

Data analysis using R for Psychology and Social Science

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2021-12-14

Contents

Introduction	9
Why R?	9
Why Tidyverse	10
About the seminar	11
Thinking like a computer	11
About the material	12
 Software	 13
0.1 Installing R	13
0.2 Installing R-Studio	13
0.3 Installing RTools	13
Installing packages	14
0.4 Minimal set of packages	15
0.5 Keeping R and packages up-to-date	16
 1 Reproducible Research: Projects and RMarkdown Notebooks	 17
1.1 Projects	17
1.2 RMarkdown	19
1.3 Exercise	22
 2 Vectors! Vectors everywhere!	 23
2.1 Variables as boxes	23
2.2 Assignment statement in detail	24
2.3 Vectors and singular values (scalars, which are also vectors) . . .	25

2.4	Vector indexes (subsetting)	28
2.5	Names as an Index	30
2.6	Slicing	32
2.7	Colon Operator and Sequence Generation	34
2.8	Working with two vectors of <i>equal</i> length	35
2.9	Working with two vectors of <i>different</i> length	35
2.10	Applying functions to a vector	37
2.11	Wrap up	38
3	Tables and Tibbles (and Tribbles)	39
3.1	Primary data types	39
3.2	All vector values must be of the same type	41
3.3	Lists	41
3.4	Subsetting, a fuller version	41
3.5	Yet another subsetting via <code>\$</code>	46
3.6	Tables, a.k.a. data frames	47
3.7	Subsetting tables	49
3.8	Using libraries	52
3.9	Tibble, a better data.frame	54
3.10	Tribble, table from text	55
3.11	Reading example tables	55
3.12	Reading csv files	56
3.13	Reading Excel files	59
3.14	Reading files from other programs	60
3.15	Writing and reading a single object	61
3.16	Wrap up	61
4	Functions! Functions everywhere!	63
4.1	Functions	63
4.2	Writing a function	65
4.3	Scopes: Global versus Local variables	67
4.4	Function with two parameters	69

<i>CONTENTS</i>	5
4.5 Table as a parameter	69
4.6 Named versus positional arguments	70
4.7 Default values	71
4.8 Nested calls	71
4.9 Piping	72
4.10 Function is just a code stored in a variable	73
4.11 Functions! Functions everywhere!	74
4.12 Using (or not using) explicit return statement	74
5 Grammar of Graphics	77
5.1 Tidy data	77
5.2 ggplot2	79
5.3 Auto efficiency: continuous x-axis	86
5.4 Auto efficiency: discrete x-axis	87
5.5 Mammals sleep: single variable	88
5.6 Mapping for all visuals versus just one visual	89
5.7 Mapping on variables versus constants	89
5.8 Themes	90
5.9 You ain't seen nothing yet	90
5.10 Further reading	90
5.11 Extending ggplot2	90
5.12 ggplot2 cannot do everything	90
6 Tidyverse: dplyr	93
6.1 Tidyverse philosophy	93
6.2 <code>select()</code> columns by name	94
6.3 Conditions	98
6.4 Logical indexing	99
6.5 <code>filter()</code> rows by values	100
6.6 <code>arrange()</code> rows in a particular order	101
6.7 <code>mutate()</code> columns	102
6.8 <code>summarize()</code> table by <code>groups</code>	104

6.9	Putting it all together	108
6.10	Should I use Tidyverse?	108
7	Working with Factors	109
7.1	How to write code	109
7.2	Implementing a typical analysis	110
7.3	Factors	112
7.4	Forcats	114
7.5	Plotting group averages	116
7.6	Plotting our confidence in group averages via quantiles	119
7.7	Looking at similarity	121
8	Glueing and sprinting	123
8.1	Comparing effect between two studies	123
8.2	Gluing in correlation strength information.	125
8.3	sprintf	126
8.4	Wrap up	127
9	Tidying your data: joins and pivots	129
9.1	Joining tables	129
9.2	Pivoting	136
9.3	Pivot longer	136
9.4	Pivot wider	142
10	Controlling computation flow	147
10.1	rep()	147
10.2	Repeating combinations	148
10.3	For loop	149
10.4	Conditional statement	151
10.5	Breaking out of the loop	154
10.6	Using for loop to load and join multiple data files	155
10.7	Apply	156
10.8	Purrr	157

11 Statistical modeling	159
11.1 Formula notation	160
11.2 Correlation	160
11.3 Pairwise comparisons	162
11.4 ANOVA	165
11.5 (Generalized) Linear Models	167
11.6 (Generalized) Linear Mixed Models	169
11.7 Practice	172
 12 Practice	 185
12.1 Bad names to good names	186
12.2 Participant ID	186
12.3 Factors	186
12.4 Response times	187
12.5 Accuracy	190
12.6 Physiological signal	193
12.7 Wrap up	197

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 that¹ but, unfortunately, philosophy of R is about have 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 one². 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. I will mention some widely used packages and functions for performing statistical analysis but I will not go into the details of how they work or how to interpret their output. 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 analysis that we will perform using Python

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

²Talking from a personal experience here.

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 methods (my impression is that even Python is lagging behind it in that respect).

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 R³. 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 re-implements 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. 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.

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 an overpowered `summarise()` function, a warning generated by `readr` package was adapted for humans but now require an extra step to be used for column specification, 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.

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

⁴Just ask about “base R vs. Tidyverse” on Twitter and see the thread set itself on fire

About the seminar

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

The material is **free to use** and is licensed under the Creative Commons Attribution-NonCommercial-NoDerivatives V4.0 International License.

Software

0.1 Installing R

Go to r-project.org and download a current stable version of R for your platform. Run the installer, accepting all defaults. The installer will ask you whether you also want a 32-bit version to be installed alongside 64-bit. You probably won't need 32-bit, so if space is at premium you can skip it. Otherwise, it will make very little difference.

0.2 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.

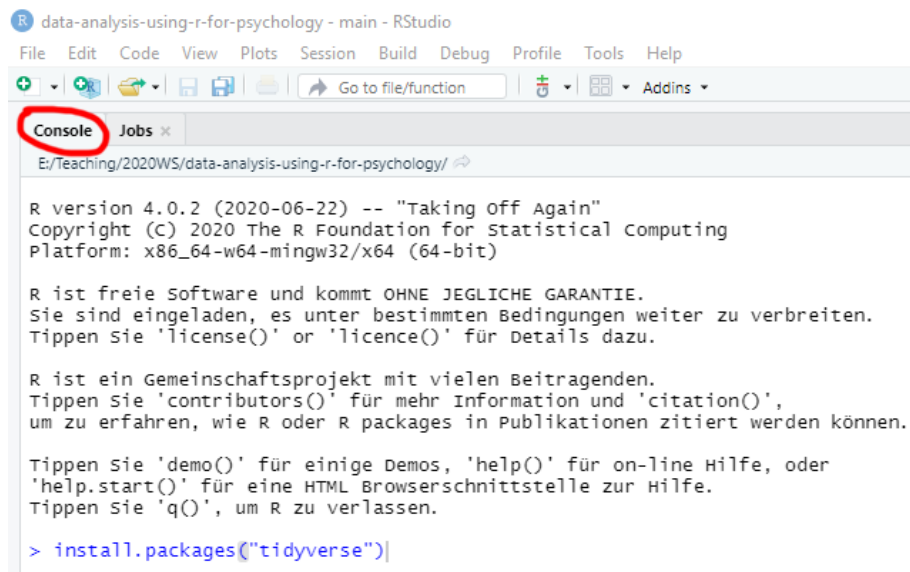
0.3 Installing RTools

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 at 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**.

The image is a screenshot of the RStudio application window. The title bar reads "data-analysis-using-r-for-psychology - main - RStudio". The menu bar includes File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, and Help. The toolbar contains various icons for file operations and running code. The "Console" tab is selected and highlighted with a red circle. The console output shows the R version (4.0.2), copyright information, and German text about the software's license and community. At the bottom, the command `> install.packages("tidyverse")` has been entered.

```
R version 4.0.2 (2020-06-22) -- "Taking off Again"
Copyright (C) 2020 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

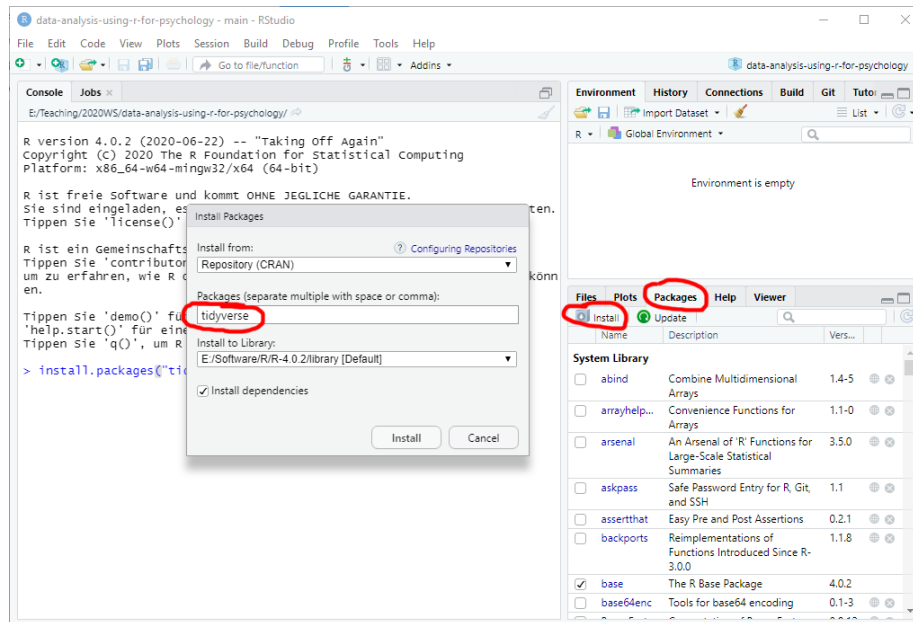
R ist freie Software und kommt OHNE JEGliche GARANTIE.
Sie sind eingeladen, es unter bestimmten Bedingungen weiter zu verbreiten.
Tippen Sie 'license()' or 'licence()' für Details dazu.

R ist ein Gemeinschaftsprojekt mit vielen Beitragenden.
Tippen Sie 'contributors()' für mehr Information und 'citation()',
um zu erfahren, wie R oder R packages in Publikationen zitiert werden können.

Tippen Sie 'demo()' für einige Demos, 'help()' für on-line Hilfe, oder
'help.start()' für eine HTML Browserschnittstelle zur Hilfe.
Tippen Sie 'q()', um R zu verlassen.

> install.packages("tidyverse")
```

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 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 (also make sure it is *x64*). Then, I use `install.packages()` to install and update everything I need.

0.4 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.

0.5 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

Reproducible Research: Projects and RMarkdown Notebooks

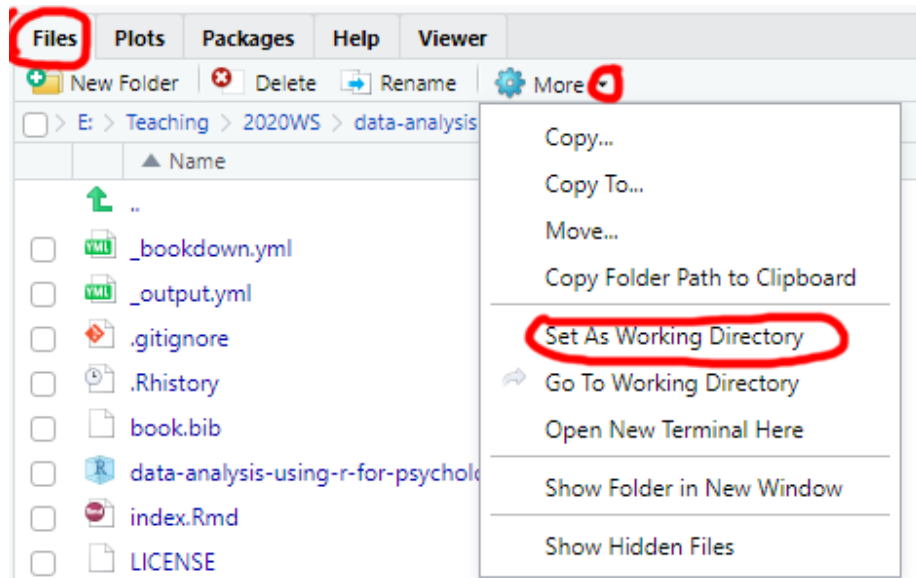
Our aim is to create reproducible research and analysis. It is a crucial component of the open science movement but is even more important for your own research or study projects. You want to create a self-contained well-documented easy-to-understand reproducible analysis. A complete self-sufficient 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.

1.1 Projects

One of the most annoying features of R is that 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 (something we won't talk about just yet). 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 `the.Rproj` file in that folder.

1.2 RMarkdown

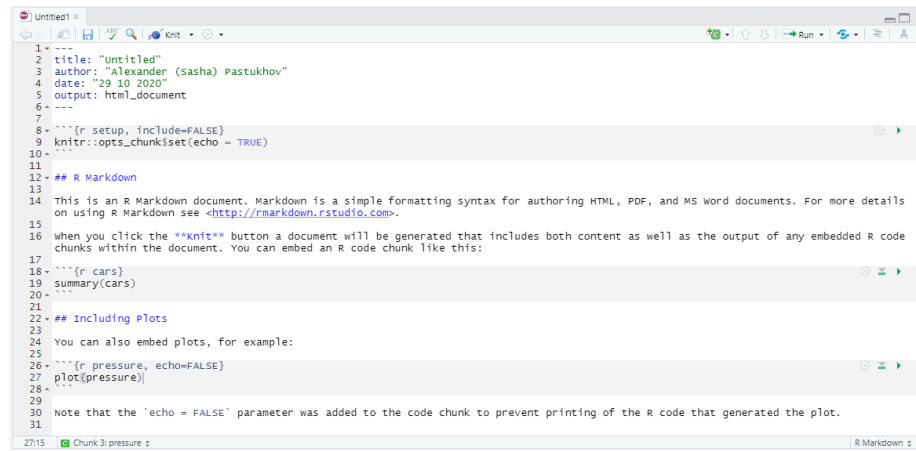
RMarkdown notebooks combine formatted text, figures, references (via bibtex) and cross-references with code¹. When a notebook is knitted, all the code is ran and its output, such as tables and figures, is inserted into the final document. This allows you to combine the narrative (the background, the methodology, comments, discussion, conclusions, etc.) with the actual code that implements what you described.

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 design 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 / 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 **.Rmd** extension automatically). The file you created is not empty, as R Studio is kind 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).

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



Let us go through the default notebook that R Studio created for us.

```

1 ---
2 title: "Untitled"
3 author: "Alexander (Sasha) Pastukhov"
4 date: "29 10 2020"
5 output: html_document
6 ---

```

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.

```

8 ```{r setup, include=FALSE}
9 knitr::opts_chunkset(echo = TRUE)
10 ```

```

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).

```

12 ## R Markdown
13
14 This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS word documents. For more details
15 on using R Markdown see <http://rmarkdown.rstudio.com>.
16
17 When you click the "Knit" button a document will be generated that includes both content as well as the output of any embedded R code
18 chunks within the document. You can embed an R code chunk like this:

```

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.

```

18 ```{r cars}
19 summary(cars)
20 ```
21

```

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 second 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.

```

26 ```{r, pressure_echo=FALSE}
27
28 # Untitled
29
30 # Chunk 1: setup
31
32 # R Markdown
33
34 # Chunk 2: cars
35
36 # Including Plots
37
38 # Chunk 3: pressure
39

```

= FALSE' parameter was added to the code chunk to prevent printing of the R code that generated the plot.

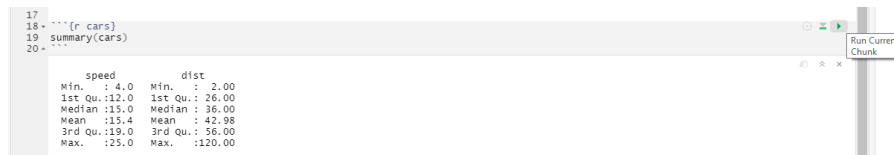
There are additional options that you can specify per chunk (whether to run the code, to show the output, what size the figures should be, etc.). Generally we won't need these options but you can get an idea about them by looking at the official manual. You can create a chunk by hand or click on “Create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

```

1 # Untitled1
2
3 title: "Untitled"
4 author: "Alexander (Sasha) Pastukhov"
5 date: "29 10 2020"
6 output: html_document
7
8 ```{r setup, include=FALSE}
9 knitr::opts_chunk$set(echo = TRUE)
10 ```
11
12 ## R Markdown
13

```

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.



```

17.  ...
18.  ```{r cars}
19.  summary(cars)
20.  ...

