

Workshop: R for datascience

Laurent Rouvière

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<https://lrouviere.github.io/R-for-datascience-lecture/>

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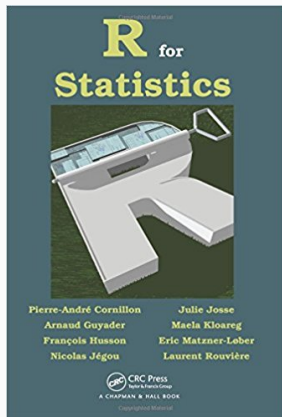
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 - import and concatenate datasets, manipulate individuals and variables
 - visualize data
 - implement some of the most important statistical algorithms on real data (IML lecture)

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 - visualize data
 - implement some of the most important statistical algorithms on real data (IML lecture)
- **Teacher:** Laurent Rouvière, laurent.rouviere@univ-rennes2.fr
 - **Research interests:** nonparametric statistics, statistical learning
 - **Teaching:** statistics and probability (University and engineer school)
 - **Consulting:** energy (ERDF), banks, marketing, sport

Resources

- Slides and tutorials (1 tutorial=1 or 2 concepts+exercises) available at <https://lrouviere.github.io/R-for-datascience-lecture/>
- The web
- Book: R for statistics, Chapman & Hall



Outline

1. Introduction
2. Some examples
3. Outline
4. Rstudio, Rmarkdown and R-packages
5. R objects (Review)
6. Reading data from files
7. Data manipulation with Dplyr
8. Visualize data
9. Visualization with ggplot2
10. Mapping with leaflet
11. Regression models with R
12. Conclusion

Introduction

Why R?

- More and more **data** available in many fields (energy, health, sport, economy. . . .)
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 - to import (merge) datasets
 - to manipulate data (**Data Mining**)
 - to visualize data (**Data Mining+Visualization**)
 - to choose and fit models (**Data Mining+statistical learning**)
 - to visualize models (models are more and more complex. . .)
 - to return and visualize results (web applications)

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Important remark

- **All** these topics can be addressed with **R**.
- Today, **R** (data scientists) and **Python** (computer scientists) are the most important softwares to make data science.

Few words about R

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Few words about R

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Consequence

- The software is always up to date.
- Clearly one of the reasons of the R success.

Some examples

Example: Fisher's iris

```
> data(iris)
> summary(iris)

##      Sepal.Length      Sepal.Width      Petal.Length      Petal.Width
##      Min.       :4.300      Min.       :2.000      Min.       :1.000      Min.       :0.100
##      1st Qu.:5.100      1st Qu.:2.800      1st Qu.:1.600      1st Qu.:0.300
##      Median :5.800      Median :3.000      Median :4.350      Median :1.300
##      Mean   :5.843      Mean   :3.057      Mean   :3.758      Mean   :1.199
##      3rd Qu.:6.400      3rd Qu.:3.300      3rd Qu.:5.100      3rd Qu.:1.800
##      Max.   :7.900      Max.   :4.400      Max.   :6.900      Max.   :2.500
##              Species
##      setosa      :50
##      versicolor:50
##      virginica   :50
##
##
##
```

Objectives

Goal

Explain **species** by the other variables.

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Goal

Explain **species** by the other variables.

- Species is a **categorical variable**.
- We are faced with a **supervised classification** problem.

Manipulate the data

```
> apply(iris[,1:4],2,mean)
## Sepal.Length Sepal.Width Petal.Length Petal.Width
##      5.843333      3.057333      3.758000      1.199333
> apply(iris[,1:4],2,var)
## Sepal.Length Sepal.Width Petal.Length Petal.Width
##      0.6856935      0.1899794      3.1162779      0.5810063
```

Manipulate the data

```
> apply(iris[,1:4],2,mean)
## Sepal.Length Sepal.Width Petal.Length Petal.Width
##      5.843333      3.057333      3.758000      1.199333
> apply(iris[,1:4],2,var)
## Sepal.Length Sepal.Width Petal.Length Petal.Width
##      0.6856935      0.1899794      3.1162779      0.5810063
```

Remark

Non-informative for the problem (highlight differences between species).

Data manipulation with dplyr

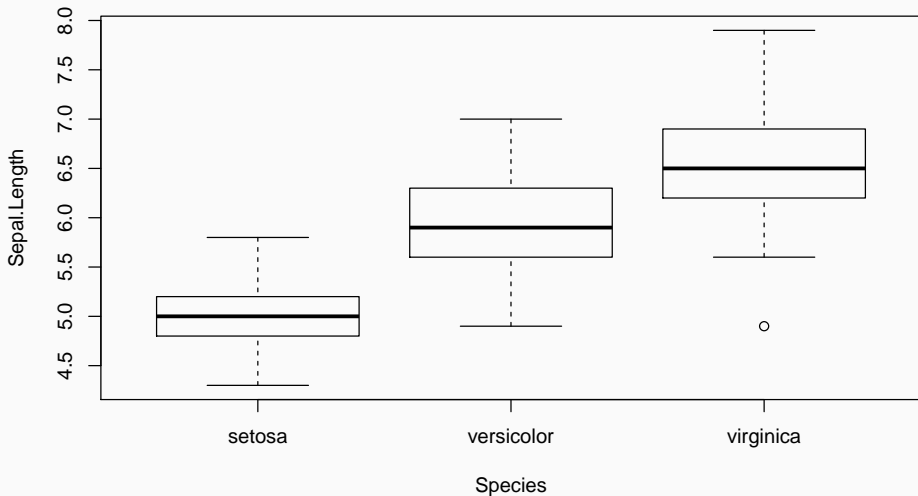
- **dplyr** is powerful R-package to transform and summarize tabular data with rows and columns.

```
> library(dplyr)
> iris %>% group_by(Species) %>% summarise_all(mean)
## # A tibble: 3 x 5
##   Species      Sepal.Length Sepal.Width Petal.Length Petal.Width
##   <fct>          <dbl>         <dbl>         <dbl>         <dbl>
## 1 setosa          5.01           3.43           1.46           0.246
## 2 versicolor      5.94           2.77           4.26           1.33
## 3 virginica       6.59           2.97           5.55           2.03
```

- **More informative:** we obtain means for **each species**.

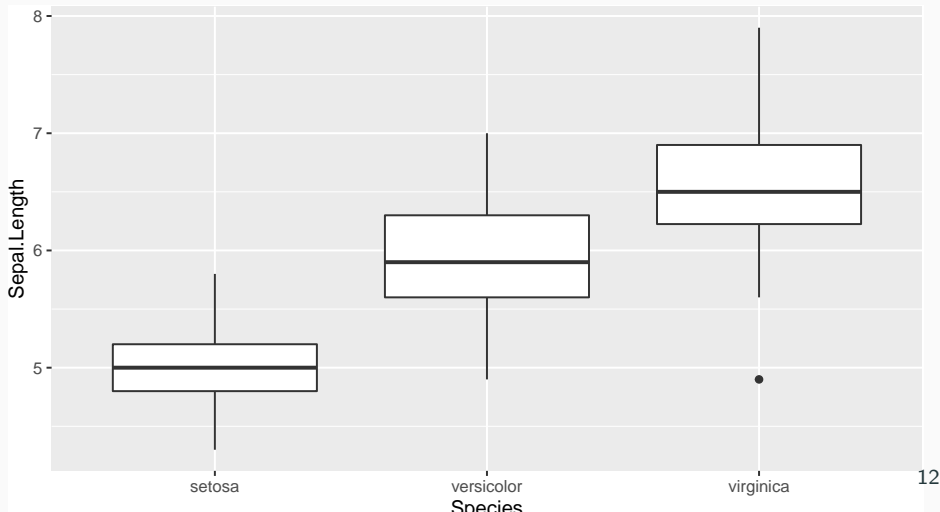
Visualization

```
> boxplot(Sepal.Length~Species,data=iris)
```



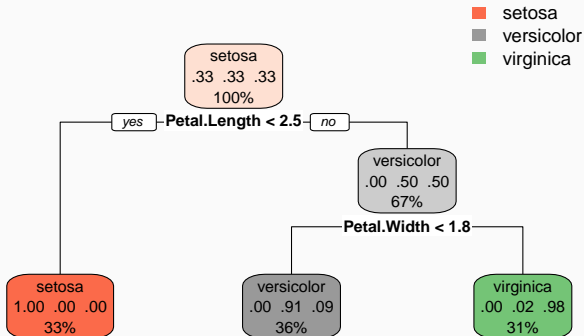
Visualization with ggplot2

```
> library(ggplot2)
> ggplot(iris)+aes(x=Species,y=Sepal.Length)+geom_boxplot()
```



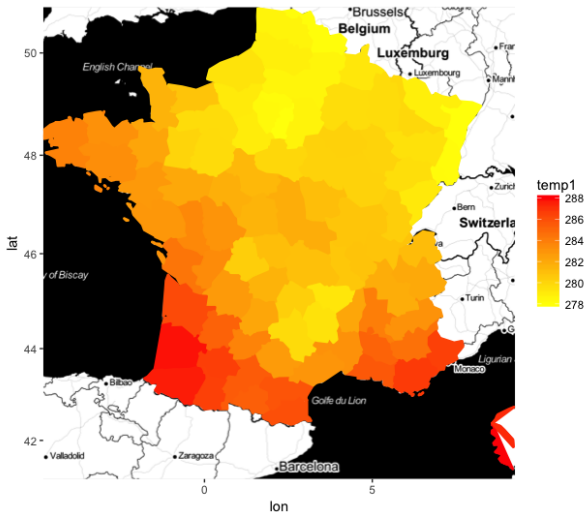
Modelling

```
> library(rpart)
> tree <- rpart(Species~.,data=iris)
> library(rpart.plot)
> rpart.plot(tree)
```



Maps with ggmap

- **Goal:** draw a map of the temperatures in france.

