with this name exists in the global environment. Do not use `mpg` as a parameter name (makes it confusing and hard to understand which table global or local you actually mean), call it something else[10]. The function should compute and return average miles-per-gallon efficiency based on city `cty` and highway `hwy` test cycles. Do it in *two* ways. First, compute and return *a vector* based on the table passed as parameter. Second, do the same computation but add the result *to the table that function received as a parameter* (call the new column `avg_mpg`) and return the entire table (remember, modifying table is not enough, as you are working *on a copy*).

Do exercise 6.

Let us write another function that computes mean efficiency for a particular cycle, either city or highway. For this, the function will take *two* parameters: 1) the table itself and 2) a string (text variable) with the name of the column. Then, you use it to access the column via simplifying `[[]]` subsetting. To summarize, your function takes 1) a table and 2) a string with a column name and returns a single number (mean for the specified column). E.g.

```
average_efficiency(mpg, "cty") # should return 16.85897
```

Do exercise 7.

4.6 Named versus positional arguments

Remember than we talked about the assignment statement, I noted that you should always use <- operator for assignments but warned you that you will encounter an alternative `=` operator when we will use functions. You also may have notice me using it, for example, in `seq(0, 2*pi, length.out = 100)`. Why did I use name for the third parameter and not the other two? Why did I have to use `length.out=` at all? This is because in R you can pass arguments by *position* (first two arguments in that example) or by *name* (that would be `length.out=`).

Then you pass arguments by *position*, values are put into corresponding arguments in the order you supplied them in. I.e., the first value goes into the first parameter, the second into the second etc. Then you specify arguments by *name*, you explicitly state which argument gets which value `arg = value`. Here, the exact order does not matter and you can put arguments in the order you need (i.,e., an order that makes understanding the code easier). You can also mix these two ways and, R being R, you can really mix them interleaving positional and named arguments any way you like[11]. Despite all the flexibility

[10] I tend to use `df`, if it is reasonably easy to deduce what sort of `data.frame` I mean.

[11] That being a case, never use named argument before positional ones. Each time you use a named argument, its position is taken out and that *changes* position index for remaining positional arguments. This is an almost certain way to put a value into a wrong parameter

that R gives you to confuse yourself and others, use only all-positional-followed-by-all-named-arguments order, e.g., `seq(0, 2*pi, length.out = 100)`.

When should you use which? That depends solely on which way is clearer or possible. For a single parameter or widely used mathematical functions, like mean or sin there is little point in using names (particularly, because the only argument is named `x`). At the same time, I *always* use named parameters for atan2 simply because I am never 100% sure about the order (i.e., `x` followed by `y` occurs far more often). At the same time, formulas for statistical models in R have a very specific look and are typically a first argument, so it is probably redundant to specify that `formula = y ~ x`.Returning to the seq() function, the `length.out` is actually its *fourth* argument with `by` (an alternative way to define how many values you will get in the sequence) being third. But because both parameters define, essentially, the same thing, it is *impossible* to specify `length.out` using positional arguments only. Finally, if a function has more than a couple of parameters, it is probably a good idea to use named arguments. In short, use you own better judgement on whatever makes understanding the code easier.

Do exercise 8.

4.7 Default values

When you write a function, you can combine simplicity of its use with flexibility via *default values*. I.e., *some* parameters can have sensible or commonly used values but, if desired, a user can specify their own values to modify functions behavior. For example, function mean has *three* parameters. You always need to specify the first one (`x`, a vector of values you are computing the mean of). But you can also specify trimming via `trim` and whether it should ignore `NA` via `na.rm`[12]. By default, you do not trim (`trim = 0`) and do not ignore `NA` (`na.rm = FALSE`). These defaults are sensible as they produce a typically expected behavior. At the same time their existence means that you can fine-tune your mean computation the way you require.

When writing your own function, you specify the default values when you define an argument. E.g., here, the second parameter `r`, the radius, has a default value of 1, so you can only specify the direction of the vector to compute (x, y) coordinates for a (default) *unit* vector.

```
polar_to_cartesian <- function(angle, r=1) {
  # ...
}
```

Do exercise 9.

---

and, at the same time, create an error that is really hard to find.

[12] If you do not ignore `NA` then the mean of a vector with at least one `NA` in it is `NA` as well

4.8 Nested calls

What if you need to call several functions in a single chain to compute a result? Think about the function from exercise #3 that converts degree to radians. Its most likely usage scenario is to convert degrees to radians and use that to compute sinus (or some other trigonometric function). There are different ways you can do this. For example, you can store the angle in radians in some temporary variable (e.g., `angle_in_radians`) and then pass it to sinus function during the next call.

```
angle_in_radians <- deg2rad(90) # function returns 1.570796, this value is stored in angle_in_rad
sin(angle_in_radians) # returns 1
```

Alternatively, you can use the value returned by `deg2rad()` *directly* as a parameter for function `sin()`

```
sin(deg2rad(90)) # returns 1
```

In this case, the computation proceeds in an *inside-out* order: The innermost function gets computed first, the function that uses its return value is next, etc. Kind of like assembling a Russian doll: you start with an innermost, put it inside a slightly bigger one, now take that one put it inside the next, etc. Nesting means that you do not need to pollute you memory with temporary variables[13] and make your code more expressive as nesting explicitly informs the reader that intermediate results are of no value by themselves and are not saved for later use.

Do exercise 10.

4.9 Piping

Although nesting is better than having tons of intermediate variables, lots of nesting can be mightily confusing. Tidyverse has an alternative way to chain or, in Tidyverse-speak, pipe a computation through a series of function calls. The magic operator is `%>%` (that's the pipe)[14] and here is how it transforms our nested call

```
sin(deg2rad(90)) # returns 1

deg2rad(90) %>% sin() # also return 1

90 %>% deg2rad() %>% sin() # also returns 1
```

[13] The worst case scenario is when you use same `temp` variable for things like that, forget to initialize / change its value properly at some point, spend half-a-day trying to understand why your code does not generate an error but results don't make sense.

[14] Starting with R version 4.1.0 there is now also a "native" pipe operator |> that works *similar* to magritt's pipe. This is a future of R piping but we will stick with `%>%` for now.

Do exercise 11.

All functions you used in the exercise had only one parameter because `single-output %>% single-input` piping is very straightforward. But what if one of the functions takes more than one parameter? By default, `%>%` puts the piped value into the *first* parameter. Thus `4 %>% radius(3)` is equivalent to `radius(4, 3)`. Although this default is very useful (the entire Tidyverse is build around this idea of piping a value into the *first* parameter to streamline your experience), sometimes you need that value as some *other* parameter (e.g., when you are pre-processing the data before piping it into a statistical test, the latter typically takes `formula` as the first parameter and `data` as second). For this, you can use a special dot variable: `.`[15], which is a hidden[16] temporary variable that holds the value you are piping through via `%>%`[17]. Thus,

```
z <- 4
w <- 3
z %>% radius(w) # is equivalent to radius(z, w)

# Note the dot!
z %>% radius(., w) # is equivalent to radius(z, w)
z %>% radius(w, .) # is equivalent to radius(w, z)
```

You can use the dot with named parameters as well

```
w %>% radius(z, y=.)
```

Note that because `.` is a variable, you can use it several times just as you can use any variable several times

```
4 %>% radius(., .) # is equivalent to radius(4, 4)
```

Do exercise 12.

4.10 Function is just a code stored in a variable

Did you spot the assignment `<-` operator in function definitions and wondered about this? Yes, this means that you are literally storing a function code in a variable. So when you call this function by name, you are asking to run the code stored inside that variable. You can appreciate that fact by typing a name of a function you wrote *without* round brackets, e.g. `double_the_value` or `radius`, and, voila, you will see the code. This means that function name is not really a name (as in some other programming languages), rather it is a name of a variable it is stored in. So you can use a variable *with a function code inside*

[15] It is `_` for the `|>` pipe.

[16] As in: It won't show up in your Global Environment tab.

[17] Yes, it is the same variable that you use over-and-over again but magrittr package makes sure to clean it up after each call, so you are not in danger of incidentally using a value from a previous call.

just the way you treat any other variable. For example, you can copy it (do `radius2 <- radius` and then `radius2` will work exactly the same way), pass it as an argument of another function (effectively, copy its code into a parameter). This will be very handy when your learn about bootstrapping (needs data and a function) or about applying/mapping functions to data.

4.11 Functions! Functions everywhere!

Every computation you perform in R is implemented as a function, even if it does not look like a function call. For example, `+` addition operation is a function. Typically, you write `2 + 3`, so no round brackets, no comma-separated list of parameters, it looks different. But this is just a special implementation of a function call (known as function operator) that makes code more readable for humans. You can actually call `+` function the way you call a normal function by using backticks around its name.

```
2 + 3
```

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

```
# note the `backticks` around +
`+`(2, 3)
```

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

Even the assignments operator `<-` is, you've guessed it, a function

```
`<-`(some_variable, 1)
some_variable
```

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

This does not mean that you should start using operators as functions (although, if it helps to make a particular code clearer, then, why not?), merely to stress that there is only one way to program any computation in R — as a function — regardless of how it may appear in the code. Later on, you will learn how to apply functions to vectors or tables (or, a Tidyversion of that, how to use functions to map inputs to outputs), so it helps to know that you can apply *any* function, even the one that does not look like a function.

4.12 Using (or not using) explicit return statement

In the code above I have always used the return function. However, explicit `return(some_value)` can be omitted if it is the *last* line in a function, you just write the value (variable) itself:

```
some_fun <- function(){
  x <- 1
  return(x)
}

some_other_fun <- function(){
  x <- 2
  x
}

yet_another_fun <- function(){
  3
}

some_fun()
```

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

```
some_other_fun()
```

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

```
yet_another_fun()
```

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

The lack of `return` function in the final line is actually an officially recommended style of Tidyverse but I am wary of this approach because "explicit is better than implicit". This omission may be reasonable if it comes at the very end of a long pipe but, in general, I would recommend using `return()`.

Chapter 5

ggplot2: Grammar of Graphics

In previous chapters, you have learned about tables that are the main way of representing data in psychological research and in R. In the following ones, you will learn how to manipulate data in these tables: change it, aggregate or transform individual groups of data, use it for statistical analysis. But before that you need to understand how to store your data in the table in the optimal way. First, I will introduce the idea of *tidy data*, the concept that gave Tidyverse its name. Next, we will see how tidy data helps you visualize relationships between variables. Don't forget to download the notebook.

5.1 Tidy data

The tidy data follows three rules:

- variables are in columns,
- observations are in rows,
- values are in cells.

This probably sound very straightforward to the point that you wonder "Can a table not by tidy?" As a matter of fact *a lot* of typical results of psychological experiments are not tidy. Imagine an experiment where participants rated a face on symmetry, attractiveness, and trustworthiness. Typically (at least in my experience), the data will stored as follows:

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M1	6	4	3
1	M2	4	7	6
2	M1	5	2	1
2	M2	3	7	2

This is a very typical table optimized for *humans*. A single row contains all responses about a single face, so it is easy to visually compare responses of individual observers. Often, the table is even wider so that a single row holds all responses from a single observer (in my experience, a lot of online surveys produce data in this format).

Participant	M1.Symmetry	M1.Attractiveness	M1.Trustworthiness	M2.Symmetry	M2.Attrac
1	6	4	3	4	7
2	5	2	1	3	7

So, what is wrong with it? Don't we have variables in columns, observations in rows, and values in cells? Not really. You can already see it when comparing the two tables above. The *face* identity is a variable, however, in the second table it is hidden in column names. Some columns are about face `M1`, other columns are about `M2`, etc. So, if you are interested in analyzing symmetry judgments across all faces and participants, you will need to select all columns that end with `.Symmetry` and figure out a way to extract the face identity from columns' names. Thus, face *is* a variable but is not a column in the second table.

Then, what about the first table, which has `Face` as a column, is it tidy? The short answer: Not really but that depends on your goals as well! In the experiment, we collected *responses* (these are numbers in cells) for different type of *judgments*. The latter are a variable but it is hidden in column names. Thus, a *tidy* table for this data would be

Participant	Face	Judgment	Response
1	M1	Symmetry	6
1	M1	Attractiveness	4
1	M1	Trustworthiness	3
1	M2	Symmetry	4
1	M2	Attractiveness	7
1	M2	Trustworthiness	6
2	M1	Symmetry	5
2	M1	Attractiveness	2
2	M1	Trustworthiness	1
2	M2	Symmetry	3
2	M2	Attractiveness	7
2	M2	Trustworthiness	2

This table is (very) tidy and it makes it easy to group data by every different combination of variables (e.g., by face and judgment, by participant and judgment), perform statistical analysis, etc. However, it may not always be the best way to represent the data. For example, if you would like to model `Trustworthiness` using `Symmetry` and `Attractiveness` as predictors, when the first table is more suitable. At the end, the table structure must fit your needs, not the other way around. Still, what you probably want is a *tidy* table because it is best suited for most things you will want to do with the data and because

it makes it easy to transform the data to match your specific needs (e.g., going from the third table to the first one via pivoting).

Most data you will get from experiments will not be tidy. We will spent quite some time learning how to tidy it up but first let us see how an already tidy data makes it easy to visualize relationships in it.

5.2 ggplot2

ggplot2 package is my main tool for data visualization in R. ggplot2 tends to make really good looking production-ready plots (this is not a given, a default-looking Matlab plot is, or used to be when I used Matlab, pretty ugly). Hadley Wickham was influenced by works of Edward Tufte when developing ggplot2. Although the aesthetic aspect goes beyond our seminar, if you will need to visualize data in the future, I strongly recommend reading Tufte's books. In fact, it is such an informative and aesthetically pleasing experience that I would recommend reading them in any case.

More importantly, ggplot2 uses a grammar-based approach of describing a plot that makes it conceptually different from most other software such as Matlab, Matplotlib in Python, etc. You need to get used to it but once you do, you probably will never want to go back.

A plot in *ggplot2* is described in three parts:

1. Aesthetics: Relationship between data and visual properties that define working space of the plot (which variables map on individual axes, color, size, fill, etc.).
2. Geometrical primitives that visualize your data (points, lines, error bars, etc.) that are *added* to the plot.
3. Other properties of the plot (scaling of axes, labels, annotations, etc.) that are *added* to the plot.

You always need the first one. But you do not need to specify the other two, even though a plot without geometry in it looks very empty. Let us start with a very simple artificial example table below. I simulate a response as

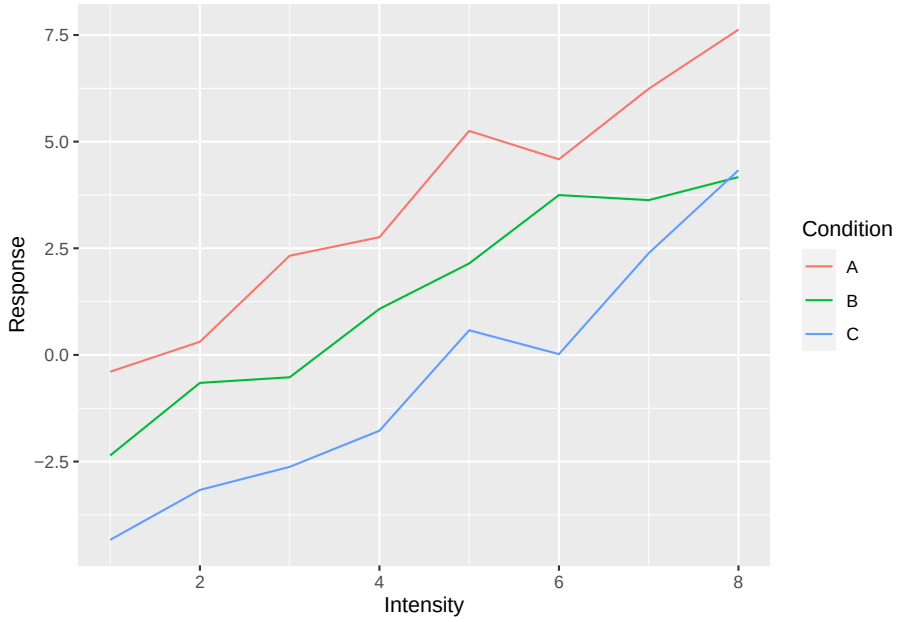
$$Response = Normal(\mu = 1, \sigma = 0.2) - Normal(\mu = 2 * ConditionIndex, \sigma = 0.4) + Normal(\mu = Intensity, \sigma = 0.4)$$

Condition	Intensity	Response
A	1	-0.3941165
B	1	-2.3569170
C	1	-4.3355756
A	2	0.3083759
B	2	-0.6553649
C	2	-3.1653605
A	3	2.3251789
B	3	-0.5241260
C	3	-2.6241035
A	4	2.7600366
B	4	1.0786012
C	4	-1.7769648
A	5	5.2519198
B	5	2.1442990
C	5	0.5783779
A	6	4.5870479
B	6	3.7475242
C	6	0.0189858
A	7	6.2393785
B	7	3.6292589
C	7	2.3854403
A	8	7.6274901
B	8	4.1691738
C	8	4.3311562

We plot this data by 1) *defining aesthetics* (mapping `Intensity` on to x-axis, `Response`on y-axis, and `Condition` on color) and 2) *adding* lines to the plot (note the plus[1] in `+ geom_line()`).

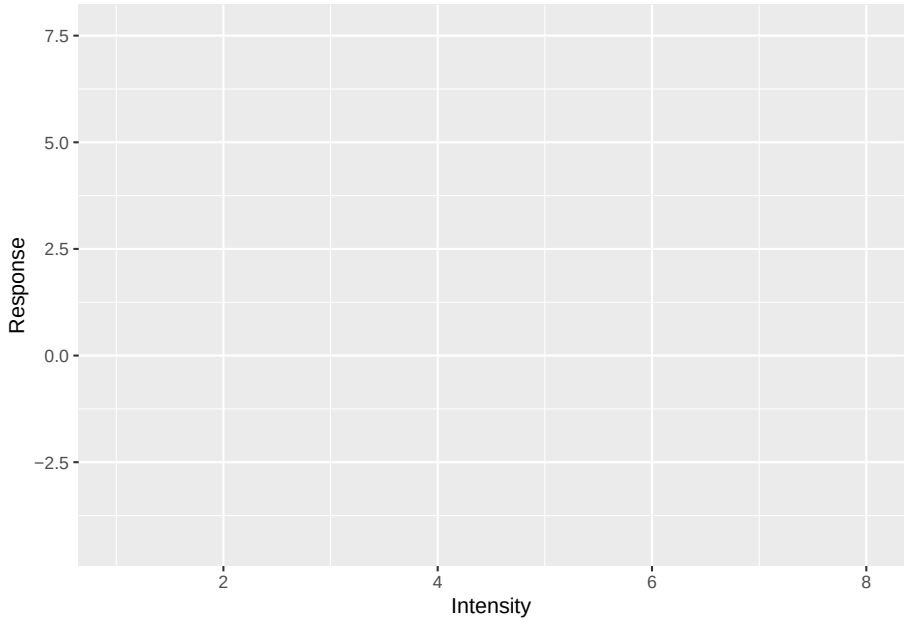
```
ggplot(data=simple_tidy_data, aes(x = Intensity, y = Response, color=Condition)) +
  geom_line()
```

[1]One of a potentially confusing bits is usage of `+` in ggplot2 but of pipe `%>%` everywhere else. The difference is deliberate and fundamental. Pipe `%>%` passes the output to the next function, `+` *adds* something to the already existing plot.



As I already wrote, technically, the only thing you need to define is aesthetics, so let us not add anything to the plot (we drop the `+geom_line()`).

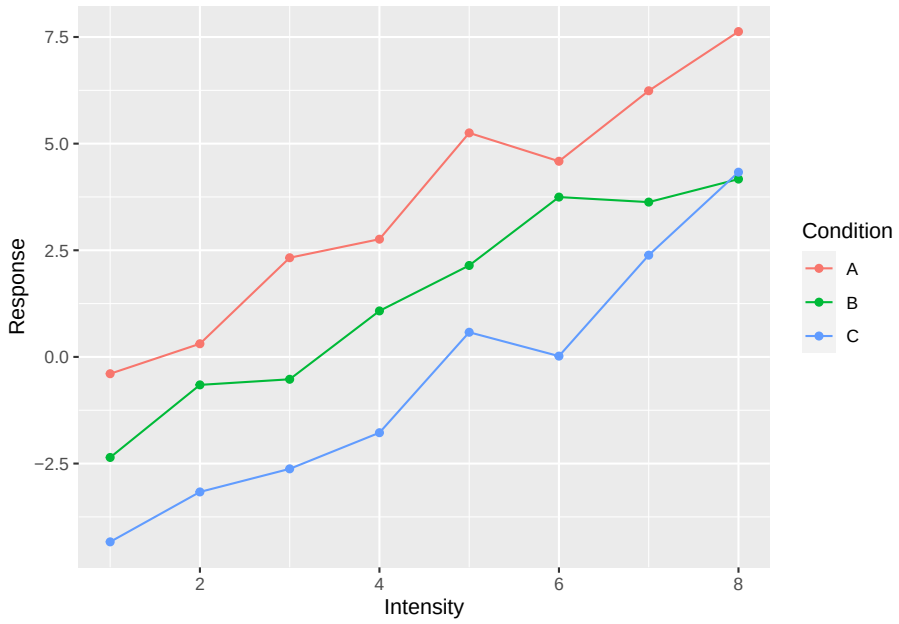
```
ggplot(data=simple_tidy_data, aes(x = Intensity, y = Response, color=Condition))
```



Told you it will look empty and yet you can already see *ggplot2* in action. Notice that axes are labeled and their limits are set. You cannot see the legend (they are not plotted without corresponding geometry) but it is also ready behind the scenes. This is because our initial call specified the most important part: how individual variables map on various properties even before we tell *ggplot2* which visuals we will use to plot the data. When we specified that x-axis will represent the `Intensity`, ggplot2 figured out the range of values, so it knows *where* it is going to plot whatever we decide to plot. Points, lines, bars, error bars and what not will span only that range. Same goes for other properties such as color. We wanted *color* to represent the condition. Again, we may not know what exactly we will be plotting (points, lines?) or even how many different visuals we will be adding to the plot (just lines? points + lines? points + lines + linear fit?) but we do know that whatever visual we add, if it can have color, its color *must* represent condition for that data point. The beauty of *ggplot2* is that it analyses your data and figures out how many colors you need and is ready to apply them *consistently* to all visuals you will add later. It will ensure that all points, bars, lines, etc. will have consistent coordinates scaling, color, size, fill mapping that are the same across the entire plot. This may sound trivial but typically (e.g., Matlab, Matplotlib), it is *your* job to make sure that all these properties match and that they represent the same value across all visual elements. And this is a pretty tedious job, particularly when you decide to change your mappings and have to redo all individual components by hand. In *ggplot2*, this dissociation between mapping and visuals means you can tinker with one of them at a time. E.g. keep the visuals but change grouping or see if effect of condition is easier to see via line type, size or shape of the point? Or you can keep the mapping and see whether adding another visual will make the plot easier to understand. Note that some mapping also *groups* your data, so when you use group-based visual information (e.g., a linear regression line) it will know what data belongs together and so will perform this computation per group.

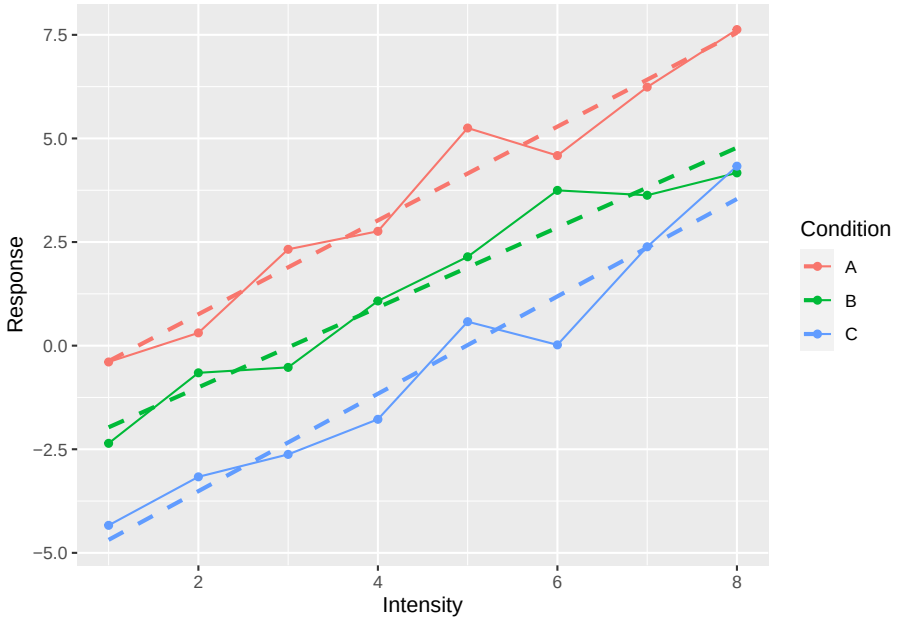
Let us see how you can keep the relationship mapping but add more visuals. Let us add both lines and points.

```
ggplot(data=simple_tidy_data, aes(x = Intensity, y = Response, color=Condition)) +
  geom_line() +
  geom_point() # this is new!
```



In the plot above, we *kept* the relationship between variables and properties but said "Oh, and throw in some points please". And ggplot2 knows how to add the points so that they appear at proper location and in proper color. But we want more!

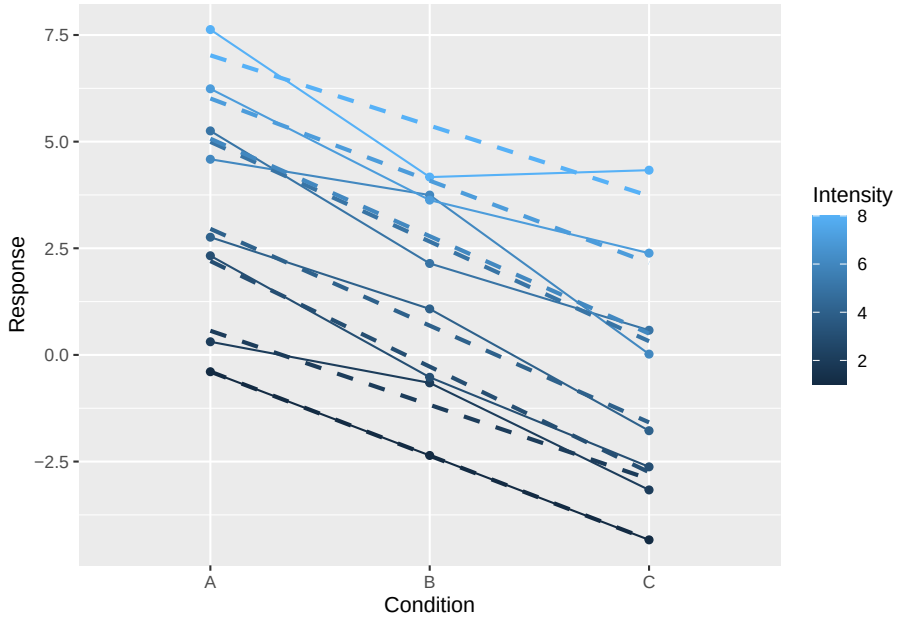
```
ggplot(data=simple_tidy_data, aes(x = Intensity, y = Response, color=Condition)) +
  geom_line() +
  geom_point() +
  # a linear regression over all dots in the group
  geom_smooth(method="lm", formula = y ~ x, se=FALSE, linetype="dashed")
```



Now we added a linear regression line that helps us to better see the relationship between `Intensity` and `Response`. Again, we simply wished for another visual to be added (`method="lm"` means that we wanted to average data via linear regression with `formula = y ~ x` meaning that we regress y-axis on x-axis with no further covariates, `se=FALSE` means no standard error stripe, `linetype="dashed"` just makes it easier to distinguish linar fit from the solid data line).

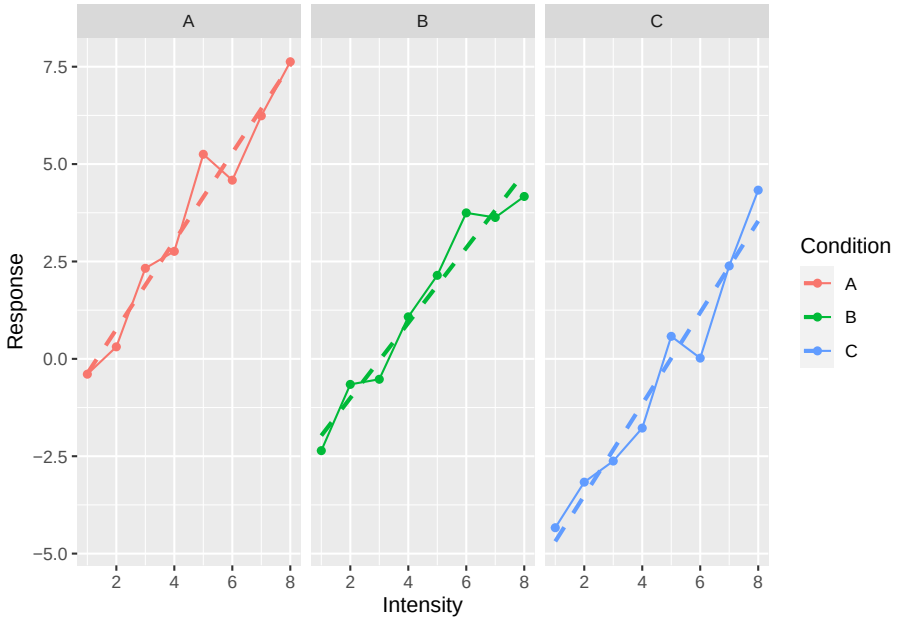
Or, we can keep the *visuals* but see whether changing *mapping* would make it more informative (we need to specify `group=Intensity` as continuous data is not grouped automatically).

```
ggplot(data=simple_tidy_data, aes(x = Condition, y = Response, color=Intensity, group=I
  geom_line() +
  geom_point() +
  geom_smooth(method="lm", se=FALSE,  formula = y ~ x, linetype="dashed")
```



Or, we can check whether splitting into several plots helps.

```
ggplot(data=simple_tidy_data, aes(x = Intensity, y = Response, color=Condition)) +
  geom_line() +
  geom_point() +
  geom_smooth(method="lm", formula = y ~ x, se=FALSE, linetype="dashed") +
  facet_grid(. ~ Condition) # makes a separate subplot for each group
```



Again, note that all three plots live on the same scale for x- and y-axis, making them easy to compare (you fully appreciate this magic if you ever struggled with ensuring optimal and consistent scaling by hand in Matlab). I went through so many examples to stress how ggplot allows you to think about the aesthetics of variable mapping *independently* of the actual visual representation (and vice versa).

Now lets us explore *ggplot2* by doing exercises. I recommend using ggplot2 reference page and cheatsheet when you are doing the exercises.

5.3 Auto efficiency: continuous x-axis

We start by visualizing how car efficiency, measured as miles-per-gallon, is affected by various factors such as production year, size of the engine, type of transmission, etc. The data is in the table mpg, which is part of the *ggplot2* package. Thus, you need to first import the library and then load the table via data() function. Take a look at the table description to familiarize yourself with the variables.

First, let us look at the relationship between car efficiency in the city cycle (`cty`), engine displacement (`displ`), and drive train type (`drv`) using color points. Reminder, the call should look as

```
ggplot(data_table_name, [aes](https://ggplot2.tidyverse.org/reference/aes.html)(x = va
  geom_primitive1() +
  geom_primitive2() +
```

. . .

Think about which variables are mapped on each axes and which is best depicted as color.

Do exercise 1.

Do you see any clear dependence? Let us try to making it more evident by adding geom_smooth geometric primitive.

Do exercise 2.

Both engine size (displacement) and drive train have a clear effect on car efficiency. Let us visualize the number of cylinders (`cyl`) as well. Including it by mapping it on the *size* of geometry.

Do exercise 3.

Currently, we are mixing together cars produced at different times. Let us visually separate them by turning each year into a subplot via facet_wrap function.

Do exercise 4.

The dependence you plotted does not look linear but instead is saturating at certain low level of efficiency. This sort of dependencies could be easier to see on a logarithmic scale. See functions for different scales and use logarithmic scaling for y-axis.

Do exercise 5.

Note that by now we managed to include *five* variables into our plots. We can continue this by including transmission or fuel type but that would be pushing it, as too many variables can make a plot confusing and cryptic. Instead, let us make it prettier by using more meaningful axes labels (`xlab()`, `ylab()` functions) and adding a plot title (labs).

Do exercise 6.

5.4 Auto efficiency: discrete x-axis

The previous section use a continuous engine displacement variable for x-axis (at least that is my assumption on how you mapped the variables). Frequently, you need to plot data for discrete groups: experimental groups, conditions, treatments, etc. Let us practice on the same mpg data set but visualize relationship between the drive train (`drv`) and highway cycle efficiency (`hwy`). Start by using point as visuals.

Do exercise 7.

One problem with the plot is that all points are plotted at the same x-axis location. This means that if two points share the location, they overlap and appear as just one dot. This makes it hard to understand the density: one

point can mean one point, or two, or a hundred. A better way to plot such data is by using box or violin plots. Experiment by using them instead of points.

Do exercise 8.

Again, let's up the ante and split plots via both number of cylinders and year of manufacturing. Use facet_grid function to generate grid of plots.

Do exercise 9.

Let us again improve our presentation by using better axes labels and figure title.

Do exercise 10.

5.5 Mammals sleep: single variable

Now lets us work on plotting a distribution for a single variable using mammals sleep dataset. For this, you need to map `sleep_total` variable on x-axis and plot a histogram. Explore the available options, in particular `bins` that determines the bins number and, therefore, their size. Note that there is no "correct" number of bins to use. *ggplot2* defaults to 30 but a small sample would be probably better served with fewer bins and, vice versa, with a large data set you can afford hundred of bins.

Do exercise 11.

Using a histogram gives you exact counts per each bin. However, the appearance may change quite dramatically if you would use fewer or more bins. An alternative way to represent the same information is via smoothed density estimates. They use a sliding window and compute an estimate at each point but also include points *around* it and weight them according to a kernel (e.g., a Gaussian one). This makes the plot look smoother and will mask sudden jumps in density (counts) as you, effectively, average over many bins. Whether this approach is better for visualizing data depends on the sample you have and message you are trying to get across. It is always worth checking both (just like it is worth checking different number of bins in histogram) to see which way is the best for your specific case.

Do exercise 12.

Let us return to using histograms and plot a distribution per `vore` variable (it is `carnivore`, `omnivore`, `herbivore`, or `NA`). You can map it on the `fill` color of the histogram, so that each *vore* kind will be binned separately.

Do exercise 13.

The plot may look confusing because by default *ggplot2* colors values for each group differently but stacks all of them together to produce the total histogram

counts. One way to disentangle the individual histograms is via facet_grid function. Use it to plot `vore` distribution in separate rows.

Do exercise 14.

That did the trick but there is an alternative way to plot individual distributions on the same plot by setting `position` argument of geom_histogram to `"identity"` (it is `"stack"` by default).

Do exercise 15.

Hmm, shouldn't we have more carnivores, what is going on? Opacity is the answer. A bar "in front" occludes any bars that are "behind" it. Go back to the exercise and fix that by specifying `alpha` argument that controls transparency. It is `1` (completely opaque) by default and can go down to `0` (fully transparent as in "invisible"), so see which intermediate value works the best.

5.6 Mapping for all visuals versus just one visual

In the previous exercise, you assigned a constant value to `alpha` (transparency) argument. You could do this in *two* places, inside of either `ggplot()` or `geom_histogram()` call. In the former case, you would have set `alpha` level for *all* geometric primitives on the plot, whereas in the latter you do it only for the histogram. To better see the difference, reuse your code for plotting city cycle efficiency versus engine size (should be exercise #6) and set `alpha` either for all visuals (in `ggplot2`) or in some visuals (e.g. only for points) to see the difference.

Do exercise 16.