```

speed		dist	
Min. : 4.0	Min. : 2.00		
1st Qu.:12.0	1st Qu.: 26.00		
Median :15.0	Median : 36.00		
Mean :15.4	Mean : 42.98		
3rd Qu.:19.0	3rd Qu.: 56.00		
Max. :25.0	Max. :120.00		

1.3 Exercise

For the today's exercise, I want you to familiarize yourself with markdown. 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 file to MS Teams.

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” concept 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
```


2.3. VECTORS AND SINGULAR VALUES (SCALARS, WHICH ARE ALSO VECTORS)²⁵

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 is 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)!

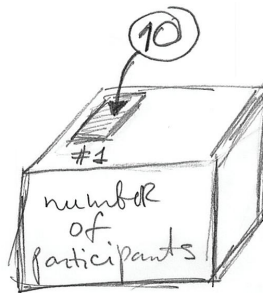
Do exercise 1.

2.3 Vectors and singular 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 #1². Therefore, the example above `number_of_participants <- 10` creates a *vector* variable with one (1) slot and stores the value in it.

¹Multiplication 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.

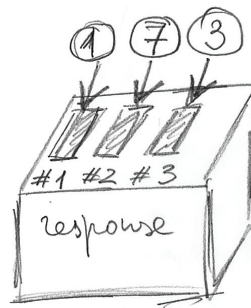
²If you have experience with programming languages like Python, C, or Java: indexes in R start with 1, not with 0.



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 concatenating (or combining) values³. The figure below illustrates the idea:



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
```

³I 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.

2.3. VECTORS AND SINGULAR VALUES (SCALARS, WHICH ARE ALSO VECTORS)²⁷

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

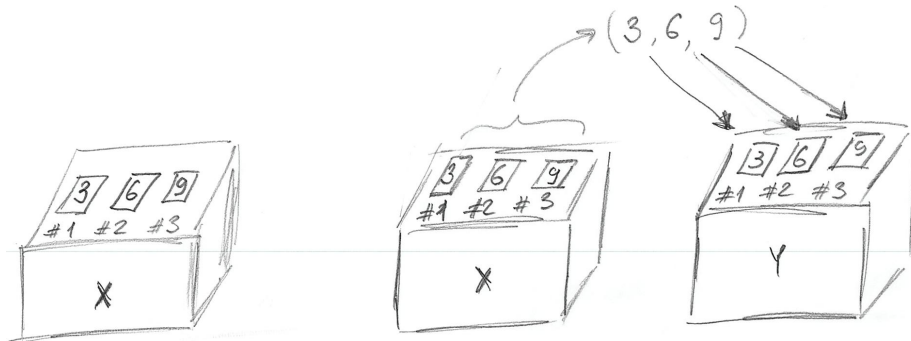
```
x <- c(3, 6, 9)
y <- x
print(x)
```

```
## [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 may⁴ catch you by surprise. Or, even worse, you will not even notice that your indexing does not work and screws 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).

⁴Who am I kidding? Will!

```
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 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 rest⁵.

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

```
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 `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 nor 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 guess 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.

```
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:

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

```
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 repeated N -times (where $N = \text{length}(\text{longer vector}) / \text{length}(\text{shorter vector})$) and this length-matched vector is then used for the mathematical operation. 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 $N = \text{ceiling}(\text{length}(\text{longer vector})/\text{length}(\text{shorter vector}))$ (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 vector⁷.

⁷No idea!

```
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.

```
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 everything¹ 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 `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

¹Terms and conditions apply.

' 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 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 if 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.

²Be 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)[#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 objects³. 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 you requested *as is*. I.e., if you used them to access part of a vector, you get a vector. If you used them to access a list or a table, you get a list or a table.

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

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 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 a 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.

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

```
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.
ex ”

```
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 indexes.

```
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 content⁵ but just `NULL` for simplifying one (`[]`). And none of them will generate an error.

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

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

⁵And `NA` as a name. Don't ask.

```
1[["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 the 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
```

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

```
## NULL
```

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

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

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

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

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

3.6 Tables, a.k.a. data frames

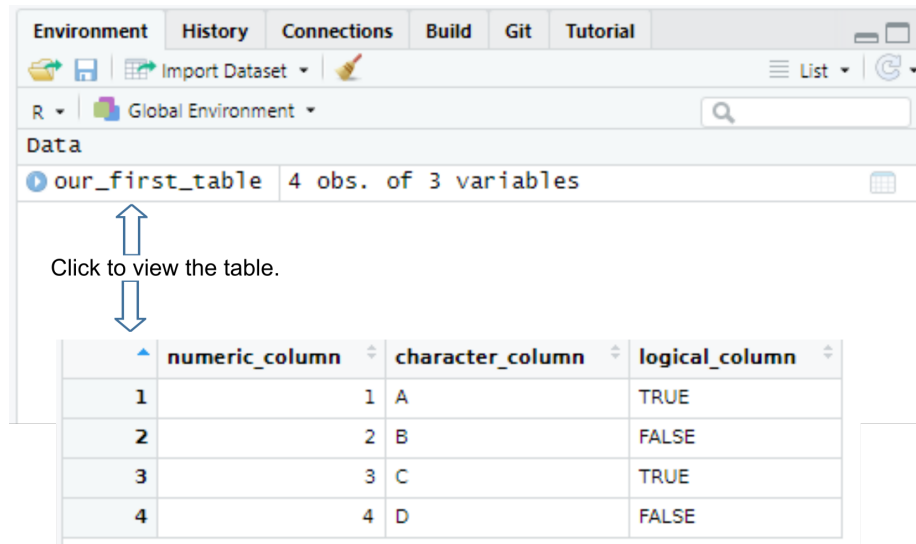
R tables are a mix between lists and matrices. You can think about it as a list of vectors (columns) of *identical* length. The default way to construct a table, which are called *data frames* in R, is via `data.frame()` function.

```
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()`).



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 *multiple-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_table\$N
the_table[[1]]
the_table[["N"]]

1 2 3 4 5

The only new thing is that, because tables are two-dimensional, 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 -> this gives you a VECTOR
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
```

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[2,] →

	N	C	L
1	2	B	FALSE

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[2:3, 1:2] →

	N	C
1	2	B
2	3	C

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. For that you use `library()` function (it has a sister function `require()` but it should be used inside functions and packages not in scripts or notebooks). 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 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)⁶. 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'
```

⁶There is also a filter function in stats library.

```
## 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
##       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 *setup* chunk of the notebook. 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 `$` notation⁷.

```
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
```

```
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.

⁷Arbitrariness strikes again! But this also means that `$` is safer to use with tibbles but not with data.frames.

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

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

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?). 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 libraries, 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 save-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

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

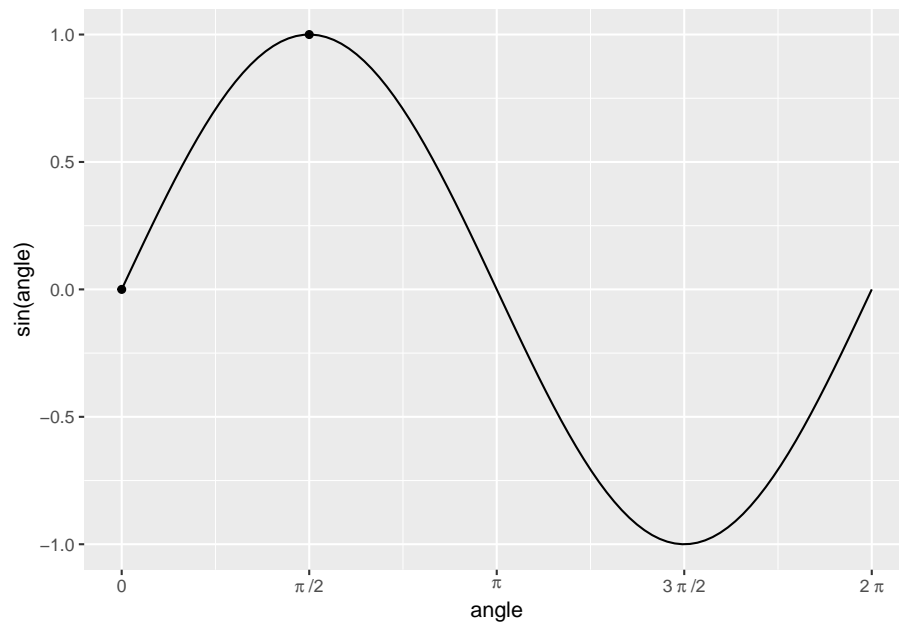
Functions! Functions everywhere!

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 value¹. 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.

¹Function 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
```

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

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))
```

```
## [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 zero³, 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 name⁴ 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

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

⁴`double_or_nothing?`

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 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 formula⁵ is

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

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

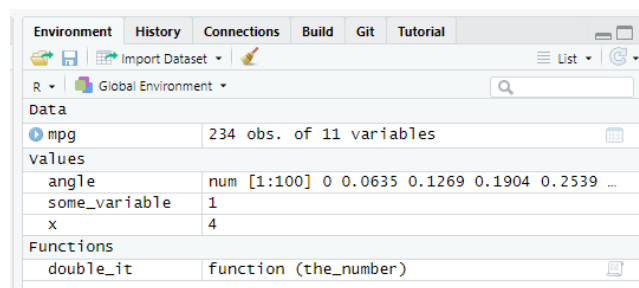
Do exercise 3

⁵Hint: Constants

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 its 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 there. You can see what you have in the global scope at any time by looking at *Environment* tab (note the *Global Environment* tag).



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 its 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* variables⁶. 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

⁶You 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 it depends not only on local things but on global variables that may or may not be where at any given moment.

⁷These rules — a **copy** of a global scope is accessible inside a function but function scope

```

# 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}"))

  # 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 itself.
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.

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.

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 tables⁹. Let us use `mpg` table from the *ggplot2* package. Write 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 else¹⁰. 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.

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

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

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

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 like¹¹. Despite all the flexibility 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.

¹¹That 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 and, at the same time, create an error that is really hard to find.

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 most 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 simply 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.

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_radians
sin(angle_in_radians) # returns 1
```

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

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

```
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 variables¹³ 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) 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
```

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: `.`, which is a hidden¹⁴ temporary

¹³The 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.

¹⁴As in: It won't show up in your Global Environment tab.

variable that holds the value you are piping through via `%>%`¹⁵. 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* 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 you learn about bootstrapping (needs data and a function) or about applying/mapping functions to data.

¹⁵Yes, 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.

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

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 be 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 be 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.Attractiveness
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

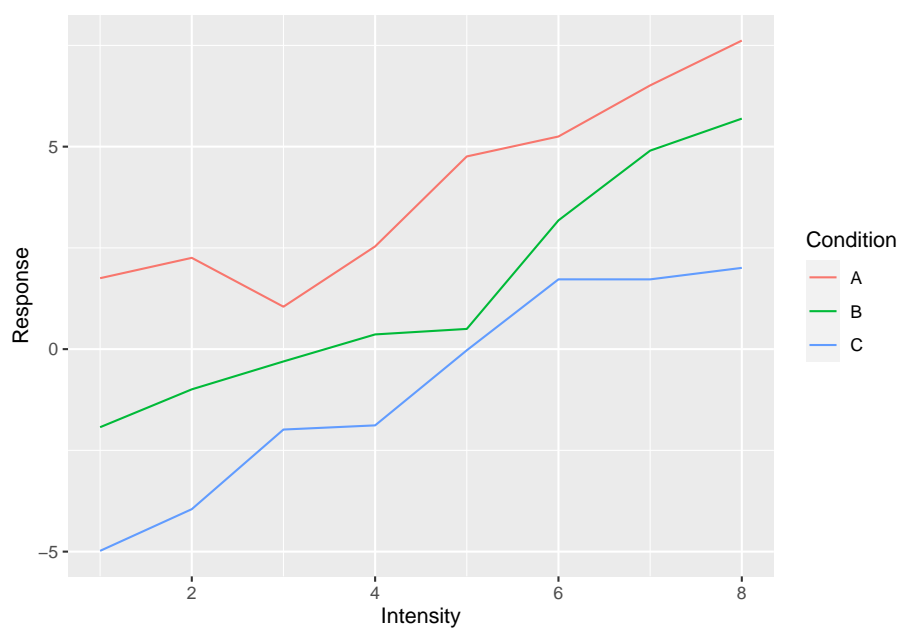
$$Response = Normal(\mu = 1, \sigma = 0.2) - Normal(\mu = 2 * ConditionIndex, \sigma = 0.4) + Normal(\mu = Intensity, \sigma = 0.4)$$

Condition	Intensity	Response
A	1	1.7516298
B	1	-1.9278857
C	1	-4.9813202
A	2	2.2539910
B	2	-0.9930058
C	2	-3.9516230
A	3	1.0472038
B	3	-0.3041480
C	3	-1.9860405
A	4	2.5361472
B	4	0.3629890
C	4	-1.8830268
A	5	4.7577832
B	5	0.4988250
C	5	-0.0289219
A	6	5.2501143
B	6	3.1792592
C	6	1.7229062
A	7	6.5118674
B	7	4.9012505
C	7	1.7225922
A	8	7.6191077
B	8	5.6919127
C	8	2.0063772

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 plus¹ in `+ geom_line()`).

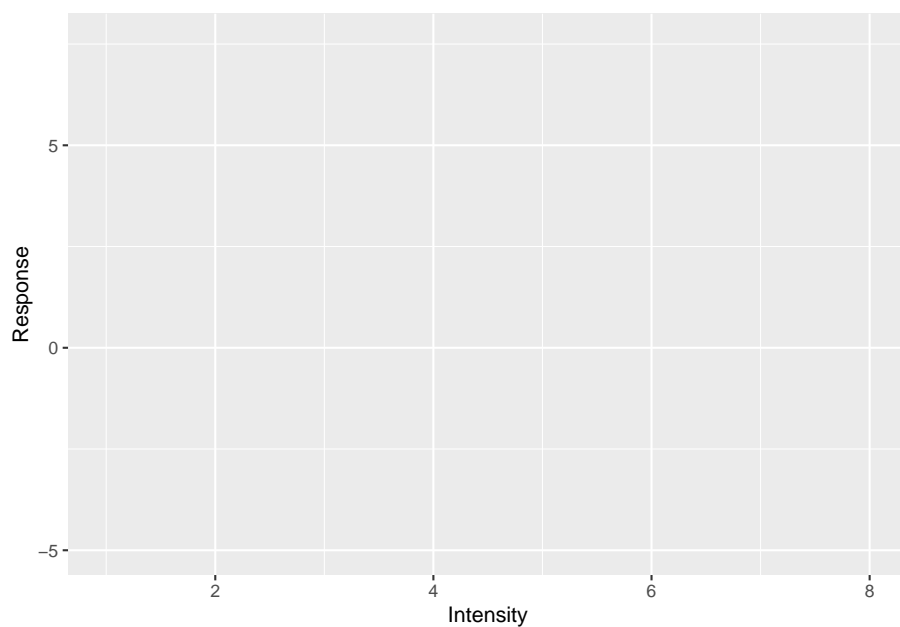
```
ggplot(data=simple_tidy_data, aes(x = Intensity, y = Response, color=Condition)) +
  geom_line()
```

¹One 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()`).