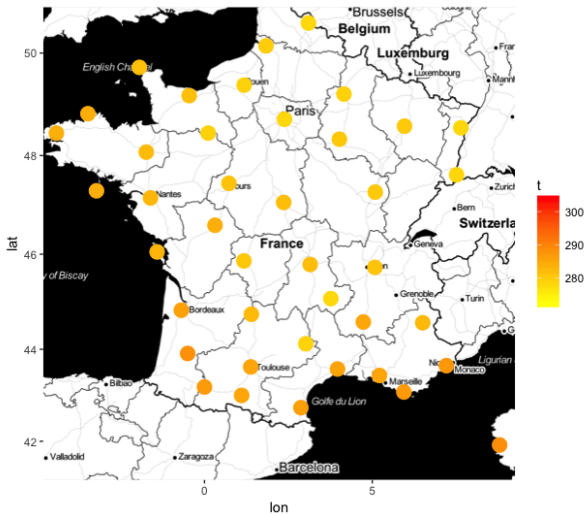


Load the data + background map

- Data are downloaded from meteofrance (temperatures for about 60 stations).

```
> temp <- fread("https://donneespubliques.meteofrance.fr/  
+             donnees_libres/Txt/Synop/synop.2019082815.csv")  
> station <- fread("https://donneespubliques.meteofrance.fr/  
+                 donnees_libres/Txt/Synop/postesSynop.csv")  
> back.fr <- get_map("France",maptype="toner",zoom=6)  
> ggmap(back.fr)+geom_point(data=D,  
+   aes(y=Latitude,x=Longitude,color=t),size=5)+  
+   scale_color_continuous(low="yellow",high="red")
```

A first map



Model

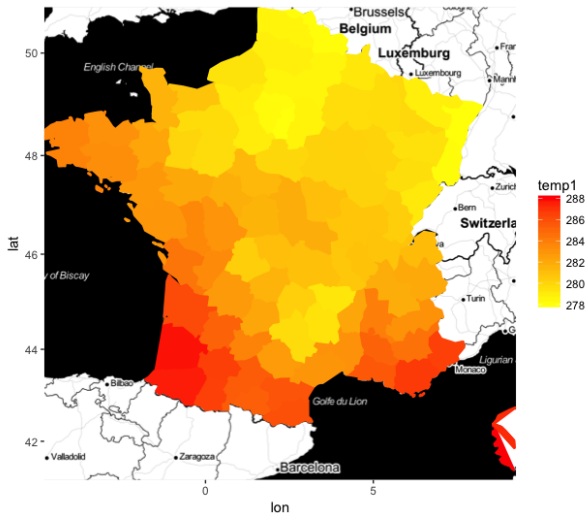
- **model** of **nearest neighbors** to estimate temperatures for all longitudes and latitudes.

```
> library(FNN)
> mod <- knn.reg(train=D[,.(Latitude,Longitude)],y=D[,t],
+               test=Test1[,.(Latitude,Longitude)],k=1)$pred
```

- Visualisation with **ggmap**.

```
> library(ggmap)
> ggmap(back.fr)+geom_polygon(data=Test5,
+   aes(y=Latitude,x=Longitude,
+       fill=temp1,color=temp1,group=dept),size=1)+
+   scale_fill_continuous(low="yellow",high="red")+
+   scale_color_continuous(low="yellow",high="red")
```

The temperature map



Interactive web apps with shiny

- **Shiny** is a R package that makes it easy to build interactive web apps straight from R.
- **Example:** basic graphics for a dataset.

```
> library(shiny)
> runApp('desc_app.R')
```

Outline

In this workshop

- 15 hours for 5 (or 6) topics
- 1 topic = slides + tutorial (notebook) to complete (add comments and do exercises)

R Notebook

- document which combines R code and comments.
- code can be **executed independently and interactively**, with **output visible** immediately beneath the input.
- very nice to make high quality reports.

Schedule

- Introduction to R lecture: basics of R (objects, apply, matrices, date, control flow statements)

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- **Introduction to R** lecture: basics of R (objects, apply, matrices, date, control flow statements)

R for datascience

- Tuto 1: Rstudio (notebook and presentations) (1 hour)
- Tuto 2: R objects (review, 1 or 2 hours)
- Tuto 3: data manipulation with dplyr (4 hours)
- Tuto 4: data visualization with ggplot2 (4 hours)
- Tuto 5: mapping with leaflet (2 hours)
- Tuto 6: modeling with R (transition with the ISL lecture, 2 hours).

- When ???
- combined with the machine learning lecture
 - Multiple choice test (50%)
 - Data science project (50%)

- Require personal efforts.
- **To Practice**, to make mistakes and to correct these mistakes: **only way** to learn a software.

- Require personal efforts.
- **To Practice**, to make mistakes and to correct these mistakes: **only way** to learn a software.
- You need to **work alone** between the sessions.
- Everyone can develop at its own pace (the goal is to progress, not to become a specialist of R in 15 hours), and **ask questions** during the sessions.
- I'm here to (**try**) to answer.

Rstudio, Rmarkdown and R-packages

- **RStudio** is an **integrated development environment** for R.
- It makes **R** easier to practice.
- It includes a console, syntax-highlighting editor that supports direct code execution, tools for plotting, history, debugging and workspace management.
- It is also **freely distributed** at the address <https://www.rstudio.com>.

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The screen is divided into 4 windows:

- **Console**: where you enter command and see output
- **Workspace and History**: show the active objects
- **Files Plots...**: show all files and folders in the workspace, see output graph, install packages. . .
- **R script**: where you keep a record of your work. Don't forget to **regularly save this files!**

Rmarkdown

Rmarkdown?

- An Rmarkdown (.Rmd) file is a record of your work.
- It contains code, output and comments of your work.
- It produces high quality report in many format (text documents, slides, etc...).
- These slides have been made with Rmarkdwon.

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-
- **Reproducible Research**: at the click of a button, you can rerun the code in an R Markdown file to reproduce your work and **export the results as a finished report**.
 - **Dynamic Documents**: you can choose to export the finished report in a **wide range of outputs**, including html, pdf, MS Word, or RTF documents; html or pdf based slides, Notebooks, and more.

Packages

- Set of R programs which supplements and enhances the functions of R.
- Generally reserved for specific methods or fields of applications
- More than 15 000 packages available at <https://cran.r-project.org>.
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2 steps

- Installation: `install.packages(package.name)` (just one time)
- Loading: `library(package.name)` (each time)

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⇒ work on Tuto 1.

Tuto 1

- Download the *.Rmd* file **Tuto1.Rmd** in https://lrouviere.github.io/stat_grand_dim/
- Open the file in **Rstudio**.
- Click on **File + Reopen with encoding** and select **utf8**
- Add in the beginning of the file

```
---  
title: 'Tuto 1: RStudio environment'  
output: html_notebook  
---
```


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---
```

- Save the file in the repository of your choice and click on **Preview**.
- **Read** the tutorial and **do exercices**.

R objects (Review)

Numeric and characters

- Numeric (easy)

```
> x <- pi
> x
## [1] 3.141593
> is.numeric(x)
## [1] TRUE
```

- Characters

```
> b <- "X"
> paste(b, 1:5, sep="")
## [1] "X1" "X2" "X3" "X4" "X5"
```

Vectors

- Creation: `c`, `seq`, `rep`

```
> x1 <- c(1,3,4)
> x2 <- 1:5
> x3 <- seq(0,10,by=2)
> x4 <- rep(x1,3)
> x5 <- rep(x1,3,each=3)
```

- Extraction:

```
> x3[c(1,3,4)] # same as x3[x1]
## [1] 0 4 6
```

Logical

```
> 1<2
## [1] TRUE
> 1==2
## [1] FALSE
> 1!=2
## [1] TRUE
```

```
> x <- 1:3
> test <- c(TRUE,FALSE,TRUE)
> x[test]
## [1] 1 3
```

```
> size <- runif(5,150,190) #5 sizes randomly generated between  
> #150 and 190  
> size  
## [1] 178.8362 185.0309 180.4393 185.4450 168.2592
```

Problem

Select size more than 174.

```
> size <- runif(5,150,190) #5 sizes randomly generated between  
#150 and 190  
> size  
## [1] 178.8362 185.0309 180.4393 185.4450 168.2592
```

Problem

Select size more than 174.

```
> size>174  
## [1] TRUE TRUE TRUE TRUE FALSE  
> size[size>174]  
## [1] 178.8362 185.0309 180.4393 185.4450
```

- For **categorical variables** in datasets:

```
> x1 <- factor(c("a","b","b","a","a"))
> x1
## [1] a b b a a
## Levels: a b
> levels(x1)
## [1] "a" "b"
```


Data not properly collected

- Assume that data are collected: 0=man, 1=woman

```
> X <- c(1,1,0,0,1)
```

```
> summary(X)
```

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	0.0	0.0	1.0	0.6	1.0	1.0

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- Problem:** R reads X as a continuous vector \Rightarrow it could generate problems for some statistical studies.

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##      0.0    0.0    1.0    0.6    1.0    1.0
```

- Problem:** R reads X as a continuous vector \Rightarrow it could generate problems for some statistical studies.