5.7 Mapping on variables versus constants

In the previous exercise, you assigned a constant value to `alpha` (transparency) argument. However, transparency is just a property just like `x`, `color`, or `size`. Thus, there are *two* ways you can use them:

- *inside* `aes(x=column)`, where `column` is column in the table you supplied via `data=`
- *outside* of `aes` by stating `x=value`, where value is some constant value or a variable *that is not in the table*.

Test this but setting the `size` in the previous plot to a constant outside of aesthetics or to a variable inside of it.

Do exercise 17.

5.8 Themes

Finally, if you are not a fan of the way the plots look, you can quickly modify this by using some other theme. You can define it yourself (there are lots of options you can specify for your theme) or can use one of the ready-mades. Explore the latter option, find the one you like the best.

Do exercise 18.

5.9 You ain't seen nothing yet

What you explored is just a tip of the iceberg. There are many more geometric primitive, annotations, scales, themes, etc. It will take an entire separate seminar to do *ggplot2* justice. However, the basics will get you started and you can always consult reference, books (see below), or me once you need more.

5.10 Further reading

If plotting data is part of your daily routine, I recommend reading ggplot2 book. It gives you an in-depth view of the package and goes through many possibilities that it offers. You may need all of them but I find useful to know that they exists (who knows, I might need them one day). Another book worth reading is Data Visualization: A Practical Introduction. by Kieran Healy.

5.11 Extending ggplot2

There are 102 (as of 21.10.2021) extensions that you find at ggplot2 website. They add more ways to plot your data, more themes, animated plots, etc. If you feel that *ggplot2* does not have the geometric primitives you need, take a look at the gallery and, most likely, you will find something that fits your bill.

One package that is *not* in the gallery is patchwork. It was created "to make it ridiculously simple to combine separate ggplots into the same graphic". It is a bold promise but authors do make good on it. It is probably the easiest way to combine multiple plots but you can also consider cowplot and gridExtra packages.

5.12 ggplot2 cannot do everything

There are many different plotting routines and packages for R but I would recommend to use *ggplot2* as your main tool. However, that does not mean that it must be your only tool, after all, CRAN is brimming with packages. In particular, *ggplot2* is built for plotting data from a single tidy table, meaning it is less optimal for plotting data in other cases. E.g., you can use it to combine

information from several tables in one plot but things become less automatic and consistent. Similarly, you can plot data which is stored in non-tidy tables or even in individual vectors but that makes it less intuitive and more convoluted. No package can do everything and *ggplot2* is no exception.

Chapter 6

Tidyverse: dplyr

Now that you understand vectors, tables, functions and pipes, and you know what our end goal (a tidy table) is, we can start with data analysis and Tidyverse way of doing it. All functions discussed below are part of dplyr[1] "grammar of data manipulation" package. Grab the exercise notebook!

6.1 Tidyverse philosophy

Data analysis is different from "normal" programming as it mostly involves a series of sequential operations on the same table. You might load the table, transform some variables, filter data, select smaller subset of columns, aggregate by summarizing across different groups of variables before plotting it or formally analyzing it via statistical tests. Tidyverse is built around this serial nature of data analysis of piping a table through a chain of functions. Accordingly, Tidyverse functions take a *table* (`data.frame` or `tibble`) as their *first* parameter, which makes piping simpler, and return a *modified table* as an output. This *table-in* $\rightarrow$ *table-out* consistency makes it easy to pipe these operations one after another. For me, it helps to think about Tidyverse functions as *verbs*: Actions that I perform on the table at each step.

Here is quick teaser of how such sequential piping works. Below, we will examine each verb/function separately and I will also show you how same operations can be carried out using base R. Note that I put each verb/function on a separate line. This makes it easier to understand how many different operations you perform (number of lines), how complex they are (how long individuals lines of code are), and makes them easy to read line-by-line.

[1] The name should invoke an image of data pliers. According to Hadley Wickham, you can pronounce it any way you like.

```
mpg2lpk <- 2.82481061

mpg %>%
  # we filter the table by rows,
  # only keeping rows for which year is 2008
  filter(year == 2008) %>%

  # we change cty and hwy columns by turning
  # miles/gallon into liters/kilometer
  mutate(cty = cty / mpg2lpk,
         hwy = hwy / mpg2lpk) %>%

  # we create a new column by computing an
  # average efficiency as mean between city and highway cycles
  mutate(avg_mpg = (cty + hwy) / 2) %>%

  # we reduce the table to only two columns
  # class (of car) and avg_mpg
  select(class, avg_mpg) %>%

  # we group by each class of car
  # and compute average efficiency for each group (class of car)
  group_by(class) %>%
  summarise(class_avg_mpg = mean(avg_mpg), .groups="keep") %>%

  # we sort table rows to go from worst to best on efficiency
  arrange(class_avg_mpg) %>%

  # we kable (Knit the tABLE) to make it look nicer in the document
  knitr::kable()
```

class	class_avg_mpg
pickup	5.299679
suv	5.707006
minivan	6.655313
2seater	7.139122
subcompact	8.153201
midsize	8.386572
compact	8.721421

6.2 `select()` columns by name

Select verb allows you to select/pick columns in a table using their names. This is very similar to using columns names as indexes for tables that you have learned in seminar 3.

First, let us make a shorter version of `mpg` table by keeping only the first five rows. Note that you can also pick first N rows via head() function.

```
short_mpg <- mpg[1:5, ]

# same "first five rows" but via head() function
short_mpg <- head(mpg, 5)

knitr::kable(short_mpg)
```

manufacturer	model	displ	year	cyl	trans	drv	cty	hwy	fl	class
audi	a4	1.8	1999	4	auto(l5)	f	18	29	p	compact
audi	a4	1.8	1999	4	manual(m5)	f	21	29	p	compact
audi	a4	2.0	2008	4	manual(m6)	f	20	31	p	compact
audi	a4	2.0	2008	4	auto(av)	f	21	30	p	compact
audi	a4	2.8	1999	6	auto(l5)	f	16	26	p	compact

Here is how you can select only `model` and `cty` columns via preserving `[]` subsetting

```
short_mpg[, c("model", "cty")]
```

model	cty
a4	18
a4	21
a4	20
a4	21
a4	16

And here is how it is done via `select()`.

```
short_mpg %>%
  select(model, cty)
```

model	cty
a4	18
a4	21
a4	20
a4	21
a4	16

The idea of Tidyverse functions is to adopt to you, so you *can* use quotes or pass a vector of strings with column names. All calls below produce the same effect, so pick the style you prefer (mine, is in the code *above*) and stick to it[2].

```
short_mpg %>%
  select(c("model", "cty"))
```

[2]In general, bad but consistent styling is better than an inconsistent mix of good styles.

```
short_mpg %>%
  select("model", "cty")

short_mpg %>%
  select(c(model, cty))
```

As you surely remember, you can use negation to select *other* indexes within a vector (`c(4, 5, 6)[-2]` gives you `[4, 6]`). For the single brackets `[]` this mechanism does not work with column *names* (only with their indexes). However, `select` has you covered, so we can select everything *but* `cty` and `model`

```
short_mpg %>%
  select(-cty, -model)
```

manufacturer	displ	year	cyl	trans	drv	hwy	fl	class
audi	1.8	1999	4	auto(l5)	f	29	p	compact
audi	1.8	1999	4	manual(m5)	f	29	p	compact
audi	2.0	2008	4	manual(m6)	f	31	p	compact
audi	2.0	2008	4	auto(av)	f	30	p	compact
audi	2.8	1999	6	auto(l5)	f	26	p	compact

In the current version of `dplyr`, you can do the same negation via `!` (a `logical not` operator, you will meet later), moreover, it is now a recommended way of writing the selection[3]. The `-` and `!` are not synonyms and the difference is subtle but important, see below.

```
# will produce the same result as above
short_mpg %>%
  select(!cty, !model)
```

As with the direct selection above, you can use negation with names as strings, you can negate a vector of names, etc. Again, it is mostly a matter of taste with consistency being more important than a specific choice you make.

```
# will produce the same result as above
short_mpg %>%
  select(!c("cty", "model"))

short_mpg %>%
  select(!"cty", !"model")

short_mpg %>%
  select(!c(cty, model))
```

Unlike vector indexing that forbids mixing positive and negative indexing, `select` does allow it. However, **do not use it**[4] because results can be fairly

[3] At least, `-` is not mentioned anymore, even though it still works.

[4] Unless you know what you are doing and that is the simplest and clearest way to achieve

counter-intuitive and, on top of that, `-` and `!` work somewhat differently. Note the difference between `!` and `-`: In the former case only the `!model` part appears to have the effect, whereas in case of `-` only `cty` works.

```
short_mpg %>%
  select(cty, !model)
```

cty	manufacturer	displ	year	cyl	trans	drv	hwy	fl	class
18	audi	1.8	1999	4	auto(l5)	f	29	p	compact
21	audi	1.8	1999	4	manual(m5)	f	29	p	compact
20	audi	2.0	2008	4	manual(m6)	f	31	p	compact
21	audi	2.0	2008	4	auto(av)	f	30	p	compact
16	audi	2.8	1999	6	auto(l5)	f	26	p	compact

```
short_mpg %>%
  select(cty, -model)
```

cty
18
21
20
21
16

To make things even, worse `select(-model, cty)` work the same way as `select(cty, !model)` (sigh…)

```
short_mpg %>%
  select(-model, cty)
```

manufacturer	displ	year	cyl	trans	drv	cty	hwy	fl	class
audi	1.8	1999	4	auto(l5)	f	18	29	p	compact
audi	1.8	1999	4	manual(m5)	f	21	29	p	compact
audi	2.0	2008	4	manual(m6)	f	20	31	p	compact
audi	2.0	2008	4	auto(av)	f	21	30	p	compact
audi	2.8	1999	6	auto(l5)	f	16	26	p	compact

So, bottom line, do not mix positive and negative indexing in `select`! I am showing you this only to signal the potential danger.

Do exercise 1.

Simple names and their negation will be sufficient for most of your projects. However, I would recommend taking a look at the official manual just to see that `select` offers a lot of flexibility (selecting range of columns, by column type, by partial name matching, etc), something that might be useful for you in your work.

---

this.

6.3 Conditions

Before we can work with the next verb, you need to understand conditions. Conditions are statements about values that are either `TRUE` or `FALSE`. In the simplest case, you can check whether two values (one in a variable and one hard-coded) are equal via `==` operator

```
x <- 5
print(x == 5)
```

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

```
print(x == 3)
```

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

For numeric values, you can use all usual comparison operators including *not equal* `!=`, *less than* `<`, *greater than* `>`, *less than or equal to* `<=` (note the order of symbols!), and *greater than or equal to* `>=` (again, note the order of symbols).

Do exercise 2.

You can negate a statement via *not* `!` symbol as `!TRUE` is `FALSE` and vice versa. However, note that round brackets in the examples below! They are critical to express the *order* of computation. Anything *inside* the brackets is evaluated first. And if you have brackets inside the brackets, similar to nested functions, it is the innermost expression that get evaluated first. In the example below, `x==5` is evaluated first and logical inversion happens only after it. In this particular example, you may not need them but I would suggest using them to ensure clarity.

```
x <- 5
print(!(x == 5))
```

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

```
print(!(x == 3))
```

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

Do exercise 3.

You can also combine several conditions using *and* `&` and *or* `|` operators. Again, note round brackets that explicitly define what is evaluated first.

```
x <- 5
y <- 2

# x is not equal to 5 OR y is equal to 1
print((x != 5) | (y == 1))
```

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

```
# x less than 10 AND y is greater than or equal to 1
print((x < 10) & (y >= 1))
```

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

Do exercise 4.

All examples above used scalars but you remember that *everything is a vector*, including values that we used (they are just vectors of length one). Accordingly, same logic works for vectors of arbitrary length with comparisons working element-wise, so you get a vector of the same length with `TRUE` or `FALSE` values for each *pairwise* comparison.

Do exercise 5.

6.4 Logical indexing

In the second seminar, you learned about vector indexing when you access *some* elements of a vector by specifying their index. There is an alternative way, called *logical indexing*. Here, you supply a vector of equal length with *logical values* and you get elements of the original vector whenever the logical value is `TRUE`

```
x <- 1:5
x[c(TRUE, TRUE, FALSE, TRUE, FALSE)]
```

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

This is particularly useful, if you are interested in elements that satisfy certain condition. For example, you want all *negative* values and you can use condition `x<5` that will produce a vector of logical values that, in turn, can be used as index

```
x <- c(-2, 5, 3, -5, -1)
x[x<0]
```

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

You can have conditions of any complexity by combining them via *and* `&` and *or* `|` operators. For example, if you want number below -1 or above 3 (be careful to have space between `<` and `-`, otherwise it will be interpreted as assignment `<-`).

```
x <- c(-2, 5, 3, -5, -1)
x[(x< -1) | (x>3)]
```

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

Do exercise 6.

Sometimes you may want to know the actual index of elements for *which* some condition is `TRUE`. Function which() does exactly that.

```
x <- c(-2, 5, 3, -5, -1)
which( (x< -1) | (x>3) )
```

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

6.5 `filter()` rows by values

Now that you understand conditions and logical indexing, using filter() is very straightforward: You simply put condition that describes rows that you want to *retain* inside the `filter()` call. For example, we can look at efficiency only for two-seater cars.

```
mpg %>%
  filter(class == "2seater")
```

manufacturer	model	displ	year	cyl	trans	drv	cty	hwy	fl	class
chevrolet	corvette	5.7	1999	8	manual(m6)	r	16	26	p	2seater
chevrolet	corvette	5.7	1999	8	auto(l4)	r	15	23	p	2seater
chevrolet	corvette	6.2	2008	8	manual(m6)	r	16	26	p	2seater
chevrolet	corvette	6.2	2008	8	auto(s6)	r	15	25	p	2seater
chevrolet	corvette	7.0	2008	8	manual(m6)	r	15	24	p	2seater

You can use information from any row, so we can look for midsize cars with four-wheel drive.

```
mpg %>%
  filter(class == "midsize" & drv == "4")
```

manufacturer	model	displ	year	cyl	trans	drv	cty	hwy	fl	class
audi	a6 quattro	2.8	1999	6	auto(l5)	4	15	24	p	midsize
audi	a6 quattro	3.1	2008	6	auto(s6)	4	17	25	p	midsize
audi	a6 quattro	4.2	2008	8	auto(s6)	4	16	23	p	midsize

Do exercise 7.

Note that you can emulate `filter()` in a very straightforward way using single-brackets base R, the main difference is that you need to prefix every column with the table name, so `mpg[["class"]]` instead of just `class`[5].

```
mpg[mpg[["class"]] == "midsize" & mpg[["drv"]] == "4", ]
```

manufacturer	model	displ	year	cyl	trans	drv	cty	hwy	fl	class
audi	a6 quattro	2.8	1999	6	auto(l5)	4	15	24	p	midsize
audi	a6 quattro	3.1	2008	6	auto(s6)	4	17	25	p	midsize
audi	a6 quattro	4.2	2008	8	auto(s6)	4	16	23	p	midsize

[5] You can sidestep this issue via with() function, although I am not a big fan of this approach.

So why use `filter()` then? In isolation, as a single line computation, both options are equally compact and clear (apart from all the extra `table[["..."]]` in base R). But pipe-oriented nature of the `filter()` makes it more suitable for chains of computations, which is the main advantage of Tidyverse.

6.6 `arrange()` rows in a particular order

Sometimes you might need to sort your table so that rows go in a particular order[6]. In Tidyverse, you arrange rows based on values of specific variables. This verb is very straightforward, you simply list all variables that must be used for sorting in the order the sorting must be carried out. I.e., first the table is sorted based on values of the first variable. Then, for equal values of that variable, rows are sorted based on the second variable, etc. By default, rows are arranged in ascending order but you can reverse it by putting a variable inside of desc() function. Here is the `short_mpg` table arranged by city cycle highway efficiency (ascending order) and engine displacement (descending order, note the order of the last two rows).

```
short_mpg %>%
  arrange(cty, desc(displ))
```

manufacturer	model	displ	year	cyl	trans	drv	cty	hwy	fl	class
audi	a4	2.8	1999	6	auto(l5)	f	16	26	p	compact
audi	a4	1.8	1999	4	auto(l5)	f	18	29	p	compact
audi	a4	2.0	2008	4	manual(m6)	f	20	31	p	compact
audi	a4	2.0	2008	4	auto(av)	f	21	30	p	compact
audi	a4	1.8	1999	4	manual(m5)	f	21	29	p	compact

Do exercise 8.

You can arrange a table using base R via order() function that gives index of ordered elements and can be used inside of preserving subsetting via single brackets `[]` notation. You can control for ascending/descending of a specific variable using rev() function that is applied *after* ordering, so `rev(order(...))`.

```
short_mpg[order(short_mpg[["cty"]], rev(short_mpg[["displ"]])), ]
```

manufacturer	model	displ	year	cyl	trans	drv	cty	hwy	fl	class
audi	a4	2.8	1999	6	auto(l5)	f	16	26	p	compact
audi	a4	1.8	1999	4	auto(l5)	f	18	29	p	compact
audi	a4	2.0	2008	4	manual(m6)	f	20	31	p	compact
audi	a4	2.0	2008	4	auto(av)	f	21	30	p	compact
audi	a4	1.8	1999	4	manual(m5)	f	21	29	p	compact

Do exercise 9.

[6] In my experience, this mostly happens when you need to print out or view a table.

6.7 `mutate()` columns

In Tidyverse, mutate function allows you to both add new columns/variables to a table and change the existing ones. In essence, it is equivalent to a simple column assignment statement in base R.

```
# base R
short_mpg[["avg_mpg"]] <- (short_mpg[["cty"]] + short_mpg[["hwy"]]) / 2

# Tidyverse equivalent
short_mpg <-
  short_mpg %>%
  mutate(avg_mpg = (cty + hwy) / 2)
```

Note two critical differences. First, `mutate()` takes a table as an input and returns a table as an output. This is why you start with a table, pipe it to mutate, and assign the results *back* to the original variable. If you have more verbs/lines, it is the output of the *last* computation that is assigned to the variable on the left-hand side of assignment[7]. Look at the listing below that indexes each line by when it is executed.

```
some_table <-    # 3. We assign the result to the original table, only once all the co
  some_table %>% # 1. We start here, with the original table and pipe to the next comp
  mutate(...)    # 2. We add/change columns inside of the table. The output is a table
```

Second, you are performing a computation *inside* the call of the `mutate()` function, so `avg_mpg = (short_mpg$cty + short_mpg$hwy) / 2` is a *parameter* that you pass to it (yes, it does not look like one). This is why you use `=` rather than a normal assignment arrow `<-`. Unfortunately, you *can* use `<-` inside the `mutate` and the computation will work as intended but, for internal-processing reasons, the *entire statement*, rather than just the left-hand side, will be used as a column name. Thus, use `<-` *outside* and `=` *inside* of Tydiverse verbs.

```
short_mpg %>%
  select(cty, hwy) %>%
  mutate(avg_mpg =  (cty + hwy) / 2,      # column name will be avg_mpg
         avg_mpg <- (cty + hwy) / 2) %>% # column name will be `avg_mpg <- (short_mpg$
  knitr::kable()
```

[7] R does have `->` statement, so, technically, you can pipe your computation and then assign it to a variable `table %>% mutate() -> table`. However, this style is generally discouraged as starting with `table <- table %>%` makes it clear that you modify and store the computation, whereas `table %>%` signals that you pipe the results to an output: console, printed-out table, plot, etc.

cty	hwy	avg_mpg	avg_mpg <- (cty + hwy)/2
18	29	23.5	23.5
21	29	25.0	25.0
20	31	25.5	25.5
21	30	25.5	25.5
16	26	21.0	21.0

As shown in the example above, you can perform several computations within a single `mutate` call and they are executed one after another, just as they would be when using base R.

Do exercise 10.

Finally, `mutate` has two cousin-verbs called transmute and add_column. The former (`transmute`) works the same way but *discards* all original columns that were not modified. You probably won't use this verb all too often but I want you to be able to recognize it, as its name and function are very similar to `mutate` and the two are easy to confuse.

```
short_mpg %>%
  transmute(avg_mpg = (cty + hwy) / 2) %>%
  knitr::kable(align = "c")
```

avg_mpg
23.5
25.0
25.5
25.5
21.0

The latter — `add_column` — is *similar* to `mutate` if you need to add a new column rather than to modify a new one. Its advantage is that it will produce an error, if you try to overwrite an existing column. Its disadvantage is that it does not appear to respect data grouping (see below), which can be very confusing. In short, stick to `mutate` unless you need either of these two functions specifically.

6.8 `summarize()` table by `groups`

This verb is used when you *aggregate* across *all* rows, reducing them to a *single value*. Some examples of aggregating functions that are probably already familiar to you are mean, median, standard deviation, min/max. However, you can "aggregate" by taking a first or a last value or even by putting in a constant. Important is that you should assign a *single* value to the column when using `summarize`[8].

[8] In the old times, summarize would only accept a single value and raise an error in any other case. That was good, as it made role of `summarize` very clear (aggregation) and it was clearly different from `mutate` (modification). Unfortunately, at certain point of time `summarize`

If you use `summarize` on an *ungrouped* table (these are the only tables we've been working on so far), it keeps only the computed columns, which makes you wonder "what's the point?"

```
mpg %>%
  summarise(avg_cty = mean(cty),
            avg_hwy = mean(hwy))
```

```
## # A tibble: 1 x 2
##   avg_cty avg_hwy
##     <dbl>   <dbl>
## 1    16.9    23.4
```

However, the real power of `summarize` (and of `mutate`) becomes evident when it is applied to the data that is *grouped by* certain criteria. group_by() verb groups rows of the table based on values of variables you specified. Behind the scenes, this turns your single table into set of tables, so that your Tidyverse verbs are applied to *each* table *separately*. This ability to parse your table into different groups of rows (all rows that belong to a particular participant, or participant and condition, or rows per block, or per trial), change that grouping on the fly, return back to the original full table, etc. makes analysis a breeze. Here is how we can compute average efficiency not across all cars (as in the code above) but for each car class separately.

```
mpg %>%
  # there are seven different classes of cars, so group_by(cars)  will
  # create seven hidden independent tables and all verbs below will be
  # applied to each table separately
  group_by(class)  %>%

  # same mean computation but per table and we've got seven of them
  summarise(avg_cty = mean(cty),
            avg_hwy = mean(hwy),
            .groups = "keep") %>%
  knitr::kable()
```

got a power up, so now it will accept *any* number of values per table/group. This means that, technically, you can use it instead of `mutate` with no loss of functionality. It also means that it won't warn you that you are doing something wrong in your aggregation, if you return more than one value per group/column. Happened to me often enough to make me wonder why this unfortunate decision was made.

class	avg_cty	avg_hwy
2seater	15.40000	24.80000
compact	20.12766	28.29787
midsize	18.75610	27.29268
minivan	15.81818	22.36364
pickup	13.00000	16.87879
subcompact	20.37143	28.14286
suv	13.50000	18.12903

Note that we compute a *single* value per table but because we do it for *seven tables*, we get *seven rows* in our resultant table. And `group_by` makes it easy to group data in any way you want. Are you interested in manufacturers instead car classes? Easy!

```
mpg %>%
  group_by(manufacturer)  %>%
  # same mean computation but per table and we've got seven of them
  summarise(avg_cty = mean(cty),
            avg_hwy = mean(hwy), .groups = "keep") %>%
  knitr::kable()
```

manufacturer	avg_cty	avg_hwy
audi	17.61111	26.44444
chevrolet	15.00000	21.89474
dodge	13.13514	17.94595
ford	14.00000	19.36000
honda	24.44444	32.55556
hyundai	18.64286	26.85714
jeep	13.50000	17.62500
land rover	11.50000	16.50000
lincoln	11.33333	17.00000
mercury	13.25000	18.00000
nissan	18.07692	24.61538
pontiac	17.00000	26.40000
subaru	19.28571	25.57143
toyota	18.52941	24.91176
volkswagen	20.92593	29.22222

How about efficiency per class *and* year? Still easy!

```
mpg %>%
  group_by(class, year)  %>%
  # same mean computation but per table and we've got seven of them
  summarise(avg_cty = mean(cty),
            avg_hwy = mean(hwy), .groups = "keep") %>%
  knitr::kable()
```

class	year	avg_cty	avg_hwy
2seater	1999	15.50000	24.50000
2seater	2008	15.33333	25.00000
compact	1999	19.76000	27.92000
compact	2008	20.54545	28.72727
midsize	1999	18.15000	26.50000
midsize	2008	19.33333	28.04762
minivan	1999	16.16667	22.50000
minivan	2008	15.40000	22.20000
pickup	1999	13.00000	16.81250
pickup	2008	13.00000	16.94118
subcompact	1999	21.57895	29.00000
subcompact	2008	18.93750	27.12500
suv	1999	13.37931	17.55172
suv	2008	13.60606	18.63636

Finally, `ungroup()` verb removes all the grouping and turns your data into a single table.

Do exercise 11.

You have probably notice the `.groups="keep"` parameter in all `summarize` calls and wondered what is it for and what other options exist? Current (21.10.2021) it is still an experimental feature of summarize that determines what happens to grouping of the table *after* summarized finished the computation. The four options are:

- `.groups = "drop"` ungroups the data and is equivalent to using `ungroup` immediately after a `summarize`.
- `.groups = "keep"` keeps grouping as is.
- `.groups = "rowwise"` each row becomes its own group. If you returned one value per group, this would be identical to `.groups = "keep"`.
- `.groups = "drop_last"` drops the *last* level of grouping you specified. E.g., if you grouped by `class`, `manufacturer`, and `year`, using this option will produce a table that is grouped only by `class` and `manufacturer`. On the one hand, this is a *default* option. On the other hand, I am not quite sure why this would be preferable over `keep"` or when would I actually require this.

My suggestions would be to *always* use `.groups="keep"` in conjunction with an explicit `ungroup()`. This way `summarize` would always behave the same way, making it easier to stop regrouping and ungrouping. I went into details only because you must specify this parameter to avoid a warning that looks both ominous and confusing. And a brief look in the manual did not help me much (you can play with different options while looking at the resultant grouping via groups() function to explore outcomes). At the moment, it is unclear whether this options stays or how it will be transformed in the future (remember, it is still an experimental one).

You can replicate the functionality of `group_by` + `summarize` in base R via aggregate() and `group_by` + `mutate` via by functions. However, they are somewhat less straightforward in use as they rely on functional programming (which you haven't learned about yet) and require both grouping and summary function within a single call.

6.9 Putting it all together

Now you have enough tools at your disposal to start programming a continuous analysis pipeline!

Do exercise 12.

6.10 Should I use Tidyverse?

As you saw above, whatever Tidyverse can do, base R can do as well. So why use a non-standard family of packages? If you are using each function in isolation, there is probably not much sense in this. Base R can do it equally well and *each individual* function is also compact and simple. However, if you need to *chain* your computation, which is almost always the case, Tidyverse's ability to pipe the entire sequence of functions in a simple consistent and, therefore, easy to understand way is a game-changer. In the long run, pick your style. Either go "all in" with Tidyverse (that is my approach), stick to base R, or find some alternative package family (e.g., data.table). However, as far as the book is concerned, it will be almost exclusively Tydiverse from now on.

Chapter 7

Working with Factors

Let us start with a "warm up" exercise that will require combining various things that you already learned. Download persistence.csv file (remember, Chrome/Edge browsers may change the extension to *.xls*, just rename it back to *.csv*) and put it into *data* subfolder in your seminar project folder. This is data from a Master thesis project by Kristina Burkel, published as an article in Attention, Perception, & Psychophysics. The work investigated how change in object's shape affected perceptual stability during brief interruptions (50 ms blank intervals). The research question was whether the results will match those for one other two history effects, which work at longer time scales. Such match would indicate that both history effects are likely to be produced by the same or shared neuronal representations of 3D rotation. Grab the exercise notebook before we start.

7.1 How to write code

From now on, you will need to implement progressively longer analysis sequences. Unfortunately, the longer and the more complex the analysis is, the easier it is to make a mistake that will ruin everything after that stage. And you will make mistakes, simply because no one is perfect and everyone makes them. I make them all the time. Professional programmers make them. So the skill of programming is not about writing the perfect code on your first attempt, it is writing your code in an iterative manner, so that any mistake you make (and, again, you will make them!) will be spotted and fixed immediately, before you continue adding more code. It should be like walking blind through uncertain terrain: One step a time, no running, no jumping, as you have no idea what awaits you.

What does this mean in practical terms? In a typical analysis (such as in the exercise below), you will need to do many things: read data, select columns,

filter it, compute new variables, group data and summarize it, plot it, etc. You might be tempted to program the whole thing in one go but it is a terrible idea. Again, if your step #2 does not do what you think it should, your later stages will work with the wrong data and tracing it back to that step #2 may not be trivial (it almost never is). Instead, implement one step at a time and check that the results look as they should. E.g., in the exercise below, read the table. Check, does it look good, does it even have the data? Once you are sure that your reading bit works, proceed to columns selection. Run this two-step code and then check that it works and the table looks the way it should. It does (it has only the relevant columns)? Good, proceed to the next step.

Never skip these checks! Always look at the results of each additional step, do not just *hope* that they will be as they should. They might, they might not. In the latter case, if you are lucky, you will see that and are in for a long debugging session. But you may not even notice that computation is subtly broken and use its results to draw erroneous conclusions. It may feel overly slow to keep checking yourself continuously but it is a *faster* way to program in a long term. Moreover, if you do it once step at a time, you actually *know*, not hope, that it works.

I've spent three paragraphs on it (and now adding even the forth one!), because, in my opinion, this approach is the main difference between novice and experienced programmers (or, one could go even further and say between good and bad programmers). And I see this mistake of writing everything in one go repeated again and again irrespective of the tool people use (you can make a really fine mess using SPSS!). So, pace yourself and let's start programming in earnest!

7.2 Implementing a typical analysis

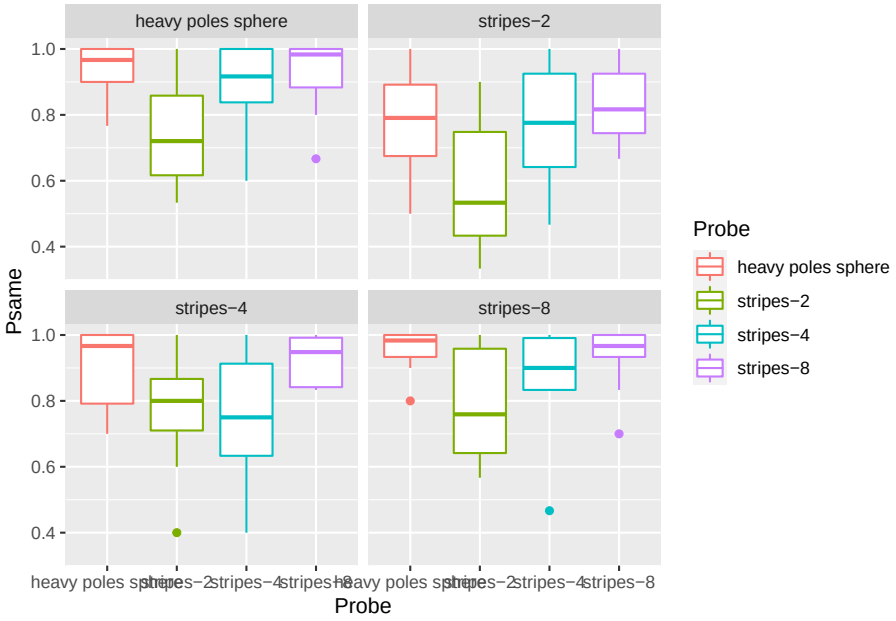
In the first exercise, I want you to implement the actual analysis performed in the paper. Good news is that by now you know enough to program it!

1. Load the data in a table. Name of the variable is up to you. Typically, I use names like `data`, `reports`, `results`, etc. Don't forget to specify columns' type.
2. Exclude `filename` column (it duplicates `Participant` and `Session` columns).
3. Compute a new variable `SameResponse` which is `TRUE` when `Response1` and `Response2` match each other (in the experiment, that means that an object was rotating in the same direction before and after the intervention).
4. For every combination of `Participant`, `Prime` and `Probe` compute proportion of same responses. You can do this in to ways. Recall that `as.integer(TRUE)` is `1` and `as.integer(FALSE)` is `0`. Thus, you can either compute proportion as mean or compute the sum of same responses

and divide it by total number of trials. Use function n() for the latter, it returns the total number of rows in the table or the group. Try doing it both ways.

5. Plot the results with `Probe` variable on x-axis, proportion of same responses on y-axis, and use `Prime` to facet plots. Use box plots (or violin plots) to visualize the data. Try adding color, labels, etc. to make plots look nice.

Your final plot should look something like this



Do exercise 1.

When you examine the plot, you can see some sort of non-monotonic dependence with a dip for `"stripes-2"` and `"stripes-4"` objects. In reality, the dependence is monotonic, it is merely the order of values on the x-axis that is wrong. The correct order, based on the area of an object covered with dots, is `"heavy poles sphere"`, `"stripes-8"`, `"stripes-4"`, `"stripes-2"`. Both `Prime` and `Probe` are *ordinal* variables called *factors* in R. Thus, to fix the order and to make object names a bit better looking, we must figure out how to work with factors in R.

7.3 Factors

Factors are categorical variables, thus variables that have a finite fixed and known set of possible values. They can be either *nominal* (cannot be ordered) or *ordinal* (have a specific order to them). An example of the former is the

drive train (`drv`) variable in mpg table. There is a finite set of possible values (`"f"` for front-wheel drive, `"r"` for rear wheel drive, and `"4"` for a four-wheel drive) but ordering them makes no sense. An example of an ordinal variable is a Likert scale that has a finite set of possible responses (for example, `"disagree"`, `"neither agree, nor disagree"`, `"agree"`) with a specific fixed order (participant's support for a statement is progressively stronger so that `"disagree"` < `"neither agree, nor disagree"` < `"agree"`).

You can convert *any* variable to a factor using factor() or `as.factor()` functions. The latter is a more limited version of the former, so it makes little sense to ever use it. Below, I will only use factor(). When you convert a variable (a vector) to factor, R:

1. figures out all unique values in this vector
2. sorts them in an ascending order
3. assigns each value an integer index, a.k.a. "level"
4. uses the actual value as a "label".