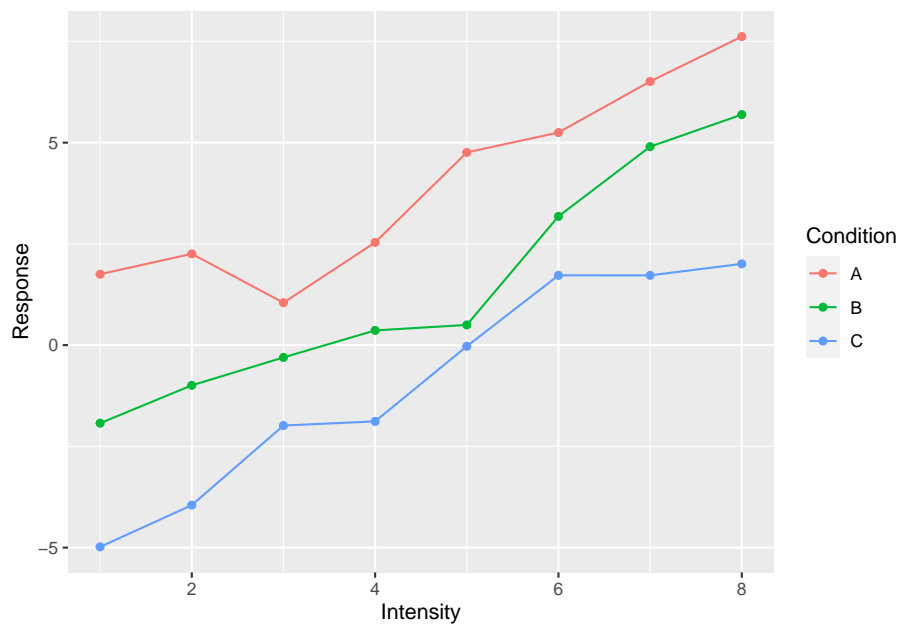
```
ggplot(data=simple_tidy_data, aes(x = Intensity, y = Response, color=Condition))
```



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.

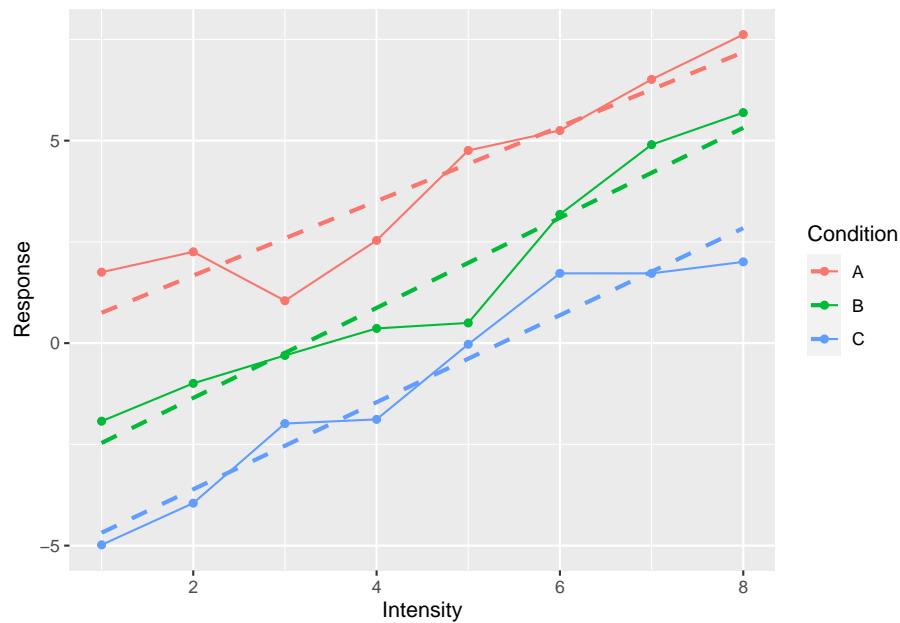
Let us see how you can keep the relationship mapping but add more visuals. Let us add both lines and points.

```
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!

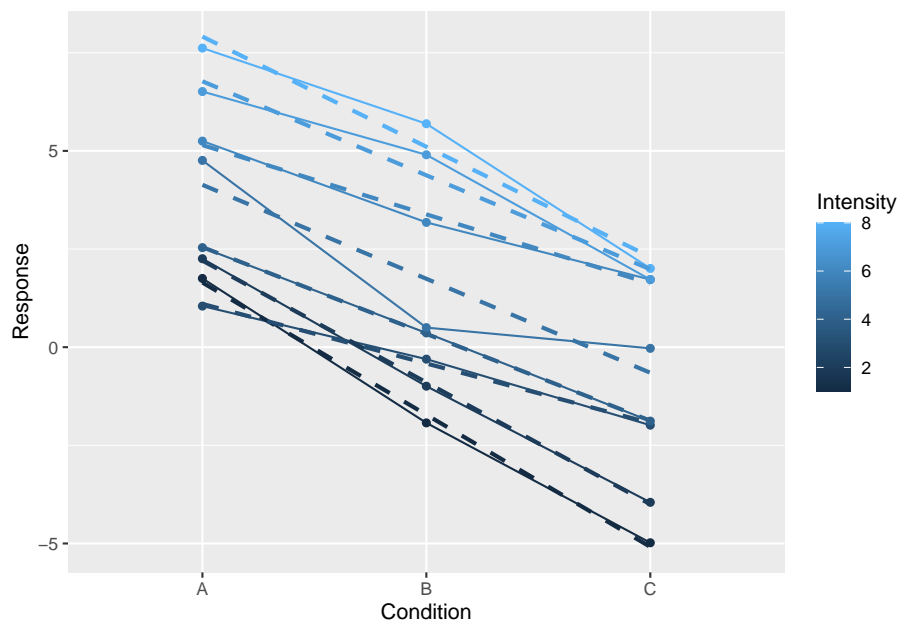
```
ggplot(data=simple_tidy_data, aes(x = Intensity, y = Response, color=Condition)) +
  geom_line() +
  geom_point() +
  # a linear regression over all dots in the group
  geom_smooth(method="lm", formula = y ~ x, se=FALSE, linetype="dashed")
```



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 linear fit from the solid data line).

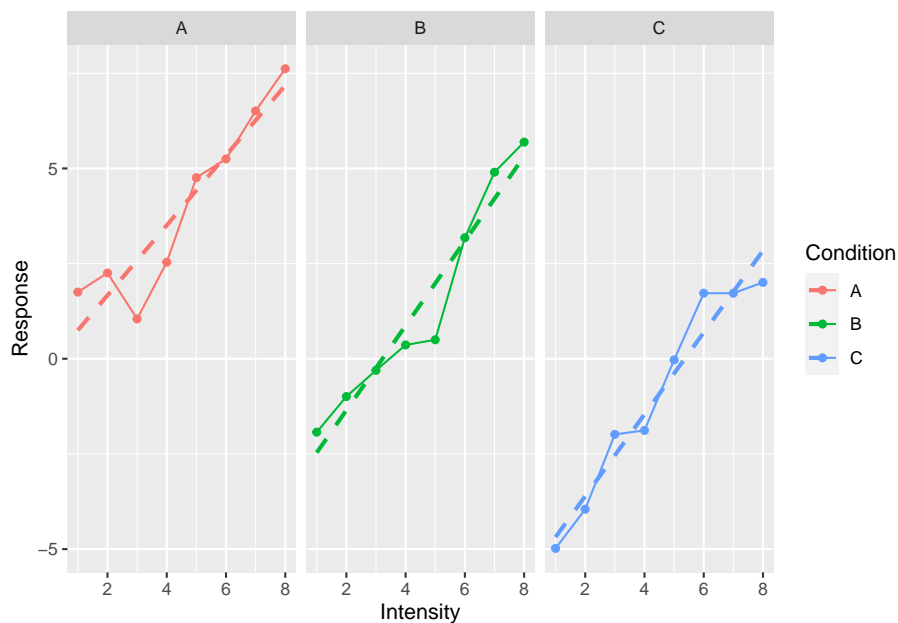
Or, we can keep the *visuals* but see whether changing *mapping* would make it more informative (we need to specify `group=Intensity` as continuous data is not grouped automatically).

```
ggplot(data=simple_tidy_data, aes(x = Condition, y = Response, color=Intensity, group=Intensity)) +
  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 let's 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 = var
```

```
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 let's 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 dplyr¹ “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* → *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.

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

```

mpg2lpg <- 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 / mpg2lpg,
         hwy = hwy / mpg2lpg) %>%

  # 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 `[]` sub-setting

```
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 it².

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

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

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 selection³. 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")
```

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


```
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 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

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

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.

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<0` 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

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 order⁶. In Tidyverse, you arrange rows based on values of specific variables.

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

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

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.

6.7 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 assignment⁷. 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 code below has
  some_table %>%   # 1. We start here, with the original table and pipe to the next computation
  mutate(...)      # 2. We add/change columns inside of the table. The output is a table which we r
```

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 Tidyverse 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$cty + short
  knitr::kable()
```

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

⁷R 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.

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.

⁸In 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` 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.

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()
```

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 Tidyverse 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

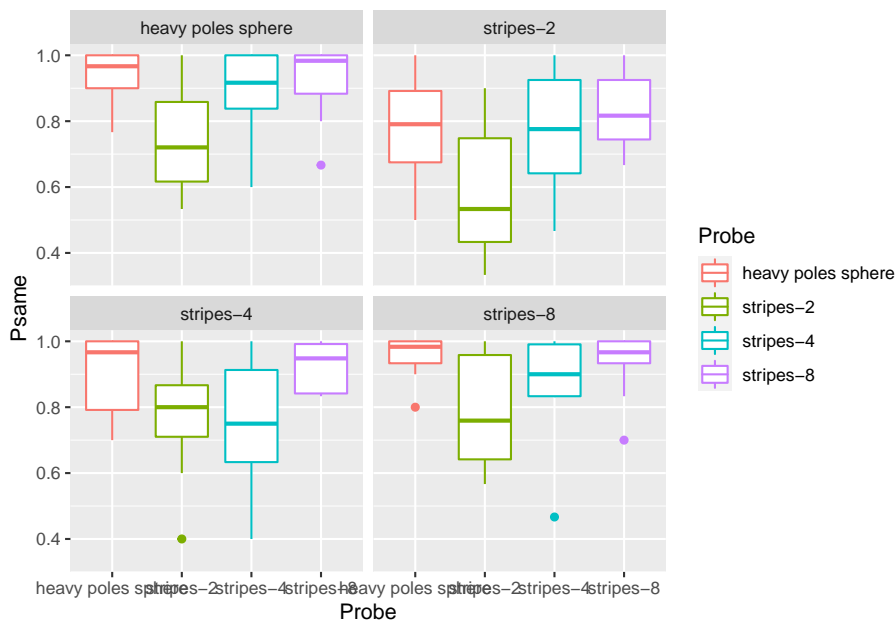
In the first exercise, I want you to implement the actual analysis performed in the paper. Good news is that by now you know enough to program it!

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 extract 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", "positive"))
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 `letters_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
```

¹At least I tend to always think that.