- Solution:**

```
> X <- as.factor(X)
```

```
> levels(X) <- c("man", "woman")
```

```
> X
```

```
## [1] woman woman man    man    woman
```

```
## Levels: man woman
```

```
> summary(X)
```

```
##      man woman
```

```
##      2      3
```

Matrix

■ Creation

```
> m <- matrix(1:4,nrow=2,byrow=TRUE)
> m
##      [,1] [,2]
## [1,]    1    2
## [2,]    3    4
```

■ Extraction

```
> m[1,2]
> m[1,] #First row
> m[,2] #Second column
```

List

- Allow to manage different objects

```
> mylist <- list(vector=1:5,mat=matrix(1:8,nrow=2))
> mylist
## $vector
## [1] 1 2 3 4 5
##
## $mat
##      [,1] [,2] [,3] [,4]
## [1,]    1    3    5    7
## [2,]    2    4    6    8
```

- Extraction:

```
> mylist[[1]]
> mylist$vector
> mylist[["vector"]]
```

Dataframe

- Objects for representing **data** in **R**

```
> name <- c("Paul", "Mary", "Steven", "Charlotte", "Peter")
> sex <- c(0, 1, 0, 1, 0)
> size <- c(180, 165, 168, 170, 175)
> data <- data.frame(name, sex, size)
> data
```

##	name	sex	size
## 1	Paul	0	180
## 2	Mary	1	165
## 3	Steven	0	168
## 4	Charlotte	1	170
## 5	Peter	0	175

```
> summary(data)
```

##	name	sex	size
##	Charlotte:1	Min. :0.0	Min. :165.0
##	Mary :1	1st Qu.:0.0	1st Qu.:168.0
##	Paul :1	Median :0.0	Median :170.0
##	Peter :1	Mean :0.4	Mean :171.6
##	Steven :1	3rd Qu.:1.0	3rd Qu.:175.0
##		Max. :1.0	Max. :180.0

```
> summary(data)
```

##	name	sex	size
##	Charlotte:1	Min. :0.0	Min. :165.0
##	Mary :1	1st Qu.:0.0	1st Qu.:168.0
##	Paul :1	Median :0.0	Median :170.0
##	Peter :1	Mean :0.4	Mean :171.6
##	Steven :1	3rd Qu.:1.0	3rd Qu.:175.0
##		Max. :1.0	Max. :180.0

Problem

Here **sex** is considered as a **numeric variable**. It is a **categorical variable**.


```

> data$sex <- as.factor(data$sex)
> levels(data$sex) <- c("man", "woman")
> summary(data)
##           name           sex           size
## Charlotte:1   man    :3   Min.      :165.0
## Mary          :1   woman:2   1st Qu.:168.0
## Paul          :1                Median :170.0
## Peter         :1                Mean    :171.6
## Steven        :1                3rd Qu.:175.0
##                Max.      :180.0

```

```

> data$sex <- as.factor(data$sex)
> levels(data$sex) <- c("man", "woman")
> summary(data)
##           name           sex           size
## Charlotte:1   man   :3   Min.      :165.0
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## Paul          :1           Median :170.0
## Peter         :1           Mean    :171.6
## Steven        :1           3rd Qu.:175.0
##              Max.      :180.0

```

Problem

Here **name** is considered as a **variable**. It is the individual names (the ID of individuals)!

```
> row.names(data) <- data$name
> data <- data[,-1] #delete column name
> data
```

<i>##</i>	<i>sex</i>	<i>size</i>
<i>## Paul</i>	<i>man</i>	<i>180</i>
<i>## Mary</i>	<i>woman</i>	<i>165</i>
<i>## Steven</i>	<i>man</i>	<i>168</i>
<i>## Charlotte</i>	<i>woman</i>	<i>170</i>
<i>## Peter</i>	<i>man</i>	<i>175</i>

Conclusion

We always have to check that data are **correctly interpreted** by **R** (with **summary** for instance).

Tibbles

- A **tibble** is a **modern** reimagining of the **data.frame**, keeping what time has proven to be effective, and throwing out what is not.
- We need to load the package **tidyverse** to use **tibble**.

Example: data frame

```
> name <- c("Paul","Mary","Steven","Charlotte","Peter")
> sex <- c(0,1,0,1,0)
> size <- c(180,165,168,170,175)
> age <- c("old","young","young","old","old")
> data <- data.frame(name,sex,size,age)
> summary(data)
```

##	name	sex	size	age
##	Charlotte:1	Min. :0.0	Min. :165.0	old :3
##	Mary :1	1st Qu.:0.0	1st Qu.:168.0	young:2
##	Paul :1	Median :0.0	Median :170.0	
##	Peter :1	Mean :0.4	Mean :171.6	
##	Steven :1	3rd Qu.:1.0	3rd Qu.:175.0	
##		Max. :1.0	Max. :180.0	

Example: tibble

```
> library(tidyverse)
> data1 <- tibble(name,sex,size,age)
> summary(data1)
```

##	name	sex	size	age
##	Length:5	Min. :0.0	Min. :165.0	Length:5
##	Class :character	1st Qu.:0.0	1st Qu.:168.0	Class :character
##	Mode :character	Median :0.0	Median :170.0	Mode :character
##		Mean :0.4	Mean :171.6	
##		3rd Qu.:1.0	3rd Qu.:175.0	
##		Max. :1.0	Max. :180.0	

dataframe vs tibbles

Main difference: no factor in tibbles.

⇒ work on tuto 2.

Reading data from files

- Data is generally contained within a **file** in which individuals are presented in rows and variables in columns.
- Functions **read.table** and **read.csv** allow to **import data** from *.txt* or *.csv* files.
- **.xls** files need to be **converted** into **.csv** files.

```
> data <- read.table("file",...)  
> data <- read.csv("file",...)
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> data <- read.table("file",...)  
> data <- read.csv("file",...)
```

- ... corresponds to many **options**. Options are **very important** since the data file always contains **specificities** (missing data, names of the variables...)

Indicating the path

- The **data file** needs to be located in the **working directory**. Otherwise, we have to indicate the **path** in **read.table**.
- **Example:** Read the file **data.csv** located in **/lectureR/Part1** :
 - Change the working directory

```
> setwd("~/lectureR/Part1")  
> df <- read.csv("data.csv",...)
```

Indicating the path

- The **data file** needs to be located in the **working directory**. Otherwise, we have to indicate the **path** in **read.table**.
- **Example:** Read the file **data.csv** located in **/lectureR/Part1** :
 - Change the working directory

```
> setwd("~/lectureR/Part1")  
> df <- read.csv("data.csv",...)
```

- Specify the directory in **read.csv**

```
> df <- read.csv("~/lecture_R/Part1/data.csv",...)
```

Indicating the path

- The **data file** needs to be located in the **working directory**. Otherwise, we have to indicate the **path** in **read.table**.
- **Example**: Read the file **data.csv** located in **/lectureR/Part1** :
 - Change the working directory

```
> setwd("~/lectureR/Part1")  
> df <- read.csv("data.csv",...)
```

- Specify the directory in **read.csv**

```
> df <- read.csv("~/lecture_R/Part1/data.csv",...)
```

- Use the **file.path** function

```
> path <- file.path("~/lecture_R/Part1/", "data.csv")  
> df <- read.csv(path,...)
```

Some important options

There are many important **options** in **read.table** and **read.csv**:

- **sep**: the field separation character (space, comma...)
- **dec**: the character used for decimal points (comma, points...)
- **header**: a logical value indicating whether the file contains the names of the variables as its first line
- **row.names**: a vector of row names (to identify individuals if needed)
- **na.strings**: a character vector of strings which are to be interpreted as NA values.
- ...

Example

- File `data_imp.txt`

name;size;age

John;174;32

Peter;?;28

Mary;165.5;NA

Example

- File `data_imp.txt`

name;size;age

John;174;32

Peter;?;28

Mary;165.5;NA

Characteristics

- 3 variables
- First line=name of the variables
- Missing values: NA, ?

First try

```
> path <- file.path("~COURS/EDHEC/R/SLIDES/", "data_imp.txt")
```

```
> df <- read.table(path)
```

```
> summary(df)
```

```
##           V1  
## John;174;32 :1  
## Mary;165.5;NA:1  
## name;size;age:1  
## Peter;?;28 :1
```


First try

```
> path <- file.path("~COURS/EDHEC/R/SLIDES/", "data_imp.txt")
```

```
> df <- read.table(path)
```

```
> summary(df)
```

```
##              V1  
## John;174;32   :1  
## Mary;165.5;NA:1  
## name;size;age:1  
## Peter;?;28   :1
```

Problem

R considers four line with **one** column!

Solution

```
> df <- read.table(path,header=TRUE,sep=";",dec=".",
+                  na.strings = c("NA","?"),row.names = 1)
> df
##           size age
## John  174.0  32
## Peter   NA  28
## Mary  165.5  NA
> summary(df)
##           size           age
##  Min.    :165.5  Min.    :28
##  1st Qu.:167.6  1st Qu.:29
##  Median :169.8  Median :30
##  Mean    :169.8  Mean    :30
##  3rd Qu.:171.9  3rd Qu.:31
##  Max.    :174.0  Max.    :32
##  NA 's    :1      NA 's    :1
```

readr package

- This package makes **data importation easier**.
- It includes **read_table** and **read_csv** functions instead of **read.table** and **read.csv** (underscores instead of points).
- In **Rstudio**, we can read data with **readr** by clicking on the **Import Dataset** icon (it does not work when things are too complicated).