Here is an example of this sequence: there four levels sorted alphabetically (note that R prints out not only the vector but also its levels).

```
letters <- c("C", "A", "D", "B", "A", "B")
letters_as_factor <- factor(letters)
letters_as_factor
```

```
## [1] C A D B A B
## Levels: A B C D
```

You can extracts levels of a factor variable by using the function of the same name

```
levels(letters_as_factor)
```

```
## [1] "A" "B" "C" "D"
```

You can specify the order of levels either during the factor() call or later using forcats library (more on that later). For example, if we want to have levels in the reverse order we specify it via `levels` parameter. Note the opposite order of levels.

```
letters <- c("C", "A", "D", "B", "A", "B")
letters_as_factor <- factor(letters, levels = c("D", "C", "B", "A"))
letters_as_factor
```

```
## [1] C A D B A B
## Levels: D C B A
```

We can also specify `labels` of individual labels instead of using values themselves. Note that the labels must match levels in *number* and *order*.

```
responses <- c(1, 3, 2, 2, 1, 3)
responses_as_factor <- factor(responses, levels = c(1, 2, 3), labels = c("negative", "neutral", "
responses_as_factor
```

```
## [1] negative positive neutral  neutral  negative positive
## Levels: negative neutral positive
```

You can see *indexes* that were assigned to each level by converting `letter_as_factor` to a numeric vector. In this case, R throws away labels and returns indexes.

```
as.numeric(letters_as_factor)
```

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

However, be careful when level labels are numbers. In the example below, you might think that `as.numeric(tens)` should give you `[20, 40, 30]`[1] but these are labels! If you need to convert labels to numbers, you have to do it in two steps `as.numeric(as.character(tens))`: `as.character()` turns factors to strings (using labels) and `as.numeric()` converts those labels to numbers (if that conversion can work).

```
tens <- factor(c(20, 40, 30))
print(tens)
```

```
## [1] 20 40 30
## Levels: 20 30 40
```

```
print(as.numeric(tens))
```

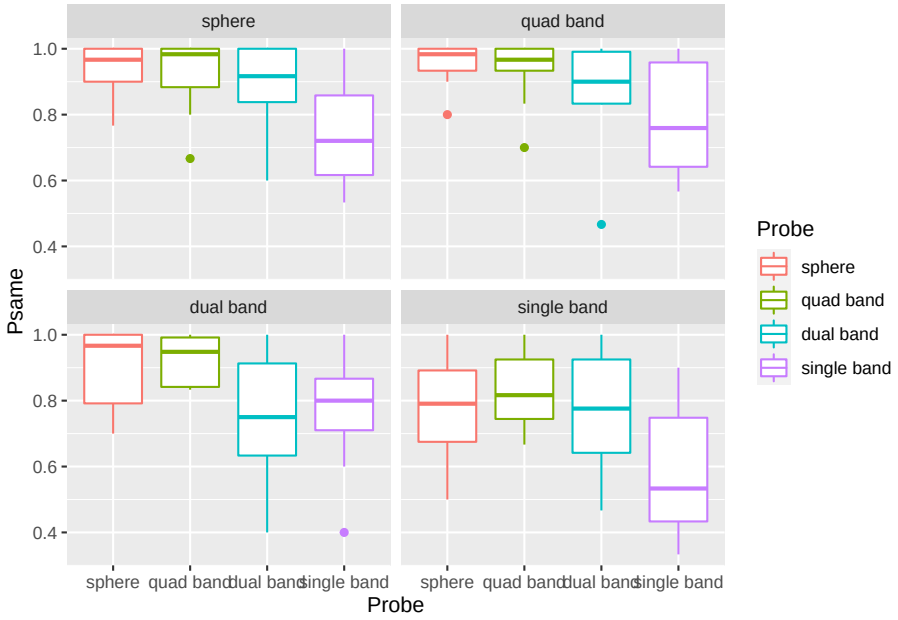
```
## [1] 1 3 2
```

```
print(as.numeric(as.character(tens)))
```

```
## [1] 20 40 30
```

For the next exercise, copy-paste the code from exercise #1 and alter it so the labels are `"sphere"` (for `"heavy poles sphere"`), `"quad band"` (for `"stripes-8"`), `"dual band"` (`"stripes-4"`), `"single band"` (for `"stripes-2"`) and levels are in that order. Your plot should look something like this.

[1] At least I tend to always think that.



Do exercise 2.

7.4 Forcats

Tidyverse has a package forcats[2] that makes working with factors easier. For example, it allows to reorder levels either by hand or automatically based on the order of appearance, frequency, value of other variable, etc. It also gives you flexible tools to changes labels either by hand, by lumping some levels together, by anonymising them, etc. In my work, I mostly use reordering (fct_relevel()) and renaming (fct_recode()) of factors by hand. You will need to use these two functions in exercise #3. However, if you find yourself working with factors, it is a good idea to check other forcats functions to see whether they can make your life easier.

To reorder factor by hand, you simply state the desired order of factors, similar to they way you specify this via `levels=` parameters in `factor()` function. However, in fct_relevel() you can move only *some* factors and others are "pushed to the back".

```
letters <- c("C", "A", "D", "B", "A", "B")
letters_as_factor <- factor(letters, levels = c("B", "C", "D", "A"))
print(letters_as_factor)
```

```
## [1] C A D B A B
```

[2]The package's name is anagram of *factors*.

```
## Levels: B C D A
```

```
# specifying order for ALL levels
letters_as_factor <- fct_relevel(letters_as_factor, "D", "C", "B", "A")
print(letters_as_factor)
```

```
## [1] C A D B A B
## Levels: D C B A
```

```
# specifying order for just ONE level, the rest are "pushed back"
# "A" should now be the first level and the rest are pushed back in their original order
letters_as_factor <- fct_relevel(letters_as_factor, "A")
print(letters_as_factor)
```

```
## [1] C A D B A B
## Levels: A D C B
```

You can also put a level at the very back, as second level, etc. fct_relevel() is very flexible, so check reference whenever you use it.

To rename individual levels you use fct_recode() by providing `new = old` pairs of values.

```
letters_as_factor <- factor(c("C", "A", "D", "B", "A", "B"))
letters_as_factor <- fct_recode(letters_as_factor, "_A_" = "A", "_C_" = "C")
print(letters_as_factor)
```

```
## [1] _C_ _A_ D   B   _A_ B
## Levels: _A_ B _C_ D
```

Note that this allows you to merge levels by hand.

```
letters_as_factor <- factor(c("C", "A", "D", "B", "A", "B"))
letters_as_factor <- fct_recode(letters_as_factor, "_AC_" = "A", "_AC_" = "C")
print(letters_as_factor)
```

```
## [1] _AC_ _AC_ D    B    _AC_ B
## Levels: _AC_ B D
```

For exercise #3, redo exercise #2 but using fct_relevel() and fct_recode(). You still need to use `factor()` function to convert `Prime` and `Probe` to factor but do not specify levels and labels. Use fct_relevel() and fct_recode() inside mutate() verbs to reorder and relabel factor values (or, first relabel and then reorder, whatever is more intuitive for you). The end product (the plot) should be the same.

Do exercise 3.

7.5 Plotting group averages

Let us keep practicing and extend our analysis to compute and plots averages for each condition (`Prime`×`Probe`) over all participants. Use preprocessing code from exercise #3 but, once you compute a proportion per `Participant`×`Prime`×`Probe`, you need to group data over `Prime`×`Probe` to compute average performance across observers. Advice, *do not* reuse the name of the column, e.g., if you used `Psame` for proportion per `Participant`×`Prime`×`Probe`, use some *other* name for `Prime`×`Probe` (e.g. `Pavg`). Otherwise, it may turn out to be very confusing (at least, this is a mistake a make routinely). Take a look at the code below, what will the `Range` values be?

```
tibble(ID = c("A", "A", "B", "B"),
       Response = c(1, 2, 4, 6)) %>%

  group_by(ID) %>%
  summarise(Response = mean(Response),
            Range = max(Response) - min(Response))
```

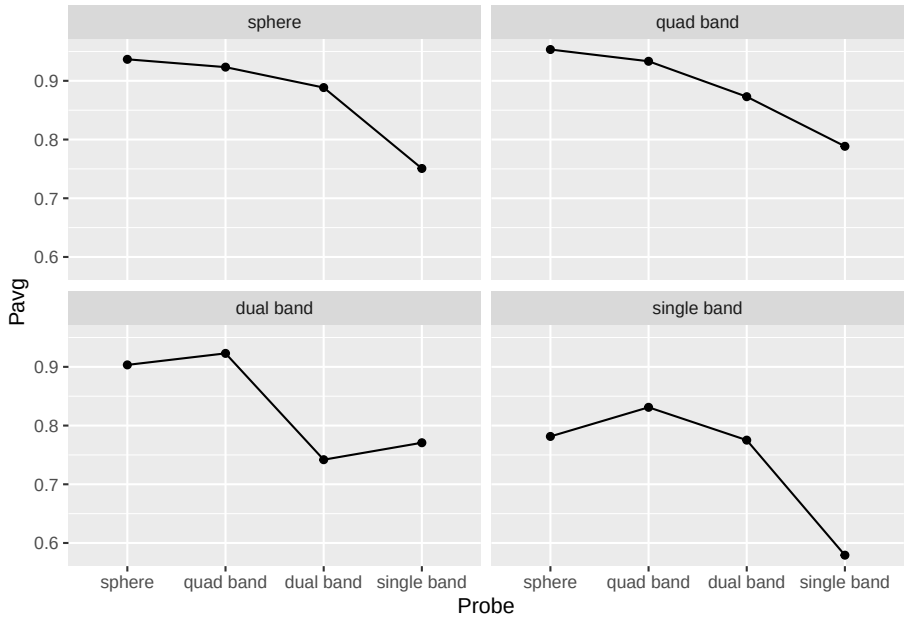
I routinely assume that they should be `1` for `"A"` (because `2-1`) and `2` for `"B"` (`6-4`). Nope, both are `0` because by the time `Range = max(Response) - min(Response)` is executed, original values of `Response` are overwritten by `Response = mean(Response)`, so it has just **one** value, the mean. And `min()` and `max()` of a single value is that value, so their difference is `0`. It is obvious once you carefully consider the code but it is *not* obvious (at least to me) straightaway. In short, be **very careful** when you are reusing column names. Better still, do not reuse them, be creative, come up with new ones!

Getting back to the exercise, compute average performance per `Prime`×`Probe`. Store the result of the computation in a new variable (I've called it `persistence_avg`) and check that results makes sense, e.g. you have just three columns `Prime`, `Probe`, and `Pavg` (or however you decided to name the column). They should look like this:

Prime	Probe	Pavg
sphere	sphere	0.9366667
sphere	quad band	0.9233333
sphere	dual band	0.8885185
sphere	single band	0.7507407
quad band	sphere	0.9533333
quad band	quad band	0.9333333
quad band	dual band	0.8729630
quad band	single band	0.7885185
dual band	sphere	0.9033333
dual band	quad band	0.9229630
dual band	dual band	0.7418519
dual band	single band	0.7707407
single band	sphere	0.7814815
single band	quad band	0.8311111
single band	dual band	0.7751852
single band	single band	0.5792593

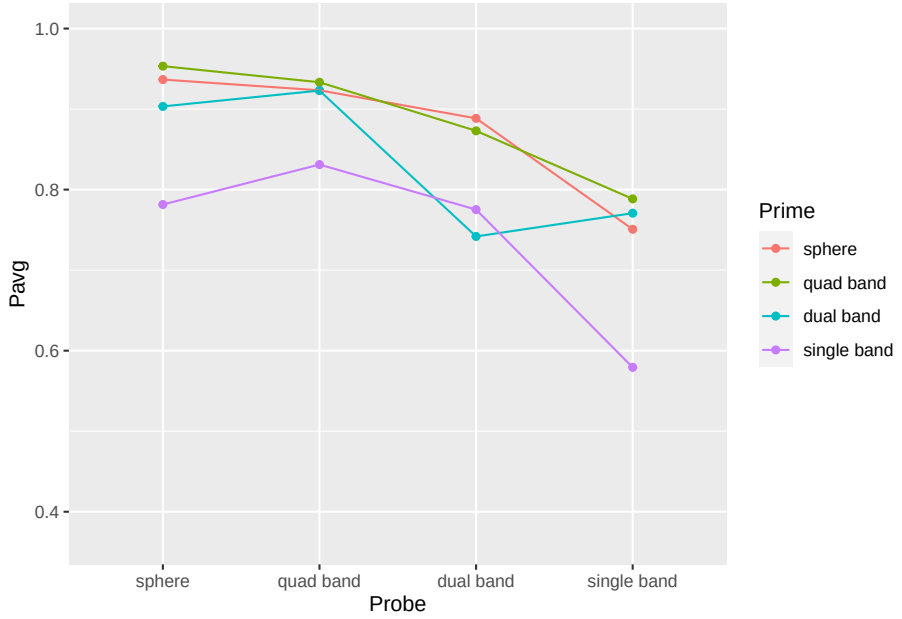
Do exercise 4.

Then, plot the results. Use geom_point() plus geom_line() to plot the mean response The plot should like like this (hint, drop color mapping and map `Prime` to `group` property).



Do exercise 5.

Tweak code from exercise 4 to plot all lines on the same plot and use color property to distinguish between different primes.



Do exercise 6.

7.6 Plotting our confidence in group averages via quantiles

From the plots above, you get a sense that identities of the probe and prime (objects before and after the interruption) matter. Single band appears to be the poorest prime (its line is lowest) and probe (its dots are lower than the rest). Conversely, sphere is an excellent prime (line at the top) and probe (dots are very high). However, averages that we plotted is just a point estimate for most likely effect strength but they alone cannot tell us whether differences in objects' shape do matter. For this, you need to perform statistical analysis but to get at least a feeling of how confident can you be about these differences, you need to plot a measure of variability associated with that *statistics*. I.e., `[1, 5, 9]` and `[4, 5, 6]` both have identical mean of 5 but their standard deviation is 4.5 *times* different (4.51 vs. 1). In the second case, the true mean is likely to be somewhere very near to 5, whereas we would have much less confidence in the former one.

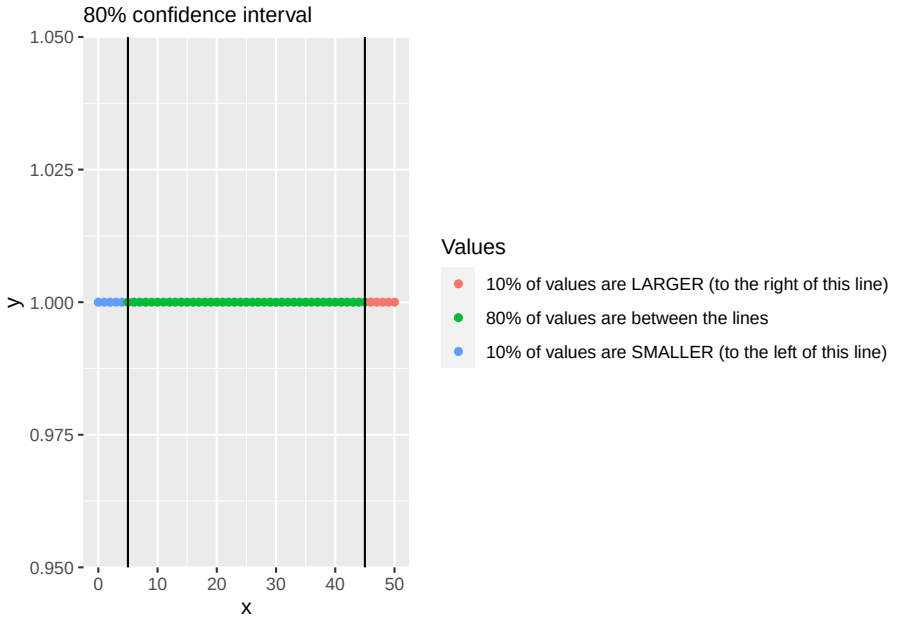
One way to characterize the mean is by computing its standard error. However, it is best used when actual data is distributed normally or, at least, symmetrically around the mean, i.e., the distance from an observation to the mean could

be the same irrespective of whether it is larger or smaller. This is a luxury you can expect only for variables that live on $\pm\infty$ range (support) or if the practically observed range of values is very far from either the floor or the ceiling. Adult height is an example of the latter: You cannot have height below 0 but an average adult height is far enough from that limit so its distribution is normal and symmetric enough. Unfortunately, a lot of data that we collect in psychology or social science research does not fit this description: Binomial data with yes/no or correct/incorrect responses lives on 0..1 range, response times have long right tail because they cannot be negative or even particularly short (200 ms would be a realistic floor for key presses, ~120 ms for eye saccadic response under *very* specific experimental conditions.)[3]

In our case the outcome variable is a *proportion* limited to 0 to 1 range. From practical point of view this means that our measure of variability is unlikely to be symmetric relative to the mean (with a unique exception of the mean exactly 0.5). I.e., think about a group average $P_{avg} = 0.8$, points *below* that average can be further away from the mean (up to 0.8) than points *above* it (0.2 away at most). This compression is called either a ceiling (when you get squashed by the upper range) or flooring (when you cannot go below certain value) effect. Thus, we need a measure that would take this asymmetry into account. Later on you will learn how to do it using bootstrapping but we will start with a simpler approach of just using quantiles of a distribution to understand its variability.

To compute this quantiles-based interval, you need to compute its lower and upper limits separately via quantiles. A quantile for 0.1 (10%) returns a value, so that 10% of all values in the vector are below it, the quantile of 0.9 (90%) means that only 10% of values are above it (or 90% are below). So, an 80% confidence intervals includes values that are between 10% and 90% or, alternatively, between 0.1 and 0.9 quantiles.

[3]I did not mention Likert scale data because it is an ordered categorical type data, so you cannot use raw data to compute even the mean, let alone its error.



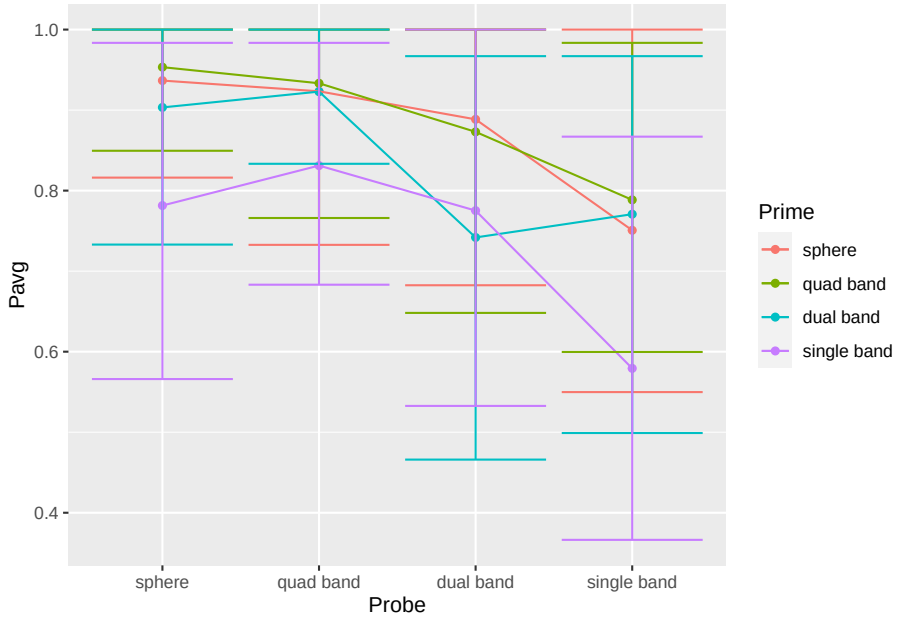
To compute this, R has function quantile().

```
x <- 0:50
quantile(x, 0.1)
```

```
## 10%
##   5
```

Modify code from from exercise #5 to compute two additional variables/columns for lower and upper limits of the *89%*[4] interval (think about what these limits are for 89% interval). Then, use geom_errorbar() to plot 89% interval (you will need to map the two variable you computed to `ymin` and `ymax` properties). The plot should look like this (hint, drop color mapping and map `Prime` to `group` property).

[4]Why 89%? Because it is a prime number! If you think that it sounds arbitrary, you are perfectly correct. But so is using 95% and for that one you do not even have the "prime number" excuse!

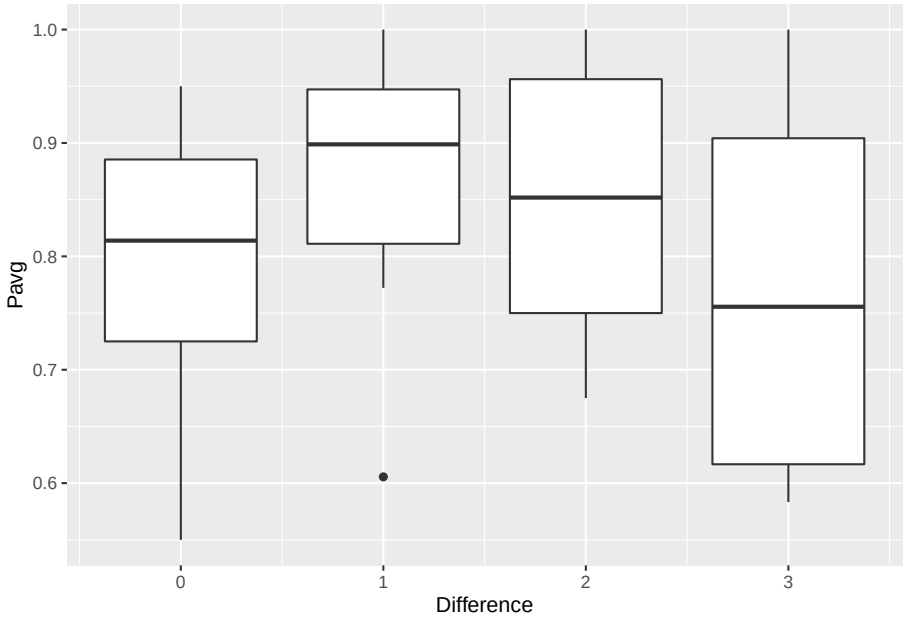


Do exercise 7.

7.7 Looking at similarity

A different study, which used same four objects, showed that a similar looking history effect but for longer interruptions (1000 ms rather than 50 ms) was modulated by objects similarity. Let us check that hypothesis by computing a rough difference measure. It will assume that their difference is proportional to the absolute "distance" between them on x-axis in the above plot[5]. E.g., distance between a sphere and a sphere is 0, but between sphere and quad-band or single-band and dual-band is 1. Difference between sphere and dual-band is 2, etc. You can compute it by converting *factor* variables `Prime` and `Probe` to integers (this assumes that levels are in the correct order). Then, you can compute the absolute difference between those indexes and store it as a new column (e.g. `Difference`). Next, group by `Difference` and `Participant` to compute average probability of the same response. Your plot should look like this (you will need to map `Difference` on `group` to get four box plots rather than one).

[5]This measure assumes metric distance, which is a very strong assumption.



Do exercise 8.

Chapter 8

Tidyng your data: joins and pivots

It is fun to work with tidy complete data. Unfortunately, more often than not you will need to preprocess and tidy it up before you can analyze it. In addition to dplyr, Tidyverse has tidyr package that helps you with some of the problems. Grab the exercise notebook and let's get started.

8.1 Joining tables

Sometimes, results of a study are stored in separate tables. For example, demographic information can be stored separately from responses, as the former is the same for all trials and conditions, so it makes little sense to duplicate it. For the actual analysis, you may eed to add this information, merging or, in SQL/Tidyverse-speak, joining two tables (I'll use term "join" from hereon).

Examples make joining operations much easier to understand, so let us create two tables.

```
demographics <- tibble(ID = c("A", "B", "C", "D"),
                       Age = c(20, 19, 30, 22))
reports <-
  tibble(ID = c("A", "B", "C", "D", "A", "B", "C", "D")) %>%
  mutate(Report = runif(length(ID), 1, 7)) %>%
  arrange(ID)
```

To join two tables, you require "key" columns: columns that contain values that will be used to identify matching rows in the two tables. You can use multiple and differently named columns for that purpose but we will start with a simplest case: a single column with same name `"ID"`. A join function (`inner_join()`

Table 8.1: demographics (left) and report (right) tables

ID	Age
A	20
B	19
C	30
D	22

ID	Report
A	4.577031
A	6.427745
B	5.267120
B	3.816742
C	3.152527
C	5.650791
D	3.521926
D	3.388860

Table 8.2: Joining/merging tables with fully matching keys via join (left) and merge (right). Note how a different order of tables results in a different order of columns.

ID	Age	Report
A	20	4.577031
A	20	6.427745
B	19	5.267120
B	19	3.816742
C	30	3.152527
C	30	5.650791
D	22	3.521926
D	22	3.388860

ID	Report	Age
A	4.577031	20
A	6.427745	20
B	5.267120	19
B	3.816742	19
C	3.152527	30
C	5.650791	30
D	3.521926	22
D	3.388860	22

here, see below for details on different joins) takes a first row in `demographics` table that has `"A"` in `ID` column and will look for all rows in table `reports` that has `ID == "A"`. Then, it will do the same for all remaining rows for `demographics` table, one row at a time. It takes three parameters: table `x` (first table), table `y` (second table), and `by` - a vector with key column names argument[1]. A call to merge() function is very similar and produces identical results. Note how column order has changed for merge(), because I used a different order of tables, but the content itself is the same.

```
via_join <- inner_join(demographics, reports, by="ID")
via_merge <- merge(reports, demographics, by="ID")
```

Things are easy when every key in the first table has its counterpart in the second one and vice versa. Things get tricky, if that is not the case. Which is why there are *four* different ways to join tables (note that they will all produce

[1] Theoretically, you can skip it and *dplyr* will do its best to find matching columns. However, this is a dangerous thing to leave out, as your intuition and *dlpyr's* matching rules may lead to different results. I strongly recommend to always specify key columns.

Table 8.3: Now demographics (left) and reports (right) table have unique keys ("D" for demographics, "E" for reports) without a match in the second table.

ID	Age
A	20
B	19
C	30
D	22

ID	Report
A	3.314145
A	1.887727
B	2.510888
B	1.834510
C	5.392972
C	6.448728
E	2.164366
E	1.604730

identical results for fully matching set of keys, as in the example above):

- **inner** join: uses only key values that are present in both tables.
- **full** join: uses all key values from both tables, if matching keys are missing in one of the tables, rows are filled with `NA`.
- **left** join: uses only key values that are present in the left (first) table, if matching keys are missing in the *right* table, , rows are filled with `NA`.
- **right** join: mirror twin of the left join, uses only key values that are present in the right (second) table, if matching keys are missing in the *left* table, , rows are filled with `NA`.

To see each join in action, let us slightly modify the `reports` table to include `ID` "E" instead of "D". Now, the "D" is missing the second table but "E" is missing in the `demographics`:

```
reports <-
  tibble(ID = c("A", "B", "C", "E", "A", "B", "C", "E")) %>%
  mutate(Report = runif(length(ID), 1, 7)) %>%
  arrange(ID)
```

Inner join is most conservative and excludes any non-matching keys, note that rows with *both* `ID == "D"` and `ID == "E"` are missing. This is the *default* behavior for the merge function.

```
inner_tidy <- inner_join(reports, demographics, by="ID")
inner_base <- merge(reports, demographics, by="ID")
```

In contrast, **full join** is the most liberal as it includes all rows from both tables, filling in missing values with `NA` (e.g., see `Report` for `ID == "D"` and `Age` for `ID == "E"`). In base R merge() function, you turn an inner join into a full one using `all=TRUE`.

```
full_tidy <- full_join(demographics, reports, by="ID")
full_base <- merge(demographics, reports, by="ID", all=TRUE)
```

Table 8.4: Inner join. Only rows for matching keys are merged

ID	Report	Age
A	3.314145	20
A	1.887727	20
B	2.510888	19
B	1.834510	19
C	5.392972	30
C	6.448728	30

Table 8.5: Full join. All rows are merged, 'NA' are used for missing values in rows from a complementary table

ID	Age	Report
A	20	3.314145
A	20	1.887727
B	19	2.510888
B	19	1.834510
C	30	5.392972
C	30	6.448728
D	22	NA
E	NA	2.164366
E	NA	1.604730

Table 8.6: Left join. All rows from demographics tables are used and missing matching rows are filled with 'NA'

ID	Age	Report
A	20	3.314145
A	20	1.887727
B	19	2.510888
B	19	1.834510
C	30	5.392972
C	30	6.448728
D	22	NA

Table 8.7: Right join. All rows from reports tables are used and missing matching rows are filled with 'NA'

ID	Age	Report
A	20	3.314145
A	20	1.887727
B	19	2.510888
B	19	1.834510
C	30	5.392972
C	30	6.448728
E	NA	2.164366
E	NA	1.604730

Left join uses only rows from the left (first) table, dropping extra rows from the second one. Note `NA` in `Report` column for `ID == "D"` and no rows for `ID == "E"`. To do a left join via merge(), you need to specify `all.x=TRUE`.

```
left_tidy <- left_join(demographics, reports, by="ID")
left_base <- merge(demographics, reports, by="ID", all.x=TRUE)
```

Right join is a mirror twin of the left join, so now rows for `ID == "D"` are missing and there are missing values for `ID=="E"`. You include `all.y=TRUE` for a right join via merge().

```
right_tidy <- right_join(demographics, reports, by="ID")
right_base <- merge(demographics, reports, by="ID", all.y=TRUE)
```

As noted above, you can also use more than one key.

```
demographics <- tibble(ID = c("A", "B", "A", "B"),
                       Gender = c("M", "F", "F", "M"),
                       Age = c(20, 19, 30, 22))
reports <- tibble(ID = c("A", "B", "A", "B"),
```

Table 8.8: Two identically named key columns: ID and Gender.

ID	Gender	Age	ID	Gender	Report
A	M	20	A	M	6.361287
B	F	19	B	F	2.127766
A	F	30	A	F	2.736973
B	M	22	B	M	1.288939

Table 8.9: Joining/merging two tables by ID and Gender.

ID	Gender	Age	Report
A	M	20	6.361287
B	F	19	2.127766
A	F	30	2.736973
B	M	22	1.288939

```
                  Gender = c("M", "F", "F", "M"),
                  Report = runif(length(ID), 1, 7))
```

```
inner_multi_tidy <- inner_join(demographics, reports, by=c("ID", "Gender"))
inner_multi_base <- merge(demographics, reports, by=c("ID", "Gender"))
```

Finally, key columns can be named *differently* in two tables. In this case, you need to "match" them explicitly. For dplyr joins, you use a named vector to match pairs of individual columns. For merge(), you supply two vectors: one for columns in the first table (parameter `by.x`) and one columns in the the second one (parameter `by.y`). Here, you need to be careful and check that columns order matches in both parameters.

```
demographics <- tibble(VPCode = c("A", "B", "A", "B"),
                       Sex = c("M", "F", "F", "M"),
                       Age = c(20, 19, 30, 22))

reports <- tibble(ID = c("A", "B", "A", "B"),
                  Gender = c("M", "F", "F", "M"),
                  Report = runif(length(ID), 1, 7))
```

```
inner_diff_tidy <- inner_join(demographics, reports, by=c("VPCode"="ID", "Sex"="Gender"
inner_diff_base <- merge(demographics, reports, by.x=c("VPCode", "Sex"), by.y=c("ID", "
```

As you saw from examples above, dplyr joins and merge() produce identical results. However, I would recommend to use the former, simply because function names make it explicit which kind of join you perform (something you can figure out only by checking additional parameters of merge()).

Table 8.10: Differently named key columns. VPCode in demographics table corresponds to ID in reports; sex in demographics corresponds to Gender in reports

VPCode	Sex	Age
A	M	20
B	F	19
A	F	30
B	M	22

ID	Gender	Report
A	M	6.958555
B	F	1.583676
A	F	3.782942
B	M	4.311466

Table 8.11: Joining tables by matching VPCode to ID and Sex to Gender.

VPCode	Sex	Age	Report
A	F	30	3.782942
A	M	20	6.958555
B	F	19	1.583676
B	M	22	4.311466

Download files IM.csv and GP.csv that you will need for exercise #1[2]. These are participants responses on two questionnaires with each participant identified by their ID (`Participant` in *IM.csv* and `Respondent` in *GP.csv*), `Condition` (which experimental group they belong to), and their `Gender`. Read both tables and join them so that there no missing values in the table (some participants are missing in `GP.csv`, so there are *three* joins that can do this, which one will you pick?). Then, turn `Condition` and `Gender` into factors, so that for `Condition` levels are `"control"` (`2`) and `"game"` (`1`) and for `Gender` levels are `"female"` (`1`) and `"male"` (`2`). Your final table should look as follows (I've dropped most of the columns for `IM.csv`, so they would fit to the page):

Participant	Condition	Gender	IM01_01	IM01_02	IM01_03	GP01_01	GP02_01	GP02_02	GP
TMM1990w	game	female	3	2	5	1	1	1	
VEH1985w	control	female	3	4	4	1	4	4	
CEN2000w	control	female	2	3	6	1	1	1	
IDK1985w	control	female	2	5	6	1	1	5	
AKB1996w	control	female	2	1	7	1	1	1	
SSF1993w	game	female	1	3	3	1	1	3	

Do exercise 1.

Repeat the same exercise but use merge(). ::: {.infobox .practice} Do exercise 2. :::

Now let us practice joining and simulating data as well. Create two tables that need to be joined by a single key column. In the first table, Use rnorm()

[2]Remember, if you end up with `.xls` extension, just rename to `.csv`.

Table 8.12: Wide non-tidy table.

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M-1	6	4	3
1	M-2	4	7	6
2	M-1	5	2	1
2	M-2	3	7	2

function to generate normally distributed data with mean of 180 and standard deviation of 50 for column `x` (or use some other name that you like) (what range would you expect to cover 95% of the data?). In the second table, use same normal distribution but with mean of 10 and standard deviation of 2 for column `y` (again, you can pick another name). When filling in key column for both tables, do it so that *inner* and *right* join would give the same final table but *left* and *full* would give you a longer one (test this explicitly!). After joining two tables, plot `x` against `y` and superimpose linear regression fit. Are two columns correlated? Should they be? ::: {.infobox .practice} Do exercise 3. :::

8.2 Pivoting

Recall the idea of tidy data:

- variables are in columns,
- observations are in rows,
- values are in cells.

And, also recall, that quite often data is stored in a wide format that is easier for humans read.

Here, `Symmetry`, `Attractiveness`, `Trustworthiness` are different face properties participants responded on, whereas values are `Response` they gave. You can work with a table like that but it is often more convenient to have a column `Scale` that will code which face property participants respond on and a column `Response` to hold values. Then, you can easily split or group your data by property while performing the same analysis on all of them.

You can do pivoting using base R reshape() function. But pivoting is a fairly confusing business, so Tidyverse alone offers three different solutions starting with reshape2 package [3], and continuing with original gather() and spread() functions in tidyr to modern pivot_longer() and pivot_wider() functions in the same package.

[3] It uses `melt` and `cast` functions for this.

8.3 Pivot longer

pivot_longer() takes a table, which you can pipe to the function Tidyverse-style, and a vector of column names that need to be transformed. All *column names* go to one new column and all the *values* go to another new column. Defaults names of these two columns are, respectively, `"name"` and `"value"` but you can specify something more suitable via, respectively, `names_to` and `values_to` parameters.

There are many more bells-and-whistles (name and value transformations, removing a prefix via regular expressions, etc.), so I recommend looking at the manual and a vignette. However, in most cases these four parameters will be all you need, so let us see pivot_longer in action.

I assume that table presented above is in `widish_df` table defined above. The columns that we want to transform are `Symmetry`, `Attractiveness`, `Trustworthiness`. Thus, the simplest call with all defaults is

```
long_tidy <- tidyr::pivot_longer(widish_df,
                                 cols=c("Symmetry", "Attractiveness", "Trustworthiness"))
```

Participant	Face	name	value
1	M-1	Symmetry	6
1	M-1	Attractiveness	4
1	M-1	Trustworthiness	3
1	M-2	Symmetry	4
1	M-2	Attractiveness	7
1	M-2	Trustworthiness	6
2	M-1	Symmetry	5
2	M-1	Attractiveness	2
2	M-1	Trustworthiness	1
2	M-2	Symmetry	3
2	M-2	Attractiveness	7
2	M-2	Trustworthiness	2

When you compare the two tables, you will see that original three columns × four rows are now stretched into twelve rows and name-value pairs are consistent across the two tables[4]. As noted above, we can improve on that by specifying proper names for new columns.

```
long_tidy <- tidyr::pivot_longer(widish_df,
                                 cols=c("Symmetry", "Attractiveness", "Trustworthiness"),
                                 names_to = "Scale",
                                 values_to = "Response")
```

[4]By the way, this simple check may seem as a trivial point but this is a kind of simple sanity check that you should perform routinely. This way you *know* rather than *hope* that transformation did what it should. I also check value is a few rows to make sure that I didn't mess things up. Catching simple errors early saves you a lot of time!