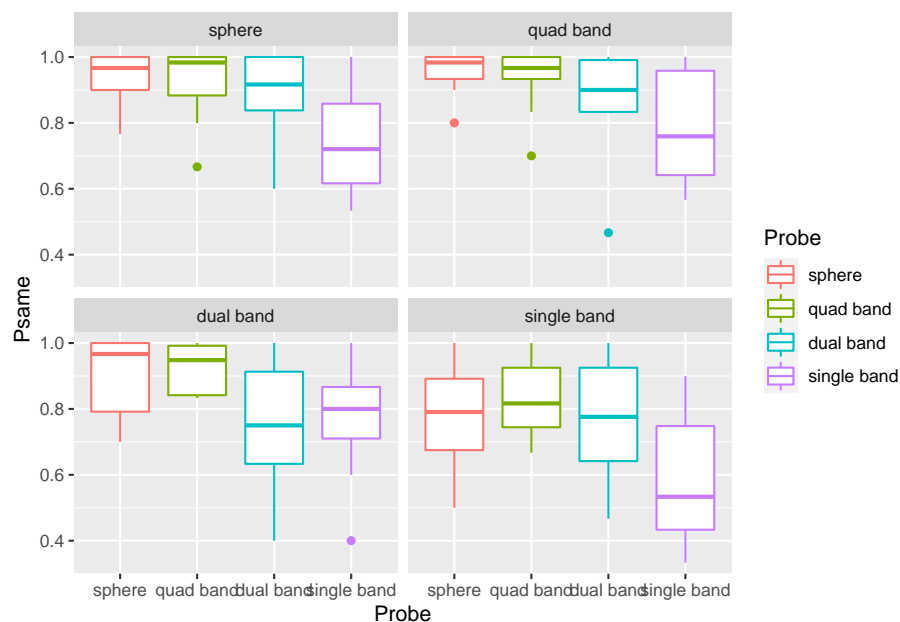
```
print(as.numeric(tens))
```

```
## [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.



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

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

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
## 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)`

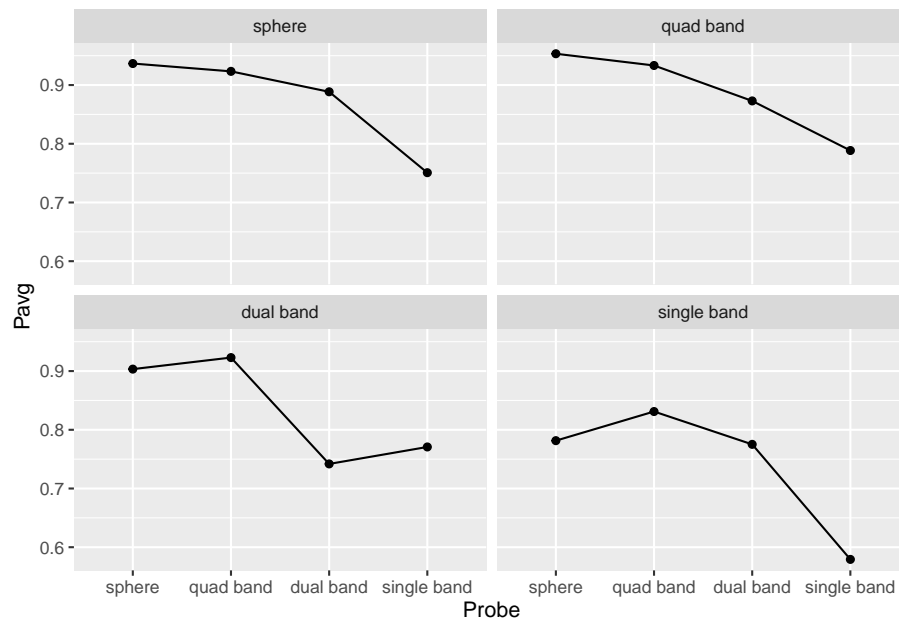
- `min(Response)` is executed, original values of `Response` are overwritten by `Response = mean(Response)`, so it has just **one** value, the mean. And `min()` and `max()` of a single value is that value, so their difference is 0. It is obvious once you carefully consider the code but it is *not* obvious (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

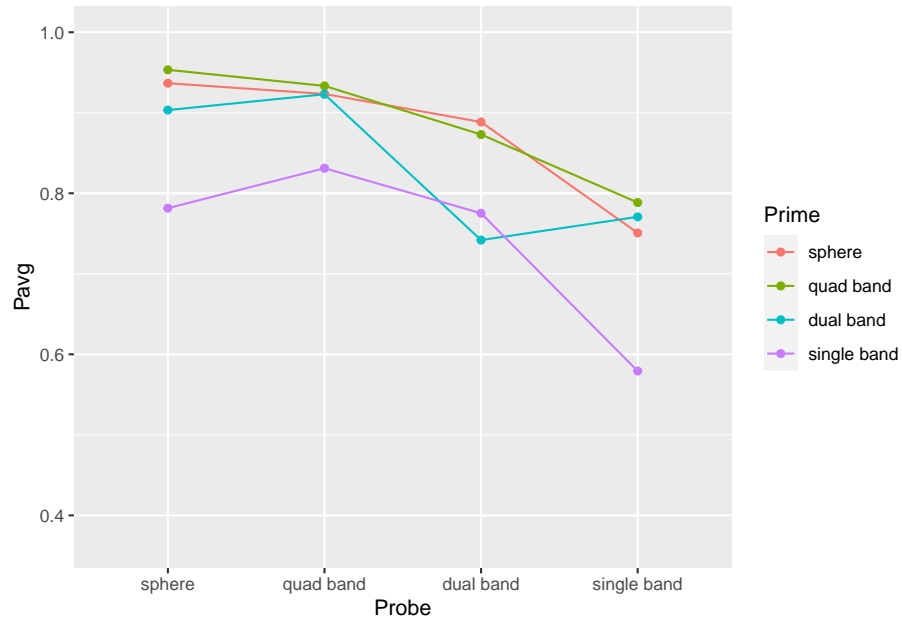
Do exercise 4.

Then, plot the results. Use `geom_point()` plus `geom_line()` to plot the mean response. The plot should look 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.

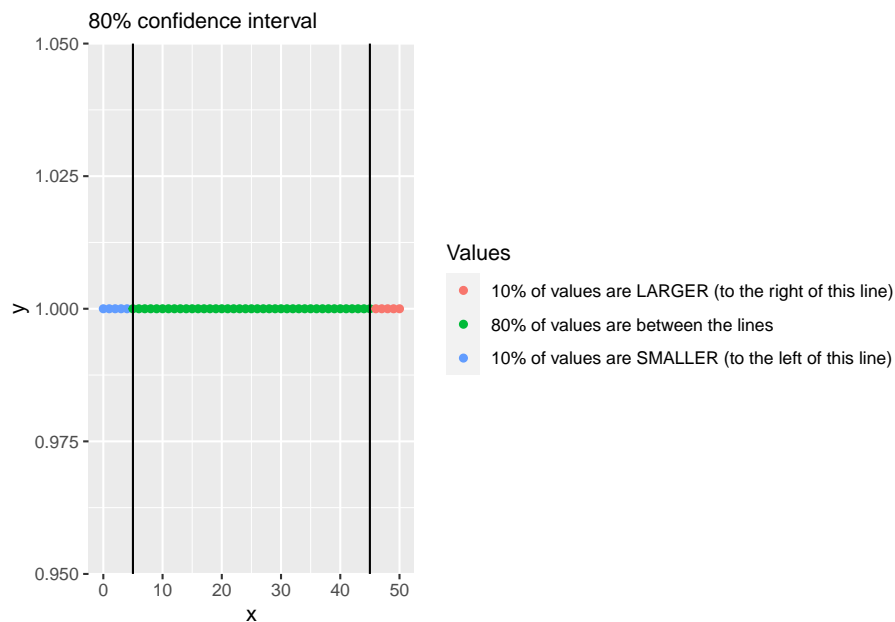
One way to characterize the mean is by computing its standard error. However, it is best used when actual data is distributed normally or, at least, symmetrically around the mean, i.e., the distance from an observation to the mean could be the same irrespective of whether it is larger or smaller. This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

³I 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.

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.



To compute this, R has function `quantile()`.

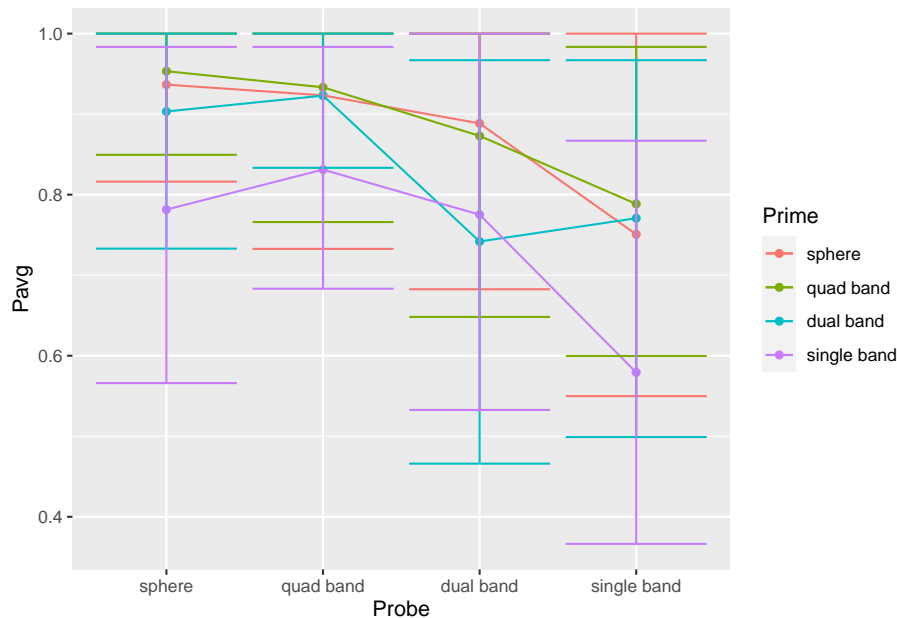
```
x <- 0:50
quantile(x, 0.1)
```

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

Modify code 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

⁴Why 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!

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).

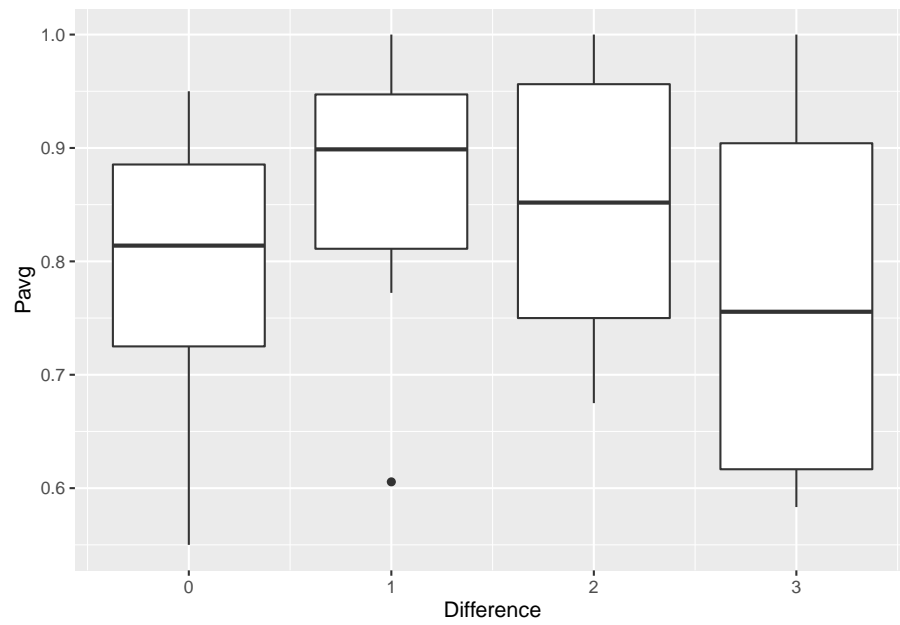


Do exercise 7.

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 plot⁵. 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).

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



Do exercise 8.

Chapter 8

Glueing and sprintfing

Let us practice more, utilizing knowledge and skill from previous seminars! Grab the exercise notebook and let's get started.

8.1 Comparing effect between two studies

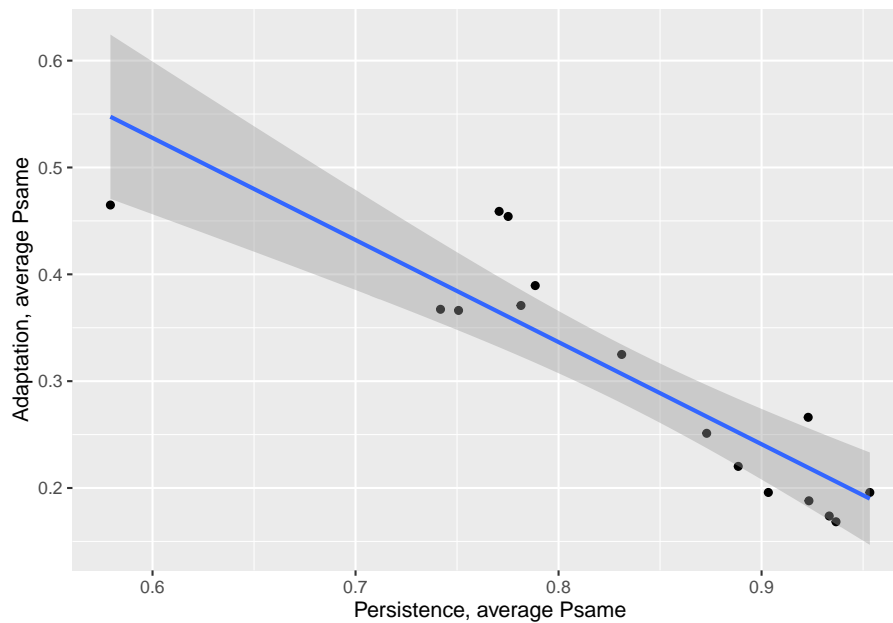
In the previous seminar, you analyzed how perceptual stability was influenced by change of object's shape for very brief interruptions (50 ms). For those brief interval, your perception is determined primarily by *neural persistence*, a lingering neural activity of neurons that represented 3D rotation before the interruption. However, you can curtail it using *a mask*, another object rotating around orthogonal axis. In this case, perception dominated by *neural fatigue* (also known as habituation or adaptation) of previously active neurons. Here, the measurement is the same (but the an intervening mask) but the expectations about similarity of reports is opposite: The stronger is the influence of the previous object, the *lower* is the probability of the same direction of rotation report (a tired neuron should be overwhelmed by competition that codes for the opposite direction of rotation). Long story short, if same groups of neurons are involved in both *neural persistence* and *neural fatigue*, we expect negative correlation, so that higher proportion of same reports in persistence lead to lower proportion for fatigue and vice versa.

Here is the outline of the analysis:

- Load and analyze persistence.csv. You can reuse your code from the previous seminar, however, I strongly recommend redoing it here from scratch. If it is easy, it won't take much time. If it is not, you definitely need to practice more, so do it! Compute the following in a single sequence using piping and store results in a variable `persistence`. The table must have

only three columns **Prime**, **Probe** and column for average proportion of same responses, and 16 rows (four primes \times four probes).

1. read the data in a table.
 2. 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).
 3. Convert **Prime** and **Probe** to factors and use labels “sphere” (for “heavy poles sphere”), “quad band” (for “stripes-8”), “dual band” (“stripes-4”), “single band” (for “stripes-2”).
 4. For every combination of **Participant**, **Prime** and **Probe** compute proportion of same responses.
 5. For every combination of **Prime** and **Probe** compute *average* proportion of same responses.
- Load and analyze bands-adaptation.csv. First, load the table and take a look at its contents or just open the file and text editor *but not in Excel* (the latter might change it, if you accidentally agree to save the file). Again, implement all steps in a single sequence using piping and store results in a variable **adaptation**. The table must have only three columns **Prime**, **Probe** and column for average proportion of same responses, and 16 rows (four primes \times four probes).
 1. Convert **Prime** and **Probe** to factors and use same labels as for persistence. So “sphere” (for “Sphere”), “quad band” (for “Quadro”), “dual band” (“Dual”), “single band” (for “Single”).
 2. Compute proportion of same responses per **Participant**, **Prime**, and **Probe** using number of same responses (**Nsame**) and the total number of trials (**Ntotal**).
 3. Compute average proportion of same responses per **Prime** and **Probe**.
 - Merge two tables by **Prime** and **Probe**, store results in a new variable (the name is up to you). Note that each table has column with average proportion of same responses. You probably used the same name for this variable for both columns (if not, do use the same name, like **Pavg**). Joining functions are average of this possibility and use *suffixes* to differentiate which table the original column came from. By defaults **suffix** = **c(“x”, “y”)**, so that that column **Pavg** from the first (left) table will become **Pavg.x** and the other one **Pavg.y**. We can do better than **c(“x”, “y”)**! Use suffix parameter but use meaningful suffixes. The table should have four columns and sixteen rows.
 - Plot average proportion of same responses for adaptation versus persistence. Use points for individual values and add linear regression line via **geom_smooth()**. The final plot should look approximately like this:



Do exercise 1.

8.2 Gluing in correlation strength information.

Let us be more precise about the strength of the correlation between the two variables. First, compute it via `cor` function. Use function `round` to round it to just two decimal places. Then, use `glue()` (see below) to make the title look nice and put it as a title or subtitle of the plot via `labs`.

Function `glue()` lives in the package of the same name that you will need to import separately (it is part of the tidyverse but is not imported automatically). It makes it simple to “glue” values directly into a string. You simply surround the R code by wiggly brackets and the result of the code execution is glued in. If you use just a variable, its value will be glued-in.

```
answer <- 42
bad_answer <- 41
glue("The answer is {answer}, not {bad_answer}")
```

```
## The answer is 42, not 41
```

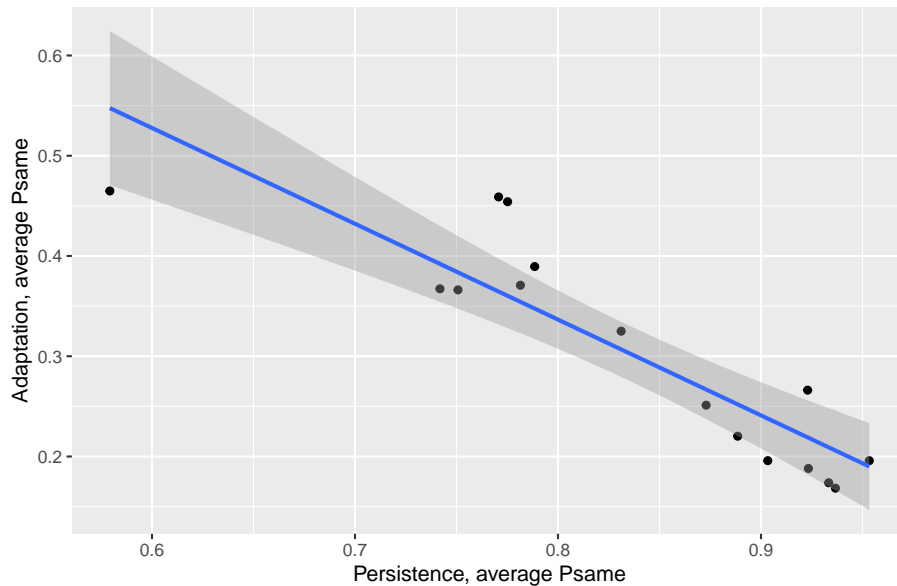
But, you can put *any* code inside, although, the more code you put, the harder it will be to read and understand it.

```
single_package_weight <- 1.2
glue("Ten packages weight {single_package_weight * 10} kg")
```

```
## Ten packages weight 12 kg
```

So, compute the correlation, glue it into the text and put it as a title of the plot.

Pearson correlation is -0.89



Do exercise 2.

8.3 sprintf

Simplicity makes glue a great tool to insert values into, because there isn't much more to know about. However, because it is so simple to use, it is not the most flexible way for formatting strings. Instead, you can use sprintf function that provides C-style string formatting (same as Python's original string formatting).

The general function call is `sprintf("string with formatting", value1, value2, value)`, where values 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 an exponential notation (e.g., `1e2`).
- **g** for an “optimally” printed float value, so that exponential notation is used for large values (e.g., `10e5` instead of `100000`).

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 right number of values. Before running it, can you figure out which call will actually work (and what will be the output) and which will produce an error?

```
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 pancakes and %d stakes for dinner", 1, 7, 10)
```

Do exercise 3.

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] "Euler's number is roughly 2.7183"
```

Repeat exercise #2 but use `sprintf()` in place of `glue()`. ::: {.infobox .practice} Do exercise 4. :::

8.4 Wrap up

That's it for today! See you after the Christmas break!

Chapter 9

Tidying 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.

9.1 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 need 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

Table 9.1: demographics (left) and report (right) tables

ID	Age	ID	Report
A	20	A	3.719993
B	19	A	3.171843
C	30	B	6.691370
D	22	B	5.142820
		C	4.128087
		C	1.893055
		D	3.433498
		D	2.419368

Table 9.2: 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	ID	Report	Age
A	20	3.719993	A	3.719993	20
A	20	3.171843	A	3.171843	20
B	19	6.691370	B	6.691370	19
B	19	5.142820	B	5.142820	19
C	30	4.128087	C	4.128087	30
C	30	1.893055	C	1.893055	30
D	22	3.433498	D	3.433498	22
D	22	2.419368	D	2.419368	22

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()` 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 argument¹. 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")
```

¹Theoretically, 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 `dplyr`'s matching rules may lead to different results. I strongly recommend to always specify key columns.

Table 9.3: 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	ID	Report
A	20	A	3.482151
B	19	A	1.051506
C	30	B	6.068382
D	22	B	6.843066
		C	1.406945
		C	4.297865
		E	6.580686
		E	6.778709

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 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")
```

Table 9.4: Inner join. Only rows for matching keys are merged

ID	Report	Age
A	3.482151	20
A	1.051506	20
B	6.068382	19
B	6.843066	19
C	1.406945	30
C	4.297865	30

Table 9.5: Full join. All rows are merged, 'NA' are used for missing values in rows from a complementary table

ID	Age	Report
A	20	3.482151
A	20	1.051506
B	19	6.068382
B	19	6.843066
C	30	1.406945
C	30	4.297865
D	22	NA
E	NA	6.580686
E	NA	6.778709

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)
```

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()`.

Table 9.6: Left join. All rows from demographics tables are used and missing matching rows are filled with ‘NA’

ID	Age	Report
A	20	3.482151
A	20	1.051506
B	19	6.068382
B	19	6.843066
C	30	1.406945
C	30	4.297865
D	22	NA

Table 9.7: Right join. All rows from reports tables are used and missing matching rows are filled with ‘NA’

ID	Age	Report
A	20	3.482151
A	20	1.051506
B	19	6.068382
B	19	6.843066
C	30	1.406945
C	30	4.297865
E	NA	6.580686
E	NA	6.778709

```
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"),
  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

Table 9.8: Two identically named key columns: ID and Gender.