Other tools to import data

- `readxl`: for `xls` files
- `sas7bdat`: for `sas` dataset
- `foreign`: for `SPSS` or `STATA` datasets
- `jsonlite`: for `json` files
- `rvest`: webscrapping (to import data from website)

Combine tables

- Information comes (always) from **several data tables**.
- We need to **correctly merge these tables** before a statistical analysis.
- **Standard R functions**: `rbind`, `cbind`, `cbind.data.frame`, `merge`...

Combine tables

- Information comes (always) from **several data tables**.
- We need to **correctly merge these tables** before a statistical analysis.
- **Standard R functions**: `rbind`, `cbind`, `cbind.data.frame`, `merge`...
- **Tidyverse functions**: `bind_rows`, `bind_cols`, `left_join`, `inner_join` (from `dplyr` or `tidyverse` package).

An example with 2 tables

```
> df1
## # A tibble: 4 x 2
##   name nation
##   <chr> <chr>
## 1 Peter USA
## 2 Mary GB
## 3 John Aus
## 4 Linda USA
```

```
> df2
## # A tibble: 3 x 2
##   name    age
##   <chr> <dbl>
## 1 John    35
## 2 Mary    41
## 3 Fred    28
```

An example with 2 tables

```
> df1
## # A tibble: 4 x 2
##   name nation
##   <chr> <chr>
## 1 Peter USA
## 2 Mary GB
## 3 John Aus
## 4 Linda USA

> df2
## # A tibble: 3 x 2
##   name age
##   <chr> <dbl>
## 1 John 35
## 2 Mary 41
## 3 Fred 28
```

Goal

One dataset with three columns: **name**, **nation** and **age**.

bind_rows

```
> bind_rows(df1,df2)
## # A tibble: 7 x 3
##   name nation age
##   <chr> <chr> <dbl>
## 1 Peter USA      NA
## 2 Mary  GB         NA
## 3 John  Aus         NA
## 4 Linda USA         NA
## 5 John  <NA>       35
## 6 Mary  <NA>       41
## 7 Fred  <NA>       28
```

bind_rows

```
> bind_rows(df1,df2)
## # A tibble: 7 x 3
##   name nation age
##   <chr> <chr> <dbl>
## 1 Peter USA      NA
## 2 Mary  GB         NA
## 3 John  Aus         NA
## 4 Linda USA         NA
## 5 John  <NA>       35
## 6 Mary  <NA>       41
## 7 Fred  <NA>       28
```

⇒ **not a safe choice** here (two lines for some individuals).

full_join

```
> full_join(df1,df2)
## # A tibble: 5 x 3
##   name nation age
##   <chr> <chr> <dbl>
## 1 Peter USA      NA
## 2 Mary  GB        41
## 3 John  Aus       35
## 4 Linda USA      NA
## 5 Fred  <NA>     28
```

full_join

```
> full_join(df1,df2)
## # A tibble: 5 x 3
##   name nation age
##   <chr> <chr> <dbl>
## 1 Peter USA      NA
## 2 Mary  GB        41
## 3 John  Aus       35
## 4 Linda USA      NA
## 5 Fred  <NA>     28
```

⇒ we keep all the individuals (NA are added for missing data)

left_join

```
> left_join(df1,df2)
## # A tibble: 4 x 3
##   name  nation  age
##   <chr> <chr>  <dbl>
## 1 Peter  USA      NA
## 2 Mary   GB       41
## 3 John   Aus      35
## 4 Linda  USA      NA
```

⇒ we keep only individuals of the first (left) dataset.

inner_join

```
> inner_join(df1,df2)
## # A tibble: 2 x 3
##   name nation   age
##   <chr> <chr>   <dbl>
## 1 Mary  GB       41
## 2 John  Aus       35
```

⇒ we keep only individuals for which both nation and age are observed.

inner_join

```
> inner_join(df1,df2)
## # A tibble: 2 x 3
##   name nation age
##   <chr> <chr> <dbl>
## 1 Mary  GB      41
## 2 John  Aus      35
```

⇒ we keep only individuals for which both nation and age are observed.

Conclusion

- Many options to merge datasets.
- Find the good function according to our problem.

⇒ work on tuto 3 - Part 1

Data manipulation with Dplyr

- **dplyr** is a powerful R-package to **transform and summarize** tabular data with rows and columns.
- It offers a **clear syntax** (based on a grammar) to manipulate data.

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- It offers a **clear syntax** (based on a grammar) to manipulate data.
- For instance, to compute the mean of *Sepal.Length* for *setosa*, we usually use

```
> mean(iris[iris$Species=="setosa",]$Sepal.Length)
## [1] 5.006
```

- **dplyr** is a powerful R-package to **transform and summarize** tabular data with rows and columns.
- It offers a **clear syntax** (based on a grammar) to manipulate data.
- For instance, to compute the mean of *Sepal.Length* for *setosa*, we usually use

```
> mean(iris[iris$Species=="setosa",]$Sepal.Length)
## [1] 5.006
```

- We can do the same with **dplyr**

```
> library(dplyr)
> iris %>% filter(Species=="setosa") %>%
+   summarise(mean(Sepal.Length))
##   mean(Sepal.Length)
## 1                5.006
```

dplyr contains a **grammar** with the following verbs:

- **select()** select columns (variables)
- **filter()** filter rows (individuals)
- **arrange()** re-order or arrange rows
- **mutate()** create new columns (new variables)
- **summarise()** summarise values (compute statistics summaries)
- **group_by()** allows for group operations in the “split-apply-combine” concept

Don't forget to look at the **cheat sheet**

Select

Goal

To select **variables**.

```
> df <- select(iris,Sepal.Length,Petal.Length)
```

```
> head(df)
```

```
##   Sepal.Length Petal.Length
## 1           5.1           1.4
## 2           4.9           1.4
## 3           4.7           1.3
## 4           4.6           1.5
## 5           5.0           1.4
## 6           5.4           1.7
```

Filter

Goal

To filter **individuals**.

```
> df <- filter(iris,Species=="versicolor")
```

```
> head(df)
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	7.0	3.2	4.7	1.4	versicolor
## 2	6.4	3.2	4.5	1.5	versicolor
## 3	6.9	3.1	4.9	1.5	versicolor
## 4	5.5	2.3	4.0	1.3	versicolor
## 5	6.5	2.8	4.6	1.5	versicolor
## 6	5.7	2.8	4.5	1.3	versicolor

Arrange

Goal

To order **individuals** according to a variable.

```
> df <- arrange(iris,Sepal.Length)
> head(df)
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	4.3	3.0	1.1	0.1	setosa
## 2	4.4	2.9	1.4	0.2	setosa
## 3	4.4	3.0	1.3	0.2	setosa
## 4	4.4	3.2	1.3	0.2	setosa
## 5	4.5	2.3	1.3	0.3	setosa
## 6	4.6	3.1	1.5	0.2	setosa

Mutate

Goal

To define **new variables** in the dataset.

```
> df <- mutate(iris,diff_petal=Petal.Length-Petal.Width)
> head(select(df,Petal.Length,Petal.Width,diff_petal))
```

	<i>Petal.Length</i>	<i>Petal.Width</i>	<i>diff_petal</i>
## 1	1.4	0.2	1.2
## 2	1.4	0.2	1.2
## 3	1.3	0.2	1.1
## 4	1.5	0.2	1.3
## 5	1.4	0.2	1.2
## 6	1.7	0.4	1.3

Summarise

Goal

To compute **statistical summaries**.

```
> summarise(iris, mean=mean(Petal.Length), var=var(Petal.Length))  
##      mean      var  
## 1 3.758 3.116278
```

group_by

Goal

To apply operations for **group of data**.

```
> summarise(group_by(iris,Species),mean(Petal.Length))  
## # A tibble: 3 x 2  
##   Species      `mean(Petal.Length)`  
##   <fct>                <dbl>  
## 1 setosa                1.46  
## 2 versicolor            4.26  
## 3 virginica            5.55
```

The pipe operator

- The pipe operator `%>%` allows to organize commands **step by step**.
- For instance, to calculate the **mean** of variable **Sepal.Length** for **setosa**, we can do

```
> mean(iris[iris$Species=="setosa","Sepal.Length"])  
## [1] 5.006
```

or (more readable)

```
> df1 <- iris[iris$Species=="setosa",]  
> df2 <- df1$Sepal.Length  
> mean(df2)  
## [1] 5.006
```

or (more readable with **dplyr**)

```
> df1 <- filter(iris, Species=="setosa")
> df2 <- select(df1, Sepal.Length)
> summarize(df2, mean(Sepal.Length))
##    mean(Sepal.Length)
## 1                5.006
```

- With the **pipe operator**, we expand the operations:

1. the data

```
> iris
```

2. Filter individuals according to **setosa specie**

```
> iris %>% filter(Species=="setosa")
```

3. Select the variable of interest

```
> iris %>% filter(Species=="setosa") %>% select(Sepal.Length)
```

4. Compute the mean

```
> iris %>% filter(Species=="setosa") %>%  
+   select(Sepal.Length)%>% summarize_all(mean)  
##   Sepal.Length  
## 1          5.006
```

More generally

- The pipe operator `%>%` merge the left object with the first component of the right object.

```
> X <- as.numeric(c(1:10,"NA"))  
> mean(X,na.rm = TRUE)  
## [1] 5.5
```

or equivalently

```
> X %>% mean(na.rm=TRUE)  
## [1] 5.5
```


Reshaping data

- Some statistical analysis requires a particular shape for the data
- A toy example

```
> df <- iris %>% group_by(Species) %>%  
+   summarize_all(funs(mean))  
> head(df)
```

A tibble: 3 x 5

##	Species	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
##	<fct>	<dbl>	<dbl>	<dbl>	<dbl>
## 1	setosa	5.01	3.43	1.46	0.246
## 2	versicolor	5.94	2.77	4.26	1.33
## 3	virginica	6.59	2.97	5.55	2.03

gather

- Gather columns into rows with **gather**:

```
> df1 <- df %>% gather(key=variable,value=value,-Species)
> head(df1)
## # A tibble: 6 x 3
##   Species      variable      value
##   <fct>       <chr>       <dbl>
## 1 setosa     Sepal.Length  5.01
## 2 versicolor Sepal.Length  5.94
## 3 virginica  Sepal.Length  6.59
## 4 setosa     Sepal.Width   3.43
## 5 versicolor Sepal.Width   2.77
## 6 virginica  Sepal.Width   2.97
```

Remark

Same information with a different shape.