Participant	Face	Scale	Response
1	M-1	Symmetry	6
1	M-1	Attractiveness	4
1	M-1	Trustworthiness	3
1	M-2	Symmetry	4
1	M-2	Attractiveness	7
1	M-2	Trustworthiness	6
2	M-1	Symmetry	5
2	M-1	Attractiveness	2
2	M-1	Trustworthiness	1
2	M-2	Symmetry	3
2	M-2	Attractiveness	7
2	M-2	Trustworthiness	2

If you want to stick to base R, you can pivot longer via reshape() function that can do both pivot to longer and wider tables. It is more flexible and, therefore, much more confusing (at least for me). Here are some parameters that we need to specify in order to emulate pivot_longer() call above:

- `direction`. Either `"long"` (here), or `"wide"`.
- `idvar`: names of variables that identify multiple records in the long format. In contrast, pivot_longer(), assumes that all columns that you did not transform are identity columns.
- `varying`: names of columns that will be turned into a single variable that contains only **values** in a new long table. Corresponds to `cols` argument in pivot_longer()
- `v.names`: name of the column with values. Corresponds to `values_to` parameter of pivot_longer().
- `timevar` : sort of corresponds to `names_to` parameter of pivot_longer(), so it is the name of the column where *indexes* or *labels* of transformed columns will go.
- `times` : by default, reshape() does not put column names into `timevar` column but uses their relative *indexes* instead. E.g., `Symmetry` column will get index of 1, `Attractiveness` will get 2, `Trustworthiness` will be 3. You can replaces these indexes with *any* labels. Below, I used the same labels as column names but I could have used *any* three values for this.

```
long_base <- reshape(widish_df,
                     direction = "long",
                     idvar = c("Participant",  "Face"),
                     varying = c("Symmetry", "Attractiveness", "Trustworthiness"),
                     v.names="Response",
                     times = c("Symmetry", "Attractiveness", "Trustworthiness"),
                     timevar = "Scale")
```

I strongly suggest experimenting with parameters of reshape() to get a feeling for how it should be (and should not be!) used.

Table 8.13: Same table pivoted via reshape.

Participant	Face	Scale	Response
1	M-1	Symmetry	6
1	M-2	Symmetry	4
2	M-1	Symmetry	5
2	M-2	Symmetry	3
1	M-1	Attractiveness	4
1	M-2	Attractiveness	7
2	M-1	Attractiveness	2
2	M-2	Attractiveness	7
1	M-1	Trustworthiness	3
1	M-2	Trustworthiness	6
2	M-1	Trustworthiness	1
2	M-2	Trustworthiness	2

Let us put this new knowledge to practice, using GP.csv file. These is a questionnaire on gaming habits, which was conducted prior to an experiment to check whether two groups of participants assigned to *Game* and *Experiment* conditions have similar gaming habits. We would like to visually inspect responses to individual items in a questionnaire appear for different conditions, as this will tell us whether we should expect a difference. Split the computations below into two pipelines. One that loads and pre-processes the data (steps 1-3). Another one that produces a summary and stores it into a different table (step 4). Advice, implement it one step at a time, checking the table and making sure that you get expected results before piping it and adding the next operation.

1. Read the file, make sure you specify column types.
2. Convert `Condition` column to a factor with "game" (1) and "control" (2).
3. Pivot all `GP..` columns. You should get a table with five columns: `Respondent`, `Condition`, `Gender`, `name` (or a column name that you specified), and `value` (or a column name that you specified). Hint, you can use slicing `:` to specify the range of columns or starts_with() function to specify a common prefix. Try both approaches.
4. Group data by condition and GP item and compute median and median absolute deviation of responses. These are robust versions of mean and standard deviation, better suitable for data with potential outliers.

You first table, in long format, should look like this (I show only first four rows)

Respondent	Condition	Gender	Item	Response
SBS1992w	game	1	GP01_01	1
SBS1992w	game	1	GP02_01	1
SBS1992w	game	1	GP02_02	1
SBS1992w	game	1	GP02_03	3

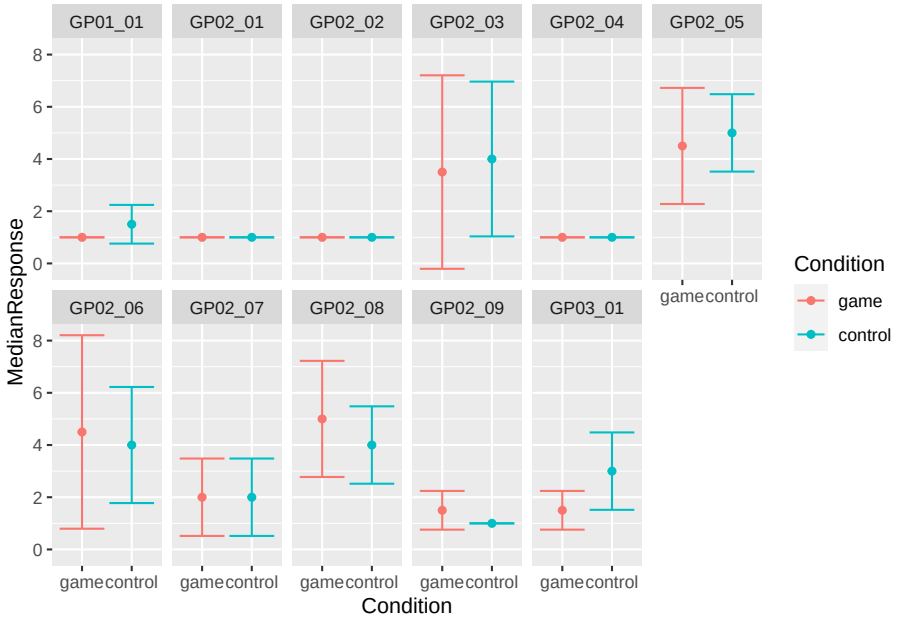
And your second table, with aggregated results, show be like this

Condition	Item	MedianResponse	ResponseMAD
game	GP01_01	1.0	0.0000
game	GP02_01	1.0	0.0000
game	GP02_02	1.0	0.0000
game	GP02_03	3.5	3.7065

Do exercise 4.

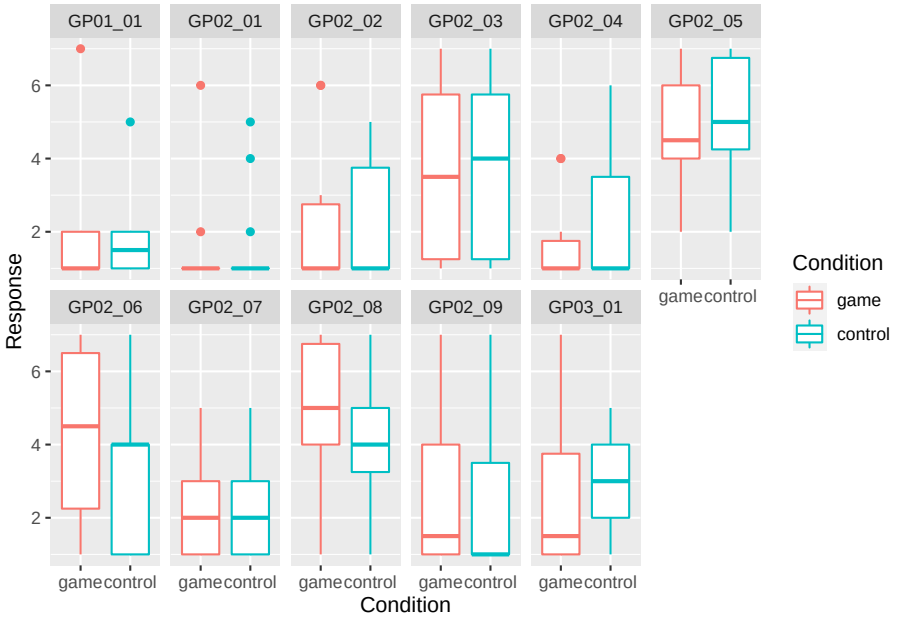
Repeat the exercise but now using base R reshape() function. ::: {.infobox .practice} Do exercise 5. :::

Now you have a table that has median and MAD values for each combination and item. Plot them to compare them visually. Use median responses for y-value of points and median±MAD for error bars. Use facets and color to make it easier to identify the items and conditions. My take on the plot is below, do you think we should expect to find difference between the conditions?



Do exercise 6.

Perform similar analysis but do not group data and summarize the data. Instead, use box plots to show the variability. Which visualization do you prefer?



Do exercise 7.

8.4 Pivot wider

You can also always go from a long to a wide representation via pivot_wider() or reshape functions. The logic is reverse, you need to specify which columns *identify* different rows that belong together, which columns contain column names, and which contain their values. For our example table the names of the columns are in the column `Scale` and values are in `Response`. But what about columns that identify the rows that belong together? In our case, these are `Participant` and `Face`, so all rows from a *long* table that have same combination of `Participant` and `Face` values should be merged together into a single row. If you do not explicitly specify `id_cols`, then by default, pivot_wider() will use *all other remaining columns* to identify which rows belong together. This is irrelevant in this toy example, as `Participant` and `Face` is all we have left anyhow but below I will show you how things can get confusing and how to overcome this.

Let us undo our previous wide-to-long transformation and get our original wide table back![5]

[5] I used table as an explicit first argument for `pivot_longer()` but piped it to `pivot_wider()`, why? To remind you that these two ways are the interchangeable and that both put the table as a parameter into the function.

Table 8.14: Our table is wide again!

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M-1	6	4	3
1	M-2	4	7	6
2	M-1	5	2	1
2	M-2	3	7	2

```
wide_again_tidy <-
  long_tidy %>%
  pivot_wider(names_from = "Scale", values_from="Response")
```

Or, using explicit `id_cols`

```
wide_again_tidy <-
  long_tidy %>%
  pivot_wider(id_cols = c("Participant", "Face"), names_from = "Scale", values_from="Re
```

You can pivot wider using reshape() as well. However, note that, as of 01.11.2021, it works correctly *only* with data frames, so if you have a tibble (as I do), you need to convert it to a data frame via data.frame() or as.data.frame(). Otherwise, you need to specify

- `direction = "wide"`
- `idvar` : different rows that belong together. Same as `id_cols` for pivot_wider() but no defaults here.
- `timevar` : same as `names_from` for pivot_wider(), column with values that will be used as column names.
- `v.names` : same as `values_from`.
- `sep`: the new column names will constructed as `v.names` + `sep` + `timevar`. By default `sep="."`.

The main difference, as compared to pivot_wider(), is how the column names are constructed. With reshape() function, the `v.names` + `sep` + `timevar` rule means that you end up with column names such as `Response.Symmetry` instead of just `Symmetry`.

```
wide_again_base <- reshape(as.data.frame(long_tidy),
                           direction = "wide",
                           idvar = c("Participant", "Face"),
                           timevar = "Scale",
                           v.names = "Response",
                           sep = "_")
```

Let us take a look at the importance of `id_cols`. Imagine that we have *another* column, say, response times. So, our long table will look like this

```
long_tidy_rt <-
  long_tidy %>%
  ungroup() %>%
  mutate(RT = round(rgamma(n(), 4, 3), 2))
```

Participant	Face	Scale	Response	RT
1	M-1	Symmetry	6	1.26
1	M-1	Attractiveness	4	0.45
1	M-1	Trustworthiness	3	0.69
1	M-2	Symmetry	4	1.29
1	M-2	Attractiveness	7	2.97
1	M-2	Trustworthiness	6	1.38
2	M-1	Symmetry	5	1.02
2	M-1	Attractiveness	2	1.17
2	M-1	Trustworthiness	1	1.08
2	M-2	Symmetry	3	1.49
2	M-2	Attractiveness	7	0.62
2	M-2	Trustworthiness	2	0.74

For pivot_wider, if we do not specify which columns identify rows that belong together, `RT` will be used as well. But, because it is different for every response, each row in the original table will be unique and we will end up with a weird looking table wit lots of `NAs`.

```
wide_odd_rt <-
  pivot_wider(long_tidy_rt, names_from = "Scale", values_from="Response")
```

Participant	Face	RT	Symmetry	Attractiveness	Trustworthiness
1	M-1	1.26	6	NA	NA
1	M-1	0.45	NA	4	NA
1	M-1	0.69	NA	NA	3
1	M-2	1.29	4	NA	NA
1	M-2	2.97	NA	7	NA
1	M-2	1.38	NA	NA	6
2	M-1	1.02	5	NA	NA
2	M-1	1.17	NA	2	NA
2	M-1	1.08	NA	NA	1
2	M-2	1.49	3	NA	NA
2	M-2	0.62	NA	7	NA
2	M-2	0.74	NA	NA	2

To remedy that, we need to specify id columns explicitly, so that `pivot_wider()` can ignore and *drop* the rest:

```
wide_rt <-
  pivot_wider(long_tidy_rt,
              id_cols = c("Participant", "Face"),
```

```
                names_from = "Scale",
                values_from="Response")
```

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M-1	6	4	3
1	M-2	4	7	6
2	M-1	5	2	1
2	M-2	3	7	2

For practice, let us take adaptation data and turn it onto a wide format that is easier for humans to read. In the original form, the table is a long format with a row for each pair of prime and probe stimuli.

Participant	Prime	Probe	Nsame	Ntotal
LUH-1992-M	Sphere	Sphere	22	119
LUH-1992-M	Sphere	Quadro	23	118
LUH-1992-M	Sphere	Dual	15	120
LUH-1992-M	Sphere	Single	31	115

Let us turn it into a wider table, so that a single row corresponds to a single prime and four new column contain proportion of same responses for individual probes. The table will look like this (use round() function to reduce the number of digits):

Participant	Prime	Sphere	Quadro	Dual	Single	Average
LUH-1992-M	Sphere	0.18	0.19	0.12	0.27	0.1900
LUH-1992-M	Quadro	0.21	0.22	0.14	0.34	0.2275
LUH-1992-M	Dual	0.25	0.30	0.27	0.48	0.3250
LUH-1992-M	Single	0.34	0.30	0.48	0.39	0.3775

The overall procedure is fairly straightforward:

1. Read the file (don't forget to specify column types)
2. Computer `Psame` proportion of same responses given number of total responses for each .
3. Pivot the table wider, think about your id columns. Also try this without specifying any and see what you get.
4. Compute an average stability across all probes and put it into a new `Average` column. You can do it "by hand" but, instead, use rowSums() to compute it. Here, use `.` to refer to the table inside the `mutate()` function and you will need to normalize it by the number of probes to get an average instead of the sum.
5. Pipe it to the output, using knitr::kable().

Use pivot_wider() in exercise 8.

Do exercise 8.

Repeat the analysis but now using the reshape() function.

Do exercise 9.

Let us practice more and create group average summary as a square 5×4 table with a single row per *Prime* and four columns for *Probe* plus a column that says which prime the row corresponds to. As a value for each cell, we want to code a _median value. The table should look like this:

Prime	Sphere	Quadro	Dual	Single
Sphere	0.13	0.13	0.17	0.32
Quadro	0.19	0.12	0.21	0.38
Dual	0.15	0.30	0.27	0.48
Single	0.34	0.30	0.48	0.51

You know almost everything you need, so think about how you would implement this as a *single* pipeline. Hints: to match my table you will definitely to convert `Prime` and `Probe` to factors to ensure consistent ordering (otherwise, they will be sorted alphabetically), you will need to group individual combinations of prime and probe before computing a summary statistics. And, of course, you will need to pivot the table wider (use your preferred method).

Do exercise 10.

Chapter 9

Controling computation flow

Grab the exercise notebook before we start.

One the most powerful features of R is that it is vector-based. Remember, everything is a vector (or a list). In the previous seminars you saw you can apply a function, a filter, or perform a computation on all values of a vector or all rows in a table in a single call. However, sometimes, you need to go over one value or row at a time explicitly. For example, if you working with a time-series, it might be easier to use an explicit for loop to compute current value based on previous state of the system. However, such instances are fairly rare, so the general rule for R is "you probably do not need a loop". Below, we will go through various tools that render explicit loops redundant.

9.1 `rep()`

The most basic repetition mechanism in R is rep() function. It takes a vector and repeats it specified number of *times*.

```
rep(c(1, 2, 3), times=4)
```

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

Alternatively, you can repeat each element specified number of times before repeating the next one via `each` parameter. The difference between options lies only in the *order* of elements in the new vector. As you can see both vectors have the same length and each individual value is repeated four times.

```
rep(c(1, 2, 3), each=4)
```

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

You can specify length of the output vector via `length.out`. When combined with `times` it can be useful for producing truncated vectors. E.g., when we repeat a three element vector but we want to get ten values. Using `times` only, we can get either nine (`times=3`) or twelve (`times=4`), not ten. `length.out=10` makes it happen.

```
rep(c(1, 2, 3), times=4, length.out = 10)
```

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

However, you can also use subsetting of a new vector to achieve the same end.

```
rep(c(1, 2, 3), times=4)[1:10]
```

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

You should be more careful when combining `length.out` with `each`, as each value is repeated `each` times and, if `length.out` is longer, the same sequence is repeated again. Could be confusing and you might get a very unbalanced repeated sequence.

```
rep(c(1, 2, 3), each=8, length.out = 10)
```

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

Do exercise 1.

9.2 Repeating combinations

To create a table with all combinations of values, you can use either base R expand.grid() or tidyr's implementation expand_grid(). The latter is a bit more robust and can expand even tables and matrices (but see the documentation for subtle differences in implementation and output).

The usage is very straightforward, you provide column names and values and you get all combinations of their values.

```
knitr::kable(grid_base)
```

gender	handidness	colorblindness
female	right	TRUE
male	right	TRUE
female	left	TRUE
male	left	TRUE
female	right	FALSE
male	right	FALSE
female	left	FALSE
male	left	FALSE

expand_grid() works the same they but for the order in the values vary within columns.

```
expand_grid(gender=c("female", "male"),
            handidness=c("right", "left"),
            colorblindness=c(TRUE, FALSE))
```

```
knitr::kable(grid_tidyr)
```

gender	handidness	colorblindness
female	right	TRUE
female	right	FALSE
female	left	TRUE
female	left	FALSE
male	right	TRUE
male	right	FALSE
male	left	TRUE
male	left	FALSE

Do exercise 2.

9.3 For loop

You can loop (iterate) over elements of a vector or list via a for loop, which is very similar to for-loops in other programming languages. However, use of the `for` loop in R is fairly rare, because vectors are a fundamental building block of R and, therefore, it is inherently vectorized (you can do the same thing to all values, not to one value at a time). In a sense, `for` loop is very un-R, so if you find yourself using it, consider whether there is a simpler or more expressive way to do this. At the same time, if `for` loop *is* the simplest or clearest way to write you code, by all means, use it!

The general format is

```
for(loop_variable in vector_or_list){
  ...some operations using loop_variable that
  changes its value on each iteration using
  values from the vector or list...
}
```

Note the curly brackets. We used them before to put the code inside a function. Here, we use them to put the code inside the loop. The loop (the code inside curly brackets) is repeated as many times as the number of elements in a vector or a list with a loop variable[1] getting assigned each vector/list value on each iteration. Thus, to print each value of a vector we can do

[1] Just a reminder, the loop variable can have *any* name. Often, you see people using `i` but I would strongly recommend going for a more meaningful name.

```
for(a_number in c(1, 5, 200)){
  print(a_number)
}
```

```
## [1] 1
## [1] 5
## [1] 200
```

Here, we have three elements in a vector, therefore the code inside curly brackets is repeated three times with the variable `a_number` taking each value in turn. I.e., `a_number` is equal to 1 on a first iteration, 5 on a second, 200 on the third. Note that the code above is equivalent to just assigning one value at a time to `a_number` and calling `print()` function three times.

```
a_number <- 1
print(a_number)
```

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

```
a_number <- 5
print(a_number)
```

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

```
a_number <- 200
print(a_number)
```

```
## [1] 200
```

As you can see, it does not really matter *how* you assign a value to a variable and repeat the code. However, the `for` loop approach is much more flexible, is easier to read and to maintain. I.e., imagine that you decided to alter the `print()` call with `cat()` instead. In the `for` loop version there is just one line to take care of. In the copy-paste version, there are three lines you need to alter. And imagine if you need to repeat the same code a hundred or thousand times, copy-paste is clearly not a viable solution.

Also note that you might be interested in repeat the code inside the for loop given number of times but are not interested in a loop variable and values that it takes. For example, we might want to repeat `print("Ho!")` three times (because it is Christmas time and "Ho! Ho! Ho!" is what Santa Clause says). In this case, we still need a vector with three elements that we can loop over but we do not care what these three elements are.

```
for(temp in 1:3){
  print("Ho!")
}
```

```
## [1] "Ho!"
## [1] "Ho!"
```

```
## [1] "Ho!"
```

Note that we are not using variable `temp` inside of the loop and it has no effect on the code inside the curly brackets. Which is why we can use *any* three values, as it is their total number that matters, not the values themselves.

```
for(temp in c("A", "B", "C")){
  print("Ho!")
}
```

```
## [1] "Ho!"
## [1] "Ho!"
## [1] "Ho!"
```

or

```
for(temp in seq(100, 300, length.out=3)){
  print("Ho!")
}
```

```
## [1] "Ho!"
## [1] "Ho!"
## [1] "Ho!"
```

In short, number of elements in the vector determines how many times the code inside the loop will be repeat. Vector elements are stored in the loop variable on each iteration and you can either use it (`a_number` example above) or ignore them ("Ho! Ho! Ho!") example.

Do exercises 3 and 4.

A typical scenario is for the loop variable to be an *index* that can be used to access an element of a vector or a list. You can build a vector of indexes via `start:stop` sequence tool we used for slicing. You can compute a length of an object via length() function. For a `data.frame` or a `tibble`, you can figure out number of rows and columns via, respectively, nrow() and ncol() functions.

```
vector_of_some_numbers <- c(1, 5, 200)
for(index in 1:length(vector_of_some_numbers)){
  print(vector_of_some_numbers[index])
}
```

```
## [1] 1
## [1] 5
## [1] 200
```

Do exercise 5.

You can also *nest* loops (wondering what cat() does? Concatenates and prints, so read the manual!).

```
for(letter in c("A", "B", "C")){
  for(number in 1:2){
    cat(letter, number, "\n")
  }
}
```

```
## A 1
## A 2
## B 1
## B 2
## C 1
## C 2
```

Do exercise 6.

As I have noted above, loops are particularly useful when you current value depends on a previous one (or many previous values). In the next exercise, use `for` loop to create a random walk. It should start at zero (so, initial value for your variable should be zero). For each next step, draw a random value from a normal distribution with zero mean and standard deviation computed as `exp(value_on_previous_step)` (the function you are looking for is rnorm()). Generate a ten-step random walk, that might look like this

```
##  [1]  0.00000000 -0.56902925 -0.23326972  0.04788655 -0.26527382  0.05453601
##  [7]  0.21423641 -1.36139599 -0.27036963  0.76728873
```

Do exercise 7.

9.4 Conditional statement

As for all other programming languages, you can control the flow of execution using if-else statements. The general usage is as follows.

```
if (some_condition) {
  # code runs if some_condition is TRUE
} else {
  # code runs if some_condition is FALSE
}
```

The rules are the same as for logical indexing, so we can define our condition using mathematical comparisons.

```
x <- -3
if (x > 0) {
  cat("X is definitely greater than  zero")
} else {
  cat("X is not greater than zero.")
}
```

```
## X is not greater than zero.
```

However, be aware that the if uses a *single* logical value. If you have more than one value, it stops with an error[2].

```
x <- c(10,  -3)
if (x < 0) {
  cat("Bingo!")
} else {
  cat("I don't like this x.")
}
```

```
## Error in if (x < 0) {: the condition has length > 1
```

As in logical indexing, you can combine several conditions using logical operators such as *and* `&` or *or* `|`. For example, we can check whether x is smaller than zero but larger than -10.

```
x <- -3
if ((x < 0) & (x > -10)) {
  cat("Bingo!")
} else {
  cat("I don't like this x.")
}
```

```
## Bingo!
```

However, be aware that R has both `&`/`|` and `&&`/`||` versions of *and* and *or* logical operators (single versus double symbols). Both perform logical operations on vectors but double-symbol ones return only the *first* value. E.g., single-symbol returns `TRUE`/`FALSE` for each value of `x`

```
x <- c(10, -3, -11)
(x < 0) & (x > -10)
```

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

But double-symbol returns it only for the *first* value *without warning you about discarding the rest of the values.*

```
x <- c(10, -3, -11)
(x < 0) && (x > -10)
```

```
## Warning in (x < 0) && (x > -10): 'length(x) = 3 > 1' in coercion to 'logical(1)'
```

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

I am sure there is a perfectly logical explanation for this bizarre implementation but I do not know it. I am bringing this up, just so that you would *never* use double-symbol logical operators! Chances are, you will forget about this

[2]If you use an older R-version, it will use *only the first one* but, at least, it will give you a warning. Point bein that it is generally a good idea to use the latest R distribution.

"silently-return-only-the-first-value" behavior and expect them to act normally. They won't behave as you think they should, so simply stay away.

Let us combine `for` loop with `if-else` operator. Generate a vector of ten normally distributed values (again, rnorm() is the function). Loop over them in a `for` loop and print() `"Positive"` if a value is larger than zero and `"Not positive"` if not. The results should look like this[3]

```
##  [1]  0.03003683  1.22390943  1.71573769 -0.89994016  0.55507190  0.42319195
##  [7]  0.82993426 -1.28614375  1.21511589 -0.05815403
```

```
## [1] "Positive"
## [1] "Positive"
## [1] "Positive"
## [1] "Not positive"
## [1] "Positive"
## [1] "Positive"
## [1] "Positive"
## [1] "Not positive"
## [1] "Positive"
## [1] "Not positive"
```

Do exercise 8.

9.5 Breaking out of the loop

The code inside the for loop is typically repeated for every value of the vector that you have supplied. However, there is a way to break out of it using a `break` statement. This stops execution of the code *inside* of the loop immediately and continues with the code immediately *after* the loop.

```
for(y in c(1, 2, 3)){
  print("This will be exected")
  break
  print("But this won't be")
}
```

```
## [1] "This will be exected"
```

```
print("Now to the code AFTER the loop")
```

```
## [1] "Now to the code AFTER the loop"
```

Note that in this case, the code was executed (incompletely!) only once. Typically, `break` is used in combination with the `if-else` statement to break out of the loop, if a certain condition is met. Let us practice. Again, generate ten

[3] Want exact same numbers as I do? Use `set.seed(164)`. This function, see set.seed() makes random generators start at a specific point, so that the you will get the *same* sequence of *random* numbers as I did.

normally distributed numbers, loop over them and print each one. However, `break` after the *fifth* value. For this, you need to loop over indexes of values (that go from 1 to the length() of your vector). Thus, you loop variable will contain an index of each element of x (because of that I called it `ix`) and you need to use it to get a value at this position within the vector. If that index is equal to 5, break out of the loop. For the ten values I've generated above, the output will be the following ("Done for today" is printed after the loop).

```
set.seed(164)
x <- rnorm(10)
for(ix in 1:length(x)){
  if (ix == 5)  break
  print(x[ix])
}
```

```
## [1] 0.03003683
## [1] 1.223909
## [1] 1.715738
## [1] -0.8999402
```

```
print("Done for today")
```

```
## [1] "Done for today"
```

Do exercise 9.

9.6 Using for loop to load and join multiple data files

Your analysis starts with loading the data. Quite often, data for individual participants is stored in different files but with identical structure, so you need code that figures out which files you need to load, loads them on at a time and then binds them to one final table. Using a `for` loop is not the most elegant way to implement this but it does the job and gives you another example of how loops can be useful. I will walk you through details and then you We will implement the code that loads and merges individual files for persistence study. Download the persistence.zip and unzip into `Persistence` subfolder (we do not want to create a mess in your main folder!).

First, you need to have a character vector with relevant file names. Package you are looking for is fs (for File System). It has everything you need to work with the file system, including working with file names (dropping or adding path, extension, etc.), creating/moving/deleting files, checking whether file exists, and what not. One function that I use the most is dir_ls() that list files in a specified folder. The two parameters you need are `path` to your folder (you can and should use a relative path) and, optionally, `glob` filter string. The latter is a globbing wildcard pattern, where `*` stands for "any sequence of characters" and `?` stand

for "one arbitrary character. For a csv file, this pattern would be `"*.csv"`. Test this single function call using appropriate `path` and `glob` parameters and make sure you get all the files in *Persistence* folder.

Next, you need to create a full table variable (I, typically, call it `results` or `reports`) and initialize it to an empty `data.frame()` (or an empty `tibble`). You loop over file names, read one file at a time (don't forget to specify column types), and then use bind_rows() to combine the full table and the new table you loaded. Note that bind_rows() returns a *new* table, so you need to assign it back to the original full table variable. Once you are done, your table should have 5232 rows and twelve columns.

Participant	Session	Block	Trial	OnsetDelay	Bias	Shape1	Shape2
AKM1995M	2019-06-12-14-07-17	0	0	0.5746952	left	stripes-8	stripes-4
AKM1995M	2019-06-12-14-07-17	0	1	0.5741707	left	stripes-4	heavy poles sph
AKM1995M	2019-06-12-14-07-17	0	2	0.5082200	left	stripes-2	stripes-2
AKM1995M	2019-06-12-14-07-17	0	3	0.6065058	right	stripes-8	stripes-2
AKM1995M	2019-06-12-14-07-17	0	4	0.5359504	left	stripes-2	heavy poles sph
AKM1995M	2019-06-12-14-07-17	0	5	0.6435367	right	stripes-4	stripes-4

Do exercise 10.

9.7 Apply

As noted above, `for` loops do the job by might not be the most elegant way of doing things. In R, you can apply a function to each row or column of a matrix. In addition, there are more case-specific versions of it, such lapply.

The function is called `apply` because you *apply* it to values of a vector. In a sense, you have been applying functions the whole time by calling them. For example, we might compute a sinus of a sequence of numbers as

```
sin(seq(0, pi, length.out = 5))
```

```
## [1] 0.000000e+00 7.071068e-01 1.000000e+00 7.071068e-01 1.224606e-16
```

Or, we can *apply* sinus function to a number sequence (note that I pass the name of the function alone `sin` but do not call it, so no round brackets!)

```
sapply(seq(0, pi, length.out = 5), sin)
```

```
## [1] 0.000000e+00 7.071068e-01 1.000000e+00 7.071068e-01 1.224606e-16
```

You might ask, what is then the point to use `apply`? Not much for simple vector cases like this, but it is very useful when you have two dimensional data, as you can apply a function along horizontal (rows) or vertical (columns) margin. For example, imagine you need to compute an average (or median, or any other quantile) of each row or column in a matrix (something you might do fairly often for posterior samples in Bayesian statistics).

Let us create a simple 3 by 4 matrix of normally distributed random numbers.

```
a_matrix <- matrix(rnorm(12), nrow = 3)
a_matrix
```

```
##               [,1]       [,2]       [,3]       [,4]
## [1,] -1.306076e-05 -0.9815949  0.3981706 -0.1809577
## [2,]  1.880631e-02 -0.4210554 -1.2544423 -0.2319481
## [3,]  2.429102e+00 -1.1964317  0.2265607  0.5361628
```

We would expect median value of any row or column to be 0 but because we have so few data points, they will be close but not exactly zero. Computing median for each row (we should get *three* numbers)

```
apply(a_matrix, 1, median)
```

```
## [1] -0.0904854 -0.3265017  0.3813618
```

Similarly for a column (here, it should be *four* numbers)

```
apply(a_matrix, 2, median)
```

```
## [1]  0.01880631 -0.98159487  0.22656072 -0.18095773
```

I will not go into any further details on these functions, concentrating on similar functionality by purrr package. However, if you find yourself working with matrices or needing to apply a function to rows of a data frame, apply might be a simpler solution. Keep this option in mind, if you feel that either looping or purrring looks inadequate.

9.8 Purrr

Package purrr is part of the tidyverse. It provides functional programming approach similar to apply but it easier to use (IMHO) and it has a more explicit and consistent way to describe and combine the output. Language-wise, you do not *apply* a function, you use it to map inputs on outputs[4]

The basic map() function always returns a list but you can explicitly state that you expect function to return a number (`map_dbl()`) and all outputs will be combined into a numeric vector. And, unlike `apply`, `map_dbl()` will generate an error if outputs cannot be converted to numeric. Or, you can specify that you expect each output to be a `data.frame`. In this case, you can automatically bind them by rows via `map_dfr()` or by columns via `map_dfc()`. Again, if all outputs cannot be converted to a `data.frame`, either function will loudly complain (which is good!).

The basic call is similar to apply but is easier to use as you can explicitly address current value via `.` variable (as in other parts of Tidyverse) and you can write a

[4]Means the same thing but this is a linear algebra way of expressing of what a function does.

"normal" function call, prefixing it with a `~`. Here is the example of computing the sinus again. First, same a `apply`

```
map_dbl(seq(0, pi, length.out = 5), sin)
```

```
## [1] 0.000000e+00 7.071068e-01 1.000000e+00 7.071068e-01 1.224606e-16
```

Now, we a magic tilde `~`. Note an explicit call to `sin()` function with `.` as an argument.

```
map_dbl(seq(0, pi, length.out = 5), ~sin(.))
```

```
## [1] 0.000000e+00 7.071068e-01 1.000000e+00 7.071068e-01 1.224606e-16
```

Again, using `map_dbl()` in this case looks as a complete overkill. So let us do something more relevant. Let us implement loading and merging of persistence study files. You already know how to get a vector with names of relevant files. Now you can use `map_dfr()` function on this vector to combine them into a single table. When using `~` call notation, remember `.` would then correspond to a single value from the vector of file names (so, a single filename). Again, you should get a single table with twelve columns and 5232 rows.

Do exercise 11.

You have just *mapped* inputs on outputs using `read_csv()` but functional programming is particularly useful, if you program your own functions. Let us program a function that takes a filename, loads the file and returns total number of trials/rows (if you forgot how to compute number of rows in a table, see above). Once you have a function, use it with `map_dbl` and a vector of persistence filenames. You should get a vector of ten values. Now we can easily see that there was something wrong with one of the files and we must pay attention to the amount of data that we have.

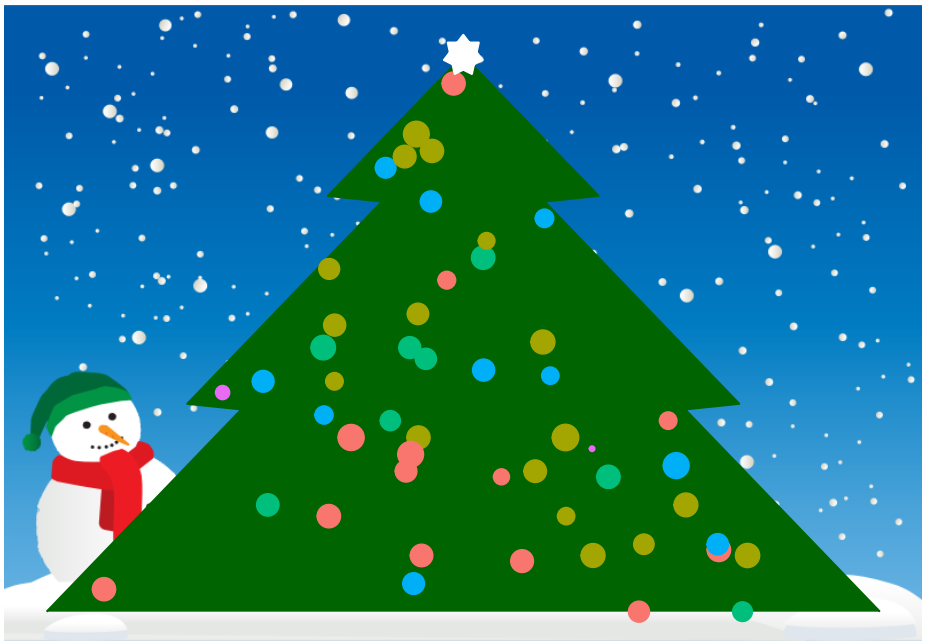
```
##  [1] 528 528 480 528 528 528 528 528 528 528
```

Do exercise 12.

Chapter 10

Christmas special

Today we will work on our Christmas spirit, while practicing in generating data and plotting. Our end-product will be a Christmas tree plot that you see below. For this project you will need png library (you should have it already but check and install, if that is not the case) and a background image created by Gordon Dylan Johnson. Grab the exercise notebook as well!



10.1 Left side of the tree

First we need a tree. We will generate its shape using a function: `x = y - 0.3 * floor(y)`, where `y` should vary between -3 and -0.3[1] (you already know how to generate a sequence, so just decide on how many point you want your shape to have). This function describes a *left* part of the tree, so create a table called `tree_left` with corresponding `x` and `y` columns and plot it via ggplot2. Note that you need to use geom_path() rather than `geom_line()`. The former connects points in the order they appear in the table, whereas the latter first sort all variables based on the x-axis variable (try it out to see what I mean). You should get a plot like the one below.