ID	Gender	Age	ID	Gender	Report
A	M	20	A	M	5.710133
B	F	19	B	F	5.673315
A	F	30	A	F	2.293083
B	M	22	B	M	1.753220

Table 9.9: Joining/merging two tables by ID and Gender.

ID	Gender	Age	Report
A	M	20	5.710133
B	F	19	5.673315
A	F	30	2.293083
B	M	22	1.753220

match pairs of individual columns. For `merge()`, you supply two vectors: one for columns in the first table (parameter `by.x`) and one column in 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", "Gender"))
```

Table 9.10: Differently named key columns. VPCode in demographics table corresponds to ID in reports; sex in demographics corresponds to Gender in reports

VPCode	Sex	Age	ID	Gender	Report
A	M	20	A	M	2.328198
B	F	19	B	F	1.072300
A	F	30	A	F	5.961688
B	M	22	B	M	6.171258

Table 9.11: Joining tables by matching VPCode to ID and Sex to Gender.

VPCode	Sex	Age	Report
A	F	30	5.961688
A	M	20	2.328198
B	F	19	1.072300
B	M	22	6.171258

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()`).

Download files `IM.csv` and `GP.csv` that you will need for exercise #1². 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()` 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

²Remember, if you end up with `.xls` extension, just rename to `.csv`.

Table 9.12: 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

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. `::`

9.2 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.

9.3 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*

³It uses `melt` and `cast` functions for this.

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"))
```

\begin{table}

\caption{Long version of `widish_df` table with default names for new columns.}

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

\end{table}

When you compare the two tables, you will see that original three columns \times four rows are now stretched into twelve rows and name-value pairs are consistent across the two tables⁴. As noted above, we can improve on that by specifying proper names for new columns.

⁴By 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!

```
long_tidy <- tidyr::pivot_longer(widish_df,
                                cols=c("Symmetry", "Attractiveness", "Trustworthiness"),
                                names_to = "Scale",
                                values_to = "Response")
```

```
\begin{table}

\caption{Long version of widish_df table with custom names for new
columns.}


```

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

```
\end{table}
```

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

Table 9.13: Same table pivoted via reshape.

	Participant	Face	Scale	Response
1.M-1.Symmetry	1	M-1	Symmetry	6
1.M-2.Symmetry	1	M-2	Symmetry	4
2.M-1.Symmetry	2	M-1	Symmetry	5
2.M-2.Symmetry	2	M-2	Symmetry	3
1.M-1.Attractiveness	1	M-1	Attractiveness	4
1.M-2.Attractiveness	1	M-2	Attractiveness	7
2.M-1.Attractiveness	2	M-1	Attractiveness	2
2.M-2.Attractiveness	2	M-2	Attractiveness	7
1.M-1.Trustworthiness	1	M-1	Trustworthiness	3
1.M-2.Trustworthiness	1	M-2	Trustworthiness	6
2.M-1.Trustworthiness	2	M-1	Trustworthiness	1
2.M-2.Trustworthiness	2	M-2	Trustworthiness	2

3. You can replace 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.

Let us put this new knowledge to practice, using GP.csv file. This 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

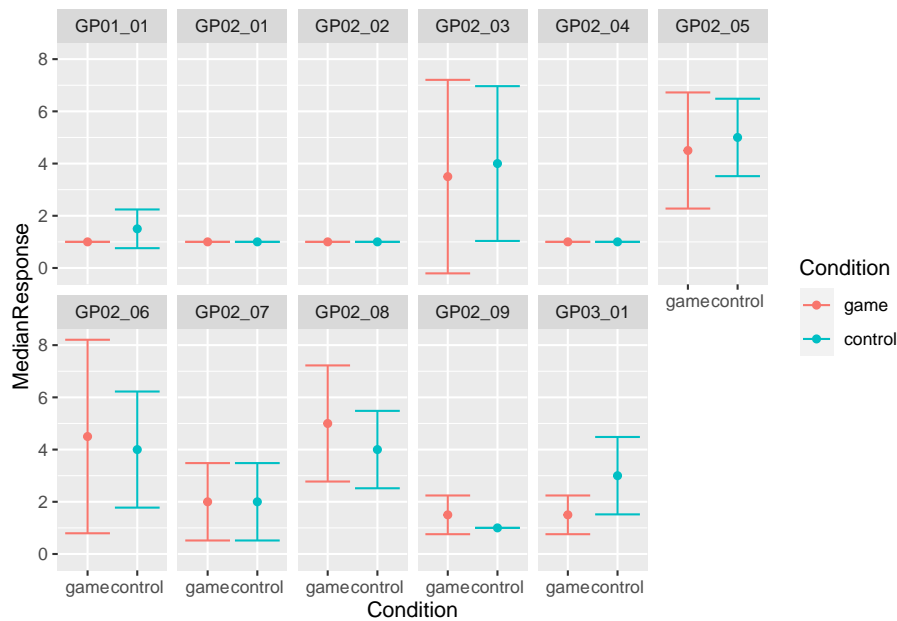
And your second table, with aggregated results, should be like this

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.

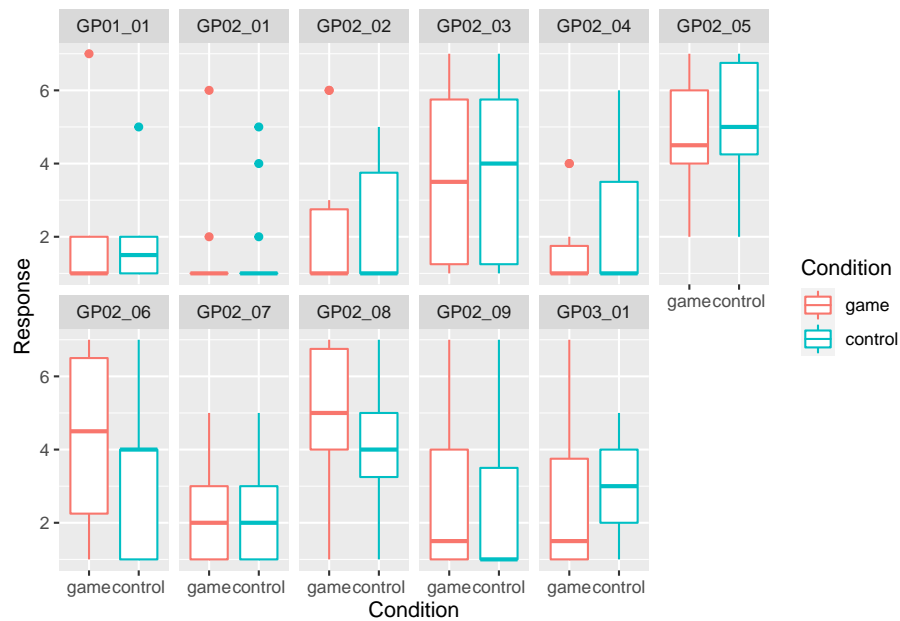
Repeat the exercise but now using base R `reshape()` function. ::: {.infobox .practice} Do exercise 5. :::

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 $\text{median} \pm \text{MAD}$ 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.

9.4 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

⁵I 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 interchangeable and that both put the table as a parameter into the function.

Table 9.14: 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="Response")
```

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 be 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	0.73
1	M-1	Attractiveness	4	1.82
1	M-1	Trustworthiness	3	1.64
1	M-2	Symmetry	4	1.08
1	M-2	Attractiveness	7	1.13
1	M-2	Trustworthiness	6	1.94
2	M-1	Symmetry	5	1.73
2	M-1	Attractiveness	2	0.39
2	M-1	Trustworthiness	1	1.00
2	M-2	Symmetry	3	0.58
2	M-2	Attractiveness	7	0.17
2	M-2	Trustworthiness	2	1.24

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 with lots of `NA`s.

```
wide_odd_rt <-
  pivot_wider(long_tidy_rt, names_from = "Scale", values_from="Response")
```

Participant	Face	RT	Symmetry	Attractiveness	Trustworthiness
1	M-1	0.73	6	NA	NA
1	M-1	1.82	NA	4	NA
1	M-1	1.64	NA	NA	3
1	M-2	1.08	4	NA	NA
1	M-2	1.13	NA	7	NA
1	M-2	1.94	NA	NA	6
2	M-1	1.73	5	NA	NA
2	M-1	0.39	NA	2	NA
2	M-1	1.00	NA	NA	1
2	M-2	0.58	3	NA	NA
2	M-2	0.17	NA	7	NA
2	M-2	1.24	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
ma2	Sphere	Sphere	22	119
ma2	Sphere	Quadro	23	118
ma2	Sphere	Dual	15	120
ma2	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
ma2	Sphere	0.18	0.19	0.12	0.27	0.1900
ma2	Quadro	0.21	0.22	0.14	0.34	0.2275
ma2	Dual	0.25	0.30	0.27	0.48	0.3250
ma2	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.
 ::: {.infobox .practice} Do exercise 8. :::

Repeat the analysis but now using the `reshape()` function. ::: {.infobox .practice} 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 10

Controlling 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.

10.1 `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.

10.2 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_tidy)
```

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.

10.3 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 variable¹ getting assigned each vector/list value on each iteration. Thus, to print each value of a vector we can do

```
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.

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
```

¹Just 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.

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 your 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.

10.4 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 will use *only the first one* but, at least, it will give you a warning.

```
x <- c(10, -3)
if (x < 0) {
  cat("Bingo!")
} else {
  cat("I don't like this x.")
}
```

```
## Warning in if (x < 0) {: the condition has length > 1 and only the first element
## will be used
```

```
## I don't like this x.
```

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)
```

```
## [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 “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 this²

```
## [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.

²Want 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.

10.5 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 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, your 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.

10.6 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 spl
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 spl
AKM1995M	2019-06-12-14-07-17	0	5	0.6435367	right	stripes-4	stripes-4

Do exercise 10.

10.7 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.

10.8 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 outputs³

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!).

³Means the same thing but this is a linear algebra way of expressing of what a function does.

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 “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 11

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 interpret¹.

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 **Statistical Rethinking** seminar or read an excellent book by Richard McElreath that the seminar is based on.

¹In 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...

11.1 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 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 (typically called `data` parameter). Same formula can be shortened by using `*` which means “all predictors and their interaction”, thus (omitting redundant intercept)

```
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, much easier to misunderstand).

```
y ~ x1*x2 - x1
y ~ x2 + x1:x2
```

11.2 Correlation

To compute correlation, use function `cor()`. You have a choice of `method`, either `"pearson"` (default, Pearson’s product moment correlation coefficient), or rank-based `"kendall"` (Kendall’s tau) or `"spearman"` (Spearman’s rho).

```
df <-
  tibble(x = rnorm(100)) %>%
  mutate(y = rnorm(n(), x, 0.5))
cor(df$x, df$y, method="pearson")
```



```
## [1] 0.9163366
```

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 = 22.655, df = 98, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.8779334 0.9430243
## sample estimates:
## cor
## 0.9163366
```

`cor.test` returns a list, so you can access its individual elements² via a double-bracket or `$` notation.

```
cor_result$p.value
```

```
## [1] 9.720871e-41
```

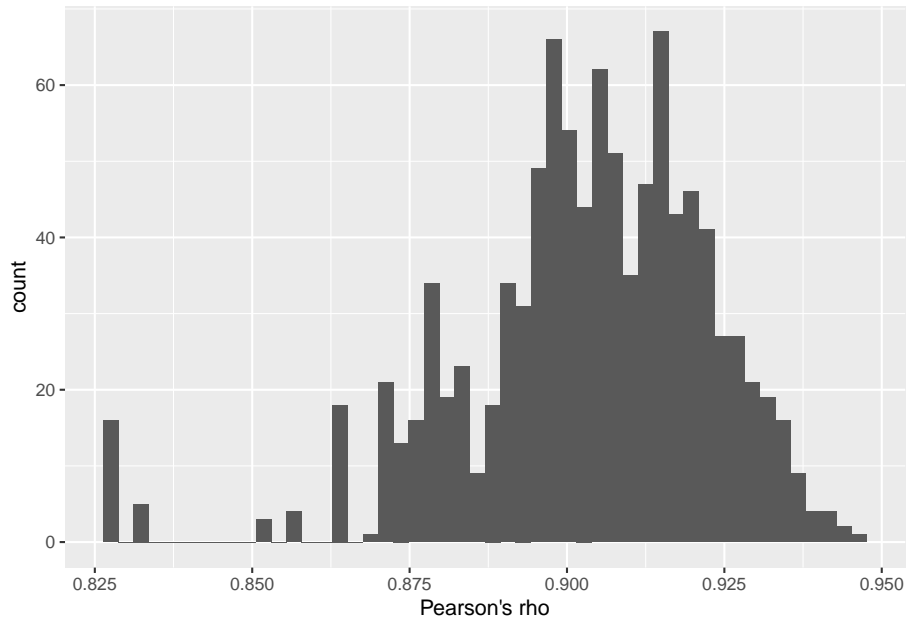
Bayesian correlation with a posterior distribution for the correlation coefficient and Bayes Factor as a measure of significance, can be computed via `correlationBF()` function, which is part of `BayesFactor` package.