Spread

- Spread rows into columns with `spread`:

```
> df1 %>% spread(variable,value)
## # A tibble: 3 x 5
##   Species      Petal.Length Petal.Width Sepal.Length Sepal.Width
##   <fct>          <dbl>         <dbl>         <dbl>         <dbl>
## 1 setosa          1.46           0.246           5.01           3.43
## 2 versicolor      4.26           1.33           5.94           2.77
## 3 virginica       5.55           2.03           6.59           2.97
```

Separate

- **Separate** one column into several

```
> df <- tibble(date=as.Date(c("01/03/2015", "05/18/2017",  
+ "09/14/2018")), "%m/%d/%Y"), temp=c(18, 21, 15))
```

```
> df
```

```
## # A tibble: 3 x 2  
##   date      temp  
##   <date>   <dbl>  
## 1 2015-01-03    18  
## 2 2017-05-18    21  
## 3 2018-09-14    15
```

```
> df1 <- df %>% separate(date, into = c("year", "month", "day"))
```

```
> df1
```

```
## # A tibble: 3 x 4  
##   year month day    temp  
##   <chr> <chr> <chr> <dbl>  
## 1 2015   01    03     18  
## 2 2017   05    18     21  
## 3 2018   09    14     15
```

- **Unite** several columns into one

```
> df1 %>% unite(date,year,month,day,sep="/")  
## # A tibble: 3 x 2  
##   date      temp  
##   <chr>    <dbl>  
## 1 2015/01/03    18  
## 2 2017/05/18    21  
## 3 2018/09/14    15
```

- **Unite** several columns into one

```
> df1 %>% unite(date,year,month,day,sep="/")  
## # A tibble: 3 x 2  
##   date      temp  
##   <chr>    <dbl>  
## 1 2015/01/03    18  
## 2 2017/05/18    21  
## 3 2018/09/14    15
```

⇒ work on **tuto 3, part 2**.

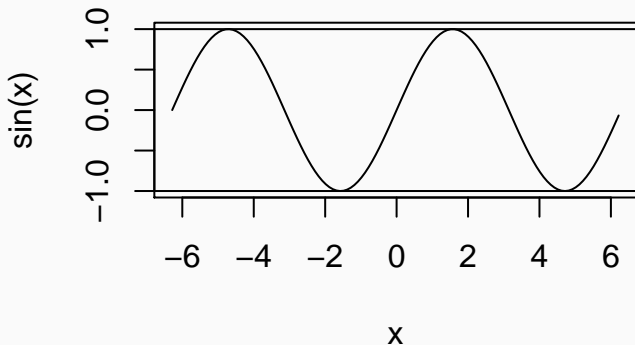
Visualize data

- **Graphs** are often the **starting point** for statistical analysis.
- One of the main advantages of **R** is how **easy** it is for the user to create many different kinds of graphs.
- We begin by a (short) review on **conventional graphs**,
- followed by an examination of some **more complex representations**, especially with **ggplot2 package**.

The plot function

- It is a **generic** function to represent all **kind of data**.
- For a **scatter plot**, we have to specify a vector for the x-axis and a vector for the y axis.

```
> x <- seq(-2*pi,2*pi,by=0.1)
> plot(x,sin(x),type="l",xlab="x",ylab="sin(x)")
> abline(h=c(-1,1))
```



Graphs for datasets

- Many kind of representations are needed according to the variables we want to visualize.
- Histogram for continuous variables, barplot for categorical variables.
- scatterplot for 2 continuous variables.
- boxplot to visualize distributions.

Graphs for datasets

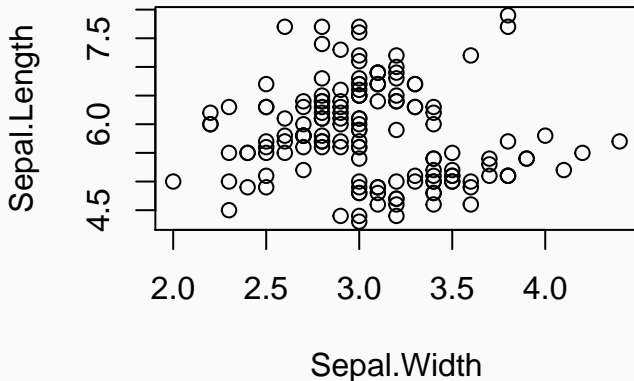
- Many kind of representations are needed according to the variables we want to visualize.
- Histogram for continuous variables, barplot for categorical variables.
- scatterplot for 2 continuous variables.
- boxplot to visualize distributions.

Fortunately

There is a R function for all the representations.

Scatter plot for dataset

```
> plot(Sepal.Length~Sepal.Width,data=iris)
```



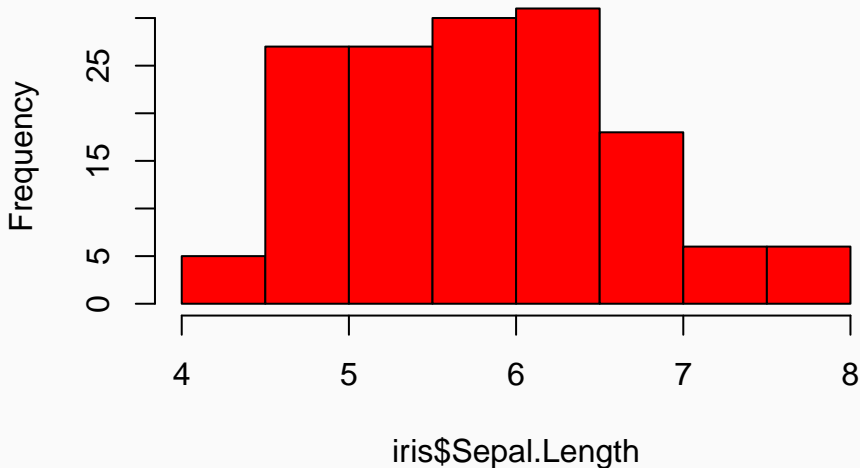
```
> #same as
```

```
> plot(iris$Sepal.Width,iris$Sepal.Length)
```

Histogram for continous variable

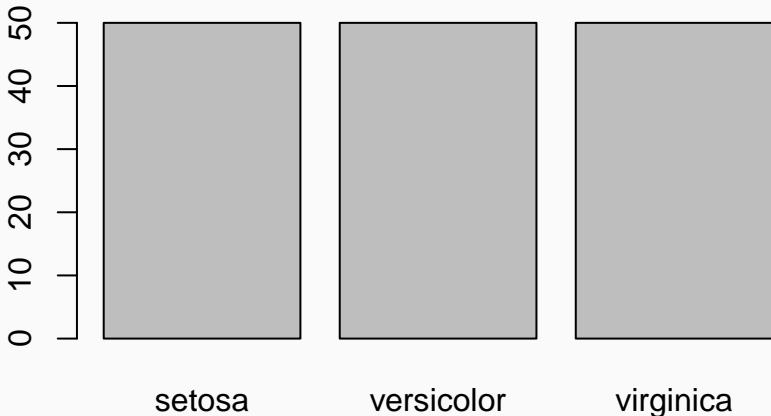
```
> hist(iris$Sepal.Length,col="red")
```

Histogram of iris\$Sepal.Length



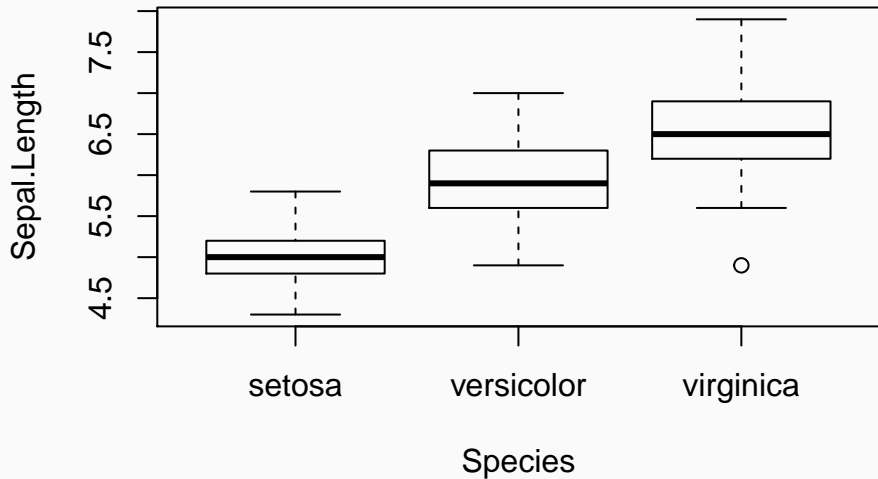
Barplot for categorical variables

```
> barplot(table(iris$Species))
```



Boxplot

```
> boxplot(Sepal.Length~Species,data=iris)
```



Visualization with ggplot2

- `ggplot2` is a plotting system for R based on the **grammar of graphics** (as **dplyr** to manipulate data).
- Graphs ggplot are clearly **nice looking** (conventionnal R graphs are not always very nice).

