

# Getting to use data in R

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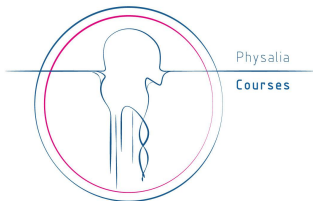
Leibniz Institute of Zoo and Wildlife Research

June 2018



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and Wildlife Research**

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# Getting started with R

- 1 Introduction
- 2 Vectors
- 3 Matrices and arrays
- 4 List
- 5 Data frames and tibbles
- 6 Importing & exporting data

# Handling data in R

There are many types of objects designed to store data in R.

We will focus on:

- vectors
- matrices (and arrays)
- data frames (and tibbles)
- lists

Note: if you master those, we are pretty much all set because most other objects derive from those!

# Handling data in R

- vectors
  - a single row of data
  - all elements have the same type (e.g. `logical`, `integer`, `double`, `character`...)
- matrices (and arrays)
  - all rows & columns have same length
  - all rows & columns have the same type
- data frames (and tibbles)
  - all rows & columns have same length
  - each column can have its own type
- lists
  - each element can have its own length
  - each element can have its own type

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# Vector

The vector is the simplest way to store data in **R**; it is a sequence of data elements of the same type.

Example of a vector:

```
height_girls <- c(178, 175, 159, 164, 183, 192)
height_girls
## [1] 178 175 159 164 183 192
```

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  - tibbles
- 6 Importing & exporting data

## Vector: general properties

They can be combined:

```
height_boys <- c(181, 189, 174, 177)
height <- c(height_boys, height_girls)
height
## [1] 181 189 174 177 178 175 159 164 183 192
```



## Vector: general properties

Subsets can be made (with indexes, booleans or names):

```
height_girls[2] ## returns element 2
## [1] 175
height_girls[-3] ## remove element 3
## [1] 178 175 164 183 192
```

## Vector: general properties

Subsets can be made (with indexes, booleans or names):

```
height_girls[2]  ## returns element 2
## [1] 175

height_girls[-3] ## remove element 3
## [1] 178 175 164 183 192
```

```
height_girls[c(1, 1, 2, 2, 2)] ## open room for bootstraps and more
## [1] 178 178 175 175 175
```

## Vector: general properties

Subsets can be made (with indexes, booleans or names):

```
height_girls[2]  ## returns element 2
## [1] 175

height_girls[-3] ## remove element 3
## [1] 178 175 164 183 192
```

```
height_girls[c(1, 1, 2, 2, 2)]  ## open room for bootstraps and more
## [1] 178 178 175 175 175
```

```
height_girls[height_girls > 168]
## [1] 178 175 183 192

height_girls[!(height_girls == min(height_girls))]
## [1] 178 175 164 183 192

height_girls[height_girls != min(height_girls)]
## [1] 178 175 164 183 192
```

## Vector: general properties

The elements of a vector can be named and those names can be used for subsetting:

```
foo <- c(alex = 1, colin = 2)
foo
##  alex colin
##    1     2
foo["colin"]
## colin
##    2
```

## Vector: general properties

The elements of a vector can be named and those names can be used for subsetting:

```
foo <- c(alex = 1, colin = 2)
foo
##  alex colin
##    1     2
foo["colin"]
## colin
##    2
```

But names behave sometimes somewhat unexpectedly:

```
foo[1] + foo[2]
## alex
##    3
```

## Vector: general properties

Vectors (as any other object) can have metadata called 'attributes' attached to them:

```
foo <- c(1, 2, 3)
attr(x = foo, which = "whatever") <- "Learning to count"
attr(x = foo, which = "something else?") <- "nope"
```

```
foo
## [1] 1 2 3
## attr(,"whatever")
## [1] "Learning to count"
## attr(,"something else?")
## [1] "nope"
```

## Vector: general properties

Vectors (as any other object) can have metadata called 'attributes' attached to them:

```
foo <- c(1, 2, 3)
attr(x = foo, which = "whatever") <- "Learning to count"
attr(x = foo, which = "something else?") <- "nope"
```

```
foo
## [1] 1 2 3
## attr(,"whatever")
## [1] "Learning to count"
## attr(,"something else?")
## [1] "nope"
```

```
attr(x = foo, which = "whatever")
## [1] "Learning to count"
```

## Vector: general properties

Vectors (as any other object) can have metadata called 'attributes' attached to them:

```
foo <- c(1, 2, 3)
attr(x = foo, which = "whatever") <- "Learning to count"
attr(x = foo, which = "something else?") <- "nope"
```

```
foo
## [1] 1 2 3
## attr(,"whatever")
## [1] "Learning to count"
## attr(,"something else?")
## [1] "nope"
```

```
attr(x = foo, which = "whatever")
## [1] "Learning to count"
```

```
attributes(foo) ## this gives a list, see later!
## $whatever
## [1] "Learning to count"
##
## $`something else?`
## [1] "nope"
```

Note: this is useful to know for handling outputs in certain packages (e.g. `spaMM`).