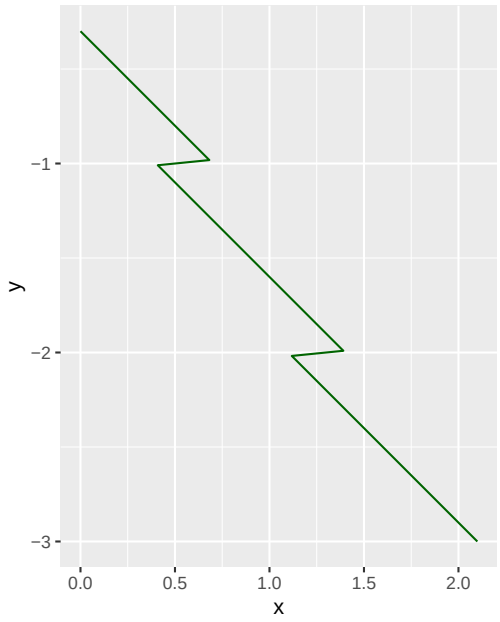
Do exercise 1.

10.2 Right side of the tree

We could use an almost the same formula to generate the right side of the tree. Or, we can create it as a mirror copy of the `tree_left`. In the latter case, we must flip the sign of the `x` (so negative `x` become positive). And, a more subtle point, we need to reverse the order of *all* rows in the table, so that `y` goes from -0.3 to -3 (it is going from -3 to -0.3 in `tree_left`, take a look yourself). You can rearrange table using subsetting or by arranging the rows based on descending

[1] You should definitely try different values for both y range and for the linear part itself to get a feeling of what it does to the shape you generate.

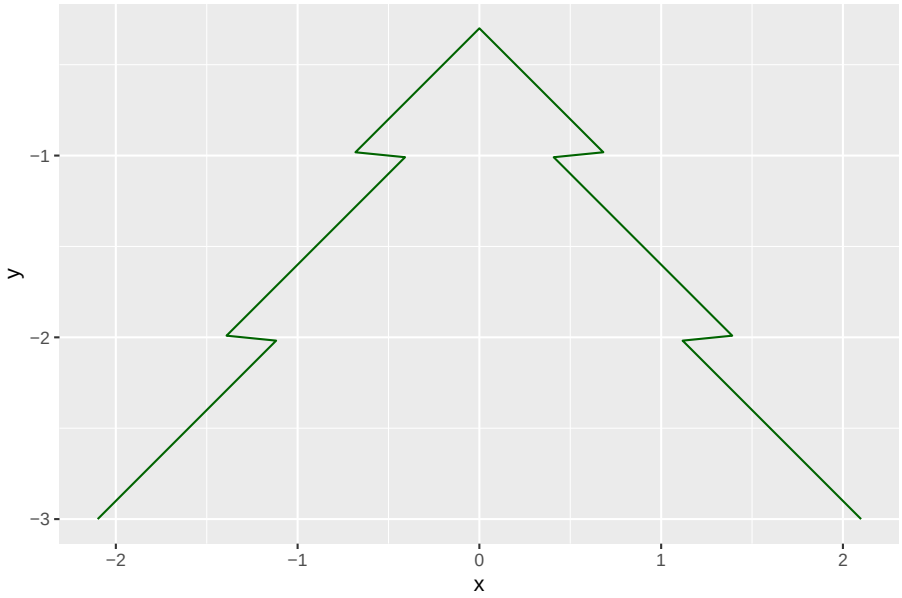
order of either `y` or row_number() (here, it will effectively give you an index for each row). The right side should look just like the left side (but mirrored!).



Do exercise 2.

10.3 The whole tree

Now let us draw the entire tree. We will do it in two ways, to practice. First, bind tables `tree_left` and `tree_right` by rows to create a new table (I called it `tree_shape`) and then reuse the same code with a single `geom_path()` call as before. Note that if you have an odd extra line going from bottom right to the top of the tree that means you did not reverse the `tree_right` table (see above).



Do exercise 3.

Alternatively, you can plot `tree_left` and `tree_right` separately by using two `geom_path()` calls. Here, you use data from *different* tables in a single plot, so you need to specify `data` parameter more than once. There are three ways to do it here. First, do not specify any data and aesthetics in the `ggplot()` call itself and use it explicitly in each `geom_path()` call. Note that you need to use named parameters via `data=...`.

```
ggplot() +
  geom_path(data=tree_left, aes(...), ...) +
  geom_path(data=tree_right, aes(...), ...)
```

Or, you can use `tree_left` (or `tree_right`) as a "main" data source and specify a different one only in one of the `geom_path()` calls:

```
ggplot(data=tree_left, aes(...), ...) +
  geom_path() +
  geom_path(data=tree_right)
```

Here, I would suggest the first option of not specifying a "main" data source, as we will use even more different tables later on.

Do exercise 4.

10.4 Filling in the tree

Now, let us "fill in" the shape between the lines. For this, we will use geom_ribbon that fills in a shape either between vertical limits (when you specify `ymin` and `ymax` aesthetics) or between the horizontal ones (`xmin` and `xmax`). The latter is our case but first we need to combine our left and right shape into a single table with three columns: `y` coordinate and `x_left` and `x_right` coordinates. Think how can you join these the two tables `tree_left` and `tree_right` to achieve this (pause and ponder before reading further).

Hint: use a join but pay attention to `suffix` parameter as it will be useful. Put the new table into the `tree` variable (we will use it later again). Take a look at the table you get before plotting it using geom_ribbon.

Do exercise 5.

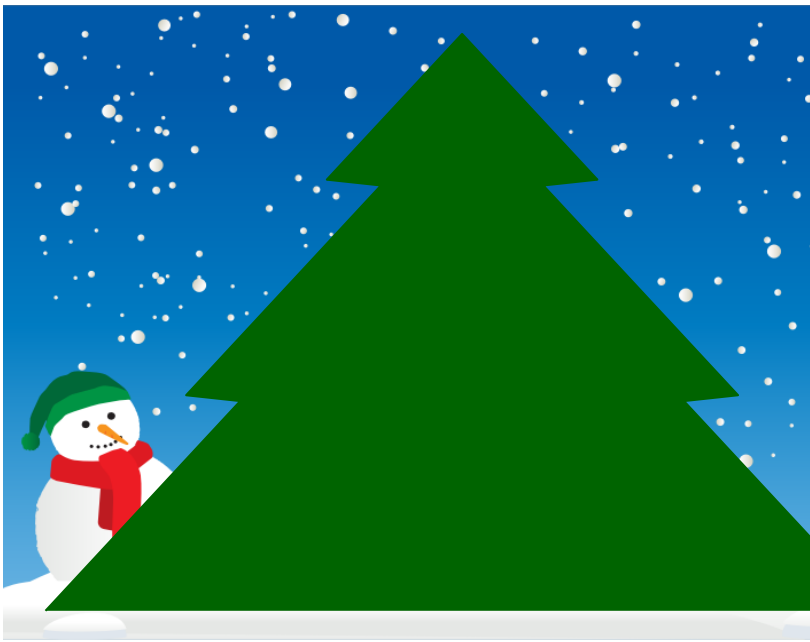
10.5 Adding background image

Our background is not very Christmasy. We should drop the grid altogether (which theme would be the best?) and replace it with a nice picture. To use this picture, you need the png library (import it in the setup chunk, not here!) and then use `readPNG()` function (see official docs or just type `?readPNG` in console). Once you read an image into a variable (I imaginatively called it `background`), you can add it to the plot in two ways. A simpler way is by using function background_image() from ggpubr library. You add it to the plot just as you

do with other geoms. However, this function is only a very thin wrapper for annotation_raster() call, so you could copy-paste it from the function body and use it directly:

```
# code from ggpubr github repository
background_image <- function(raster.img){
  annotation_raster(raster.img,
                    xmin = -Inf, xmax = Inf,
                    ymin = -Inf, ymax = Inf)
}
```

You new plot should look like this:



Do exercise 6.

10.6 Adding decoration (a boring one)

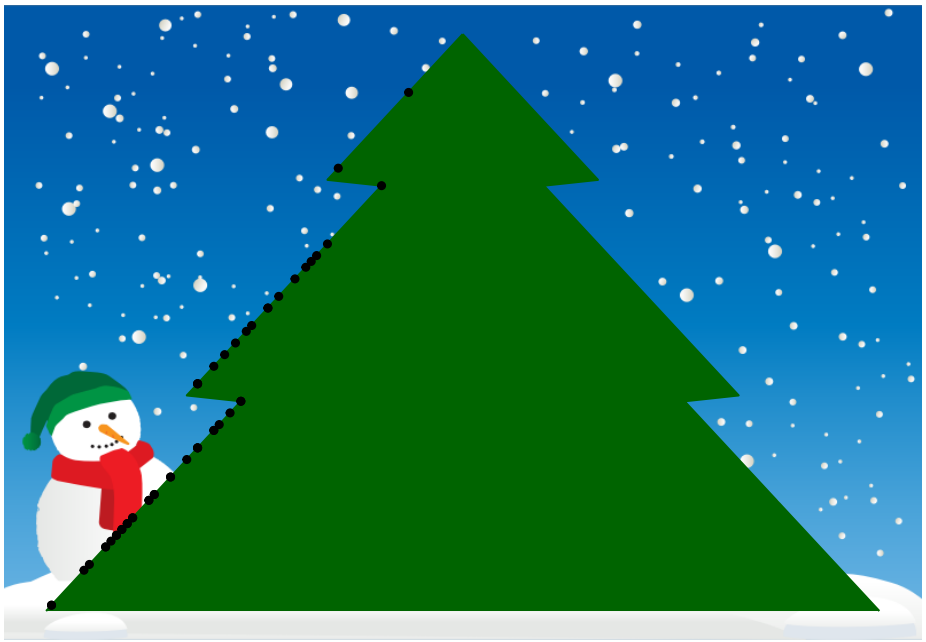
We need some decoration on our tree. Our task is to generate "Christmas balls" (geom_point()) at various locations *within* the tree. For this, we need to first randomly select rows from our `tree` table that you created in exercise 5 and then generate a random location *within* the tree limits for each sampled row. Let us deal with the first problem (randomly selecting riws, so, effectively, randomly selecting y coordinate) first.

To randomly sample rows from a table, you can use slice_sample function from dplyr. It takes a table and returns a new table with randomly sampled rows. You only need to specify a number of rows that you want to have in a new table either directly (parameter `n`) or as a proportion of number of rows in the

original table (parameter `prop`). In our case, I used the latter and sampled half of the original tree table. You also need to decide on whether the same row can be sampled more than once (so-called sampling with replacement). I opted for this via `replace=TRUE` parameter. Finally, we want rows that describe the lower part of the tree to be sampled more often than the upper ones because we can put more decoration on them (the tree is wider). For this, we need to compute width of the tree for each row (a new column that I called `x_range` but you can call it `width`) *before* the sampling. Then, we can use that `x_range` for the `weight_by` parameter of the slice_sample. Put a sampled table into a new variable (I called it `balls`) and add it to the plot via geom_point(). For the moment, use `x_left` for x-coordinate. It will put all the balls on the left edge of the tree but we will fix this shortly.

```
balls <-
  tree %>%
  mutate(x_range = x_right - x_left) %>%
  slice_sample(prop = 0.5, weight_by = x_range, replace=TRUE) %>%
  mutate(x = runif(n(), x_left, x_right),
         size = rnorm(n(), 5, 1),
         icolor = factor(sample(1:5, n(), replace=TRUE)))

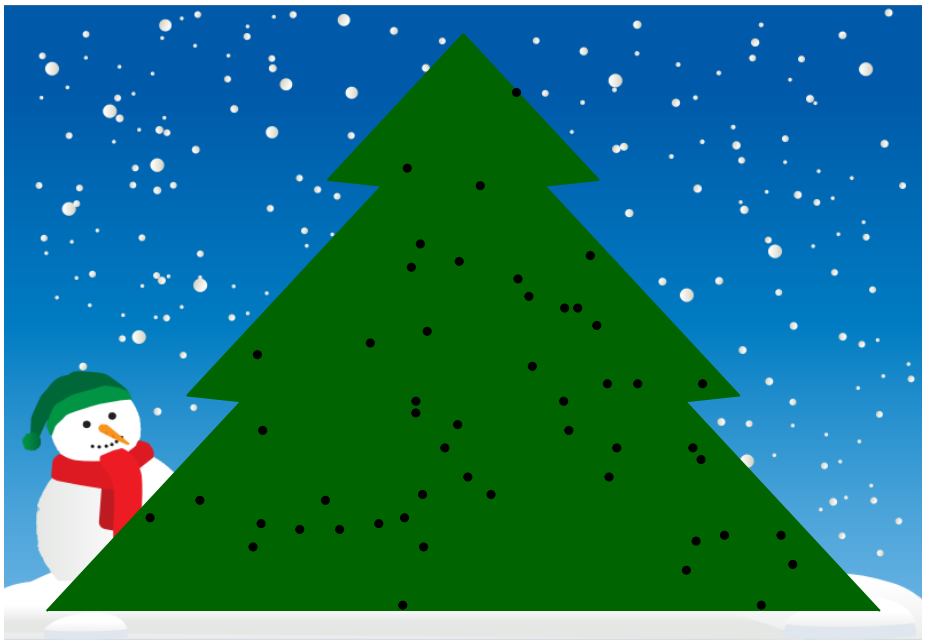
ggplot(tree_left, aes(x=x, y=y)) +
  annotation_raster(background,
                    xmin = -Inf, xmax = Inf,
                    ymin = -Inf, ymax = Inf) +
  geom_path(color="darkgreen") +
  geom_ribbon(data=tree, aes(x=x_left, xmin=x_left, xmax=x_right), fill="darkgreen") +
  geom_path(data=tree_right, color="darkgreen") +
  geom_point(data=balls, aes(x=x_left, y=y)) +
  theme_void()
```



Do exercise 7.

10.7 Adding decoration (a bit more fun one)

We created the vertical location for each ball via random sampling. Now we need to generate a valid x-position somewhere in between `x_left` and `x_right` coordinates. Use runif() function for using `x_left` and `x_right`. Note that you need to specify the number of random values to generate. That should be the number of rows in the table. If you do it within mutate, use function n(). For base R, you can use nrow(). Create a new column `x` and use it for plotting. Note how plot changes every time you re-run the sampling or randomization code.

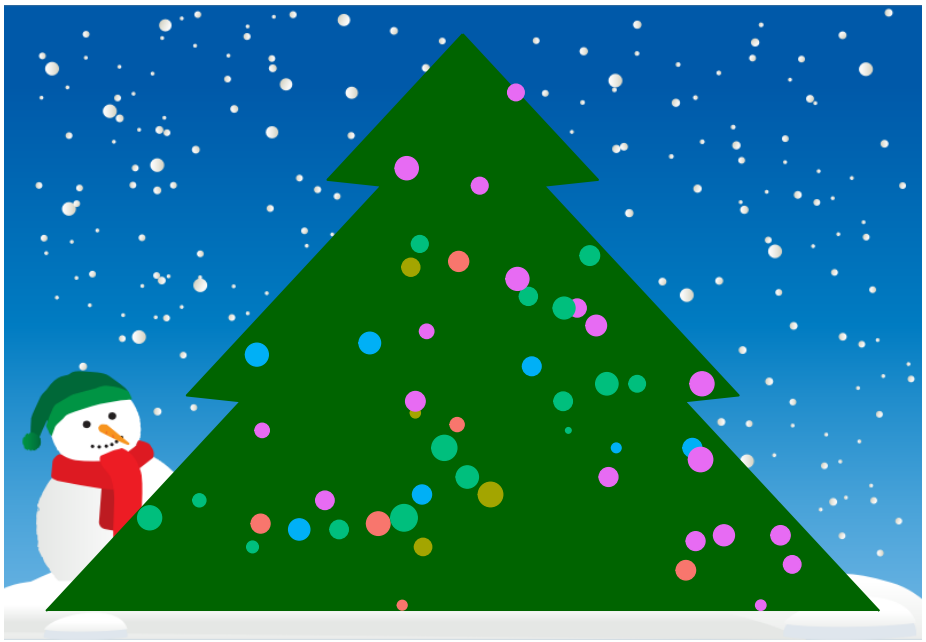


Do exercise 8.

10.8 Adding decoration (the fun ones)

Black tiny Christmas balls of the same size? That won't do! Generate a new column (I called it `size`) with random ball sizes drawn from a normal distribution. Decide on a reasonable mean and standard deviation but remember that you need to specify the number of random values that you want (just like for runif() above).

Second, let as specify color of individual balls as a factor variable. This way, we can use it for `color` aesthetics and ggplot2 will use it palettes to pick the colors for us. Just create a vector of some numbers (the number of unique entries will be your number of colors) and convert it to a factor (check what will happen, if you won't do this). Inside the geom_point() call, use `show.legend=FALSE` to suppress the legend (check what will happen, if you set it to `TRUE` or omit it).



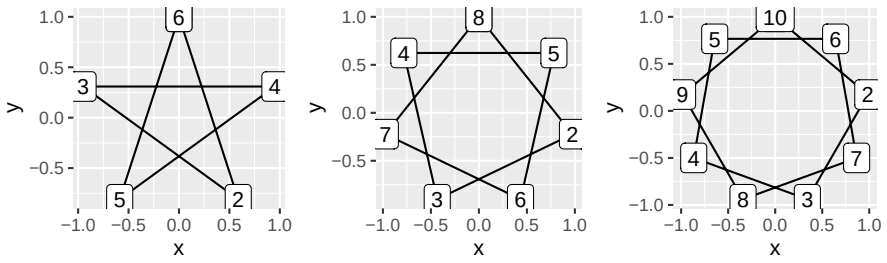
Do exercise 9.

10.9 A star on top

Our final touch will be a star on the top of the tree. We could use another geom_point but with a different shape but instead we will draw it as a regular polygon with odd number of vertices, like the ones you see below. The numbers indicate the order in which vertices are created and drawn along the path. To make a closed contour, we very first (top) vertex needs to be also the last vertex, so you cannot see a label for #1 (it is covered by #6, #8, and #10 labels) but it is definitely where. Think how you can generate such a shape by walking around the circle with a given angular step and how you can compute x and y coordinates by knowing that angle and a radius (size) of the shape (here, I assumed radius to be 1).

```
star_plots <- purrr::map(c(5, 7, 9),
                         ~tibble(theta = (0:.) * (4 * pi / .)) %>%
                          mutate(i = 1:n(),
                                 x = sin(theta),
                                 y = cos(theta)) %>%
                          ggplot(aes(x=x, y=y)) +
                          geom_path() +
                          geom_label(aes(label=i)) +
                          coord_equal())
```

```
star_plots[[1]] | star_plots[[2]] | star_plots[[3]]
```



If you examine the plots above, you will see that you go around the circle in exactly N steps, where N is 5, 7, or 9. Thus you can compute an angular step between *adjacent* vertices by diving the length of a circle in degrees or radians by the number of steps you need to make. However, for our star we are not connecting each vertex to a adjacent one but to the *next* one. Think about what it means to the step size. Once you've figured out the step size, you can generate location of each vertex in term of a *polar angle* starting at 0 (top position) using that step. Note that you need to have N+1 vertices to close the contour and that serves as a nice sanity check as the polar angle for the first and the last entry mast be the same (keeping in mind that 0 is the same angle as 360° and $2 \cdot \pi$). Later on, we want radians as we will use the angle with trigonometric functions but I suggest that you first generate a vector of angles in degrees, as it makes checking values easier.

To turn a polar angle into x/y coordinates, you need to recall basic trigonometry that is drawn below.

Pick the number of vertices that you like, generate polar angles, convert them to x and y coordinates, and plot the contour to check it visually. Try using geom_polygon with a fill color instead of geom_path.

Do exercise 10.

Our star is ready, we only need to add the geom_polygon. However, your "de-

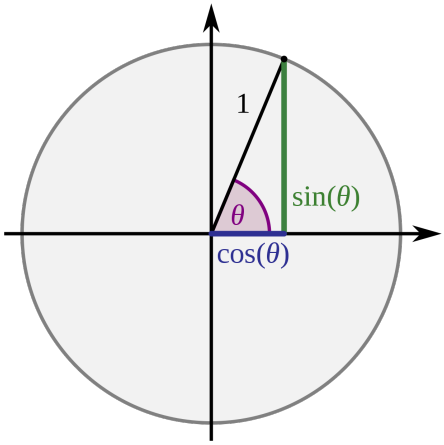
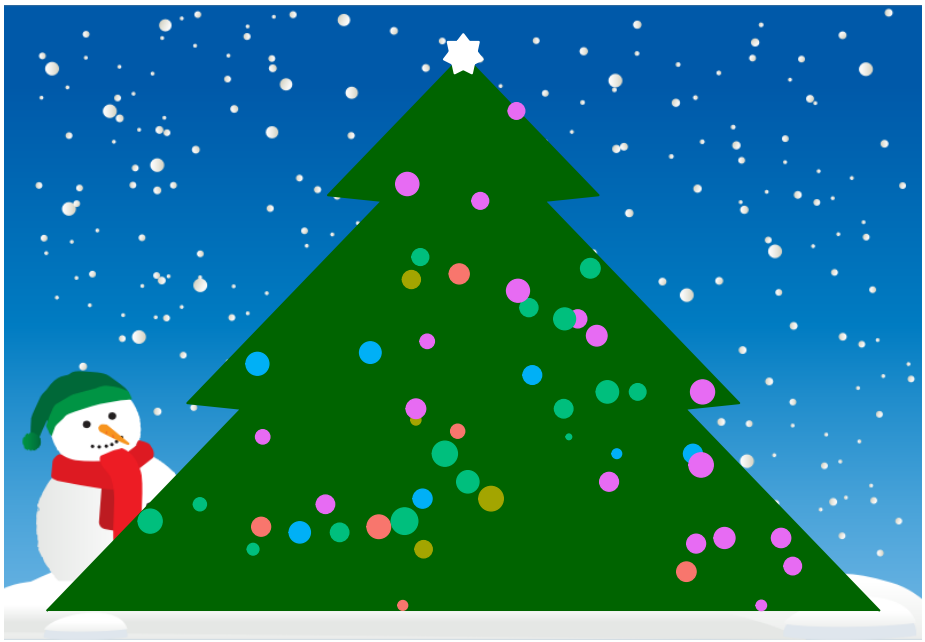


Figure 10.1: Cosine and sine on the unit circle by Stephan Kulla (User:Stephan Kulla) - Own work, CC0, https://commons.wikimedia.org/w/index.php?curid=57551646.

fault" star will look way to big and will not be on the top of the tree, as in the figure below.

Think how you can adjust the size (radius of the star) to make it smaller and what adjustment to y-coordinate do you need to make.



Do exercise 11.

10.10 Merry Christmas!

Although this assignment might look whimsical, it relies on techniques for parametrically generating data that are useful for real-life power analysis, prior predictive modelling, simulating data for model testing, etc.

Chapter 11

Missing data

Grab an exercise notebook before we start!

Sometimes data is missing. It can be missing *explicitly* with `NA` standing for Not Available / Missing data. Or, it can be missing *implicitly* when there is no entry for a particular condition. In the latter case, the strategy is to make missing values explicit first (discussed below).

Then (once) you have missing values, represented by `NA` in R, you must decide how to deal with them: you can use this information directly as missing data can be diagnostic in itself, you can impute values using either a sophisticated statistical methods or via a simple average/default value strategy, or you can exclude them from the analysis. Every option has pros and cons, so think carefully and do not use an option whose effects you do not fully understand as it will compromise the rest of your analysis.

11.1 Making missing data explicit (completing data)

To make implicit missing data explicit, *tidyr* provides a function complete() that figures out all combinations of values for columns that you specified, finds missing combinations, and adds them using `NA` (or some other specified value) for other columns. Imagine a toy incomplete table (no data for Participant `2` and Face `M-2`).

We can complete that table by specifying columns that define all required combinations.

```
complete_df <- complete(incomplete_df, Participant, Face)
```

For *non-factor* variables (`Participant` is numeric and `Face` is character/string),

Table 11.1: Table with no data for Face M2 for Participant 2.

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M-1	6	4	3
1	M-2	4	7	6
2	M-1	5	2	1

Table 11.2: Completed table with explicit NAs

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M-1	6	4	3
1	M-2	4	7	6
2	M-1	5	2	1
2	M-2	NA	NA	NA

complete finds all unique values for each column and finds all combinations of these elements. However, if a variable is a factor, complete uses it levels, even if not all levels are present in the data. E.g., we can use `Face` as a factor with three levels: "M-1", "M-2", and "F-1". In this case, information is missing for both participants (neither have responses on face "F-1") and should be filled with NAs. This approach is useful if you know all combinations that *should* be present in the data and need to ensure the completeness.

```
extended_df <-
  incomplete_df %>%
  # converting Face to factor with THREE levels (only TWO are present in the data)
  mutate(Face = factor(Face, levels = c("M-1", "M-2", "F-1"))) %>%
  # completing the table
  complete(Participant, Face)
```

Do exercise 1.

You can also supply default values via `fill` parameter that takes a named

Table 11.3: Completed missing data including F-1 face.

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M-1	6	4	3
1	M-2	4	7	6
1	F-1	NA	NA	NA
2	M-1	5	2	1
2	M-2	NA	NA	NA
2	F-1	NA	NA	NA

Table 11.4: Completed missing data with non-NA values.

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M-1	6	4	3
1	M-2	4	7	6
2	M-1	5	2	1
2	M-2	0	0	NA

list, e.g., `list(column_name = default_value)`. However, I'd like to remind you again that you should only impute values that "make sense" given the rest of your analysis. Zeros here are for illustration only and, in a real-life scenario, would ruin your inferences either by artificially lowering symmetry and attractiveness of the second face or (if you are lucky) will break and stop the analysis that expects only values within 1-7 range (rmANOVA won't be bothered at that would be the first scenario),

```
filled_df <-
  incomplete_df %>%
  complete(Participant, Face, fill=list(Attractiveness=0, Symmetry=0))
```

Do exercise 2.

The complete() is easy to use convenience function that you can easily replicate yourself. To do this, you need to create a new table that lists all combinations of variables that you are interested in (you can use either expand.grid() or expand_grid() for this) and then left joining the original table to it (why left join? Could you use another join for the same purpose?). The results is the same as with a complete() itself.

Do exercise 3.

11.2 Dropping / omitting NAs

There are two approaches for excluding missing values. You can exclude all incomplete rows which have missing values in *any* variable via na.omit() (base R function) or drop_na() (tidyr package function). Or you can exclude rows only if they have `NA` in a specific columns by specifying their names.

For a table you see below

First, we can ensure only complete cases via na.omit()

```
na.omit(widish_df_with_NA)
```

or via drop_na()

```
widish_df_with_NA %>%
  drop_na()
```

Table 11.5: Table with missing values.

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M-1	6	NA	3
1	M-2	NA	7	NA
2	M-1	5	2	1
2	M-2	3	7	2

Table 11.6: Complete cases via na.omit()

Participant	Face	Symmetry	Attractiveness	Trustworthiness
2	M-1	5	2	1
2	M-2	3	7	2

Second, we drop rows only if `Attractiveness` data is missing.

```
widish_df_with_NA %>%
  drop_na(Attractiveness)
```

Practice time. Create you own table with missing values and exclude missing values using na.omit() and drop_na().

Do exercise 4.

drop_na() is a very convenient function but you can replicate it functionality using is.na() in combination with filter dplyr function or logical indexing. Implement code that excludes rows if they contain `NA` in a specific column using these two approaches.

Do exercises 5 and 6.

Recall that you can write your own functions in R that you can use to create convenience wrappers like drop_na(). Implement code that uses logical indexing as a function that takes table (`data.frame`) as a first argument and name a of a single column as a second, filters out rows with `NA` in that column and returns the table back.

Do exercise 7.

As noted above, you can also impute values. The simplest strategy is to use

Table 11.7: Complete cases via drop_na()

Participant	Face	Symmetry	Attractiveness	Trustworthiness
2	M-1	5	2	1
2	M-2	3	7	2

Table 11.8: Complete Attractiveness via drop_na()

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M-2	NA	7	NA
2	M-1	5	2	1
2	M-2	3	7	2

Table 11.9: Missing values filled with 0 and -1

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M-1	6	0	3
1	M-2	-1	7	NA
2	M-1	5	2	1
2	M-2	3	7	2

either a fixed or an average (mean, median, etc.) value. tidyr function that performs a simple substitution is replace_na()[1] and, as a second parameter, it takes a named list of values `list(column_name = value_for_NA)`. For our toy table, we can replace missing `Attractiveness` and `Symmetry` values with some default value, e.g. `0` and `-1` (this is very arbitrary, just to demonstrate how it works, do not do things like these for real analysis unless you know what you are doing!)

```
widish_df_with_NA %>%
  replace_na(list(Attractiveness = 0, Symmetry = -1))
```

Do exercise 8.

Unfortunately, `replace_na()` works only with constant values and does not handle grouped tables very well[2] So to replace an `NA` with a mean value of a *grouped* data, we need to combine some of our old knowledge with an ifelse(conditon, value_if_true, value_if_false) function. This function is a vectorized cousin of the if-else that takes 1) a vector of logical values (`condition`), 2) a vector values that are returned if `condition` is true, 3) a vector of values that are returned if `condition` is false. Note that the usual rules of vector length-matching apply, so if the three vectors have different length, they will be automaticall (and silently) adjusted to match the length of `condition` vector.

Here is how it works to replace all negative values in a vector with a `0` and all non-negative with `1`:

```
v <- c(-1, 3, 5, -2, 5)
ifelse(v < 0, 0, 1)
```

[1] There is also an inverse function na_if() that converts a specific value to an `NA`.
[2] At least I wasn't able to figure out how to do this.

Table 11.10: adaptation_with_na.csv with missing values

Participant	Prime	Probe	Nsame	Ntotal
ma2	Sphere	Sphere	NA	119
ma2	Sphere	Quadro	23	NA
ma2	Sphere	Dual	NA	120
ma2	Sphere	Single	31	115
ma2	Quadro	Sphere	25	120
ma2	Quadro	Quadro	26	120

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

It works *per element*, so each value is replaced by its counterpart in the appropriate vector

```
v <- c(0, 0, 1, 0, 1)
ifelse(v == 1,
       c(1, 2, 3, 4, 5),
       c(-1, -2, -3, -4, -5))
```

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

As with all computations, you can use original values themselves. Here is how to replace only negative values but keep the positive ones:

```
v <- c(-1, 3, 5, -2, 5)
ifelse(v < 0, 0, v)
```

```
## [1] 0 3 5 0 5
```

We, essentially, tell the function, "if the condition is false, use the original value". Now, your turn! Using the same vector and ifelse() function, replace negative values with a mean value of the positive values in the vector.

Do exercise 9.

Now that you know how to use `ifelse()`, replacing `NA` with a mean will be (relatively) easy. Use adaptation_with_na table and replace missing information using participant-specific values.

Here is one way to approach this problem. We cannot know the number of trials for a specific Prime × Probe combination, but we can replace missing values for `Ntotal` with a participant-specific median value (a "typical" and integer number of trials but do not forget about `na.rm` option, see manual for details). `Nsame` is trickier. For this, compute proportion of same response for each condition `Psame = Nsame / Ntotal`. This will produce missing values whenever `Nsame` is missing. Now, replace missing `Psame` values (is.na()) with a mean `Psame` *per participant* (again, watch our for `na.rm`!) using ifelse() (you can use it inside `mutate()`). Finally, compute mising values for `Nsame` from `Psame` and `Ntotal`

Table 11.11: adaptation_with_na.csv with imputed values

Participant	Prime	Probe	Nsame	Ntotal	Psame
ma2	Sphere	Sphere	36	119	0.2983741
ma2	Sphere	Quadro	23	120	0.1916667
ma2	Sphere	Dual	36	120	0.2983741
ma2	Sphere	Single	31	115	0.2695652
ma2	Quadro	Sphere	25	120	0.2083333
ma2	Quadro	Quadro	26	120	0.2166667

(do not forget to round them, so you end up with integer number of trials). This entire computation should be implemented as a single pipeline. You will end up with a following table.

Do exercise 10.

Chapter 12

Working with strings

When working with strings, I strongly suggest consulting a manual and vignettes of the stringr package. It has many functions that cover most needs. Grab exercise notebook before we start.

12.1 Warming up

Before we start working with strings, let us warm up by preprocessing band-adaptation.csv that we will be working with.

1. Read it (try specifying the URL instead of the local filename).Do not forget to specify column types!
2. compute proportion of "same" responses as a using `Nsame` (number of "same" responses) and `Ntotal` (total number of trials).
3. Convert `Prime` and `Probe` column to factors with the order "Sphere", "Quadro", "Dual", "Single".
4. Compute median and median absolute deviation from the median for `Psame` for all combinations of `Prime` and `Probe`.

Your table should look as follows:

Do exercise 1.

12.2 Formatting strings via `glue()`

The table above gives us information about *median* probability of seeing the same rotation and about its absolute deviation from the median. However, it would be more convenient for a reader we would combine these two pieces of information into a single entry in form for of " ± ". Plus, it would be easier to see the pattern in a square table with one `Prime` per row and one `Probe` per column. The table I have in mind look like this:

Table 12.1: bands_df

Prime	Probe	Pmedian	Pmad
Sphere	Sphere	0.13	0.06
Sphere	Quadro	0.13	0.04
Sphere	Dual	0.17	0.10
Sphere	Single	0.32	0.08
Quadro	Sphere	0.19	0.07
Quadro	Quadro	0.12	0.12
Quadro	Dual	0.21	0.19
Quadro	Single	0.38	0.07
Dual	Sphere	0.15	0.15
Dual	Quadro	0.30	0.14
Dual	Dual	0.27	0.15
Dual	Single	0.48	0.16
Single	Sphere	0.34	0.18
Single	Quadro	0.30	0.20
Single	Dual	0.48	0.12
Single	Single	0.51	0.18

Table 12.2: Probability of persistence, median ± MAD

Prime	Sphere	Quadro	Dual	Single
Sphere	0.13 ± 0.06	0.13 ± 0.04	0.17 ± 0.1	0.32 ± 0.08
Quadro	0.19 ± 0.07	0.12 ± 0.12	0.21 ± 0.19	0.38 ± 0.07
Dual	0.15 ± 0.15	0.3 ± 0.14	0.27 ± 0.15	0.48 ± 0.16
Single	0.34 ± 0.18	0.3 ± 0.2	0.48 ± 0.12	0.51 ± 0.18

You already know how to perform the second step (pivoting table wider to turn `Probe` factor levels into columns). For the first step, you need to combine two values into a string. There are different ways to construct this string via sprintf(), paste(), or via glue package. We will start with Tidyverse's glue() and explore base R functions later.

glue package is part of the Tidyverse, so it should be already installed. However, it is not part of *core* tidyverse, so it does not get imported automatically via `library(tidyverse)` and you do need to import it separately or use `glue::` prefix. Function glue() allows you to "glue" values and code directly into a string. You simply surround *any* R code by wiggly brackets inside the string and the result of the code execution is glued in. If you use just a variable, its value will be glued-in. But you can put *any* code inside, although, the more code you put, the harder it will be to read and understand it.

```
answer <- 42
bad_answer <- 41
glue::glue("The answer is {answer}, not {abs(bad_answer / -4)}")
```

```
## The answer is 42, not 10.25
```

Use the table that you prepared during exercise 1 to compute a new column with " ± " (you will want to use round() function to restrict values to just 2 digit after the decimal point). Think about *when* you want to perform this computation (before or after pivoting?) and which column(s?) do you need to pivot wider.

Do exercise 2.