For a given dataset, a graph is defined from many **layers**. We have to specify:

- the **data**
- the **variables** we want to plot
- the **type of representation** (scatterplot, boxplot. . .).

Ggplot graphs are defined from these layers. We indicate

- the data with **ggplot**
- the variables with **aes** (aesthetics)
- the type of representation with **geom_**

The grammar

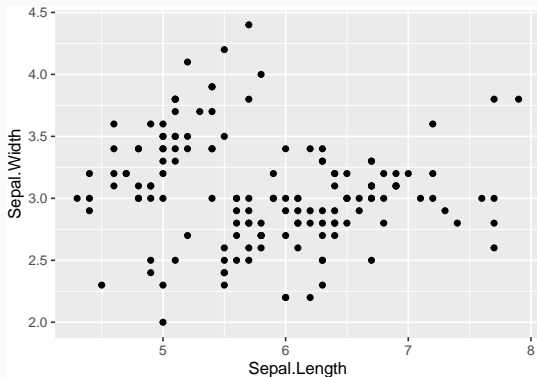
Main elements of the grammar are:

- **Data (ggplot)**: the **dataset**, it should be a dataframe or a tibble
- **Aesthetics (aes)**: to describe the way that **variables** in the data are mapped. All the variables used in the graph should be specified in **aes**
- **Geometrics (geom_...)**: to control the **type** of plot
- **Statistics (stat_...)**: to describe **transformation** of the data
- **Scales (scale_...)**: to **control the mapping** from data to aesthetic attributes (change colors, size. . .)

All these elements are combined with a **+**.

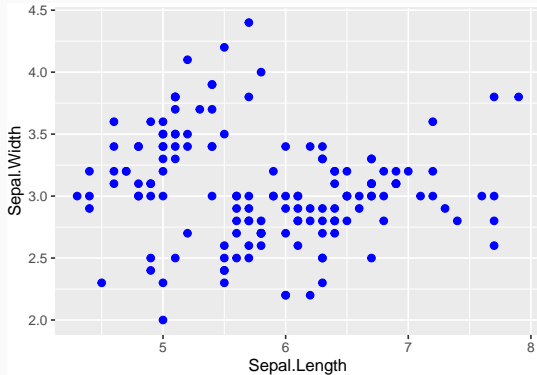
An example

```
> ggplot(iris)+aes(x=Sepal.Length,y=Sepal.Width)+geom_point()
```



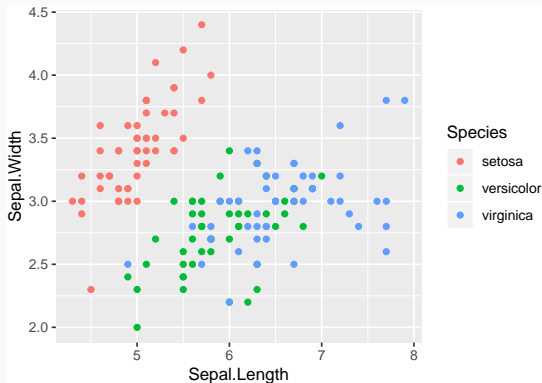
Color and size

```
> ggplot(iris)+aes(x=Sepal.Length,y=Sepal.Width)+  
+   geom_point(color="blue",size=2)
```



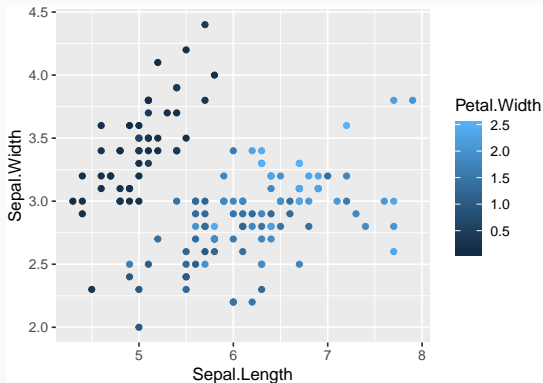
Color by (categorical) variable

```
> ggplot(iris)+aes(x=Sepal.Length,y=Sepal.Width,  
+               color=Species)+geom_point()
```



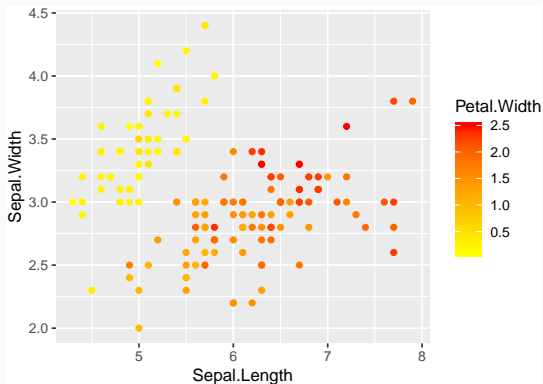
Color by (continuous) variable

```
> ggplot(iris)+aes(x=Sepal.Length,y=Sepal.Width,  
+                 color=Petal.Width)+geom_point()
```



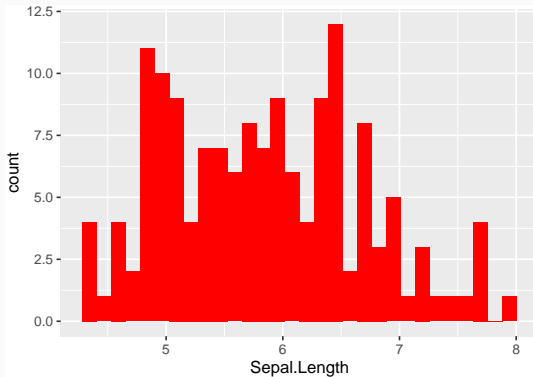
Color by (continous) variable

```
> ggplot(iris)+aes(x=Sepal.Length,y=Sepal.Width,  
+                 color=Petal.Width)+geom_point()+  
+                 scale_color_continuous(low="yellow",high="red")
```



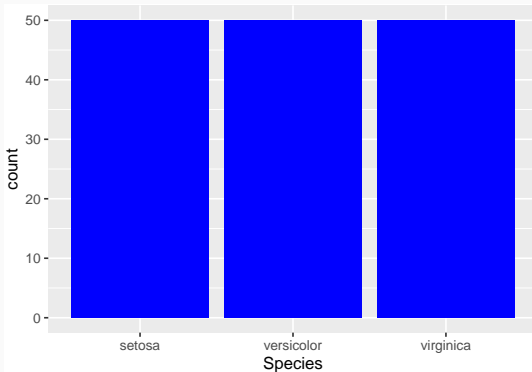
Histogram

```
> ggplot(iris)+aes(x=Sepal.Length)+geom_histogram(fill="red")
```



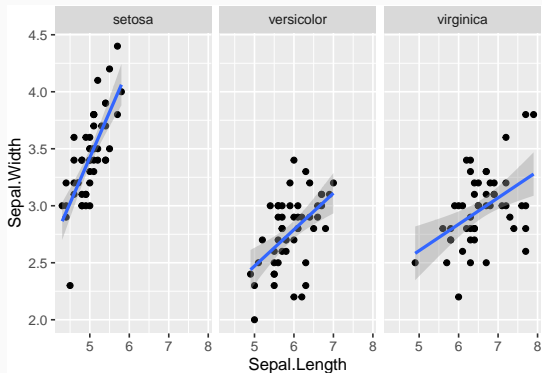
Barplot

```
> ggplot(iris)+aes(x=Species)+geom_bar(fill="blue")
```



Facetting (more complex)

```
> ggplot(iris)+aes(x=Sepal.Length,y=Sepal.Width)+geom_point()+  
+ geom_smooth(method="lm")+facet_wrap(~Species)
```

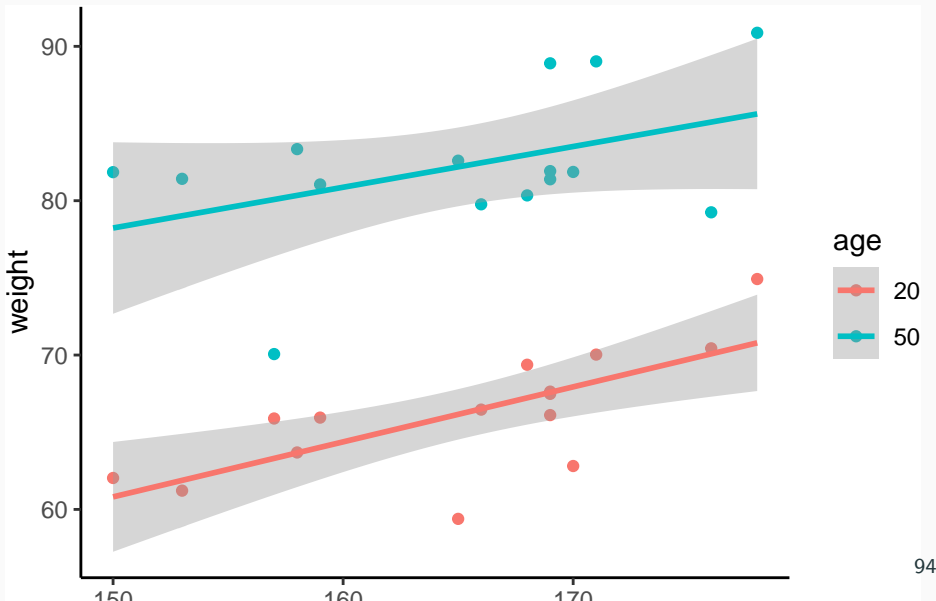


Combining ggplot with dplyr

- One has to build a **good dataframe (or tibble)** to obtain an **efficient graph**.
- For instance

```
> head(df)
## # A tibble: 6 x 3
##   size weight.20 weight.50
##   <dbl>      <dbl>      <dbl>
## 1   153      61.2      81.4
## 2   169      67.5      81.4
## 3   168      69.4      80.3
## 4   169      66.1      81.9
## 5   176      70.4      79.2
## 6   169      67.6      88.9
```