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- types & classes
- factors
- functions

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## 4 List

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- functions

## 5 Data frames and tibbles

- general properties
- challenge
- functions
- dplyr
- tidyr
- tibbles

## 6 Importing & exporting data

# Vector: types

Types refer to the internal representation of the objects:

- logicals

```
(foo <- c(TRUE, FALSE, F, T))  
## [1] TRUE FALSE FALSE TRUE  
typeof(x = foo)  
## [1] "logical"
```

# Vector: types

Types refer to the internal representation of the objects:

- logicals

```
(foo <- c(TRUE, FALSE, F, T))  
## [1] TRUE FALSE FALSE TRUE  
typeof(x = foo)  
## [1] "logical"
```

- integers

```
(foo <- c(1L, 5L, 7L, 0L))  
## [1] 1 5 7 0  
typeof(x = foo)  
## [1] "integer"
```

# Vector: types

Types refer to the internal representation of the objects:

- logicals

```
(foo <- c(TRUE, FALSE, F, T))
## [1] TRUE FALSE FALSE TRUE
typeof(x = foo)
## [1] "logical"
```

- integers

```
(foo <- c(1L, 5L, 7L, 0L))
## [1] 1 5 7 0
typeof(x = foo)
## [1] "integer"
```

- doubles

```
(foo <- c(1, 1.2, pi))
## [1] 1.000000 1.200000 3.141593
typeof(x = foo)
## [1] "double"
```

# Vector: types

Types refer to the internal representation of the objects:

- logicals

```
(foo <- c(TRUE, FALSE, F, T))
## [1] TRUE FALSE FALSE TRUE
typeof(x = foo)
## [1] "logical"
```

- integers

```
(foo <- c(1L, 5L, 7L, 0L))
## [1] 1 5 7 0
typeof(x = foo)
## [1] "integer"
```

- doubles

```
(foo <- c(1, 1.2, pi))
## [1] 1.000000 1.200000 3.141593
typeof(x = foo)
## [1] "double"
```

- characters

```
(foo <- c("bla", "bli", "blo"))
## [1] "bla" "bli" "blo"
typeof(x = foo)
## [1] "character"
```

# Vector: types

Types refer to the internal representation of the objects:

- logicals

```
(foo <- c(TRUE, FALSE, F, T))
## [1] TRUE FALSE FALSE TRUE
typeof(x = foo)
## [1] "logical"
```

- integers

```
(foo <- c(1L, 5L, 7L, 0L))
## [1] 1 5 7 0
typeof(x = foo)
## [1] "integer"
```

- doubles

```
(foo <- c(1, 1.2, pi))
## [1] 1.000000 1.200000 3.141593
typeof(x = foo)
## [1] "double"
```

- characters

```
(foo <- c("bla", "bli", "blo"))
## [1] "bla" "bli" "blo"
typeof(x = foo)
## [1] "character"
```

Note: **R** detects automatically the type of input and creates the right type of vector for you! Challenge: compare `typeof()` with `mode()`.

# Vector: classes

Classes refer to the how functions interact with the objects:

- logicals

```
(foo <- c(TRUE, FALSE, F, T))
## [1] TRUE FALSE FALSE TRUE
class(x = foo)
## [1] "logical"
```

- integers

```
(foo <- c(1L, 5L, 7L, 0L))
## [1] 1 5 7 0
class(x = foo)
## [1] "integer"
```

- numerics (from the type doubles)

```
(foo <- c(1, 1.2, pi))
## [1] 1.000000 1.200000 3.141593
class(x = foo)
## [1] "numeric"
```

- characters

```
(foo <- c("bla", "bli", "blo"))
## [1] "bla" "bli" "blo"
class(x = foo)
## [1] "character"
```

Note: many don't make the distinction between types and classes explicit but it helps to understand some weird behaviours of **R**.