```
library(BayesFactor)
correlationBF(df$x, df$y)
```

```
## Bayes factor analysis
## -----
## [1] Alt., r=0.333 : 1.049887e+36 ±0%
##
## Against denominator:
## Null, rho = 0
## ---
## Bayes factor type: BFcorrelation, Jeffreys-beta*
```

²Use `(names())`[<https://stat.ethz.ch/R-manual/R-devel/library/base/html/names.html>] function to get names of all elements.

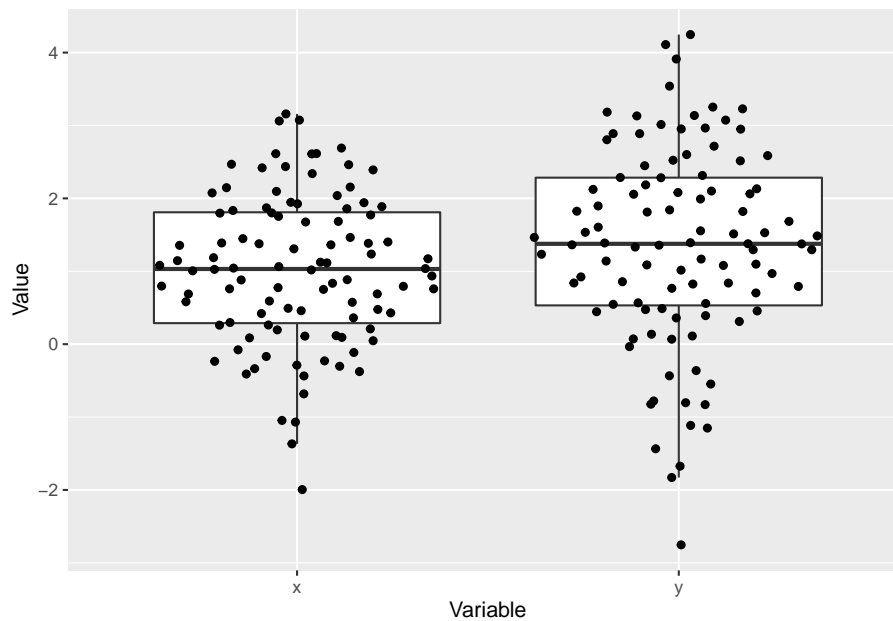
```
cor_bf <- correlationBF(df$x, df$y, posterior = TRUE, iterations=1000)
ggplot(data=NULL, aes(x=c(cor_bf[, "rho"]))) +
  geom_histogram(bins=50, ) +
  xlab("Pearson's rho")
```



11.3 Pairwise comparisons

For pairwise comparisons for normally distributed data, you can use Student's t-Test via `t.test()`. Here, I generate `x` as a normally distributed normal variable and `y`, as a normally distributed variable random whose mean is `x+0.5`. 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, 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 difference in means is not equal to 0
## 95 percent confidence interval:
## -0.5090948 -0.1298688
## sample estimates:
## mean of the differences
## -0.3194818
```

You can also use formula notation, if one variable describes grouping

```
df_group <-
  tibble(x = c(df$x, df$y),
         group = factor(c(rep("A", 100), rep("B", 100))))
```

x	group
1.3776580	A
1.8338910	A
-0.3034055	A
1.3079381	A

```
t.test(x ~ group, data=df_group, paired=TRUE)
```

```
##
## Paired t-test
##
## data: x by group
## t = -3.3432, df = 99, p-value = 0.00117
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.5090948 -0.1298688
## sample estimates:
## mean of the differences
## -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.

11.4 ANOVA

ANalysis **Of** **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).

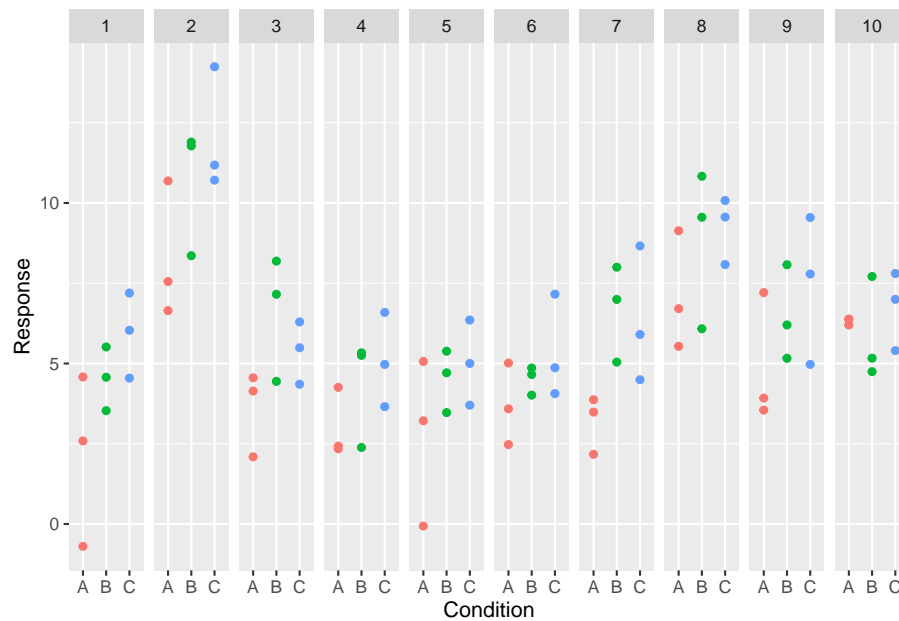
First, let us simulate data for ten participants and their responses, assuming that condition B increases their responses by 2 (arbitrary) units and C by 3³.

```
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 condition "B"
  ungroup() %>%
  mutate(Response = rnorm(n(), Intercept + 2 * as.integer(Condition == "B") + 3 * as.integer(Condition == "C"), 1))
  select(-Intercept)
```

³`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.sign
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(df_anova))

## Bayesian 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.

11.5 (Generalized) Linear Models

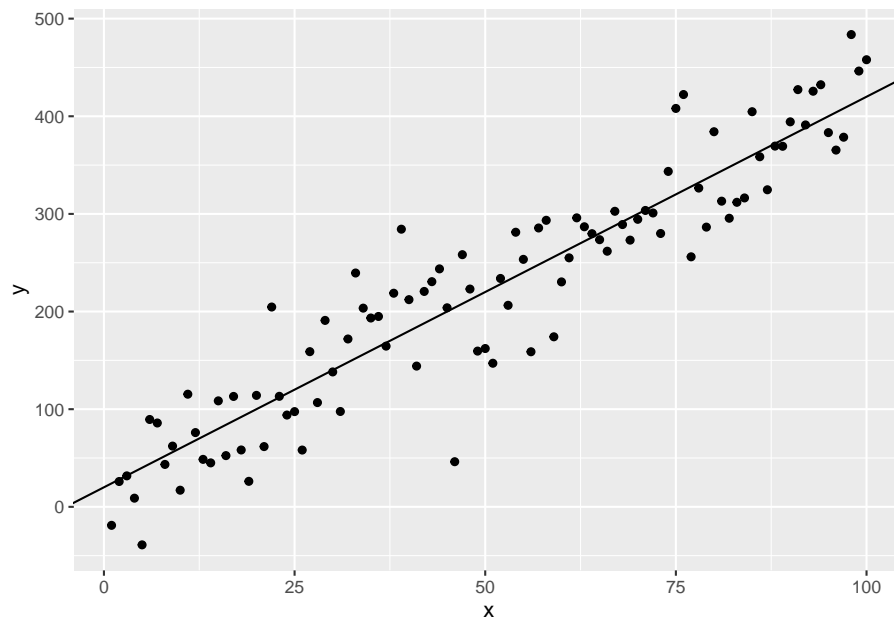
Base R provides function to perform linear regression `lm()` and generalized linear models `glm()` for binomial, count, and other types of data.

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 $y \sim x$ 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
## -157.448  -30.581   -0.077   33.018  109.173
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  16.4483     9.1389   1.80    0.075 .
## x             4.0701     0.1571  25.91 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 45.35 on 98 degrees of freedom
## Multiple R-squared:  0.8726, Adjusted R-squared:  0.8713
## F-statistic: 671.1 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 design. 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)	16.448278	9.1389367	1.799802	0.074969
x	4.070054	0.1571132	25.905235	0.000000

11.6 (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)` notation⁴.

```
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
##
## 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
##
```

⁴Here, 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.

```
## 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(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`⁵.

```
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
##
## 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.
```

⁵I use `lmerTest::` to tell R that I need function `lmer()` from package `lmerTest` and not from `lme4` as before

```
## 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.

11.7 Practice

For practice, we will use data from a gamification experiment. Participant performed the same challenging task setup as a typical (read, boring) experiment or styled as a game with trial score, combos, high score table, achievements, etc. The idea was to investigate whether this shallow gamification (there was no story and all elements were present only before or after each trial and provided no information on the task itself) would alter (hopefully, improve) their performance. We quantified it via proportion of correct responses, response time, and score achieved for each trial (that one, you will need to compute yourself). Below, we would like to understand effects of

1. Experimental group coded in variable `Condition`, either "`experiment`" or "`game`".
2. Task difficulty controller via cue-onset asynchrony. Participants could response while the stimulus was still on the scree ($COA = -100$ ms), shortly after it disappeared ($COA=100$ ms), or after a delay ($COA = 1000$ ms). We would expect that task is harder to longer COAs.
3. Perceptual learning. As participants do the task, the become better at it and are likely to become both faster and more accurate for later blocks. So we need to incorporate that improvement over different blocks into our model. The overall block index is coded in `Block` variable but we will need to create a new variable `COABlock` that will encode index of the block within each difficulty.

You will need to load data, preprocess data, plot accuracy, response times, and score relative for each condition, difficulty, and difficulty block, perform formal statistical analysis to see whether any of the factor have an effect. So, first, download `gamification.zip` and unzip into your R-seminar project folder. You should get *gamification* subfolder with all the files. There will be no template notebook, create it from scratch yourself and keep it organized, e.g., headings, comments, chunked code, etc.

Read files and preprocess data

The two steps should be a single pipe. 1. Read and merge all CSV files in *gamification* folder into a single table. It is "German Excel" formatted with :

as a delimiter and , as a decimal point. To perform it most cleanly, use `read_delim` function that allows you to specify the delimiter via `delim` parameter and the decimal point via `locale` parameter. You will need to read on how to specify the locale first. My advice, debug reading on a single file and then add reading-and-merging either via `for` loop or `purrr` mapping. 2. Compute whether response on each trial was correct (`Response` is equal to `Match` variable) and store it in `Correct` column. It is already present in the table but due to software glitch, some values are not correct. In general, it is not a bad idea to recompute such variables and compare them with table in the table, just to be on the safe side. 3. Drop columns `SessionID`, `Color0`, `Color1`, `Color2`, `Color3`, `Which` and `FlipComplimentary`. They are not relevant for the analysis and it is easier to look at uncluttered data.

Observer	Condition	Block	Trial	COA	Target	Match	Response	RT	Correct	OnsetD
AAF1997w	experiment	1	1	-100	column	TRUE	FALSE	0.9619999	FALSE	0.7110
AAF1997w	experiment	1	2	-100	column	FALSE	FALSE	0.8230000	TRUE	0.7710
AAF1997w	experiment	1	3	-100	row	FALSE	FALSE	0.9500000	TRUE	1.3230
AAF1997w	experiment	1	4	-100	column	TRUE	TRUE	0.8500001	TRUE	0.8880

Now we need to compute block index per difficulty (and per participant and condition). We will spin it off as a separate table and then join it with the main one. 1. Generate a summary table with a single row per `Observer`, `Condition`, `COA`, `Block`. Hint, you can use `summarise(.groups="drop")` with no additional arguments to get one row per group.

Observer	Condition	COA	Block
AAF1997w	experiment	-100	1
AAF1997w	experiment	-100	6
AAF1997w	experiment	-100	7
AAF1997w	experiment	-100	10

2. Regroup the table by `Observer`, `Condition`, and `COA` and compute `COABlock` block index. It is simply a sequence from 1 till number of rows in the group, you can get the latter via `n()` function.

Observer	Condition	COA	Block	COABlock
AAF1997w	experiment	-100	1	1
AAF1997w	experiment	-100	6	2
AAF1997w	experiment	-100	7	3
AAF1997w	experiment	-100	10	4
AAF1997w	experiment	100	2	1
AAF1997w	experiment	100	4	2

3. Now we can add `COABlock` to the main table by joining the two. I would strongly recommend to name the new full table differently, e.g., the original could be `results_raw` and the new one `results`. This is because if

you join to table, overwriting one of them, and try to do joining again (you fixed it and now should work properly), you will get different column names as dplyr will enforce unique column names. It can get very confusing.

4. Filter out any rows where `COABlock` is more than 4. Some participants volunteered to do more but for the analysis we need to have full data for everyone.

Observer	Condition	Block	Trial	COA	Target	Match	Response	RT	Correct
AAF1997w	experiment	1	1	-100	column	TRUE	FALSE	0.9619999	FALSE
AAF1997w	experiment	1	2	-100	column	FALSE	FALSE	0.8230000	TRUE
AAF1997w	experiment	1	3	-100	row	FALSE	FALSE	0.9500000	TRUE
AAF1997w	experiment	1	4	-100	column	TRUE	TRUE	0.8500001	TRUE

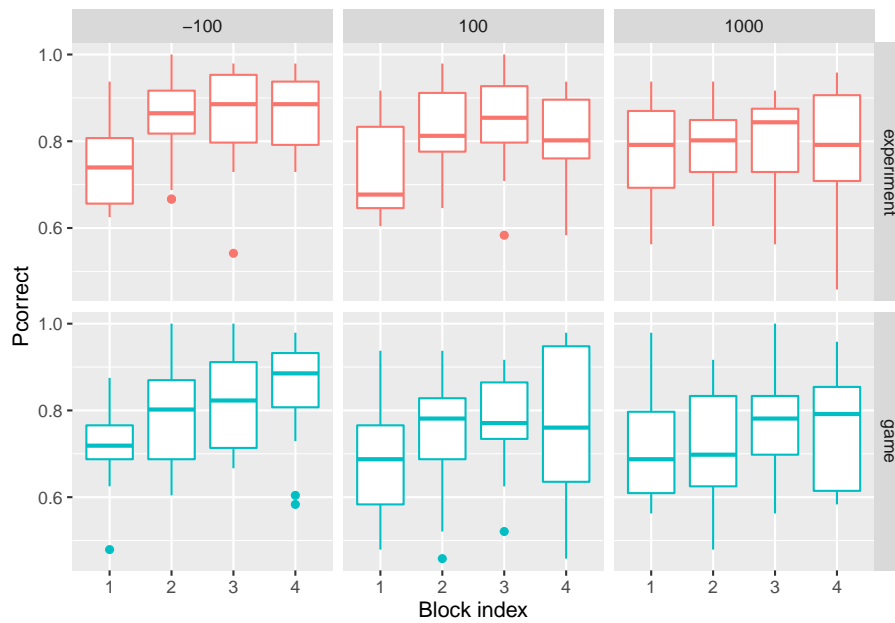
Accuracy

Let us analyze accuracy, the results should be stored in a new separate table.

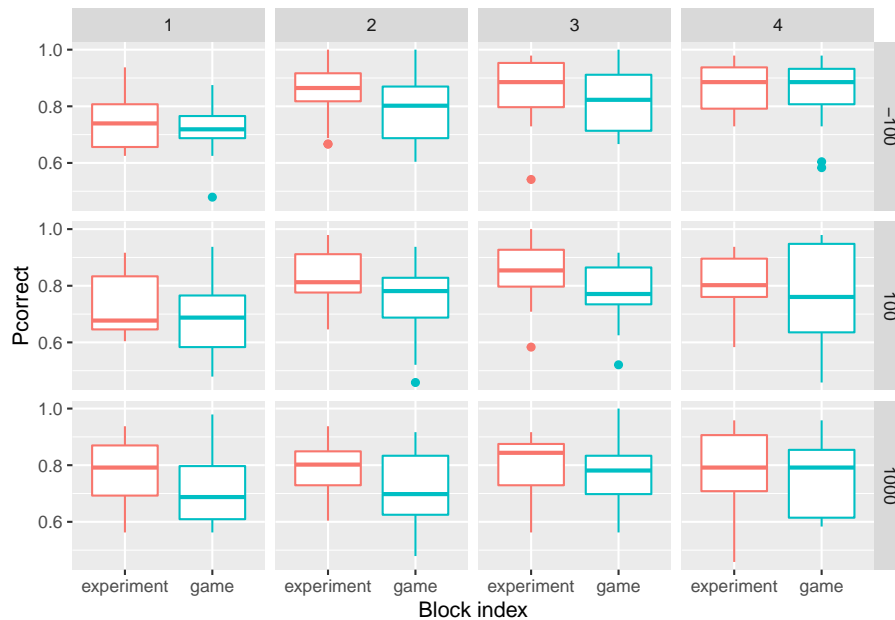
1. Compute number of correct trials each `Observer`, `Condition`, `COA` and `COABlock` combination. Also, store total number of trials for each combination in a separate variable (again, take a look at `n()` function). We need these two variables for the statistical analysis.
2. Compute proportion of correct responses. You can compute it directly from `Correct` or from the two variables you computed on the previous step. We need this variable for visualization.

Observer	Condition	COA	COABlock	Ncorrect	Ntotal	Pcorrect
AAF1997w	experiment	-100	1	38	48	0.7916667
AAF1997w	experiment	-100	2	47	48	0.9791667
AAF1997w	experiment	-100	3	47	48	0.9791667
AAF1997w	experiment	-100	4	45	48	0.9375000

Let us visualize the performance. Generate a similar looking plot



And an alternative visualization.



The first one, shows an effect of experience (note how performance gets higher for the later blocks), for second one makes it easier to compare between conditions. Here, **experiment** tends to produce higher accuracy. However, this is just eye-balling the data, we need some actual numbers. For this, we will

use Generalized Linear Mixed Model. It is *generalized* because our data is binomial (participants were successful in `Ncorrect` trials out of `Ntotal`). It is *linear* because we assume a simple linear sum of individual effects. It is *mixed*, because we will add `Observer` as a random factor⁶. We will also use `COA` as a factor variable to have a more direct comparison between individual `COA` levels.

Read documentation to figure out how you specify the formula and binomial family. You will need to use library `lmer4` and I strongly suggest using `lmer4::glmer()` notation as we will later use `lmerTest` package, which redefines some functions and it can be hard to figure out function from which package was actually called.

The summary output of the model should look like this.

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: cbind(Ncorrect, Ntotal) ~ Condition + as.factor(COA) + COABlock +
## (1 | Observer)
## Data: accuracy
##
##          AIC          BIC    logLik deviance df.resid
##    1788.8    1811.7   -888.4   1776.8     330
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.72915 -0.29164  0.02438  0.34443  1.09710
##
## Random effects:
## Groups   Name            Variance Std.Dev.
## Observer (Intercept) 0.01044  0.1022
## Number of obs: 336, groups:  Observer, 28
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.26288    0.04509  -5.830 5.55e-09 ***
## Conditiongame -0.05776    0.04539  -1.272  0.20323
## as.factor(COA)100 -0.05424    0.02905  -1.867  0.06191 .
## as.factor(COA)1000 -0.06163    0.02915  -2.115  0.03447 *
## COABlock       0.03216    0.01070   3.005  0.00265 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Cndtng as.(COA)100 a.(COA)1000
```