Goal



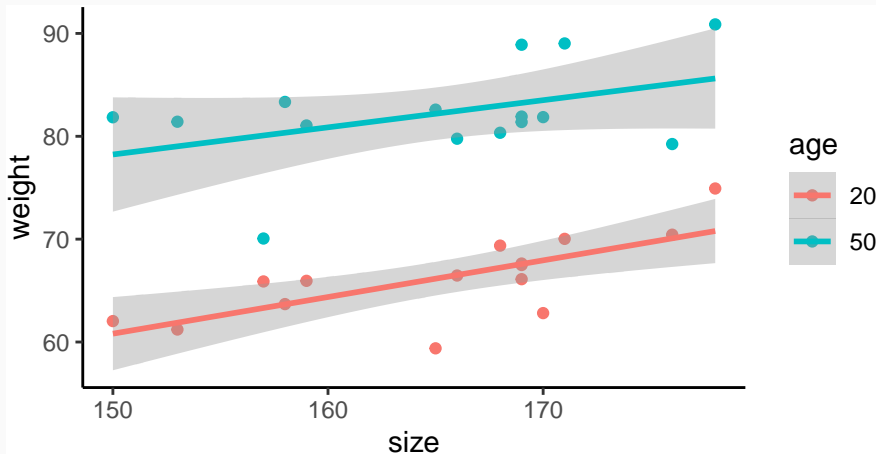
dplyr step

- Gather column `weight.M` and `weight.W` into one column `weight`:

```
> df1 <- df %>% gather(key=age,value=weight,-size)
> df1 %>% head()
## # A tibble: 6 x 3
##   size age      weight
##   <dbl> <chr>    <dbl>
## 1   153 weight.20  61.2
## 2   169 weight.20  67.5
## 3   168 weight.20  69.4
## 4   169 weight.20  66.1
## 5   176 weight.20  70.4
## 6   169 weight.20  67.6
> df1 <- df1 %>% mutate(age=recode(age,
+   "weight.20"="20", "weight.50"="50"))
```

ggplot step

```
> ggplot(df1)+aes(x=size,y=weight,color=age)+  
+   geom_point()+geom_smooth(method="lm")+theme_classic()
```



Complement: some demos

```
> demo(image)
> example(contour)
> demo(persp)
> library("lattice");demo(lattice)
> example(wireframe)
> library("rgl");demo(rgl)
> example(persp3d)
> demo(plotmath);demo(Hershey)
```


Complement: some demos

```
> demo(image)
> example(contour)
> demo(persp)
> library("lattice");demo(lattice)
> example(wireframe)
> library("rgl");demo(rgl)
> example(persp3d)
> demo(plotmath);demo(Hershey)
```

⇒ Work on **tuto 4**.

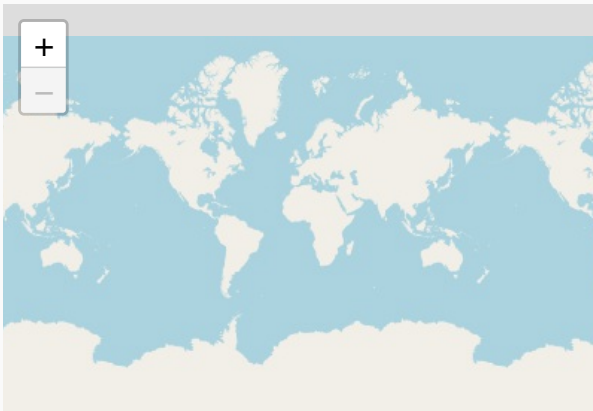
Mapping with leaflet

- In many applications, it could be interesting to make **mapping** to **visualize** a **dataset** or the result of a **model**.
- A **lot of R packages**: ggmap, RgoogleMaps, maps. . .
- In this part: **leaflet**.

Background map

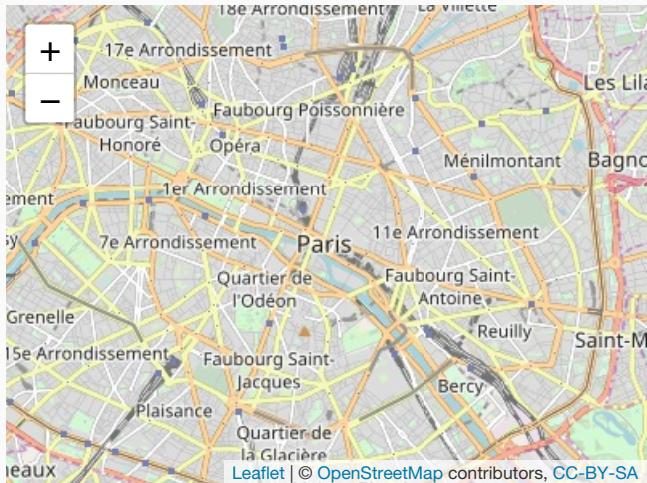
- Leaflet is one of the most popular open-source JavaScript libraries for interactive maps.
- Documentation: [here](#)

```
> library(leaflet)  
> leaflet() %>% addTiles()
```



Many background style

```
> Paris <- c(2.35222,48.856614)
> leaflet() %>% addTiles() %>%
+   setView(lng = Paris[1], lat = Paris[2],zoom=12)
```



Leaflet | © OpenStreetMap contributors, CC-BY-SA

```
> leaflet() %>% addProviderTiles("Stamen.Toner") %>%  
+   setView(lng = Paris[1], lat = Paris[2], zoom = 12)
```



Leaflet with dataset

- Location of 1000 seismic event near Fiji

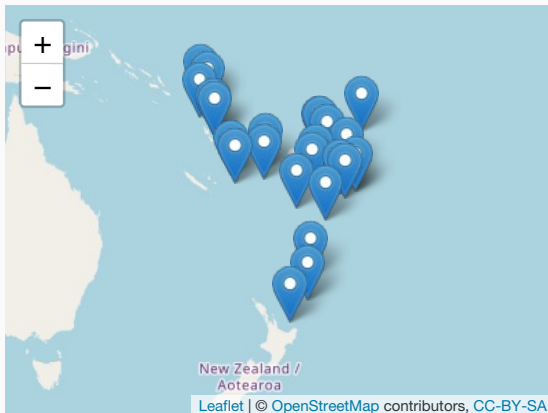
```
> data(quakes)
```

```
> head(quakes)
```

##		lat	long	depth	mag	stations
## 1		-20.42	181.62	562	4.8	41
## 2		-20.62	181.03	650	4.2	15
## 3		-26.00	184.10	42	5.4	43
## 4		-17.97	181.66	626	4.1	19
## 5		-20.42	181.96	649	4.0	11
## 6		-19.68	184.31	195	4.0	12

Visualize seismics with magnitude more then 5.5

```
> quakes1 <- quakes %>% filter(mag>5.5)
> leaflet(data = quakes1) %>% addTiles() %>%
+   addMarkers(~long, ~lat, popup = ~as.character(mag))
```

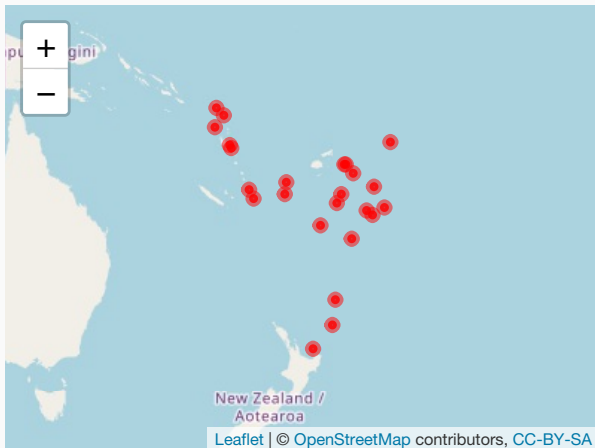


Remark

When you click on a marker, you visualize the magnitude.

addCircleMarkers

```
> leaflet(data = quakes1) %>% addTiles() %>%  
+   addCircleMarkers(~long, ~lat, popup=~as.character(mag),  
+                   radius=3,fillOpacity = 0.8,color="red")
```



⇒ work on tuto 5.

Regression models with R

- **Goal:** present classical functions to make regression with R .
- **Transition** with the Machine Learning lecture.
- Focus on **R tools**, mathematical tools will be (or have been) presented in other lectures (statistical model, data mining, machine learning).

Data

Y	X_1	X_2	\dots	X_p
y_1	$x_{1,1}$	$x_{1,2}$	\dots	$x_{1,p}$
\vdots	\vdots	\vdots	\vdots	\vdots
\vdots	\vdots	\vdots	\vdots	\vdots
y_n	$x_{n,1}$	$x_{n,2}$	\dots	$x_{n,p}$

Goal

Explain or predict **output** Y by **inputs** X_1, \dots, X_p .