12.3 Formatting strings via `paste()`

Base R has functions paste() and paste0() that are conceptually very similar to glue(). The concatenate a vector a strings into a single string. If you recall, vector values can only be of one (most flexible) type. Therefore, if you have a vector that intersperses string with other values, they will be *first* converted to strings anyhow. The difference between `paste()` and `paste0()` is that the former puts a separator string in-between each value (defaults to `' '` but you can define your own via `sep` argument), whereas `paste0()` uses no separator. We can replicate our glue() example.

```
answer <- 42
bad_answer <- 41
paste("The answer is ", answer, ", not ", abs(bad_answer / -4), sep="")
```

```
## [1] "The answer is 42, not 10.25"
```

```
paste0("The answer is ", answer, ", not ", abs(bad_answer / -4))
```

```
## [1] "The answer is 42, not 10.25"
```

Redo exercise 2 but using one of the paste functions instead of the glue().

Do exercise 3.

12.4 Formatting strings via `sprintf()`

For detailed string formatting, base R has a sprintf() function that provides a C-style string formatting (same as Python's original string formatting and a common way to format a string in many programming languages). The general function call is `sprintf("string with formatting", value1, value2, value)`, where values are are inserted into the string. In `"string with formatting"`, you specify where you want to put the value via `%` symbol that is followed by an *optional* formatting info and the *required* symbol that defines the **type** of the value. The type symbols are

- `s` for string
- `d` for an integer
- `f` for a float value using a "fixed point" decimal notation
- `e` for a float value using a scientific notation (e.g., `1e2`).
- `g` for an "optimally" printed float value, so that scientific notation is used for very large or very small values (*e.g.*, `1e+5` instead of `100000` and `1-e5` for `0.00001`).

Here is an example of formatting a string using an integer:

```
sprintf("I had %d pancakes for breakfast", 10)
```

```
## [1] "I had 10 pancakes for breakfast"
```

You are not limited to a single value that you can put into a string. You can specify more locations via `%` but you must make sure that you pass the matching number of values. If there fewer parameters when you specified in the string, you will receive an *error*. If there are too many, only a *warning*[1]. Before running it, can you figure out which call will actually work (and what will be the output) and which will produce an error or a warning?

```
sprintf("I had %d pancakes and either %d  or %d stakes for dinner", 2)
sprintf("I had %d pancakes and %d stakes for dinner", 7, 10)
sprintf("I had %d pancake and %d stakes for dinner", 1, 7, 10)
```

In case of real values you have two options: `%f` and `%g`. The latter uses scientific notation (e.g. `1e10` for `10000000000`) to make a representation more compact. When formatting floating numbers, you can specify the number of decimal points to be displayed.

```
e <- 2.71828182845904523536028747135266249775724709369995
sprintf("Euler's number is roughly %.4f", e)
```

[1] Talk about consistency…

```
## [1] "Euler's number is roughly 2.7183"
```

Note that as most functions in R, sprintf() is vectorized so when you pass a vector of values it will generate a *vector* of strings with one formatted string for a value.

```
sprintf("The number is %d", c(2, 3))
```

```
## [1] "The number is 2" "The number is 3"
```

This means that you can use sprintf() to work on column both in base R and inside mutate() Tidyverse verb.

```
tibble(Number = 1:3) %>%
  mutate(Message = sprintf("The number is %d", Number)) %>%
  knitr::kable()
```

Number	Message
1	The number is 1
2	The number is 2
3	The number is 3

Redo exercise #2 but use sprintf() instead of glue().

Do exercise 4.

12.5 Extracting information from a string

Previous exercises dealt with combining various bits of information into a single string. Often, you also need to do the opposite: extract bits of information from a single string. For example, in the toy table on face perception, we have been working with, `Face` column code gender of the face `"M"` (table is short but you can easily assume that faces of both genders were used) and the second is its index (`1` and `2`). When we worked with persistence, `Participant` column encoded year of birth and gender, whereas `Session` contained detailed information about year, month, day, hour, minutes, and seconds all merged together. There are several ways to extract this information, either by extracting one piece at a time via substr() or string processing library stringr. Alternatively, you can split a string column into several columns via separate() or extract() functions.

12.6 Splitting strings via `separate()`

Function separate() is part of tidyverse and its use is very straightforward: you pass 1) the name of the column that you want to split, 2) names of the columns it needs to be split into, 3) a separator symbol or indexes of splitting positions. Examples using the face table should make it clear. Reminder, this is the original wide table and we want to separate `Face` into `FaceGender` and `FaceIndex`.

```
widish_df <-
  tibble(Participant = c(1, 1, 2, 2),
         Face = rep(c("M-1", "M-2"), 2),
         Symmetry = c(6, 4, 5, 3),
         Attractiveness = c(4, 7, 2, 7),
         Trustworthiness = c(3, 6, 1, 2))

knitr::kable(widish_df)
```

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M-1	6	4	3
1	M-2	4	7	6
2	M-1	5	2	1
2	M-2	3	7	2

As there is a very convenient "dash" between the two, we can use it for a separator symbol:

```
widish_df %>%
  separate(Face, into=c("FaceGender", "FaceIndex"), sep="-")
```

Participant	FaceGender	FaceIndex	Symmetry	Attractiveness	Trustworthiness
1	M	1	6	4	3
1	M	2	4	7	6
2	M	1	5	2	1
2	M	2	3	7	2

Note that the original `Face` column is gone. We can keep it via `remove=FALSE` option

```
widish_df %>%
  separate(Face, into=c("FaceGender", "FaceIndex"), sep="-", remove=FALSE)
```

Participant	Face	FaceGender	FaceIndex	Symmetry	Attractiveness	Trustworthiness
1	M-1	M	1	6	4	3
1	M-2	M	2	4	7	6
2	M-1	M	1	5	2	1
2	M-2	M	2	3	7	2

We also do not need to extract *all* information. For example, we can extract only face gender or face index. To get only the gender, we only specify *one* `into` column and add `extra="drop"` parameter, telling `separate()` to drop any extra piece it obtained:

```
widish_df %>%
  separate(Face, into=c("Gender"), sep="-", remove=FALSE, extra="drop")
```

Participant	Face	Gender	Symmetry	Attractiveness	Trustworthiness
1	M-1	M	6	4	3
1	M-2	M	4	7	6
2	M-1	M	5	2	1
2	M-2	M	3	7	2

Alternatively, we can explicitly *ignore* pieces by using `NA` for their column name:

```
widish_df %>%
  separate(Face, into=c("Gender", NA), sep="-", remove=FALSE)
```

```
widish_df %>%
  separate(Face, into=c("Gender", NA), sep="-", remove=FALSE) %>%
  knitr::kable()
```

Participant	Face	Gender	Symmetry	Attractiveness	Trustworthiness
1	M-1	M	6	4	3
1	M-2	M	4	7	6
2	M-1	M	5	2	1
2	M-2	M	3	7	2

What about keeping only the *second* piece in a `FaceIndex` column? We ignore the first one via `NA`

```
widish_df %>%
  separate(Face, into=c(NA, "Index"), sep="-", remove=FALSE)
```

```
widish_df %>%
  separate(Face, into=c(NA, "Index"), sep="-", remove=FALSE) %>%
  knitr::kable(align = "c")
```

Participant	Face	Index	Symmetry	Attractiveness	Trustworthiness
1	M-1	1	6	4	3
1	M-2	2	4	7	6
2	M-1	1	5	2	1
2	M-2	2	3	7	2

Let's practice. Use separate() to preprocess persistence data and create two new columns for hour and minutes from `Session` column. Do it in a single pipeline, starting with reading all files (use tidyverse read_csv() and specify column types!) and renaming `Shape1` (`Prime`) and `Shape2` (`Probe`) columns. You results should look like this, think about columns that you drop or keep (this is only first four rows, think of how you can limit your output the same way via head() function):

Participant	Hour	Minutes	Block	Trial	OnsetDelay	Bias	Prime	Probe
AKM1995M	14	07	0	0	0.5746952	left	stripes-8	stripes-4
AKM1995M	14	07	0	1	0.5741707	left	stripes-4	heavy poles sphere
AKM1995M	14	07	0	2	0.5082200	left	stripes-2	stripes-2
AKM1995M	14	07	0	3	0.6065058	right	stripes-8	stripes-2

Do exercise 5.

As noted above, if position of individual pieces is fixed, you can specify it explicitly. Let us make out toy table a bit more explicit

Participant	Face	Symmetry	Attractiveness	Trustworthiness
1	M-01	6	4	3
1	F-02	4	7	6
2	M-01	5	2	1
2	F-02	3	7	2

For our toy faces table, the first piece is the gender and the last one is its index. Thus, we tell `separate()` starting position each pieces, starting with the *second* one:

```
widish_df %>%
  separate(Face, into=c("FaceGender", "Dash", "FaceIndex"), sep=c(1, 2))
```

```
widish_df %>%
  separate(Face, into=c("FaceGender", "Dash", "FaceIndex"), sep=c(1, 2), remove=FALSE)
  knitr::kable()
```

Participant	Face	FaceGender	Dash	FaceIndex	Symmetry	Attractiveness	Trustworthines
1	M-01	M	-	01	6	4	
1	F-02	F	-	02	4	7	
2	M-01	M	-	01	5	2	
2	F-02	F	-	02	3	7	

Here, I've create `Dash` column for the separator but, of course, I could have omitted it via `NA` column name.

```
widish_df %>%
  separate(Face, into=c("FaceGender", NA, "FaceIndex"), sep=c(1, 2))
```

```
widish_df %>%
  separate(Face, into=c("FaceGender", NA, "FaceIndex"), sep=c(1, 2)) %>%
  knitr::kable()
```

Participant	FaceGender	FaceIndex	Symmetry	Attractiveness	Trustworthiness
1	M	01	6	4	3
1	F	02	4	7	6
2	M	01	5	2	1
2	F	02	3	7	2

Practice time! Using same persistence data extract birth year and gender of

participants from `Participant` code (however, keep the code column). Put a nice extra touch by converting year to a number (separate() splits a string into strings as well) and gender into a factor type with better labels. Here is how should look like:

Participant	BirthYear	Gender	Hour	Minutes	Block	Trial	OnsetDelay	Bias	Prime	Probe
AKM1995M	1995	Female	14	07	0	0	0.5746952	left	stripes-8	stripes-4
AKM1995M	1995	Female	14	07	0	1	0.5741707	left	stripes-4	heavy pc
AKM1995M	1995	Female	14	07	0	2	0.5082200	left	stripes-2	stripes-2
AKM1995M	1995	Female	14	07	0	3	0.6065058	right	stripes-8	stripes-2

Do exercise 6.

12.7 Extracting a substring when you know its location

Base R provides a function extract a substring (or many substrings) via substr() function (you can also its alias `substring()`). It takes a string (or a vector of strings) and vectors with `start` and `stop` indexes of each substring.

```
face_img <- c("M01", "M02", "F01", "F02")
substr(face_img, 2, 3)
```

```
## [1] "01" "02" "01" "02"
```

Repeat exercise 6 but use substr() to extract each column (`BirthYear` and `Gender`) from the participant code.

Do exercise 7.

Tidyverse has its own stringr library for working with strings. Its uses a consistent naming scheme `str_<action>` for its function and covers virtually all tasks that are related to working with strings. stringr equivalent of substr() is str_sub() that behaves similarly.

```
face_img <- c("M01", "M02", "F01", "F02")
str_sub(face_img, 2, 3)
```

```
## [1] "01" "02" "01" "02"
```

Repeat exercise 7 but using str_sub() function.

Do exercise 8.

12.8 Detecting a substring using regular expressions

> Some people, when confronted with a problem, think "I know, I'll use regular expressions." Now they have two problems.
>
> *Jamie Zawinsk*

One of the most powerful ways to work with strings is via regular expressions that allow you to code a flexible pattern that is matched to a substring within a string. For example, you can detect whether a string contains a number without knowing where it is located. Here a pattern `"\\d{3}"` means that we are looking for 3 (hence the `{3}`) digits (hence the `\\d`)

```
QandA <- c("What was the answer, 42, right?", "No idea! What could it be, 423?")
grepl("\\d{3}", QandA)
```

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

Stringr library has it own version with a more obvious name str_detect()[2]. Note, however, the reverse order of arguments, as `str_` function always take (a vector of) strings as a first parameter

```
str_detect(QandA, "\\d{3}")
```

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

You can also look for 1 or more digits (which is `+`)

```
str_detect(QandA, "\\d+")
```

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

Or for a specific word

```
str_detect(QandA, "What")
```

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

Or for a specific word only at the beginning (`^`) of the string

```
str_detect(QandA, "^What")
```

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

When it comes to regular expressions, what I have shown you so far is not even a tip of an iceberg, it is a tip of a tip of an iceberg at best. They are very flexible, allowing you to code very complicated patterns but they are also hard to read and, therefore, hard to debug[3]. For example, this is a regular expression

[2] GREP stands for Global Regular Expression Print.
[3] Hence, the quote at the beginning of the section.

to check validity on an email address[4]

```
(?:[a-z0-9!#$%&'*+/=?^_`{|}~-]+(?:\.[a-z0-9!#$%&'*+/=?^_`{|}~-]+)*|"(?:[\x01-\x08\x0b\x0c\x0e-\x1
```

Still, if you need to work with text they are indispensable, so your should remember about them. When facing an actual task grab a cheatsheet and use an online expression tester to debug the pattern.

In the next exercise, use a regular expression to filter() out Primes and Probes that *end* with a *single* digit. I know that all of them end with a single digit, if digit is in them, so you can make a very simple expression that would do the job. But I want you to practice working with the cheatsheet, so it must specify that only one digit is allowed and that it must be the last symbol. When you pattern works, you should end up with a table where all Primes and Probes are `"heavy poles sphere"`.

Do exercise 9.

Now let us practice extracting the relevant information via pattern matching. Use str_extract() to extract the participants unique code, the first three letters of `Participant` column. Again, here you can simply use a substr() but I want you write a pattern that matches 1) one or more 2) upper case letters 3) at the beginning of the string.

Do exercise 10.

Finally, let us practice in replacing part of a string via regular expressions. Use str_replace() to anonymize the birth year of our participants. You need to replace the four digits that represent their birth year with a *single* `"-"`. The table should look as follows:

Participant	Hour	Minutes	Block	Trial	OnsetDelay	Bias	Prime	Probe	Response1
AKM-M	14	07	0	0	0.5746952	left	stripes-8	stripes-4	right
AKM-M	14	07	0	1	0.5741707	left	stripes-4	heavy poles sphere	left
AKM-M	14	07	0	2	0.5082200	left	stripes-2	stripes-2	right
AKM-M	14	07	0	3	0.6065058	right	stripes-8	stripes-2	right

Do exercise 11.

[4]This an official RCF 5322 standard that should work on *almost* all of the valid email addresses.

Chapter 13

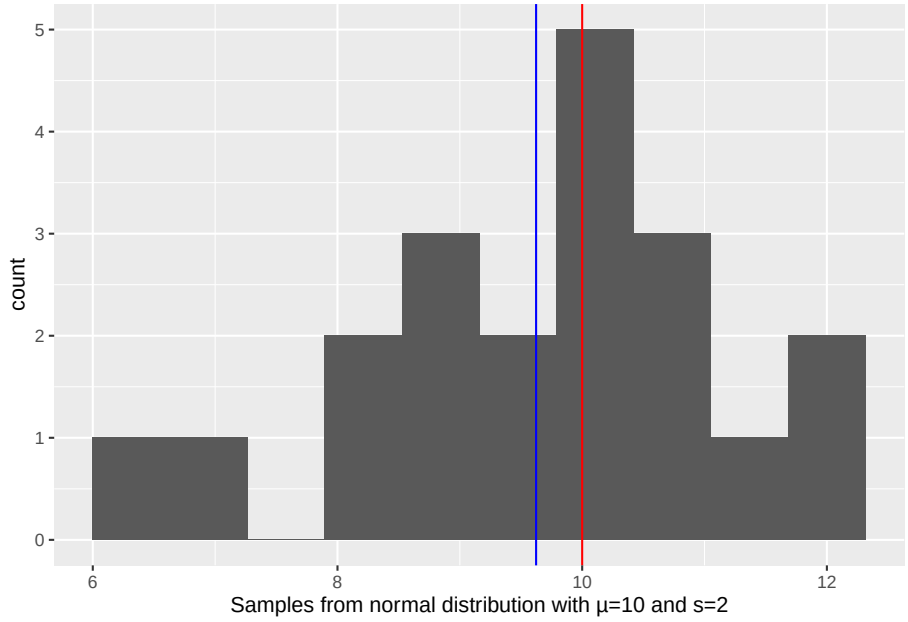
Sampling and simulations

An ability to simulate and sample data is important whenever you analyze your data. Simulating data by sampling from predefined distributions allows you develop your analysis routine and ensure that it can correctly recover the anticipated effects even before you have seen or collected the data. Or even before you designed your study as such simulations form a core of the power analysis. Sampling your data paves way for non-paramatric bootstrapping and permutation testing that helps you whenever assumptions of parametric tests are violated or when you require an estimate that is not easy to derive analytically.

Grab exercise notebook before reading on.

13.1 Estimating mean of a normal distribution via resampling

Let us start very simple. Your task will be to generate samples from a normal distribution and then use resampling approach to estimate the original mean. Step one is simple, decide on mean and standard deviation of the normal distribution and generate 20 samples using rnorm() function (`r<distribution` functions generate random number based on distribution and its parameters). Check your results visually by plotting a histogram and adding a red vertical line to indicate the true mean of the distribution. We also need to see the difference between the true mean and the sample mean. So include a blue vertical line to indicate the *sample* mean. Run your code several times to appreciate variability of the data and, therefore, of the sample mean. Your plot should look something like this.



Do exercise 1.

In the real life, we do not know the true mean which is why we need to collect the data to begin with. We also know that our sample mean is different from the true mean and we would like to know how much can we trust that value. In other words, we would like to know how much the *sample mean* would vary if we would draw some *other* samples from the same distribution. Theoretically, you want to draw samples from that "true" distribution directly. Practically, you do not have access to it, apart from replicating your experiment or study many times. Instead, you can make either an educated guess about shape and parameters of this distribution. This is a parametric approach used to compute estimators analytically, e.g., from the Student t Distribution. This is the way it is done in the t.test().

```
t.test(samples, mu = 10)
```

```
##
##  One Sample t-test
##
## data:  samples
## t = -1.1076, df = 19, p-value = 0.2819
## alternative hypothesis: true mean is not equal to 10
## 95 percent confidence interval:
##   8.911319 10.335209
## sample estimates:
## mean of x
```

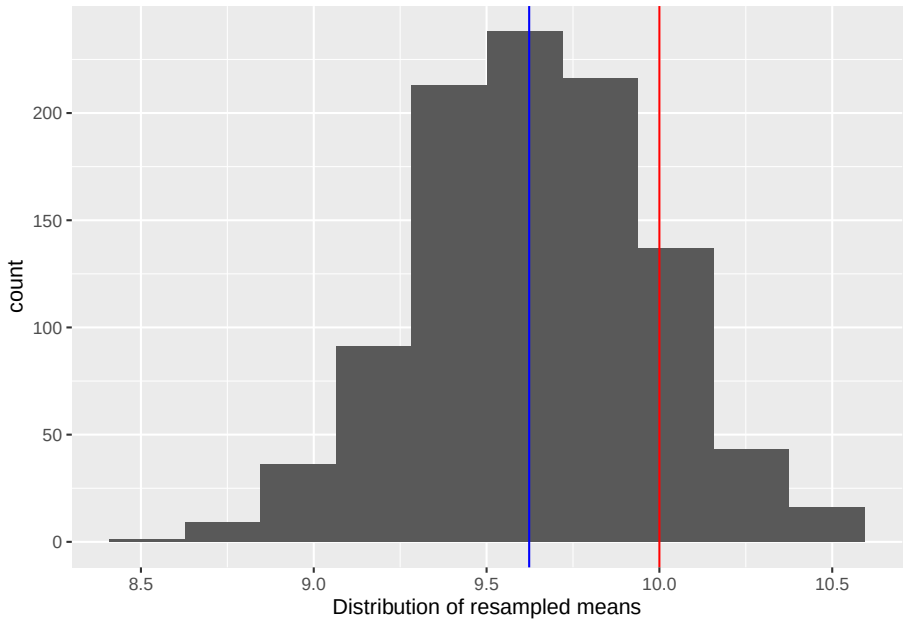
```
##  9.623264
```

The other approach is to assume that your sample and, therefore, the data you collected is representative, so sampling from the data is just like sampling from the true distribution. This is obviously a strong assumption, particularly for small samples. However, this approach can work with any data, regardless of its distribution, and can be used to estimate statistic that is not easy to derive analytically. Thus, below we will use a brute force approach that relies on sheer computer power to compute the same confidence interval through resampling from the original data that you generated.

You will need three functions for this. First, the function that samples you data: sample(). It takes the original data (first parameter `x`) and randomly samples `size` items from it either with or without replacement (controlled by `replace` parameter that defaults to `FALSE`, so no replacement). In our case we want to get a sample of the size as the original data and we want to sample *with* replacement. Again, this way we pretend that we get another data sample, as if we would run the study again, and the probability of individual entries depends on how frequently they appear in the original data. For our purposes, we want to resample data and compute its mean. Write the code that does just that. Run the chunk several times to see how computed mean value changes due to resampling. As an exercise, set `replace=FALSE` and think what value do you expect and whether and how it would change when run the chunk again.

Do exercise 2.

Our second step is to repeat out first step many times. Say, 1000 times. The function that helps you to do this is replicate(). That takes number of repetitions (first parameter `n`) and an arbitrary R code that returns a value (our step one). Once you run it, you will get a vector of 1000 means from resampled data. Plot the histogram, overlaying the true and sample means as a reference



Our final step is to use quantile() function to compute 95% confidence interval. quantile() function takes a vector and computes a value that is greater than `probs` fraction of values in that vector. E.g., if `probs=c(0.25, 0.75)`, it will return a two values, so that 25% of values are smaller than the first one and 75% of them are smaller than the second. Or, to put it differently, 50% of all values are with `probs=c(0.25, 0.75)`. In our case, we want to compute 95% confidence interval, i.e., 95% of all values should be between the lower and upper confidence interval values. Once you run the code, you should see that 95% confidence interval from resampling is very similar to what the t-test reported (you want get the same values due to random sampling but they should also be close to the t-test's analytic estimate).

```
## 95% CI: 8.940554 10.316821
```

Do exercise 3.

13.2 Bootstrapping via boot library

The approach that we used is called "bootstrapping" and R conveniently has a boot library to simplify and automate bootstrapping and the confidence interval computation. You do not need to install it (`boot` comes with base R) but you need to import it via `library(boot)`.

The key function is boot(). It has plenty of parameters that allow you to fine tune its performance but the three key compulsory parameters are

- `data`: your original data you want to use for bootstrapping.
- `statistic`: function(s) that compute desired statistic, such as mean in our case.
- `R`: the number of bootstrap replicates (we used 1000 when we did this by hand).

For non-parametric bootstraping, like the one we used above, you will need to write the `statistic` function yourself even if you want to compute a statistic for which functions already exist, like mean or standard deviation. This is because `statistic` function must take at least two arguments: 1) the data that you passed and 2) how it should be resampled. By default, the second parameter will contain indexes of elements in the data. Note that bootstrap resamples *with* replacement, so the same index can appear more than once meaning that the same element was drawn more than once (just as we did above).

Your statistic function should like as following, of course with a better name and an actual code inside.

```
your_statistic_function <- function(data, indexes){
  # here you compute desired statistic subsetting data using indexes
}
```

Once you have this function, you can bootstrap samples via

```
booted_samples <- boot(samples, statistic = your_statistic_function, R=1000)
```

Next, use function boot.ci() to compute the confidence interval. It takes your bootstrapped samples as a first parameter. You can also specify the confidence interval you are interested in (`conf`, defaults to 0.95) and `type` of the confidence interval. The one we computed above is called percentile (`type="perc"`), so this is the type you should specify. Once you run the code the output should be similar to that below.

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 1000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = booted_samples, type = "perc")
##
## Intervals :
## Level     Percentile
## 95%   ( 8.939, 10.242 )
## Calculations and Intervals on Original Scale
```

As you can see, we very similar results as above (but for variation due to sampling). Thus, either approach will work but, in most cases, `boot` is more flexible solution (but do read on bootstrapping before using advanced options).

Do exercise 4.

13.3 More samples give you more confidence

In the exercises above, we computed confidence intervals for the mean based on 20 original samples. However, this was an arbitrary number I came up with. For the real study, you would like to know how the number of samples (participants, trials per condition, etc.) affects the width of the confidence interval. For example, assuming that our data comes from a normal distribution centered at 0.5 with a standard deviation of 2, how many samples do we need to be certain that mean is not a zero (confidence interval does not overlap with zero)?

The solution is to simulate this situation using different number of samples. We will need to package the simulation into function to make it simpler to work with it but let us start with plain script code first. Assume that variable (our future parameter) `n_samples` holds number of samples that you need to generate (set it to some arbitrary value, e.g., 10). You code should

- draw `n_samples` random samples from a normal distribution with mean of 0.5 and standard deviation of 2.
- bootstrap 1000 estimates of the mean.
- compute percentile 95% confidence interval.
- store it into a tibble along with number of samples.

The only tricky part is extracting the confidence interval values from the object that boot.ci() function returns. Assuming that you computed percentile CI and stored the value in variable `CI`, the lower limit is `CI$percent[4]` and the upper is in `CI$percent[5]`. Your final tibble should look as follows (`lowerCI` and `upperCI` will be different for you because of random sampling).

lowerCI	upperCI
0.0859532	1.940723

Once you code is working, turn it into a function (I called it `CI_for_sim`) that takes `n_samples` as a parameter. Test it by calling it with `n_samples = 10`, the result should be exactly the same as before.

Do exercise 5.

Next, we need to run this function for different number of samples and we want to end up with a table, like the one below.

n_samples	lowerCI	upperCI
10	-1.0085864	1.5596448
11	0.4958008	1.6589707
12	-0.3982136	1.9194213
13	-0.5672158	2.0918783
14	-1.2831007	0.7664541
15	0.4524685	2.0642302

There are different ways to do this but we will use this as an opportunity to learn about group_modify(), a function that allows you to apply a function to each

group in your table. The only condition for such function is that it must return a table. All tables are bind together by row so you end up with a single table. A table that function returns can be of any length and have as many columns as required. Thus, group_modify() is a powerful way to compute many columns at the same time, expand, modify, or summarize the group. Here is an example of how you use it.

```
avg_mpg_per_cylinder <- function(mpg_values, cylinders_n) {
  tibble(AvgMpgPerCylinder = mean(mpg_values) / cylinders_n,
         Variance = var(mpg_values) / cylinders_n)
}

mpg %>%
  group_by(cyl, year) %>%
  group_modify(~avg_mpg_per_cylinder(.x$cty, .y$cyl)) %>%
  knitr::kable()
```

cyl	year	AvgMpgPerCylinder	Variance
4	1999	5.211111	4.4994949
4	2008	5.305556	1.3158730
5	2008	4.100000	0.0666667
6	1999	2.677778	0.4651515
6	2008	2.735294	0.6072490
8	1999	1.527778	0.3397436
8	2008	1.598837	0.4437984

The function takes a vector of values on fuel efficiency (`mpg_values`) and a number of cylinders (`cylinders_n`) and returns a table with mean and variance of fuel efficiency per cylinder. When calling this function inside the group_modify(), you need to use `~` before the function call (tells Tidyverse that you want to execute the code as is) and use `.y$` for variables that define the group (would be `cyl` and `year` in our case) and `.x$` for other columns.

Let us use group_modify() to simulate CIs for different number of samples. In a single pipe,

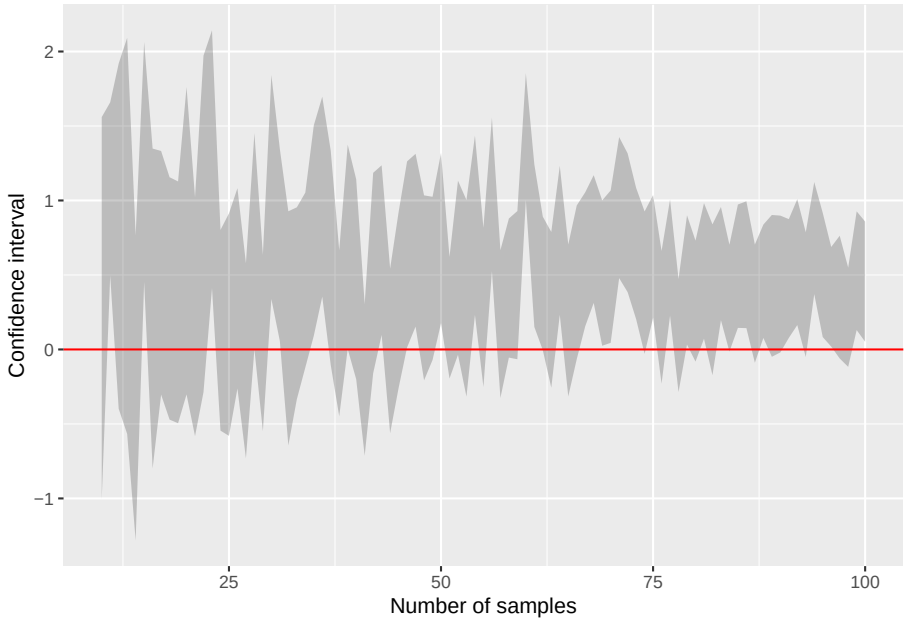
1. create a tibble with a single column `n_samples` and assign some reasonable range of values to it (I went from 10 to 100)
2. group data by the number of samples
3. simulate data and compute CI by calling your `CI_for_sim()` function inside the group_modify().

Once you are done, your table should look something like this.

n_samples	avg	lowerCI	upperCI
10	0.2716089	-1.0085864	1.5596448
11	1.0479285	0.4958008	1.6589707
12	0.7077041	-0.3982136	1.9194213
13	0.7223447	-0.5672158	2.0918783
14	-0.2562594	-1.2831007	0.7664541
15	1.2952590	0.4524685	2.0642302

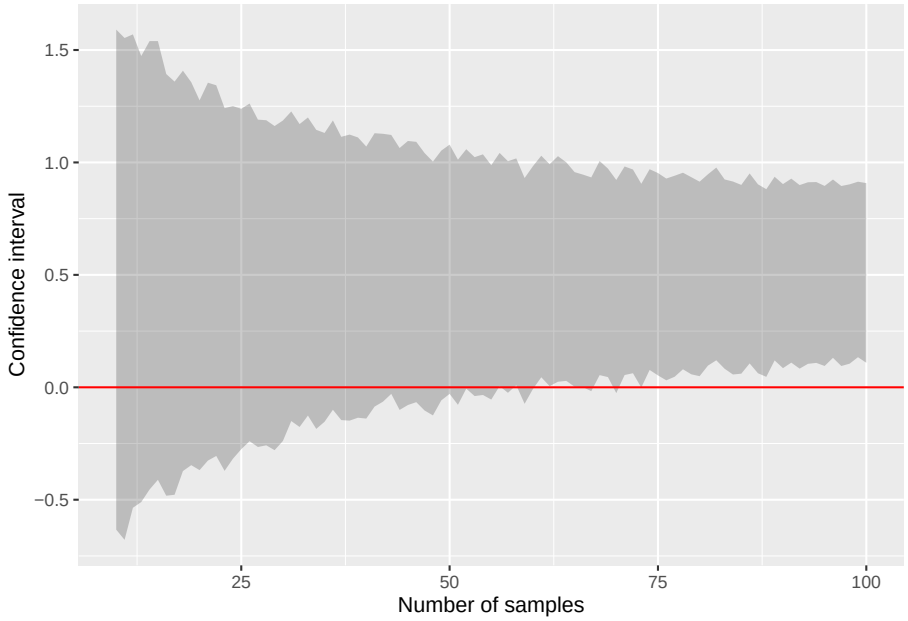
Do exercise 6.

It is much easier to understand the data once we visualize it. Plot the results using geom_ribbon() (note that you will need to set `y` aesthetics to some variable or value even though it is not used) and geom_hline(). The plot should look similar to the one below.



Do exercise 7.

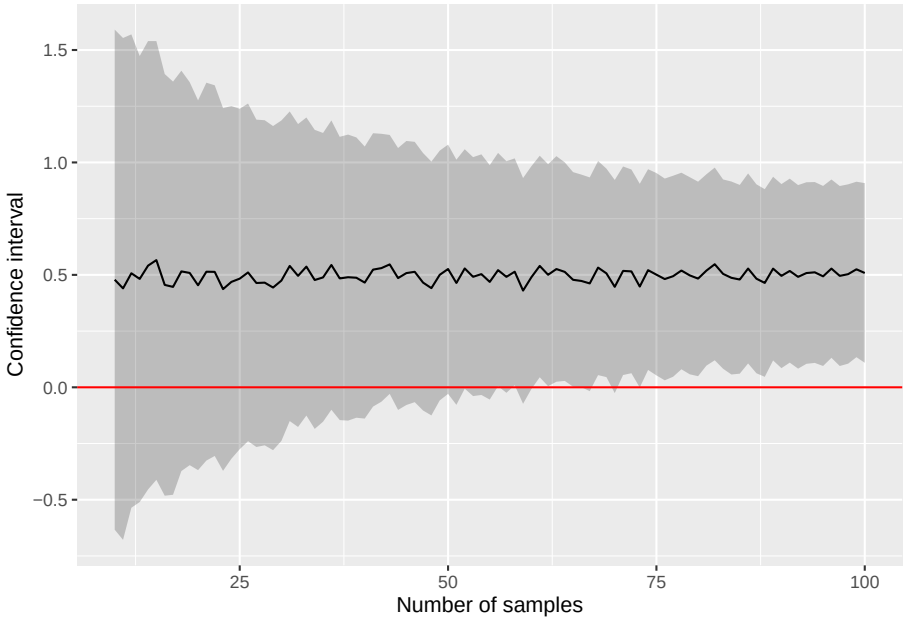
As you can see in the plot above, confidence intervals vary a lot, so it is hard to be certain about the number of samples we require. Thus, we need to sample the bootstrap as well. Redo the analysis but now create a tibble with two columns — `n_samples` (go 10 to 100) and `iteration` (go 1 to 100) — and fill the table with all combinations of these values (you should get 9100 rows). Next, simulate and compute CI for each combination of `n_samples` and `iteration` and then compute *average* lower and upper interval for each `n_samples` value. Plot these averages as we did above and you should see a much smoother plot that makes it easier to decide on the required number of samples (probably around 75). Note, if your simulations takes too long, reduce the number of iterations or use a larger step between `n_samples` (not 1 as we did before but 2 or 5).



Do exercise 8.

13.4 Adding average sample mean

Let us redo the computation but add average sample mean to the plot. For this, you need to modify your `CI_for_sim()` function to include sample mean to the tibble that it return and average over mean for different iterations. Your final plot should resemble this. Note how estimated mean remains stable (unbiased) for different number of samples. It is our certainty about the value, as expressed by the confidence interval, that changes.



Do exercise 9.

13.5 Practice makes perfect

Our simulations above used normally distributed data. In psychological research, you often use binomial responses (yes/no, correct/mistake). Here, with of a confidence intervals depends both number of samples but also the probability of success ("yes" or "correct" response). Repeat the analysis using four assumed probabilities of success: 0.6, 0.7, 0.8, and 0.9. The logic is the same but you need to use rbinom() to generate random responses. Here, the `size` parameter is the number of samples that we draw, whereas `n` is how many times we draw these samples. It return a random number of successes out of `size` number of trials. E.g., here is how to generate number of successful trials assuming total of 20 trials and probability of success being 0.8.