⁶The magic machinery underneath will mix ordinary least squares (OLS) estimates for fixed effects with Best Linear Unbiased Predictions (BLUP) for random effects.


```
## Conditiongm -0.501
## as.(COA)100 -0.320 0.002
## a.(COA)1000 -0.323 0.002 0.491
## COABlock -0.600 0.000 0.003 0.010
```

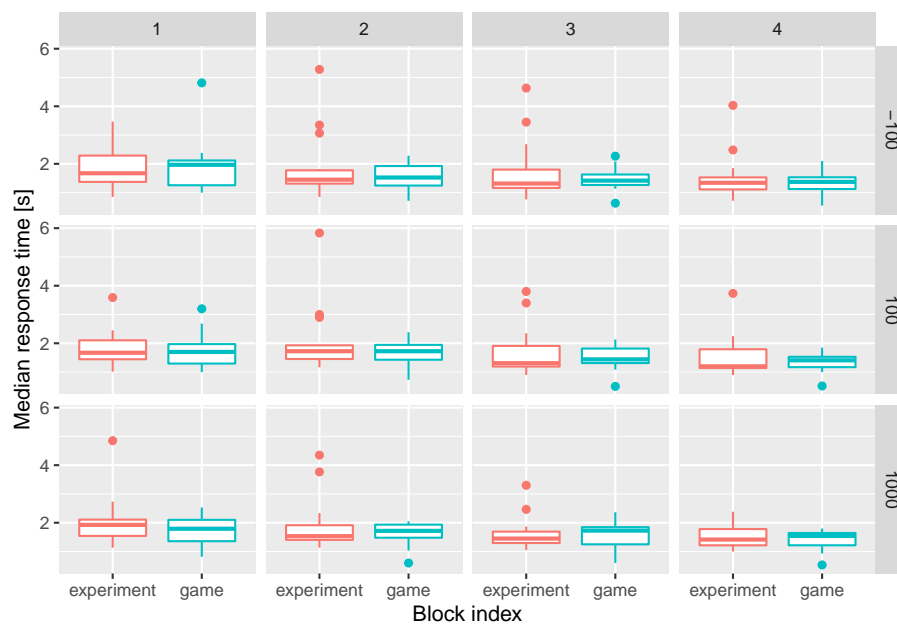
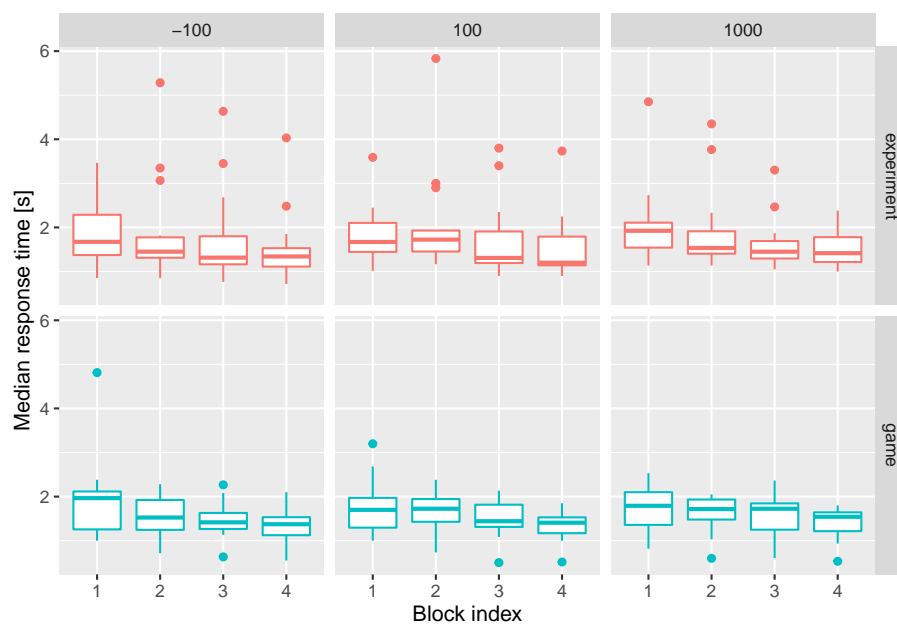
As you can see, experience definitely improves the accuracy (effect for COABlock is positive and significant), there seems to be some effect of difficulty at least between extreme cases of COA = -100 ms (baseline) and COA = 1000 ms. But, does not seem to be much of an effect of the condition. We can also confirm this ANOVA-style with a single significance value for each fixed factor via `drop1()` function, you will need to specify `test = "Chisq"` as a parameter to get significance values.

```
## Single term deletions
##
## Model:
## cbind(Ncorrect, Ntotal) ~ Condition + as.factor(COA) + COABlock +
## (1 | Observer)
##          npar    AIC    LRT Pr(Chi)
## <none>          1788.8
## Condition      1 1788.3 1.5749 0.209504
## as.factor(COA)  2 1790.1 5.3724 0.068141 .
## COABlock       1 1795.8 9.0345 0.002649 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Response times

What about response times? Repeat the analysis but with a few changes. First, we only need to compute median response time instead of proportion of correct trials. Second, for the analysis, we use linear (not generalized) mixed models via `lmer()` function from `lmerTest` package. Its advantage over the function with the same name from `lme4` package is in providing significance values. Again, use `lmerTest::lmer()` notation to use function from `lmerTest` and not the function of the same name in `lme4` package.

Observer	Condition	COA	COABlock	MedianRT
AAF1997w	experiment	-100	1	0.8500000
AAF1997w	experiment	-100	2	0.8494999
AAF1997w	experiment	-100	3	0.7660000
AAF1997w	experiment	-100	4	0.7180001



```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: MedianRT ~ Condition + as.factor(COA) + COABlock + (1 | Observer)
## Data: rt
```

```
##
## REML criterion at convergence: 376.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -4.6729 -0.4167 -0.0270  0.3736  6.0652
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
## Observer (Intercept) 0.3913   0.6255
## Residual              0.1275   0.3570
## Number of obs: 336, groups:  Observer, 28
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    2.152089   0.177100  31.010542  12.152 2.50e-13 ***
## Conditiongame -0.201307   0.239619  25.999998  -0.840   0.409
## as.factor(COA)100 -0.009205   0.047713 305.000001  -0.193   0.847
## as.factor(COA)1000 -0.008772   0.047713 305.000001  -0.184   0.854
## COABlock       -0.142757   0.017422 305.000001  -8.194 7.05e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Cndtng as.(COA)100 a.(COA)1000
## Conditiongm -0.677
## as.(COA)100 -0.135  0.000
## a.(COA)1000 -0.135  0.000  0.500
## COABlock    -0.246  0.000  0.000      0.000

## Single term deletions using Satterthwaite's method:
##
## Model:
## MedianRT ~ Condition + as.factor(COA) + COABlock + (1 | Observer)
##              Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Condition    0.0900  0.0900     1    26  0.7058    0.4085
## as.factor(COA) 0.0060  0.0030     2   305  0.0237    0.9766
## COABlock      8.5594  8.5594     1   305 67.1409 7.046e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Computing the score

First, we need to compute score for each trial. The catch is, the score depends on both participants response on a *current* trial (correct or not and how fast

was the response) and on *previous* trials (the score is multiplied by a combo: number of correct responses on a row + 1).

We begin by computing a raw score for each trial using the following rules:

- If the response is incorrect, the raw score is 0, otherwise
- $raw\ score = ceiling(10 \cdot \frac{4-RT}{3})$ but it cannot be larger than 10 or smaller than 0.

Function `ceiling(x)` returns the smallest integers not less than the corresponding elements of `x`. There is no function that could “clip” a value between 0 and 10 in R, so you need to write it yourself. It should take three parameters

1. Vector of values to be clipped.
2. Lower value limit.
3. Higher value limit.

```
example_vector <- c(-1, 15, 2, 10, 0, -4)
clip(example_vector, 0, 10)
```

```
## [1] 0 10 2 10 0 0
```

Here is the head of the table with the computed raw score

```
results %>%
  filter(RawScore==2) %>%
  select(-c(Target, Match, Response, RT, COABlock, OnsetDelay)) %>%
  head(10) %>%
  knitr::kable()
```

Observer	Condition	Block	Trial	COA	Correct	RawScore
AKB1996w	experiment	3	26	1000	TRUE	2
AKB1996w	experiment	8	47	1000	TRUE	2
AKB1996w	experiment	12	40	1000	TRUE	2
ARF1995w	game	1	42	-100	TRUE	2
ARF1995w	game	1	44	-100	TRUE	2
ARF1995w	game	2	35	100	TRUE	2
ARF1995w	game	3	4	1000	TRUE	2
ARF1995w	game	3	8	1000	TRUE	2
ARF1995w	game	3	14	1000	TRUE	2
ARF1995w	game	3	19	1000	TRUE	2

To compute combo multiplier (number of correct responses on the row), we will write another function that loops over a vector of `Correct` responses.

Every correct response (TRUE) add 1 to the multiplier for the *next* trial. Every incorrect response resets it to 1, again, for the *next* trial.

```
correct <- c(TRUE, TRUE, TRUE, FALSE, FALSE, TRUE, TRUE, FALSE, TRUE)
compute_combo(correct)
```

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

Once you have the function and it work correctly, you can use to compute combo multiplier for the table. However, note that you need to do it per block, so you need to group data by **Observer**, **Condition**, **COA**, and **COABlock** first. Otherwise, your combo score won't be 1 at the beginning of each block.

```
results %>%
  head(10) %>%
  select(-c(Target, Match, Response, RT, COABlock, OnsetDelay)) %>%
  knitr::kable()
```

Observer	Condition	Block	Trial	COA	Correct	RawScore	Combo
AAF1997w	experiment	1	1	-100	FALSE	0	1
AAF1997w	experiment	1	2	-100	TRUE	10	1
AAF1997w	experiment	1	3	-100	TRUE	10	2
AAF1997w	experiment	1	4	-100	TRUE	10	3
AAF1997w	experiment	1	5	-100	TRUE	10	4
AAF1997w	experiment	1	6	-100	TRUE	10	5
AAF1997w	experiment	1	7	-100	TRUE	10	6
AAF1997w	experiment	1	8	-100	TRUE	10	7
AAF1997w	experiment	1	9	-100	FALSE	0	8
AAF1997w	experiment	1	10	-100	TRUE	10	1

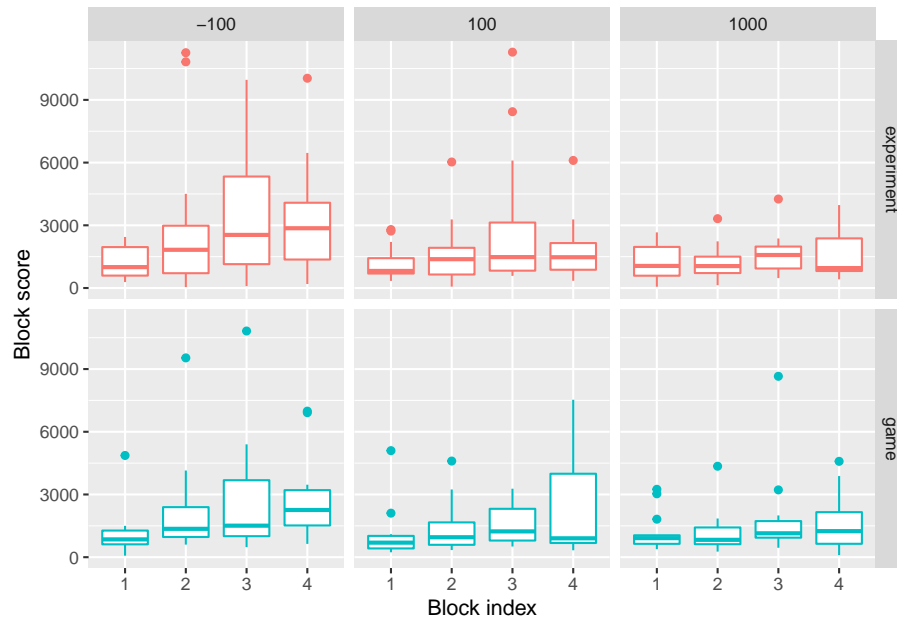
To get the actual score you just multiply raw score and multiplier

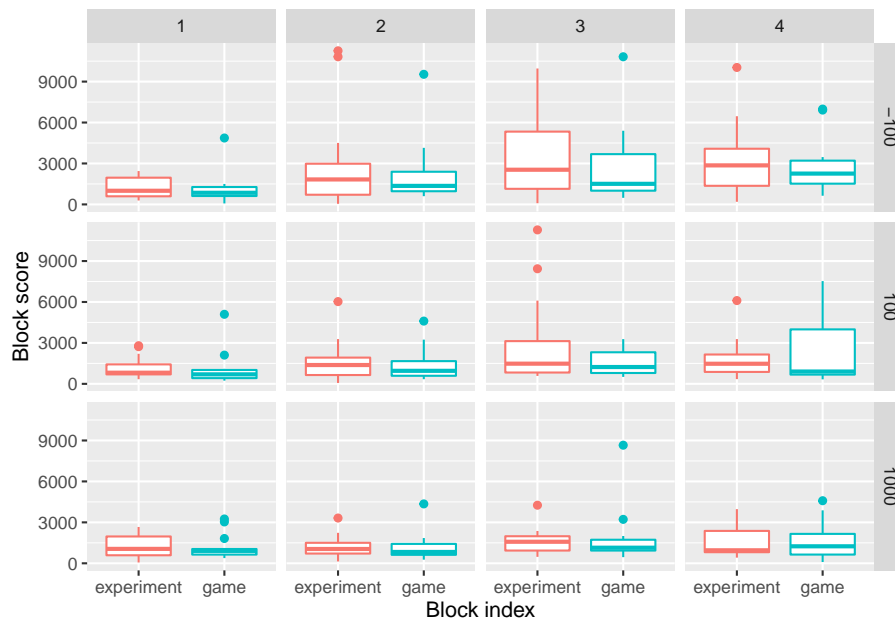
```
results %>%
  head(10) %>%
  select(-c(Target, Match, Response, RT, COABlock, OnsetDelay)) %>%
  knitr::kable()
```

Observer	Condition	Block	Trial	COA	Correct	RawScore	Combo	Score
AAF1997w	experiment	1	1	-100	FALSE	0	1	0
AAF1997w	experiment	1	2	-100	TRUE	10	1	10
AAF1997w	experiment	1	3	-100	TRUE	10	2	20
AAF1997w	experiment	1	4	-100	TRUE	10	3	30
AAF1997w	experiment	1	5	-100	TRUE	10	4	40
AAF1997w	experiment	1	6	-100	TRUE	10	5	50
AAF1997w	experiment	1	7	-100	TRUE	10	6	60
AAF1997w	experiment	1	8	-100	TRUE	10	7	70
AAF1997w	experiment	1	9	-100	FALSE	0	8	0
AAF1997w	experiment	1	10	-100	TRUE	10	1	10

Now that you have score per trial, perform analysis similar to response times but for each observer, condition, COA, and COA block compute a *total* score for each block. Otherwise, plot and analyze it similar to response times.