Example: ozone

```
> ozone <- read.table("../DATA/ozone.txt")  
> head(ozone %>% select(1:5))
```

##	maxO3	T9	T12	T15	Ne9
## 20010601	87	15.6	18.5	18.4	4
## 20010602	82	17.0	18.4	17.7	5
## 20010603	92	15.3	17.6	19.5	2
## 20010604	114	16.2	19.7	22.5	1
## 20010605	94	17.4	20.5	20.4	8
## 20010606	80	17.7	19.8	18.3	6

Goal

Explain or predict the **daily maximum one-hour-average ozone** (maxO3 column) by the other variables.

- There exists an **unknown** function $m : \mathbb{R}^p \rightarrow \mathbb{R}$ such that

$$Y = m(X_1, \dots, X_p) + \varepsilon.$$

- ε : error terms (as small as possible).

Statistical model

- There exists an **unknown** function $m : \mathbb{R}^p \rightarrow \mathbb{R}$ such that

$$Y = m(X_1, \dots, X_p) + \varepsilon.$$

- ε : error terms (as small as possible).
- Statistician's job**: find a good estimate \hat{m} of m from the data $(x_1, y_1), \dots, (x_n, y_n)$ where $x_i \in \mathbb{R}^p$ and $y_i \in \mathbb{R}$.

Statistical models

Allow to find such estimates.

An example: the linear model

- **Assumption:** the unknown function is linear

$$Y = \beta_0 + \beta_1 X_1 + \dots + \beta_p X_p + \varepsilon,$$

$\beta = (\beta_0, \beta_1, \dots, \beta_p)$ are the **unknown** parameters.

An example: the linear model

- **Assumption:** the unknown function is linear

$$Y = \beta_0 + \beta_1 X_1 + \dots + \beta_p X_p + \varepsilon,$$

$\beta = (\beta_0, \beta_1, \dots, \beta_p)$ are the **unknown** parameters.

- **Least square estimates:**

$$\hat{\beta} = (X^t X)^{-1} X^t Y.$$

- **Estimate** of m :

$$\hat{m}(x) = \hat{\beta}_0 + \hat{\beta}_1 x_1 + \dots + \hat{\beta}_p x_p.$$

Models with R

- Models on **R** are **always fitted in the same way**:

```
> method(formula,data=...,options)
```

where

- method** refers to the name of the model
- formula** specifies the input Y and the outputs X_j
- data** is the name of the dataset
- options** refers to many options depending on the method.

Methods

Remark

Each model corresponds to a **R function**.

R function	algorithm	Package	Problem
lm	linear model		Reg
glm	logistic model		Class
lda	linear discriminant analysis	MASS	Class
svm	Support Vector Machine	e1071	Class
knn.reg	nearest neighbor	FNN	Reg
knn	nearest neighbor	class	Class
rpart	tree	rpart	Reg and Class
glmnet	ridge and lasso	glmnet	Reg and Class

Formula

Remark

To specify **input** and **outputs**.

```
> lm(Y~X1+X3,data=df)
```

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To specify **input** and **outputs**.

```
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$$\Rightarrow Y = \beta_0 + \beta_1 X_1 + \beta_3 X_3 + \varepsilon$$

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> lm(Y~X1+I(X3^2),data=df)
```

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```
> lm(Y~.,data=df)
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Remark

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```

$$\Rightarrow Y = \beta_0 + \beta_1 X_1 + \beta_3 X_3 + \varepsilon$$

```
> lm(Y~X1+I(X3^2),data=df)
```

$$\Rightarrow Y = \beta_0 + \beta_1 X_1 + \beta_3 X_3^2 + \varepsilon$$

```
> lm(Y~.,data=df)
```

$$\Rightarrow Y = \beta_0 + \beta_1 X_1 + \dots + \beta_p X_p + \varepsilon$$

Example

```
> mod.lin <- lm(maxO3~T12+Ne9,data=ozone)
> mod.lin
##
## Call:
## lm(formula = maxO3 ~ T12 + Ne9, data = ozone)
##
## Coefficients:
## (Intercept)          T12           Ne9
##      7.638        4.457       -2.696
```

Example

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```

- **Model:** $\text{maxO3} = \beta_0 + \beta_1 T12 + \beta_2 \text{Ne9} + \varepsilon$.
- **Estimates:** $\hat{\beta}_0 = 7.638, \hat{\beta}_1 = 4.457, \hat{\beta}_2 = -2.696$.

Example

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- **Model:** $\text{maxO3} = \beta_0 + \beta_1 T12 + \beta_2 \text{Ne9} + \varepsilon$.
- **Estimates:** $\hat{\beta}_0 = 7.638, \hat{\beta}_1 = 4.457, \hat{\beta}_2 = -2.696$.

Estimate of m

$$\hat{m}(x) = 7.638 + 4.457 T12 - 2.696 \text{Ne9}.$$

Making predictions

- Once the model has been fitted, we can use it to make predictions.

Example

- MétéoFrance predicts for tomorrow: $T_{12}=20$ and $Ne_9=4.9$.
- What does our model predict for the ozone concentration?

Making predictions

- Once the model has been fitted, we can use it to make **predictions**.

Example

- MétéoFrance predicts for tomorrow: T12=20 and Ne9=4.9.
- What does our model predict for the ozone concentration?

- **Answer:**

$$\hat{m}(T12 = 20, Ne9 = 4.9) = 7.638 + 4.457 * 20 - 2.696 * 4.9 = 83.5676$$

.

Predict function

- `predict` is a `generic` function: we can use it to make predictions for all models (linear, logistic, tree...)

```
> predict(model.name, newdata=newdataset, ...)
```

Predict function

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```
> predict(model.name, newdata=newdataset, ...)
```

- **Example**

```
> new.df <- data.frame(T12=20, Ne9=4.9)
> predict(mod.lin, newdata=new.df)
##           1
## 83.57509
```

Very important

Use the **same structure** for both dataframes.

Estimating the mean square error (ISL lecture)

- The performance of an estimate \hat{m} can be measured by its mean square error:

$$MSE(\hat{m}) = E[(Y - \hat{m}(X))^2].$$

Estimating the mean square error (ISL lecture)

- The performance of an estimate \hat{m} can be measured by its **mean square error**:

$$MSE(\hat{m}) = E[(Y - \hat{m}(X))^2].$$

- This (**unknown**) error is generally estimated by **validation hold out**:
 - Split the data into a train set and a test set
 - Fit the model on the train set $\implies \hat{m}$
 - Estimate the MSE by

$$\frac{1}{n_{test}} \sum_{i \in test} (y_i - \hat{m}(x_i))^2.$$

An example

- Data splitting

```
> library(caret)
> set.seed(12345)
> index.train <- createDataPartition(1:nrow(ozone),p=2/3)
> train <- ozone %>% slice(index.train$Resample1)
> test <- ozone %>% slice(-index.train$Resample1)
```

An example

- Data splitting

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```

- Model fitting

```
> mod <- lm(maxO3~.,data=train)
```

An example

- Data splitting

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> test <- ozone %>% slice(-index.train$Resample1)
```

- Model fitting

```
> mod <- lm(maxO3~.,data=train)
```

- Estimated MSE

```
> pred <- predict(mod,newdata=test)
> df <- data.frame(pred=pred,obs=test$maxO3)
> df %>% summarize(MSE=mean((pred-obs)^2))
##           MSE
## 1 387.5472
```

- Very useful to choose one model.
- **Example:** many models (linear, tree, random forest...)

Method

1. Estimate MSE for all algorithms;
2. Choose the algorithm with the smallest MSE.

- Very useful to choose one model.
- **Example:** many models (linear, tree, random forest...)

Method

1. Estimate MSE for all algorithms;
2. Choose the algorithm with the smallest MSE.

⇒ Work on **tuto 6**.

Conclusion

Project

- Group of 3 or 4
- Find a dataset for a supervised learning problem (explain one variable by other variables). This dataset should contain at least 800 individuals and 30 variables (continuous or categorical)
- There are many datasets on the web, you can look at the following websites for instance:
 - UCI machine learning repository
 - kaggle datasets (you have to register but it's free)
 - other websites of your choice

- You will address the following topics in the study
 - identify the practical problem
 - translate the practical problem into a mathematical problem
 - describe the dataset according to the problem (with `dplyr`)
 - visualize the dataset according to the problem (with `ggplot`)
 - develop machine learning methods (nearest neighbor, linear/logistic models, penalized linear/logistic models, trees, random forest). You should provide a brief description of each algorithm in the context of your problem.
 - make a comparison of the different models (quadratic error, misclassification error, ROC curves, AUC...)

- From now on, you can:
 - choose the dataset
 - make the description of the dataset (**dplyr**) and the visualization of the dataset (**ggplot**).

Be careful

- The goal is **not** to provide a **list** of statistical summaries or graphs.
- Find **relevant** summaries and you should **explain** the output (with **text!**).

- Each group should provide a **notebook** (.rmd file) and send by email (laurent.rouviere@univ-rennes2.fr):
 - the notebook (only the .rmd file, not the html file)
 - the dataset (txt or csv file)
- I will run all the chunks of the notebook (the notebook should be complete!), if there is a problem with one chunk, I will not be able to see the output.

- Many (modern) tools to manipulate data.
- Sufficient to perform a wide range of statistical analysis.
- Many lectures where you will use R.
- Try to force yourself to use these tools (when you want to make a graph, try to do it in ggplot).

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Thank you