```
rbinom(n=1, size=20, prob=0.8)
```

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

Note that you can use `n` parameter to create many (iterations of) draws.

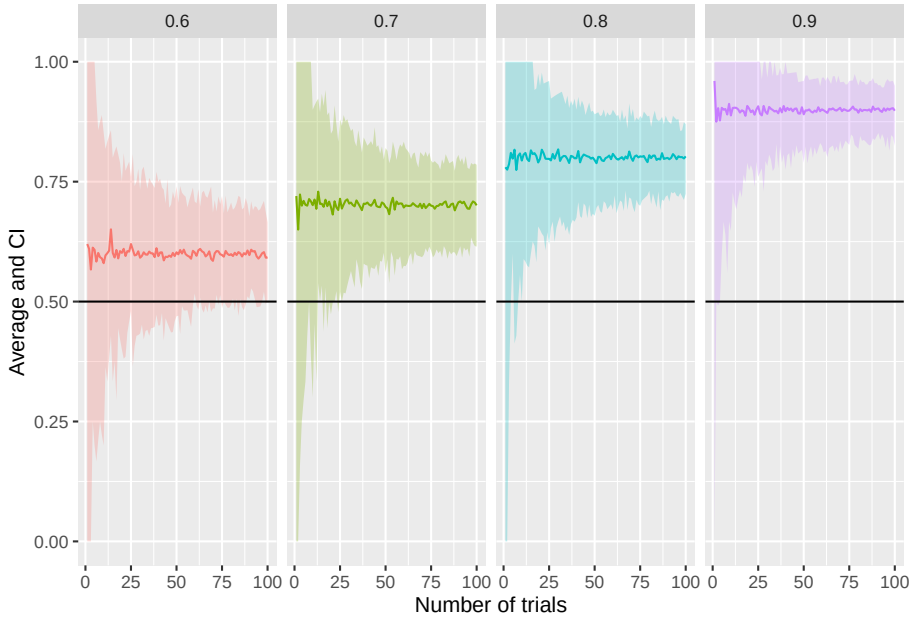
```
rbinom(n=10, size=20, prob=0.8)
```

```
##  [1] 17 18 16 15 12 18 17 14 15 14
```

```
# same as
replicate(10, rbinom(n=1, size=20, prob=0.8))
```

```
##  [1] 16 17 17 16 16 18 18 17 18 16
```

Here, I did not use `boot` library. Instead, I have utilized rbinom() to generate many draws of a given size and quantile() to compute percentile confidence interval. The final plot should look similar to this (but for quantitative differences due to sampling). As you can see, you need many trials when probability of success is closer to 0.5.



Do exercise 10.

13.6 Starting with basics

What we covered today are basics of simulations and resampling approach. However, once expanded they allow you to explore your models even before you have collected the data and perform power analysis to evalute their expected performance.

Chapter 14

Statistical modeling

I suspect that this is a seminar that you were waiting for the most as it finally tells you how to call statistical functions in R. However, from my perspective, it is the least useful seminar in the entire course because if you know statistics and you know which specific tool you need, figuring out how to use it in R is fairly trivial. Conversely, if your knowledge of statistics is approximate, knowing how to call functions will do you little good. The catch about statistical models is that they are very easy to run (even if you implement them by hand from scratch) but they are easy to misuse and very hard to interpret[1].

To make things worse, computers and algorithms do not care. In absolute majority of cases, statistical models will happily accept any input you provide, even if it is completely unsuitable, and spit out numbers. Unfortunately, it is on you, not on the computer, to know what you are doing and whether results even make sense. The only solution to this problem: do not spare any effort to learn statistics. Having a solid understanding of a basic regression analysis will help you in figuring out which statistical tools are applicable and, even more importantly, which will definitely misguide you. This is why I will give an general overview with some examples simulations but I will not explain here when and why you should use a particular tool or how to interpret the outputs. Want to know more? Attend my *Bayesian Statistics* seminar or read an excellent Statistical Rethinking by Richard McElreath that the seminar is based on.

Below, we will go through a number statistical analysis approaches and, for some, you will learn how to use resampling and permutation to obtain confidence intervals and p values, replicating the ones that parametric models produce. Hopefully, this should give you an intuition about where these values come

[1] In the Statistical Rethinking seminar we spend three seminars learning how to understand and interpret a simple linear multiple regression with just two predictors. And the conclusion is that even in this simple case, you are not guaranteed to fully understand it. And if you think that you can easily interpret an interaction term even for two continuous predictors…

from (the ones you see in the output are analytically derived solutions for when you would perform resampling and permutation for infinitely many iterations but the core idea is the same) and how you can compute them for simulations, power analysis, or when analytic estimates are not readily available. Grab the notebook.

14.1 Correlation

In base R, you can use function cor() to compute correlation. You have a choice of `method`, either `"pearson"` (default, Pearson's product moment correlation coefficient, ρ), or rank-based `"kendall"` (Kendall's rank correlation coefficient, τ) or `"spearman"` (Spearman's rank correlation coefficient, ρ).

```
df <-
  tibble(x = rnorm(100)) %>%
  mutate(y = rnorm(n(), x, 0.5))
cor(df$x, df$y, method="pearson")
```

```
## [1] 0.9019981
```

Alternatively, you can use cor.test() that also computes test statistics and significance.

```
cor_result <- cor.test(df$x, df$y, method="pearson")
cor_result
```

```
##
##  Pearson's product-moment correlation
##
## data:  df$x and df$y
## t = 20.682, df = 98, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.8575026 0.9331000
## sample estimates:
##       cor
## 0.9019981
```

`cor.test` returns a list, so you can access its individual elements[2] via a double-bracket or `$` notation.

```
cor_result$p.value
```

```
## [1] 1.587873e-37
```

Bayesian correlation with a full posterior distribution for the correlation coefficient and Bayes Factor as a measure of significance, can be computed via

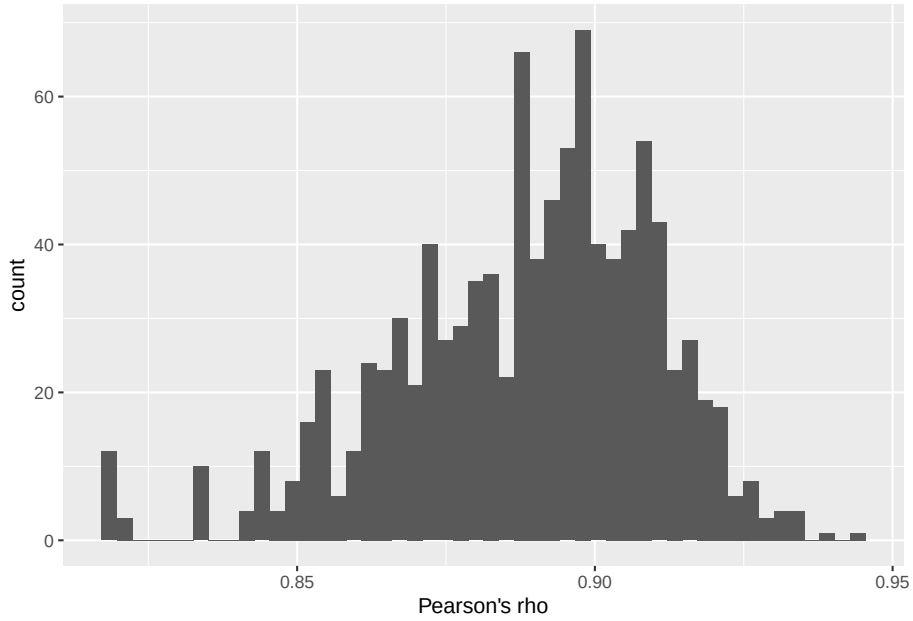
[2] Use names() function to get names of all elements.

`correlationBF()` function, which is part of BayesFactor package.

```
library(BayesFactor)
correlationBF(df$x, df$y)
```

```
## Bayes factor analysis
## --------------
## [1] Alt., r=0.333 : 1.018692e+33 ±0%
##
## Against denominator:
##   Null, rho = 0
## ---
## Bayes factor type: BFcorrelation, Jeffreys-beta*
```

```
cor_bf <- correlationBF(df$x, df$y, posterior = TRUE, iterations=1000)
ggplot(data=NULL, aes(x=c(cor_bf[, "rho"]))) +
  geom_histogram(bins=50, ) +
  xlab("Pearson's rho")
```



14.2 Correlation in practice

Let us practice computing and understanding the correlation using randomly generating data. First, let us compute Pearson's correlation coefficient by hand.

The formula is

$$r_{xy} = \frac{\sum_{i=1}^{n}(x_i - \hat{x})(y_i - \hat{y})}{\sqrt{\sum_{i=1}^{n}(x_i - \hat{x})^2}\sqrt{\sum_{i=1}^{n}(y_i - \hat{y})^2}}$$

where $\hat{x}$ and $\hat{y}$ are sample means for the corresponding variable. Thanks to vectorized nature of R, you *do not* need to use loops! Generate random data from normal distribution the way I did above. Generate variable `x` from standard normal distribution (rnorm(), $\mu = 0$, $\sigma = 1$), generate a second variable from a normal distribution with μ defined by `x` and use a value of your choice for σ. Compare your results with those of cor() function.

```
## cor(x, y) = 0.878730431189062, rxy = 0.878730431189062
```

Do exercise 1.

When interpreting correlation between two variables, your are interested not only in the estimate itself but also about your confidence about it. The cor.test() function helps you in this by returning a 95% confidence interval. Let us replicate this via resampling approach you have learned about the last time. Recall the idea is to draw more samples from the distribution but, since we do cannot do this, we resample the data we have with replacement by assuming that our original sample is representative. Generate `x` and `y` as in exercise 1 and compute a percentile 95% confidence interval. For this, you will need to sample *pairs* of values with replacement. In other words, you need to sample *index* of elements. You can do it yourself or rely on boot()). Once you computed correlation coefficients for 1000 samples drawn from original variables, compute and compare the 95% confidence interval with one reported by cor.test().

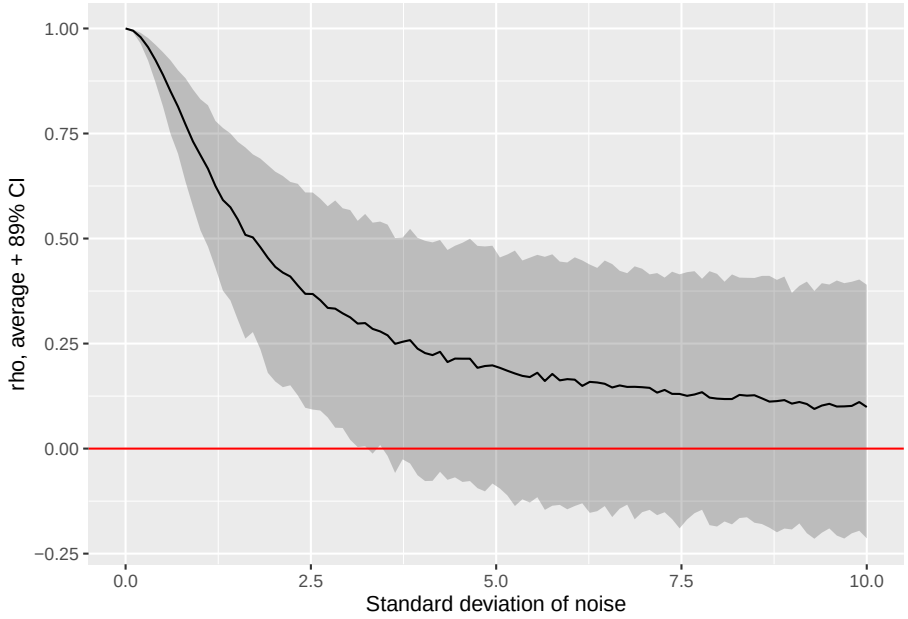
```
## 95% CI via resampling: 0.974918..0.988283
```

```
##
##  Pearson's product-moment correlation
##
## data:  x and y
## t = 52.538, df = 98, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.9743617 0.9883520
## sample estimates:
##       cor
## 0.9827071
```

Do exercise 2.

Next, let us see how noise in `y` (second variable) affect it strength. The approach will be very similar to how we explored with dependence between number of samples and our (un)certainty about the mean in the previous seminar. Write a function that will take two parameters: 1) number of samples and 2) standard deviation of noise. Generate variable `x` and `y` the same way as in exercise 1

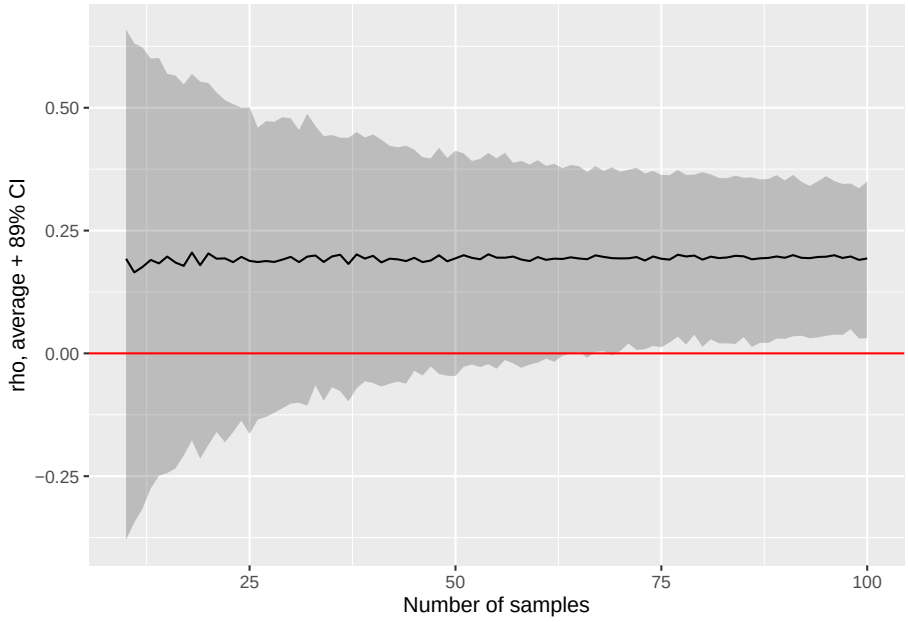
but use the function parameter for σ when generating `y`. Return the correlation coefficient. Next, create a tibble with various levels of standard deviation of noise with 1000 iterations (rows) per level. Compute correlation coefficient for every row (I have used `Nsamples = 30`) and then mean and 89%[3] confidence interval for each level of noise. Plot it, so it looks similar to the plot below.



Do exercise 3.

The analysis above explored how increased noise masks correlation between two samples of a *fixed* size. However, when you design a study you are more likely to be interested in an opposite question: what is your confidence about a *fixed strength* correlation (you figure out its value from the literature) given an increasing number of samples. This is the same logic that we applied to our confidence about mean. I have used $\sigma_{noise} = 5.0$ for the plot below.

[3]Why 89%? Because 89 is a prime number.

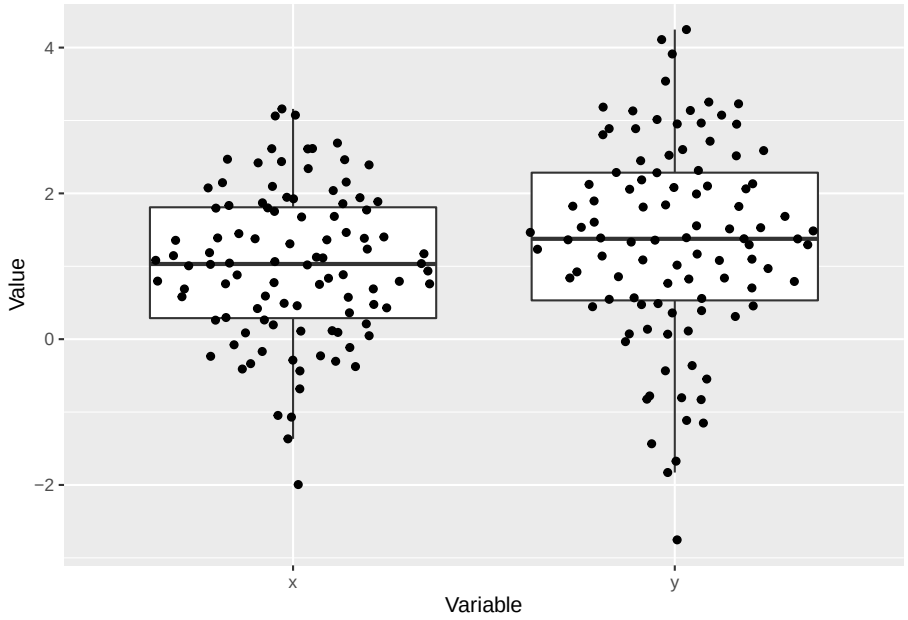


Do exercise 4.

14.3 Pairwise comparisons

For pairwise comparisons for normally distributed data, you can use Student's t-Test via t.test(). Here, I generate to `x` as a normally distributed normal variable and `y`, as a normally distributed variable random whose mean is `x + 0.3`. I am using library ggbeeswarm to generate the nicely looking cloud of dots.

```
set.seed(14454)
df <-
  tibble(x = rnorm(100, mean = 1, sd = 1)) %>%
  mutate(y = rnorm(100, mean = x + 0.3, sd = 1))
```



You can perform *t-test* assuming that samples in two variables are independent

```
t.test(df$x, df$y, paired = FALSE)
```

```
##
##  Welch Two Sample t-test
##
## data:  df$x and df$y
## t = -1.8603, df = 184.37, p-value = 0.06443
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.65829852  0.01933491
## sample estimates:
## mean of x mean of y
##  1.018298  1.337780
```

Or, that they are paired (this matches how I generated the data), i.e., repeated-measures design (note the change in estimates, statistics, and significance).

```
t.test(df$x, df$y, paired = TRUE)
```

```
##
##  Paired t-test
##
## data:  df$x and df$y
## t = -3.3432, df = 99, p-value = 0.00117
## alternative hypothesis: true mean difference is not equal to 0
```

```
## 95 percent confidence interval:
##  -0.5090948 -0.1298688
## sample estimates:
## mean difference
##      -0.3194818
```

A Bayesian version is provided via `ttestBF()` function, which is part of the BayesFactor package.

```
library(BayesFactor)
ttestBF(x = df$x, y=df$y, paired=TRUE)
```

```
## Bayes factor analysis
## --------------
## [1] Alt., r=0.707 : 19.27724 ±0%
##
## Against denominator:
##   Null, mu = 0
## ---
## Bayes factor type: BFoneSample, JZS
```

For a non-parametric pairwise test, you can use Wilcoxon Rank Sum and Signed Rank Tests wilcox.test(). Package coin implements many tests, including permutation tests, such as Two- and K-sample Fisher-Pitman permutation test via `oneway_test()` that tests for the equality of the distributions in *independent* groups, see vignette for details.

14.4 T-tests in practice

As with the correlation coefficient, let us generate data and compute the t-statistics by hand. The formula is

$$t = \frac{\bar{X} - \mu_0}{s_D/\sqrt{n}}$$

where $\bar{X}$ and s_D are the average and standard deviation of *difference* between all pairs, n is the number of pairs, and μ_0 is the null hypothesis for difference. In our case, we would like to know whether the difference is different from zero, thus, $\mu_0 = 0$.

Generate random data similarly to how I did it in the example above. Compute t-statistic and compare it to the output of a *paired* t.test().

```
## t-statistic: -2.35394746408782
```

```
##
##  Paired t-test
##
```

```
## data:  x and y
## t = -2.3539, df = 99, p-value = 0.02055
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.42255491 -0.03601326
## sample estimates:
## mean difference
##      -0.2292841
```

Do exercise 5.

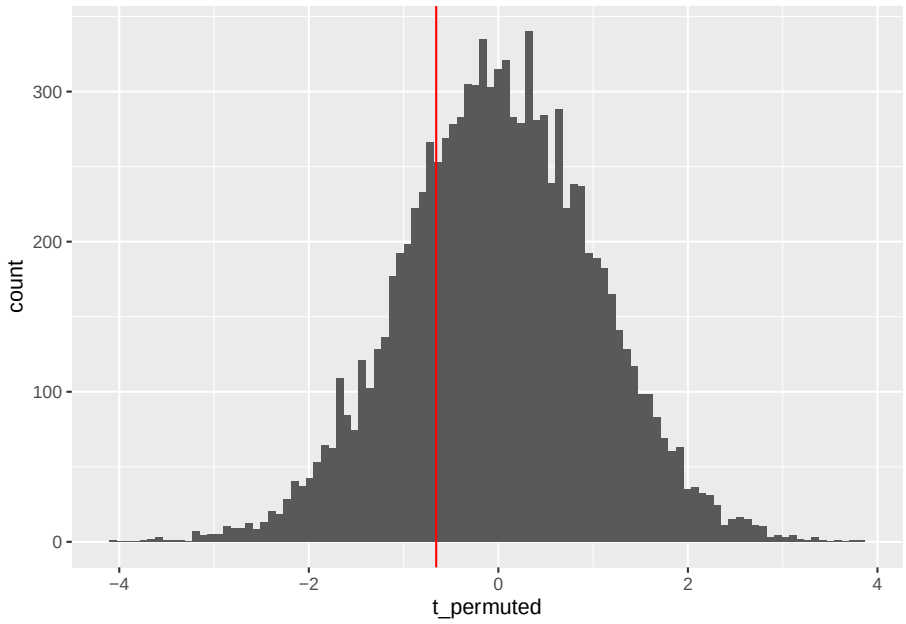
Let us use resampling approach to replicate analytically derived confidence interval of difference between the means and the p-value. We start with the 95% confidence interval for the difference. The idea is the same as before when we computed the confidence interval for correlation: We sample both variables *pairwise*, compute the average difference, store it, repeat this 1000 times. Once we have 1000 resampled average distances, compute a percentile interval and compare it to one reported by t.test().

```
## resampled 95% percentile confidence interval: -0.525506556471162..-0.124136641013539
```

```
##
##  Paired t-test
##
## data:  x and y
## t = -3.0788, df = 99, p-value = 0.00269
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.5329613 -0.1152214
## sample estimates:
## mean difference
##      -0.3240913
```

Do exercise 6.

Next comes the statistical significance testing via a *permutation test*. Here, we compute the t-statistic for the sample (you already know how to do that). Then, we pool values from both `x` and `y` into a single vector, shuffle that single vector and divide it back into permuted x (first half of the pooled vector) and permuted y (second half of the pooled vector). Then we compute the t-statistics for the difference between permuted vectors. We repeat this 10000 times to obtain a distribution of t-statistics that we would observe when pairing between `x` and `y` was random. Finally, we compute the proportion of values that are more extreme (smaller than, in our case) than the original value. This, effectively, is the probably of observing such extreme t-statistic by pure chance and is interpreted the same way as the p-value. Compare this to the output of the paired t-test using `alternative = "less"`:




```
## Proportion of t-statisic for permuted pairs < t-stat for original: 0.2573
```

```
##
##  Paired t-test
##
## data:  x and y
## t = -0.65575, df = 99, p-value = 0.2568
## alternative hypothesis: true mean difference is less than 0
## 95 percent confidence interval:
##      -Inf 0.100426
## sample estimates:
## mean difference
##     -0.06555021
```

Do exercise 7.

14.5 Formula notation

Using statistical models in R is particularly easy because most packages make use of a formula to describe a model. Different functions and packages interpret the formula *mostly* the same way with differences arising due to how random effects or additional parameters are described. Here is an example of a formula:

```
y ~ 1 + x1 + x2 + x1:x2
```

It says that the outcome variable `y` should be a modeled as a linear combination

of an intercept `1` (can be omitted in a formula), predictor variables `x1` and `x2`, plus their interaction `x1:x2`. This also assumes that all these variables are in a single table that you also supply to the function (that parameter is typically called `data`). Same formula can be shortened by using `*` which means "both predictors and their interaction" and omitting redundant intercept (it is always used unless you explicitly exclude it)

```
y ~ x1*x2
```

You can also *exclude* specific terms via `-`. So, if you insist that the intercept *must* go through 0, you write "exclude intercept term" as `-1`

```
y ~ x1*x2 - 1
```

Or you can exclude a specific term or an interaction. The two formulas below are equivalent with a main effect for `x2` and an interaction term but no main effect for `x1`. However, I would generally discourage you from using `-` as the first formula is much harder to understand (or, conversely, much easier to misunderstand).

```
y ~ x1*x2 - x1
y ~ x2 + x1:x2
```

14.6 Using t-test via formula

When we used t.test() above, we specified two vectors. However, you can also use a table where one column contains *values* and another one *group labels*. Here, we estimate difference in mean `x` between two `group`s.

```
yA <- rnorm(100, mean = 1, sd = 1)
yB <- rnorm(100, mean = yA + 0.1, sd = 1)
df_group <-
  tibble(y = c(yA, yB),
         group = factor(c(rep("A", 100), rep("B", 100))))
```

y	group
2.2309282	A
1.0449518	A
0.8420765	A
0.2378746	A

```
t.test(y ~ group, data=df_group, paired=TRUE)
```

```
##
##  Paired t-test
##
## data:  y by group
## t = -0.32625, df = 99, p-value = 0.7449
```

```
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.2185310  0.1568153
## sample estimates:
## mean difference
##     -0.03085788
```

14.7 ANOVA

ANalysis **O**f **VA**riance is probably the most widely used analysis in social sciences. However, I would strongly suggest considering generalized linear mixed models instead. Unlike ANOVA they can work when residuals are not normally distributed (binomial, count, Likert-scale ordered categorical, proportions data, etc.), they can tolerate missing values, and they tend to overfit less (their results are likely to better generalize to future data) by assuming that individual participants are more average than they appear in the raw data (so-called shrinkage).

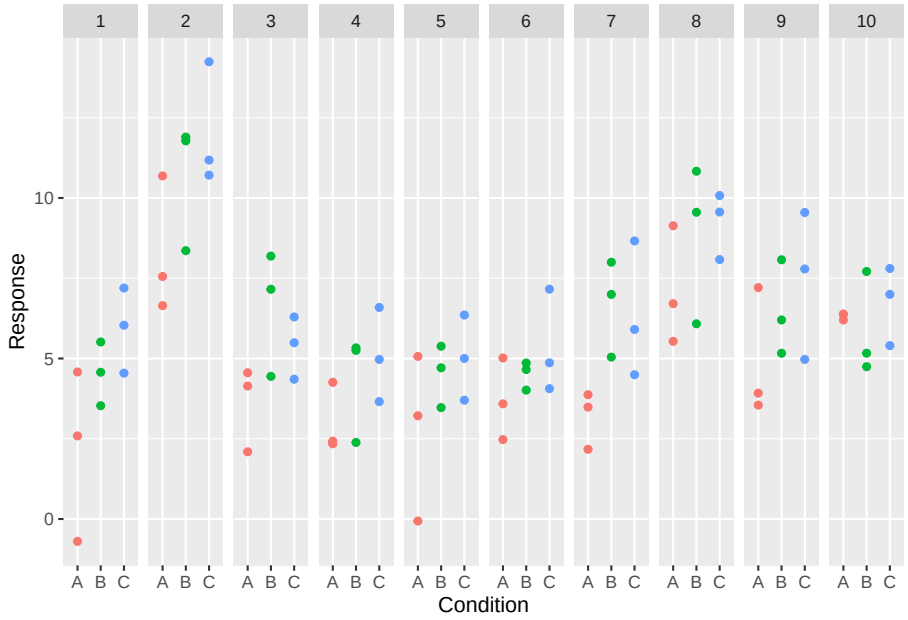
First, let us simulate data for ten participants and their responses, assuming that condition `B` increases their responses by 2 (arbitrary) units and `C` by 3[4].

```
set.seed(519264)
df_anova <-
  # generate ten participants with five trials per condition
  expand_grid(Participant  = factor(1:10),
              Condition = factor(c(rep("A", 3), rep("B", 3), rep("C", 3)))) %>%

  # decide on a SINGLE baseline (intercept) for each participant
  group_by(Participant) %>%
  mutate(Intercept = rnorm(1, 5, 2.5)) %>%

  # simulate normally distributed responses, assuming that are 3 units higher for cond
  ungroup() %>%
  mutate(Response = rnorm(n(), Intercept + 2 * as.integer(Condition == "B") + 3 * as.i
  select(-Intercept)
```

[4]set.seed() function initializes random numbers generator to a specific state to get a reproducible but random (as in, sequentially uncorrelated) sequence of values.



The base R ANOVA function is called aov(), however, it does not support repeated measures. Instead, you can use function `anova_test` from package rstatix

For the *repeated-measures* ANOVA, we need to specify column with identity of participants via parameter `wid`

```
library(rstatix)
anova_test(data=df_anova, Response ~ Condition, wid=Participant)
```

```
## ANOVA Table (type II tests)
##
##      Effect DFn DFd     F     p p<.05   ges
## 1 Condition   2  87 7.418 0.001     * 0.146
```

You can perform various pairwise post-hoc tests, e.g. Tukey

```
tukey_hsd(df_anova, Response ~ Condition)
```

```
tukey_hsd(df_anova, Response ~ Condition) %>%
  knitr::kable()
```

term	group1	group2	null.value	estimate	conf.low	conf.high	p.adj	p.adj.signif
Condition	A	B	0	1.8015391	0.2763798	3.326698	0.01640	*
Condition	A	C	0	2.3560918	0.8309325	3.881251	0.00115	**
Condition	B	C	0	0.5545527	-0.9706066	2.079712	0.66200	ns

A Bayesian ANOVA with posterior distributions for individual coefficients and significance via Bayes Factor can be performed via `anovaBF` function from

BayesFactor package.

```
anovaBF(Response ~ Condition + Participant, whichRandom="Participant", data=data.frame
```

```
## Bayes factor analysis
## --------------
## [1] Condition + Participant : 55450.04 ±0.85%
##
## Against denominator:
##   Response ~ Participant
## ---
## Bayes factor type: BFlinearModel, JZS
```

If you decide for repeated-measure ANOVA, I would suggest using and reporting results for both frequentist and Bayesian ANOVA, as it will demonstrate that they do not depend on the choice of the statistical approach.

14.8 (Almost) everything is a linear regression model

Even though linear models did not appear as the first on the list, they are. All approaches that we covered so far, correlation, t-test, ANOVA, and many more (MANOVA, ANCOVA, etc.) a linear regression models. They may not *look* like linear regression models and even the formulas that we used, e.g., for t-test, do not look as if they have anything to do with linear regression, but they are. Here is a simple demonstration where I use the same code to generate data for running a t-test on a table. For a single two-level categorical variable, a t-test is equivalent to one-way ANOVA (note matching p-values).

```
yA <- rnorm(100, mean = 1, sd = 1)
yB <- rnorm(100, mean = yA + 0.1, sd = 1)
df_group <-
  tibble(y = c(yA, yB),
         group = factor(c(rep("A", 100), rep("B", 100))))
t.test(y ~ group, data = df_group)
```

```
##
##  Welch Two Sample t-test
##
## data:  y by group
## t = 0.24858, df = 180.05, p-value = 0.804
## alternative hypothesis: true difference in means between group A and group B is not
## 95 percent confidence interval:
##  -0.2663616  0.3431457
## sample estimates:
## mean in group A mean in group B
```

```
##       0.9997196       0.9613275
```

```
summary(aov(y ~ group, data = df_group))
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## group         1   0.07  0.0737   0.062  0.804
## Residuals   198 236.15  1.1927
```

However, we can ask R to show summary *as if* it was a linear model via `summary.lm()` function (`.lm` means that we call summary method for an `lm` linear model object). Again, note matching p-value for `group` parameter but also that now we can see the slope estimate for it.

```
summary.lm(aov(y ~ group, data = df_group))
```

```
##
## Call:
## aov(formula = y ~ group, data = df_group)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.15527 -0.76406 -0.05814  0.71729  2.95763
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.99972    0.10921   9.154   <2e-16 ***
## groupB      -0.03839    0.15444  -0.249    0.804
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.092 on 198 degrees of freedom
## Multiple R-squared:  0.000312,   Adjusted R-squared:  -0.004737
## F-statistic: 0.06179 on 1 and 198 DF,  p-value: 0.8039
```

The take home message here is that virtually all of the commonly used statistical analyses are linear regression custom tailored for a specific usage case and given a cool label. Because of that it might *look* like there are big differences between methods but in reality they differ mostly in kind (only categorical, only continuous, both) and number of variables, plus on which parameters you interpret and which you "ignore" as random effects. Again, this is a very large topic in itself and I can only encourage you once again to make a deeper dive in statistics via Statistical Rethinking book (or, if you a student at Uni Bamberg, join my seminar).

14.9 (Generalized) Linear Models

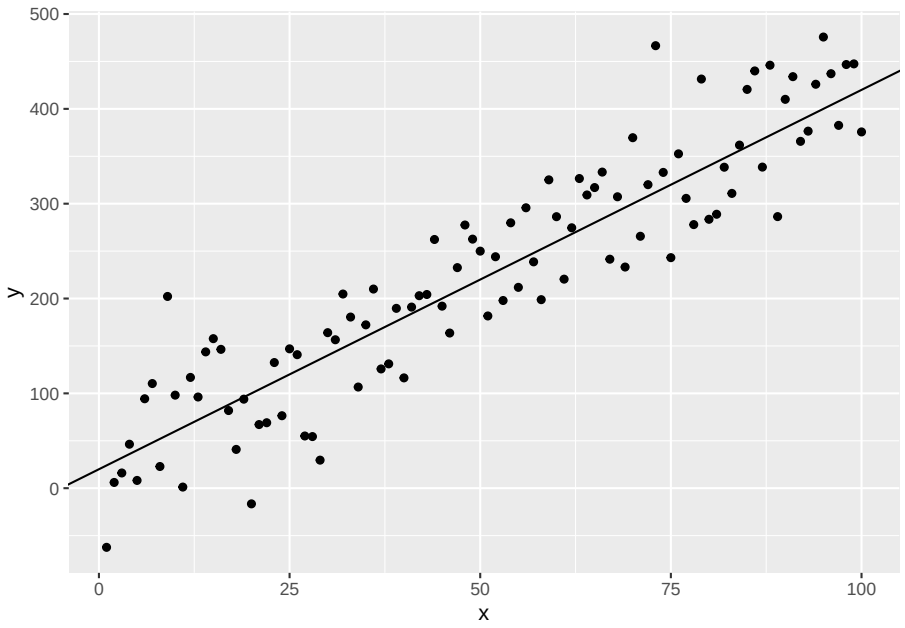
Base R provides function to perform linear regression lm() and generalized linear models glm() for binomial, count, and other types of data.

Let us generate a simple linear dependence between two parameters and see how `lm()` will infer the dependence. Our formula will be

$$y = 20 + 4 * x + \epsilon$$

where ϵ is normally distributed noise.

```
df_lm <-
  tibble(x = 1:100) %>%
  mutate(y = rnorm(n(), 20 + 4 * x, 50))
```



Now let us fit the linear model using formula `y ~ x` and use summary() function to see the details.

```
lm_fit <- lm(y ~ x, data=df_lm)
summary(lm_fit)
```

```
##
## Call:
## lm(formula = y ~ x, data = df_lm)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -117.254  -41.577    9.094   38.678  147.265
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  18.2680    10.4880   1.742   0.0847 .
## x             4.1241     0.1803  22.873   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 52.05 on 98 degrees of freedom
## Multiple R-squared:  0.8422, Adjusted R-squared:  0.8406
## F-statistic: 523.2 on 1 and 98 DF,  p-value: < 2.2e-16
```

As you can see, values for both intercept and the slope are very close to our original. If you need to extract information about individual coefficients, I recommend tidy() function from broom package that returns information about the model in a "tidy" format:

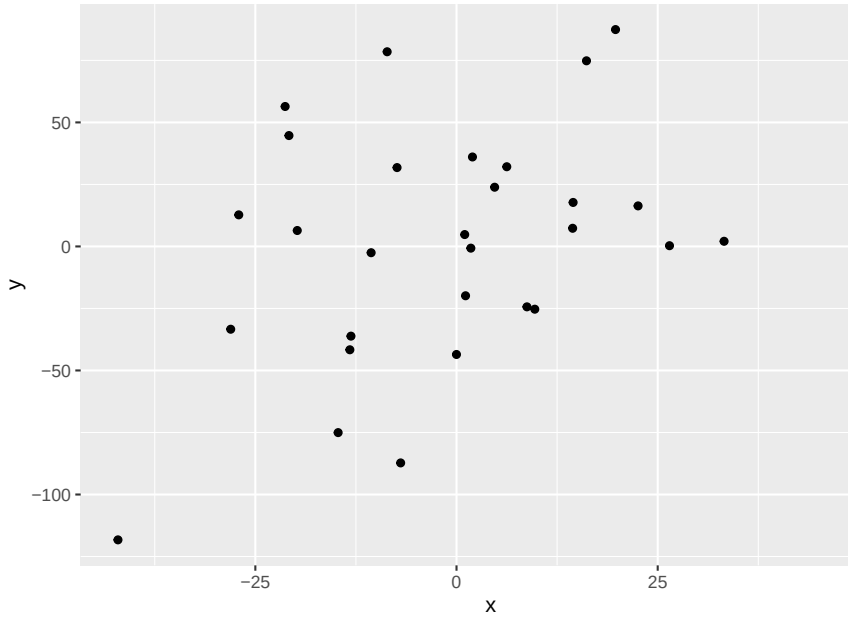
```
library(broom)
tidy(lm_fit)
```

term	estimate	std.error	statistic	p.value
(Intercept)	18.267956	10.4880101	1.741794	0.0846821
x	4.124118	0.1803059	22.872893	0.0000000

14.10 Resampling a linear model

same rules still apply when We perform linear regression explicitly as linear regression (and not packaged as some statistical test): We are not interested in estimates alone but in our confidence (uncertainty) about them and about probability of a null hypothesis (e.g., an actual parameter value is zero). lm() function produces analytically derived estimates based on the same idea of drawing (infinitely) more samples from the "true" distribution. Let us repeat the same resampling (for confidence interval) and permutation (for statistical significance) tricks.

Generate a table with data with 30 values for `x` drawn from a normal distribution with zero mean and standard deviation of 10. $y = 20 + 3 \cdot x + \epsilon$, where ϵ $Normal(0, 50)$, i.e., noise comes from a normal distribution centered at zero



with standard deviation of 50.