Observer	Condition	COA	COABlock	TotalScore
AAF1997w	experiment	-100	1	1429
AAF1997w	experiment	-100	2	10820
AAF1997w	experiment	-100	3	9960
AAF1997w	experiment	-100	4	5290
AAF1997w	experiment	100	1	2796
AAF1997w	experiment	100	2	3281





```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: TotalScore ~ Condition + as.factor(COA) + COABlock + (1 | Observer)
## Data: score
##
## REML criterion at convergence: 5871.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9447 -0.4973 -0.1420  0.2494  4.6969
##
## Random effects:
## Groups Name Variance Std.Dev.
## Observer (Intercept) 1234010 1111
## Residual 2349159 1533
## Number of obs: 336, groups: Observer, 28
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    1667.32    388.67    55.80   4.290 7.17e-05 ***
## Conditiongame   -261.00    451.94    26.00  -0.578 0.568566
## as.factor(COA)100 -704.64    204.82   305.00 -3.440 0.000662 ***
## as.factor(COA)1000 -1009.47    204.82   305.00 -4.929 1.36e-06 ***
## COABlock         366.22     74.79   305.00   4.897 1.58e-06 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Cndtng as.(COA)100 a.(COA)1000
## Conditiongm -0.581
## as.(COA)100 -0.263  0.000
## a.(COA)1000 -0.263  0.000  0.500
## COABlock    -0.481  0.000  0.000      0.000

## Single term deletions using Satterthwaite's method:
##
## Model:
## TotalScore ~ Condition + as.factor(COA) + COABlock + (1 | Observer)
##              Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Condition      783474   783474     1    26  0.3335    0.5686
## as.factor(COA) 60049893 30024946     2   305 12.7811 4.673e-06 ***
## COABlock       56330349 56330349     1   305 23.9789 1.582e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Chapter 12

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	

12.1 Bad names to good names

We have a couple of columns that are not easy to use:

- @#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

12.2 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	

12.3 Factors

First, let us do easy bits, converting several columns to factors and setting up labels.

- `sex`
 - `1 : female`
 - `2 : male`
- `Condition:`
 - `0 : control`
 - `1 : speed`
 - `2 : size`
 - `3 : random`
- `IncongruentFirst`
 - `0 : Congruent first`
 - `1 : Incongruent first`

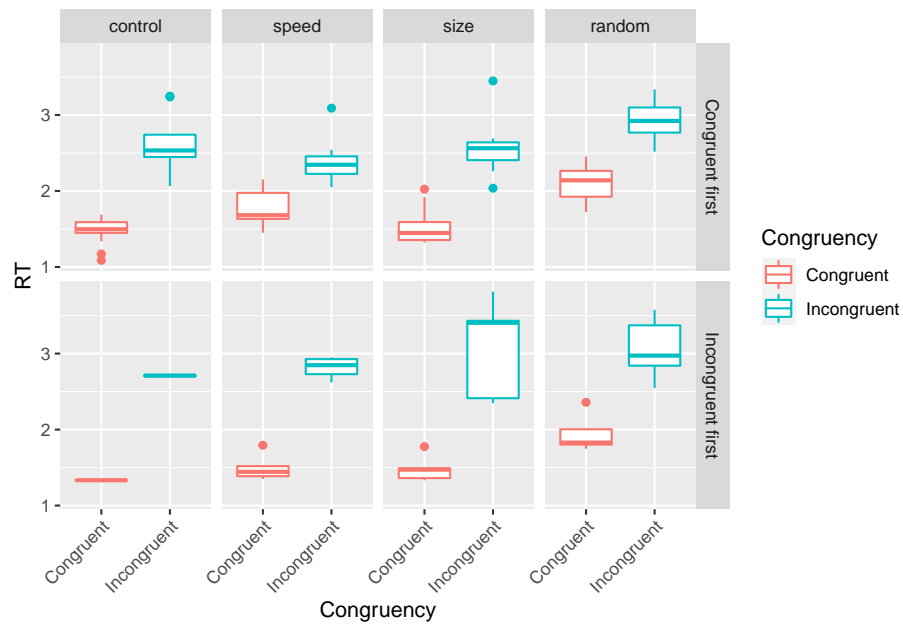
HabitNr	sex	Condition	IncongruentFirst	errorsCongruent	ReactiontimemeanCong	errorsIncongruent
1	male	control	Congruent first	2	1.477454	1
2	male	speed	Congruent first	1	2.028072	1
3	female	size	Congruent first	1	1.334083	
4	male	control	Congruent first	2	1.171517	
5	male	speed	Congruent first	0	2.097203	2
6	male	size	Congruent first	2	1.322103	

12.4 Response times

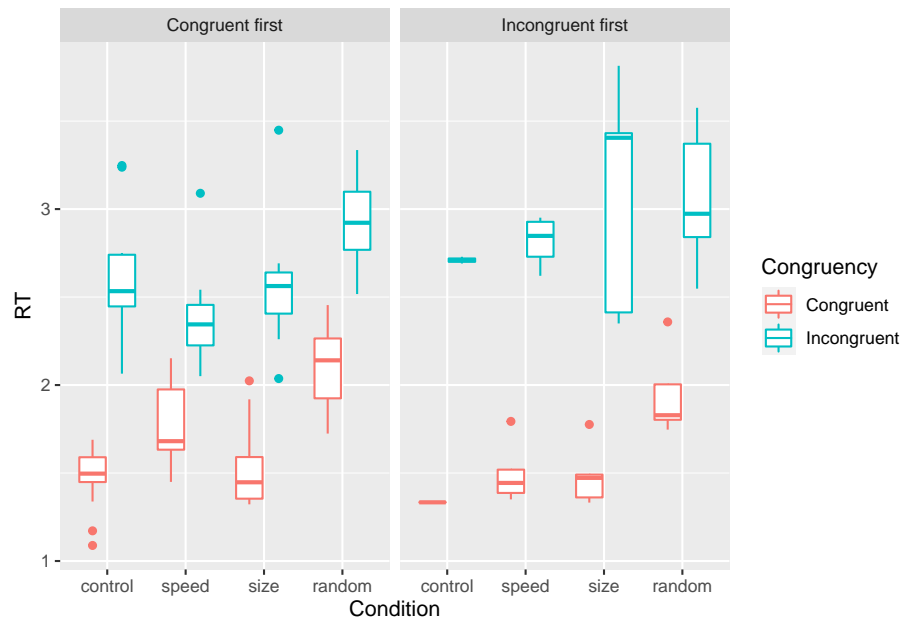
Next, we need to “spin-off” a separate table that will contain information about response times per congruency manipulation. Thus we want a table where column **Congruency** indicates whether presentation was congruent, whereas two columns (**ReactiontimemeanCong** and **ReactiontimemeanInco**) for response 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 response 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 and HabitNr (participant ID) as a random factor. We will not look at any interactions although they are most likely of interest for the follow up analysis.

```
## boundary (singular) fit: see ?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
## Conditionsized    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
## Conditionsized    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) Cndtnspd Cndtnsz Cndtnr IncFlf
## Cndtnspd -0.628
## Cndtnsz -0.628 0.539
```

```
## Conditnrndm -0.603  0.525  0.525
## IncngrntFlf -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 ?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
```

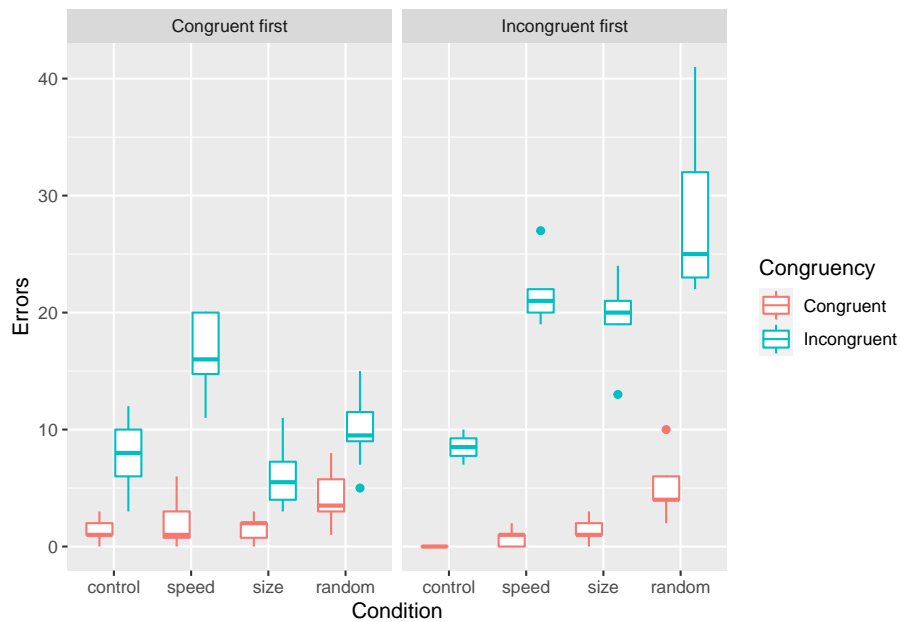
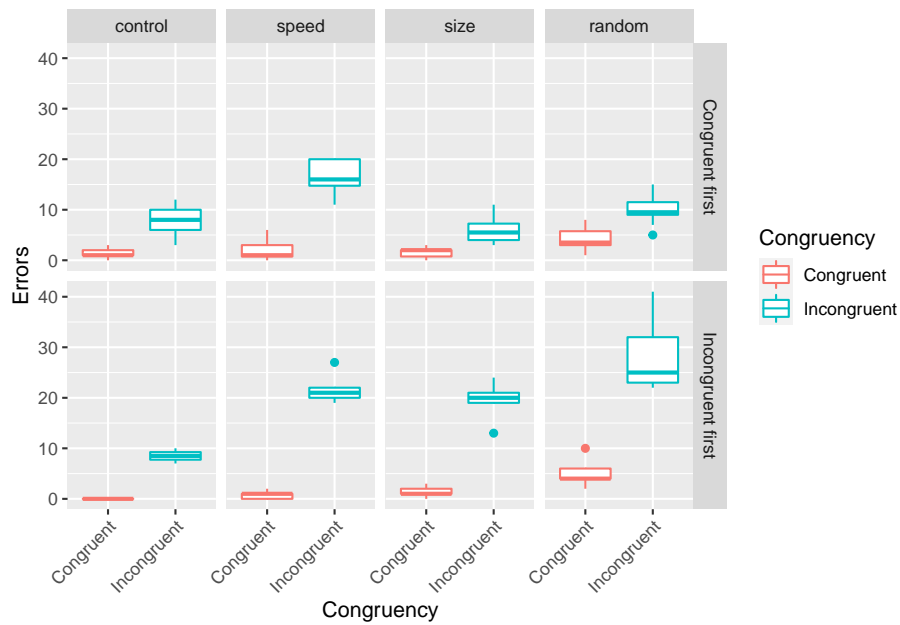
In short, we a highly significant effect of color-word congruency (good news, otherwise out Stroop task wasn't very successful) and one condition (*random*) is clear difference. However, the *order* of block (first congruent then incongruent or vice versa) did not really matter.

12.5 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 ***
## Conditionsiz      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 IncFI
## Conditinspd -0.600
## Conditionsz -0.542  0.615
## Conditnrndm -0.575  0.651  0.615
## IncngrntFI -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.

12.6 Physiological signal

Now we come to the tricky part because information about physiological signal (I'll call it 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	Bs3	Bs4
1	6.490969	4.564023	6.354532	5.224722	12.339243	6.490969	4.564023	6.354532	5.224722	12.339243
2	4.864416	7.957840	6.587935	3.044139	2.909219	4.864416	7.957840	6.587935	3.044139	2.909219
3	10.071530	1.650143	1.562964	6.156831	8.045311	10.071530	1.650143	1.562964	6.156831	8.045311
4	12.162085	4.796817	2.649034	2.019965	5.061974	12.162085	4.796817	2.649034	2.019965	5.061974
5	3.265458	7.900660	4.254162	16.426251	6.177225	3.265458	7.900660	4.254162	16.426251	6.177225
6	5.478926	5.845528	6.175421	4.388986	2.740655	5.478926	5.845528	6.175421	4.388986	2.740655

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:B4**. 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

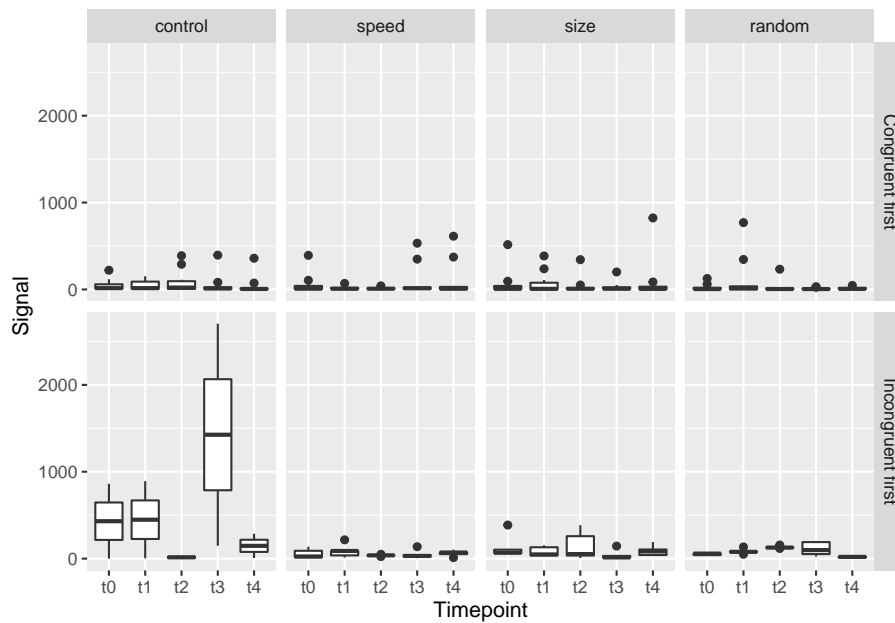
HabitNr	Condition	IncongruentFirst	Timepoint	Signal
31	control	Congruent first	t0	61.92695
31	control	Congruent first	t1	130.66799
31	control	Congruent first	t2	111.63928
31	control	Congruent first	t3	82.54038
31	control	Congruent first	t4	73.56076
32	control	Incongruent first	t0	861.35340

Again, same procedure for rows with valid **Bs0:Bs4** columns

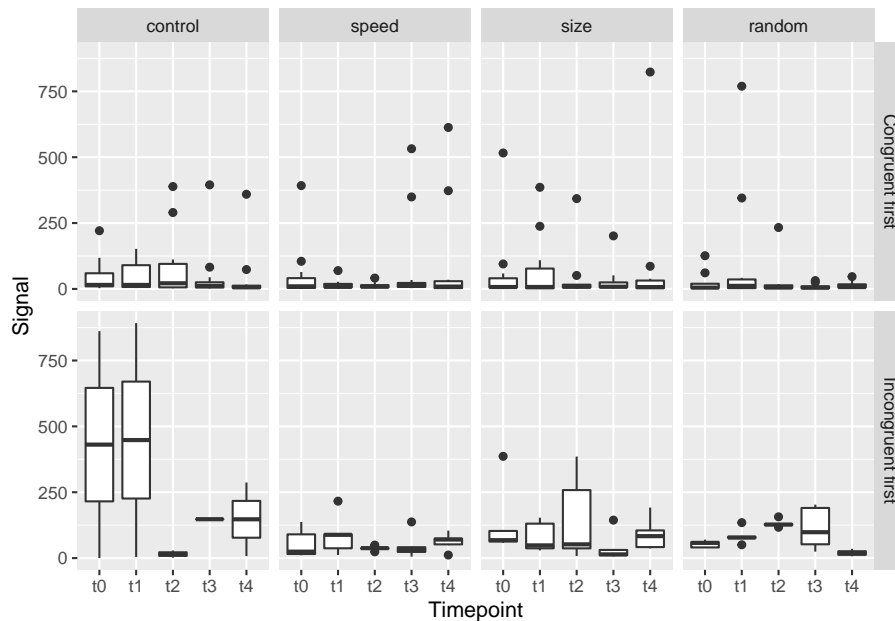
HabitNr	Condition	IncongruentFirst	Timepoint	Signal
1	control	Congruent first	t0	6.490969
1	control	Congruent first	t1	4.564023
1	control	Congruent first	t2	6.354532
1	control	Congruent first	t3	5.224722
1	control	Congruent first	t4	12.339243
2	speed	Congruent first	t0	4.864416

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
## Conditionsized -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 .
## Conditionsized
## 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
## IncngrntFlf -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
```

12.7 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.