```
##
## Call:
## lm(formula = y ~ x, data = df_lm)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -83.317 -28.098  -4.514  30.695  84.269
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.7296     8.1681   0.212   0.8338
## x             0.8722     0.4153   2.100   0.0448 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 44.74 on 28 degrees of freedom
## Multiple R-squared:  0.1361, Adjusted R-squared:  0.1053
## F-statistic: 4.411 on 1 and 28 DF,  p-value: 0.04483
```

Our first task is to resample `x` and `y` pairwise (slice_sample() is one way to do this), fit lenear model to the resampled data, and extract coefficients via tidy(). Repeat that 1000 times to obtain a table with parameters and their estimates. There are different ways you can implement this. I have opted repeat it 1000 times via map_dfr() that combines all tidy coefficient tables into a single table by row. Note that there was no need from me to write a separate function,

as I have simply nested calls to tidy(), lm(), and slice_sample()). Once you have samples it is a simple task to compute confidence interval for `estimate` of each parameter (grouping data is easy, right?). To compare this to analytically estimated 95% confidence intervals that you can compute from a fitted linear model via confint() function.

term	Lower 95% CI	Upper 95% CI
(Intercept)	-13.0543641	16.209992
x	-0.0407846	1.749849

```
##                    2.5 %    97.5 %
## (Intercept) -15.00188381 18.461150
## x             0.02155481  1.722767
```

Do exercise 8.

Next stop, statistical significance for `x`. Our null hypothesis is that pairing of `x` and `y` in our data is accidental and the statistic (that characterizes the strength of the dependence) that we observed happened just by chance. We test this idea by permuting the `x` which results in different `x`×`y` pairs, fit the model and record statistic *for* x for that random pairing. Once we repeat this process 1000 times we have our distribution of statistic assuming that pairing between `x` and `y` is accidental. Next we only need to compute the proportion of absolute) statistic values that are more extreme than the absolute value of the original statistic. Note that as we permute `x`, our inference are applicable *only* to `x`. Thus, here we only need to record t value (statistic) for `x` and it could be more convenient to put them into a single vector. Extracting this information in R is a bit cumbersome. First, you need to get a summary(), then get a `$coef` attribute with a table of coefficients, and then get the *t value* for `x`. Here's how you do this step by step.

This gives you the summary:

```
summary(lm(y ~ x, df_lm))
```

```
##
## Call:
## lm(formula = y ~ x, data = df_lm)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -83.317 -28.098  -4.514  30.695  84.269
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.7296     8.1681   0.212   0.8338
## x             0.8722     0.4153   2.100   0.0448 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 44.74 on 28 degrees of freedom
## Multiple R-squared:  0.1361, Adjusted R-squared:  0.1053
## F-statistic: 4.411 on 1 and 28 DF,  p-value: 0.04483
```

This, only the coefficients table:

```
summary(lm(y ~ x, df_lm))$coef
```

```
##              Estimate Std. Error   t value   Pr(>|t|)
## (Intercept) 1.7296329  8.1680621 0.2117556 0.83383155
## x           0.8721608  0.4152524 2.1003149 0.04483337
```

This, a single value *t value* for `x`:

```
summary(lm(y ~ x, df_lm))$coef["x", "t value"]
```

```
## [1] 2.100315
```

This way, you can use replicate(), combining all *t values* from permuted-and-fitted models into a single vector. I have used 2000 replications to get a more accurate probability (but this does take more time, of course).

```
## Probability to observe more extreme t value by chance: 0.0485
```

```
##   Estimate Std. Error    t value   Pr(>|t|)
## 0.87216077 0.41525239 2.10031487 0.04483337
```

Do exercise 9.

14.11 (Generalized) Linear Mixed Models

Generalized linear mixed models allow you to incorporate information about random factors into the model. One of the most popular packages in R is lme4. Let us use LMM on data we generated for ANOVA. Here, we specify that we would like to have individual slopes for each participants via `(1|Participant)` notation[5].

```
library(lme4)
lmer_fit <- lmer(Response ~ Condition + (1|Participant), data=df_anova)
summary(lmer_fit)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: Response ~ Condition + (1 | Participant)
##    Data: df_anova
##
## REML criterion at convergence: 359.6
```

[5]Here, each participant must have their own intercept but they all share same single slope for `Condition`. You can also specify that they individual slopes that are either correlated or uncorrelated with their intercept.

```
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3188 -0.7330 -0.1038  0.8131  2.0589
##
## Random effects:
##  Groups      Name        Variance Std.Dev.
##  Participant (Intercept) 3.966    1.991
##  Residual                2.444    1.563
## Number of obs: 90, groups:  Participant, 10
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)   4.5005     0.6914   6.509
## ConditionB    1.8015     0.4037   4.463
## ConditionC    2.3561     0.4037   5.836
##
## Correlation of Fixed Effects:
##            (Intr) CndtnB
## ConditionB -0.292
## ConditionC -0.292  0.500
```

To get tidy summary you need to use function `tidy` but from broom.mixed library

```
library(broom.mixed)
tidy(lmer_fit)
```

effect	group	term	estimate	std.error	statistic
fixed	NA	(Intercept)	4.500512	0.6914189	6.509097
fixed	NA	ConditionB	1.801539	0.4036827	4.462760
fixed	NA	ConditionC	2.356092	0.4036827	5.836495
ran_pars	Participant	sd__(Intercept)	1.991432	NA	NA
ran_pars	Residual	sd__Observation	1.563456	NA	NA

To also get information about formal statistical significance, you can use an extension package lmerTest[6].

```
library(lmerTest)
lmert_fit <- lmerTest::lmer(Response ~ Condition + (1|Participant), data=df_anova)
summary(lmert_fit)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Response ~ Condition + (1 | Participant)
##    Data: df_anova
```

[6] I use `lmerTest::` to tell R that I need function `lmer()` from package `lmerTest` and not from `lme4` as before

```
##
## REML criterion at convergence: 359.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3188 -0.7330 -0.1038  0.8131  2.0589
##
## Random effects:
##  Groups      Name        Variance Std.Dev.
##  Participant (Intercept) 3.966    1.991
##  Residual                2.444    1.563
## Number of obs: 90, groups:  Participant, 10
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   4.5005     0.6914 11.4337   6.509 3.64e-05 ***
## ConditionB    1.8015     0.4037 78.0000   4.463 2.69e-05 ***
## ConditionC    2.3561     0.4037 78.0000   5.836 1.16e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) CndtnB
## ConditionB -0.292
## ConditionC -0.292  0.500
```

Again, we can use `tidy` to get coefficients information in a single table.

```
tidy(lmert_fit)
```

effect	group	term	estimate	std.error	statistic	df	p.value
fixed	NA	(Intercept)	4.500512	0.6914189	6.509097	11.43367	3.64e-05
fixed	NA	ConditionB	1.801539	0.4036827	4.462760	78.00000	2.69e-05
fixed	NA	ConditionC	2.356092	0.4036827	5.836495	78.00000	1.00e-07
ran_pars	Participant	sd__(Intercept)	1.991432	NA	NA	NA	NA
ran_pars	Residual	sd__Observation	1.563456	NA	NA	NA	NA

Note that `lmer()` functions provide information about difference of each condition to the baseline (condition `A`) not no ANOVA-style significance for the "overall" effect of condition. For this, you can use function drop1, which test for a variable significance by dropping it from a model and checking whether it performed significantly worse *without* it.

```
drop1(lmert_fit)
```

```
## Single term deletions using Satterthwaite's method:
##
## Model:
```

```
## Response ~ Condition + (1 | Participant)
##           Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Condition 91.042  45.521     2    78  18.623 2.446e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

You can also use Bayesian generalized linear modeling via rstanarm and BRMS packages. The former is somewhat faster, as it does not require model compilation (makes big difference when data is small but you test a lot of models), but is less flexible.

14.12 Disclaimer, repeated

The material above gives an *overview* of how to carry out statistical analysis in R but it is by no means exhaustive, nor deep enough to master it. I can only encourage you to again to learn a particular statistical analysis first, building an intuition of how it works and when it is valid, and only then to figure our which package and function in R can be used to run it.

Chapter 15

Practice

Today we will practice tidying up and plotting an almost real data. The *structure* of the table is real, I've used it precisely because it is a sort of messy, untidy data you often get. The *actual values* are, however, fake. Well, not fake, simulated! But that means that you should not use this particular data to make any inferences about Stroop task, which is what the original experiment was about.

Here is the back story. Once upon a time, an experiment with the Stroop task was performed. There four different conditions, one control one, of course. And a continuous physiological signal (similar to skin conductance) was measured at five time points: 0) sometime before the task, 1) right before the task, 2) after first block, 3) after the second block, 4) 15 minutes after the task. What we would like to establish:

- Did the task work in principle? I.e., do we see more errors and longer response times for when color and word were incongruent?
- Was there an effect of conditions on either the error count or response times?
- Was out physiological signal different at different time-points? Particularly, if we compare it before the task and after a congruent or incongruent blocks?

Download stroopsim.csv the table, read it, and read on to understand what individual columns mean and how we need to transform the table before it becomes usable. Create a markdown notebook yourself, make sure it is clearly structured!

sex	Condition	IncongruentFirst	@#errorsCong	ReactiontimemeanCong	@#errorsInco	Rea
2	0	0	2	1.477454	12	
2	1	0	1	2.028072	18	
1	2	0	1	1.334083	7	
2	0	0	2	1.171517	4	
2	1	0	0	2.097203	20	
2	2	0	2	1.322103	6	

15.1 Bad names to good names

We have a couple of columns that are not easy to use in R:

- `@#errorsCong` should be `errorsCongruent`
- `@#errorsInco` should be `errorsIncongruent`

sex	Condition	errorsCongruent	errorsIncongruent
2	0	2	12
2	1	1	18
1	2	1	7
2	0	2	4
2	1	0	20
2	2	2	6

15.2 Participant ID

Currently, we have a *wide* table with one row per participant. However, we will need to tidy it up, meaning that we need to keep track of which rows belong to which participants. For this, create a new column `HabitNr` which will simply have row index. To make things easier, use relocate() verb to make it the *first* column in the table.

HabitNr	sex	Condition	IncongruentFirst	errorsCongruent	ReactiontimemeanCong	errorsIn
1	2	0	0	2	1.477454	
2	2	1	0	1	2.028072	
3	1	2	0	1	1.334083	
4	2	0	0	2	1.171517	
5	2	1	0	0	2.097203	
6	2	2	0	2	1.322103	

15.3 Factors

Convert following columns to factors setting up useful labels.

- `sex`
  - 1 : `female`
  - 2 : `male`

- `Condition`:
  - 0 : `control`
  - 1 : `speed`
  - 2 : `size`
  - 3 : `random`
- `IncongruentFirst`
  - 0 : `Congruent first`
  - 1 : `Incongruent first`

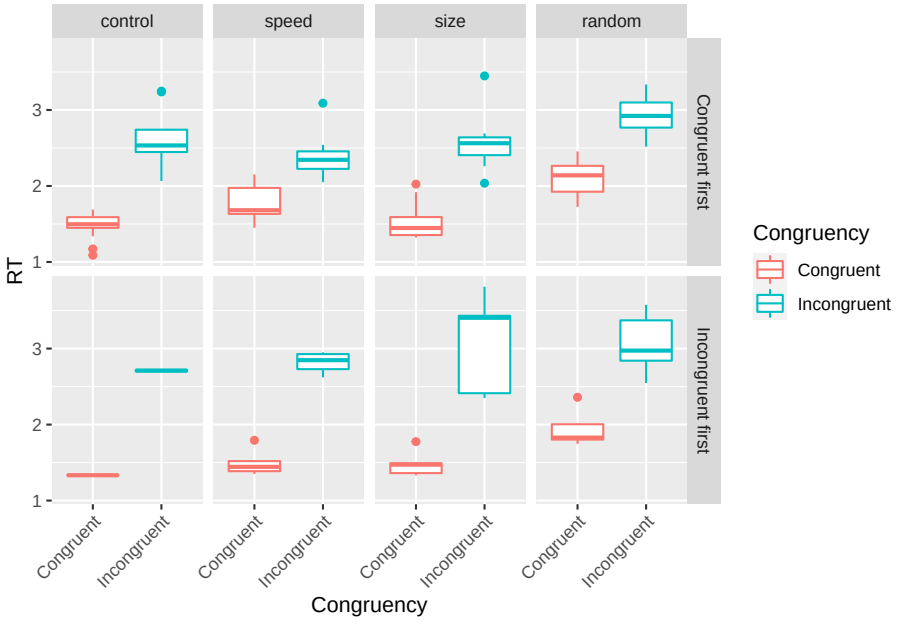
HabitNr	sex	Condition	IncongruentFirst	errorsCongruent	ReactiontimemeanCong	errorsIncongruen
1	male	control	Congruent first	2	1.477454	1
2	male	speed	Congruent first	1	2.028072	1
3	female	size	Congruent first	1	1.334083	
4	male	control	Congruent first	2	1.171517	
5	male	speed	Congruent first	0	2.097203	2
6	male	size	Congruent first	2	1.322103	

15.4 Response times

Next, we need to "spin-off" a separate table that will contain information about response times per congruency manipulation. Thus we want a table where column `Congruency` indicates whether presentation was congruent, whereas two columns (`ReactiontimemeanCong` and `ReactiontimemeanInco`) for response times become two rows (we pivot table longer). Note that I have used better labels for congruent and incongruent conditions. You can first rename them pivot or pivot and relabel (choice is yours). At the moment, we do not need all other columns, see table below to see what I decided to keep.

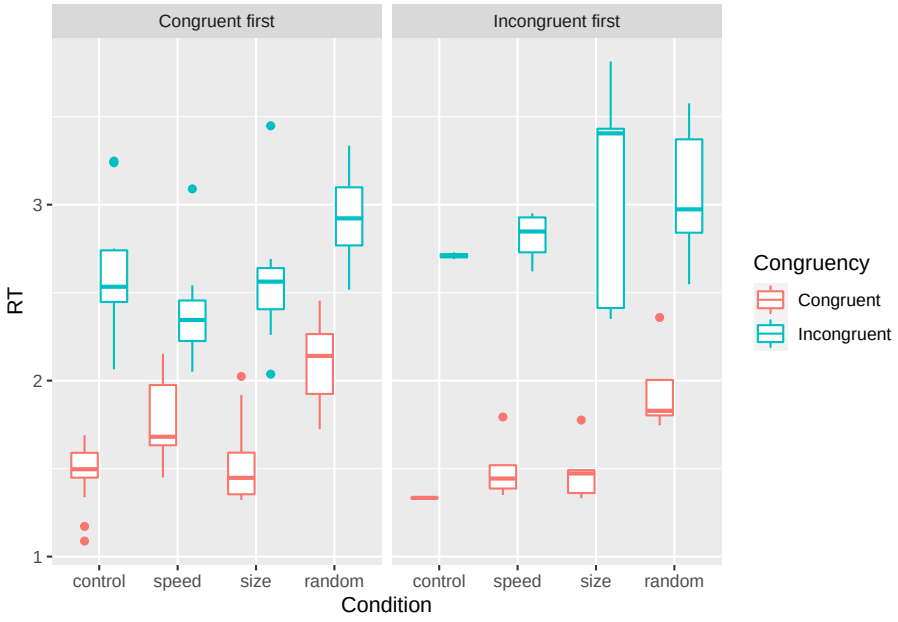
HabitNr	Condition	IncongruentFirst	Congruency	RT
1	control	Congruent first	Congruent	1.477454
1	control	Congruent first	Incongruent	3.247461
2	speed	Congruent first	Congruent	2.028072
2	speed	Congruent first	Incongruent	2.408471
3	size	Congruent first	Congruent	1.334083
3	size	Congruent first	Incongruent	2.676602

Let us see how condition and incongruency-order presentation affects our re-



sponse times.

Participants responses were clearly faster on trials when color and word were incongruent. But to better see the effect of condition, let us replot the data.



Now, we can that some conditions do appear to be different as well. Let us confirm this via statistics. We will use linear mixed models (thus, package

lmerTest) with `Condition`, `IncongruentFirst`, and `Congruency` as fixed effect, `HabitNr` (participant ID) as a random factor, and logarithm of RT as an outcome variable (using logarithm transformation on right skewed data as response times makes more symmetric). We will not look at any interactions although they are most likely of interest for the follow up analysis.

```
## boundary (singular) fit: see help('isSingular')
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: RT ~ Condition + IncongruentFirst + Congruency + (1 | HabitNr)
##    Data: rt
##
## REML criterion at convergence: 84
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.7862 -0.7005 -0.1239  0.4302  3.5893
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  HabitNr  (Intercept) 0.00000  0.0000
##  Residual             0.09852  0.3139
## Number of obs: 128, groups:  HabitNr, 64
##
## Fixed effects:
##                                    Estimate Std. Error        df t value
## (Intercept)                         1.51036    0.06423 122.00000  23.513
## Conditionspeed                      0.05433    0.07929 122.00000   0.685
## Conditionsize                       0.06613    0.07929 122.00000   0.834
## Conditionrandom                     0.45794    0.08204 122.00000   5.582
## IncongruentFirstIncongruent first   0.08994    0.06374 122.00000   1.411
## CongruencyIncongruent               1.02108    0.05549 122.00000  18.402
##                                   Pr(>|t|)
## (Intercept)                        < 2e-16 ***
## Conditionspeed                       0.495
## Conditionsize                        0.406
## Conditionrandom                   1.46e-07 ***
## IncongruentFirstIncongruent first    0.161
## CongruencyIncongruent              < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Cndtnsp Cndtnsz Cndtnr IncFIf
## Conditinspd -0.628
## Conditionsz -0.628  0.539
```

```
## Conditnrndm -0.603  0.525   0.525
## IncngrntFIf -0.132 -0.129  -0.129  -0.155
## CngrncyIncn -0.432  0.000   0.000   0.000  0.000
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')

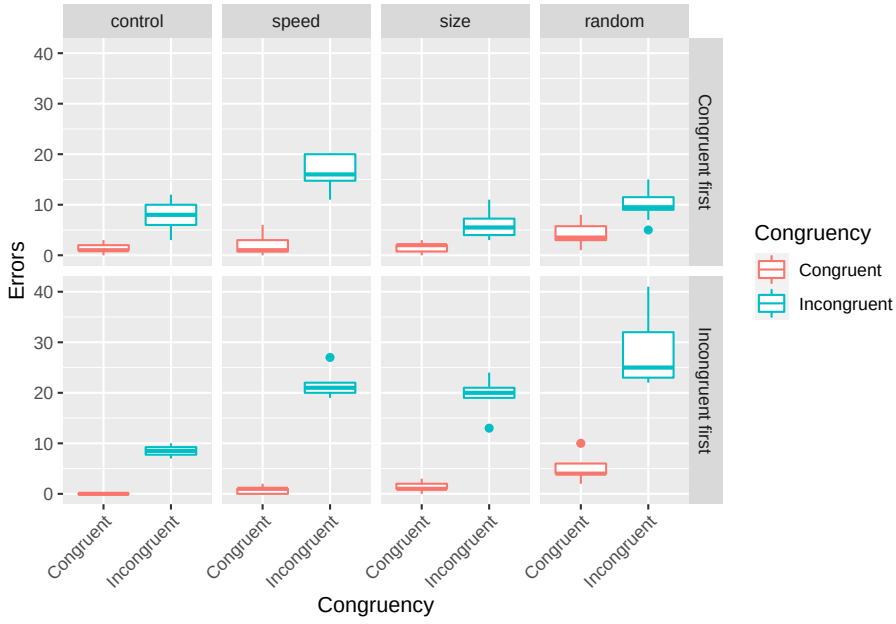

## Single term deletions using Satterthwaite's method:
##
## Model:
## RT ~ Condition + IncongruentFirst + Congruency + (1 | HabitNr)
##                  Sum Sq Mean Sq NumDF DenDF  F value    Pr(>F)
## Condition         4.012   1.337     3   122  13.5728 1.065e-07 ***
## IncongruentFirst  0.196   0.196     1   122   1.9911    0.1608
## Congruency       33.363  33.363     1   122 338.6302 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In short, we a highly significant effect of color-word congruency (good news, otherwise out Stroop task wasn't very successful) and one condition (*random*) is clear difference. However, the *order* of block (first congruent then incongruent or vice versa) did not really matter.

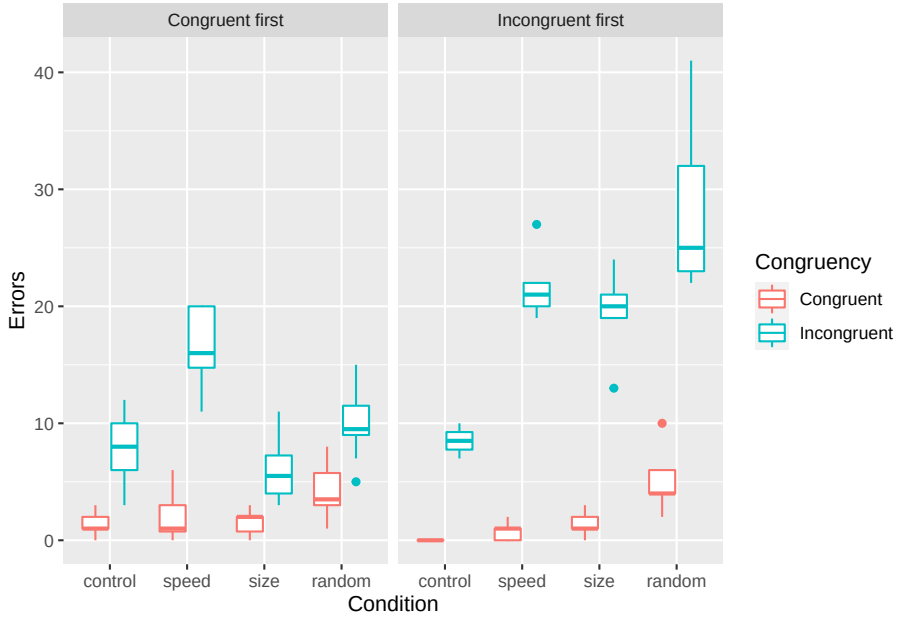
15.5 Accuracy

Now let us perform the same analysis but on correct response count. What you need to know is that there were 120 trials in total for each block. We have information about *errors* not *correct responses* but it makes no difference for analysis, only for model interpretation. Extract column and pivot table same way as you did with response times.

HabitNr	Condition	IncongruentFirst	Congruency	Errors
1	control	Congruent first	Congruent	2
1	control	Congruent first	Incongruent	12
2	speed	Congruent first	Congruent	1
2	speed	Congruent first	Incongruent	18
3	size	Congruent first	Congruent	1
3	size	Congruent first	Incongruent	7



Again, let us plot data both ways



Plots are very similar to those for response times. So let us perform the statistical analysis. This is a binomial data, so many errors per 120 trials, so use `glmer()` function (generalized linear mixed model) from `lme4` package with binomial family.

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(Errors, 120) ~ Condition + IncongruentFirst + Congruency +
##     (1 | HabitNr)
##    Data: errors
##
##      AIC      BIC   logLik deviance df.resid
##    608.9    628.9   -297.5    594.9      121
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1050 -0.8816 -0.1543  0.7427  3.5440
##
## Random effects:
##  Groups  Name        Variance Std.Dev.
##  HabitNr (Intercept) 0.02038  0.1428
## Number of obs: 128, groups:  HabitNr, 64
##
## Fixed effects:
##                                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)                      -4.64135    0.12575 -36.908  < 2e-16 ***
## Conditionspeed                    0.63983    0.11812   5.417 6.07e-08 ***
## Conditionsize                     0.07082    0.12845   0.551    0.581
## Conditionrandom                   0.65101    0.12174   5.348 8.91e-08 ***
## IncongruentFirstIncongruent first 0.59263    0.08209   7.219 5.24e-13 ***
## CongruencyIncongruent             1.82114    0.09439  19.295  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Cndtnsp Cndtnsz Cndtnr IncFIf
## Conditinspd -0.600
## Conditionsz -0.542  0.615
## Conditnrndm -0.575  0.651   0.615
## IncngrntFIf -0.120 -0.124  -0.154  -0.178
## CngrncyIncn -0.642  0.004   0.000   0.008  0.005

## Single term deletions
##
## Model:
## cbind(Errors, 120) ~ Condition + IncongruentFirst + Congruency +
##     (1 | HabitNr)
##                  npar     AIC    LRT   Pr(Chi)
## <none>                 608.92
## Condition           3  646.37  43.45 1.971e-09 ***
```

```
## IncongruentFirst    1  643.42  36.50 1.524e-09 ***
## Congruency          1 1132.52 525.60 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In comparison to response times, even the block order makes the difference with more errors if incongruent condition was presented first. For errors, `speed` condition was different from the `control` baseline. However, `size` conditions appears to be very boring, as we see no difference in neither error rate nor response times.

15.6 Physiological signal

Now we come to the tricky part because information about physiological signal (I'll call is PS for short) is stored in columns `S0A` till `S4A` for some participant but in columns `Bs0` till `Bs4` for others. I.e., `S0A` codes the same information as `Bs0`, `S1A` same as `Bs1`, etc. The digit indicates the measurement time point. How can we fix this? Either using `ifelse()` or by splitting table by rows, converting each to a common long format and then merging them. For didactic purposes, we will do both!

In case of ifelse() solution, let us store everything in first set of columns but overwrite their value only if they have `NA`. So, `S0A` is not `NA`, you leave it alone, otherwise you overwrite it with a value from `Bs0`. Here is the end-product (store data in a separate new table `clean_results`, so you can work on the original later again).

HabitNr	S0A	S1A	S2A	S3A	S4A	Bs0	Bs1	Bs2	B
1	6.490969	4.564023	6.354532	5.224722	12.339243	6.490969	4.564023	6.354532	5.2247
2	4.864416	7.957840	6.587935	3.044139	2.909219	4.864416	7.957840	6.587935	3.0441
3	10.071530	1.650143	1.562964	6.156831	8.045311	10.071530	1.650143	1.562964	6.1568
4	12.162085	4.796817	2.649034	2.019965	5.061974	12.162085	4.796817	2.649034	2.0199
5	3.265458	7.900660	4.254162	16.426251	6.177225	3.265458	7.900660	4.254162	16.4262
6	5.478926	5.845528	6.175421	4.388986	2.740655	5.478926	5.845528	6.175421	4.3889

The alternative is more challenging but still fairly straightforward. First, let us spin-off two separate tables. One which has valid values for `S0A`:`S4A` dropping all the rows when they are `NA`. And, conversely, the other table that has valid values for columns `Bs0`:`Bs4`. Then, pivot each table longer (we need to do this anyhow) and recode labels to `t0` till `t4`. After that we can merge two tables by rows via `bind_rows`.

Here is the first table after filtering

HabitNr	sex	Condition	IncongruentFirst	errorsCongruent	ReactiontimemeanCong	erro
31	female	control	Congruent first	0	1.589768	
32	female	control	Incongruent first	0	1.331935	
33	male	size	Incongruent first	3	1.331964	
34	male	speed	Incongruent first	0	1.443712	
35	male	random	Congruent first	3	2.052467	
36	male	size	Congruent first	3	1.404922	

And here it is pivoted

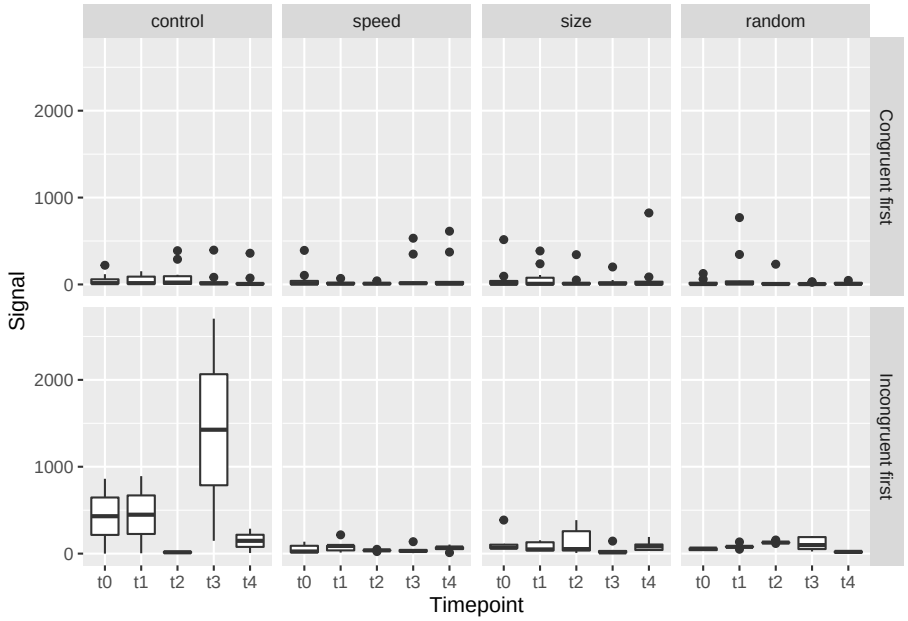
HabitNr	Condition	IncongruentFirst	Timepoint	Signal
31	control	Congruent first	t0	61.92695
31	control	Congruent first	t1	130.66799
31	control	Congruent first	t2	111.63928
31	control	Congruent first	t3	82.54038
31	control	Congruent first	t4	73.56076
32	control	Incongruent first	t0	861.35340

Again, same procedure for rows with valid `Bs0:Bs4` columns

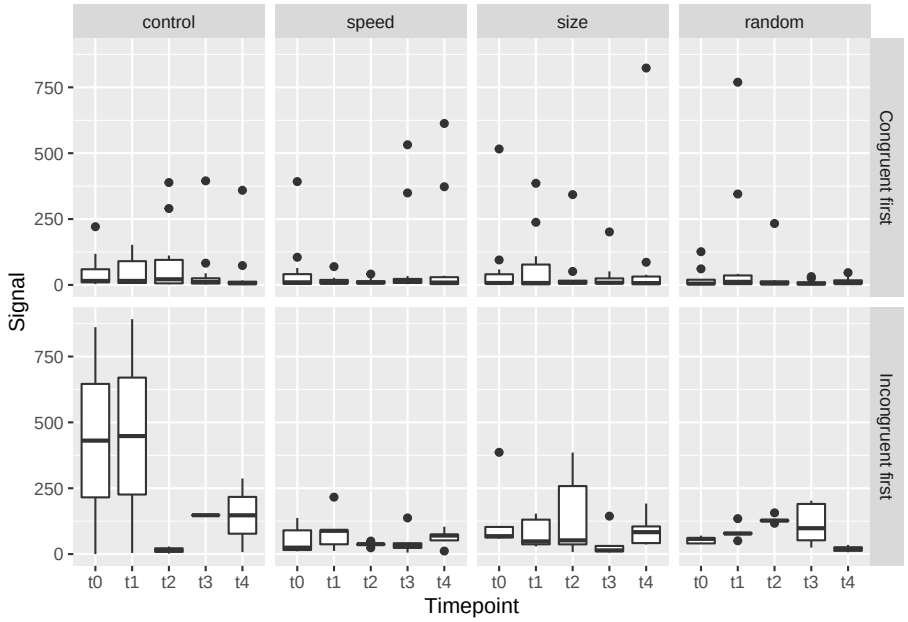
HabitNr	Condition	IncongruentFirst	Timepoint	Signal
1	control	Congruent first	t0	6.490969
1	control	Congruent first	t1	4.564023
1	control	Congruent first	t2	6.354532
1	control	Congruent first	t3	5.224722
1	control	Congruent first	t4	12.339243
2	speed	Congruent first	t0	4.864416

Once you merged two tables by rows (see bind_rows()).

let us take a look at the results.



There seems to be clear outliers, so let us drop all values above 1000 (filter inside the ggplot call) and plot again



Well, certainly hard to tell, so no clear and consistent effect. Still, let us do stats via linear mixed models.

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Signal ~ Timepoint + Condition + IncongruentFirst + (1 | HabitNr)
##    Data: signal
##
## REML criterion at convergence: 4184.7
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.0989 -0.2701 -0.1293 -0.0072 12.6054
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  HabitNr  (Intercept)  3774     61.43
##  Residual             33352    182.63
## Number of obs: 320, groups:  HabitNr, 64
##
## Fixed effects:
##                                    Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)                          95.282     33.593 137.344   2.836  0.00525
## Timepointt1                          10.906     32.284 252.000   0.338  0.73578
## Timepointt2                         -11.969     32.284 252.000  -0.371  0.71113
## Timepointt3                          25.524     32.284 252.000   0.791  0.42991
## Timepointt4                          -6.173     32.284 252.000  -0.191  0.84851
## Conditionspeed                      -71.414     36.510  59.000  -1.956  0.05520
## Conditionsize                       -55.042     36.510  59.000  -1.508  0.13699
## Conditionrandom                     -75.083     37.776  59.000  -1.988  0.05151
## IncongruentFirstIncongruent first    88.443     29.349  59.000   3.013  0.00380
##
## (Intercept)                         **
## Timepointt1
## Timepointt2
## Timepointt3
## Timepointt4
## Conditionspeed                      .
## Conditionsize
## Conditionrandom                     .
## IncongruentFirstIncongruent first **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Tmpnt1 Tmpnt2 Tmpnt3 Tmpnt4 Cndtnsp Cndtnsz Cndtnr
## Timepointt1 -0.481
## Timepointt2 -0.481  0.500
## Timepointt3 -0.481  0.500  0.500
```

```
## Timepointt4 -0.481  0.500  0.500  0.500
## Conditinspd -0.553  0.000  0.000  0.000  0.000
## Conditionsz -0.553  0.000  0.000  0.000  0.000  0.539
## Conditnrndm -0.531  0.000  0.000  0.000  0.000  0.525   0.525
## IncngrntFIf -0.116  0.000  0.000  0.000  0.000 -0.129  -0.129  -0.155
```

```
## Single term deletions using Satterthwaite's method:
##
## Model:
## Signal ~ Timepoint + Condition + IncongruentFirst + (1 | HabitNr)
##                   Sum Sq Mean Sq NumDF DenDF F value   Pr(>F)
## Timepoint          56635   14159     4   252  0.4245 0.790883
## Condition         171033   57011     3    59  1.7094 0.174862
## IncongruentFirst 302871  302871     1    59  9.0810 0.003802 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

15.7 Wrap up

That's it for today but realistically, this is still an oversimplified version of the analysis. The original study had many more predictors and even here, there is likely to be an interaction between time point and whether congruent or incongruent condition was presented first.