# Vector: classes

There are more classes than types:

- factors

```
(foo <- factor(c("bla", "bli", "blo")))  
  
## [1] bla bli blo  
## Levels: bla bli blo  
  
class(x = foo)  
## [1] "factor"  
  
typeof(x = foo)  
## [1] "integer"  
  
levels(x = foo)  
## [1] "bla" "bli" "blo"  
  
levels(x = foo) <- c(levels(x = foo), "blu") ## set extra level  
table(foo)  
  
## foo  
## bla bli blo blu  
##    1    1    1    0
```



# Vector: classes

There are more classes than types:

- factors

```
(foo <- factor(c("bla", "bli", "blo")))  
  
## [1] bla bli blo  
## Levels: bla bli blo  
  
class(x = foo)  
  
## [1] "factor"  
  
typeof(x = foo)  
  
## [1] "integer"  
  
levels(x = foo)  
  
## [1] "bla" "bli" "blo"  
  
levels(x = foo) <- c(levels(x = foo), "blu") ## set extra level  
table(foo)  
  
## foo  
## bla bli blo blu  
##    1    1    1    0
```

- dates

```
(foo <- c(as.Date(x = "2018/06/18"),  
          as.Date(x = "19-06-18", format = "%d-%m-%y")))  
  
## [1] "2018-06-18" "2018-06-19"  
  
class(x = foo)  
  
## [1] "Date"  
  
typeof(x = foo)  
  
## [1] "double"  
  
foo + 50 ## you can do simple maths on dates!  
  
## [1] "2018-08-07" "2018-08-08"
```

# Vector: classes

There are more classes than types:

- factors

```
(foo <- factor(c("bla", "bli", "blo")))

## [1] bla bli blo
## Levels: bla bli blo

class(x = foo)

## [1] "factor"

typeof(x = foo)

## [1] "integer"

levels(x = foo)

## [1] "bla" "bli" "blo"

levels(x = foo) <- c(levels(x = foo), "blu") ## set extra level
table(foo)

## foo
## bla bli blo blu
## 1 1 1 0
```

- dates

```
(foo <- c(as.Date(x = "2018/06/18"),
          as.Date(x = "19-06-18", format = "%d-%m-%y")))

## [1] "2018-06-18" "2018-06-19"

class(x = foo)

## [1] "Date"

typeof(x = foo)

## [1] "double"

foo + 50 ## you can do simple maths on dates!

## [1] "2018-08-07" "2018-08-08"
```

Note: factors are heavily used in the context of linear models!

## Vector: classes

Vectors must contain elements of the same type (otherwise errors or automatic coercion may occur):

```
foo <- 1
bar <- "A"
foo_bar <- c(foo, bar)
foo_bar
## [1] "1" "A"
```

## Vector: classes

Vectors must contain elements of the same type (otherwise errors or automatic coercion may occur):

```
foo <- 1
bar <- "A"
foo_bar <- c(foo, bar)
foo_bar
## [1] "1" "A"
```

```
foo + 1
## [1] 2
foo_bar[1] + 1
## Error in foo_bar[1] + 1: non-numeric argument to binary operator
```

## Vector: classes

Vectors must contain elements of the same type (otherwise errors or automatic coercion may occur):

```
foo <- 1
bar <- "A"
foo_bar <- c(foo, bar)
foo_bar
## [1] "1" "A"
```

```
foo + 1
## [1] 2
foo_bar[1] + 1
## Error in foo_bar[1] + 1: non-numeric argument to binary operator
```

### Challenges:

- find out why the previous call produces an error.
- try to check how the automatic coercion occurs by mixing different classes in different ways (logical, integers, numeric, characters, factors).
- find out which date is internally stored as 0?

## Vector: classes

Some coercions are straightforward:

```
as.integer(x = 1.2)
```

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

```
as.integer(x = 1.9)
```

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

```
as.integer(x = -2.1)
```

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

```
foo <- factor(x = 10:20)
```

```
foo
```

```
## [1] 10 11 12 13 14 15 16 17 18 19 20
```

```
## Levels: 10 11 12 13 14 15 16 17 18 19 20
```

```
as.character(x = foo)
```

```
## [1] "10" "11" "12" "13" "14" "15" "16" "17" "18" "19" "20"
```

# Vector: classes

Some coercions are straightforward:

```
as.integer(x = 1.2)
```

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

```
as.integer(x = 1.9)
```

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

```
as.integer(x = -2.1)
```

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

```
foo <- factor(x = 10:20)
```

```
foo
```

```
## [1] 10 11 12 13 14 15 16 17 18 19 20
```

```
## Levels: 10 11 12 13 14 15 16 17 18 19 20
```

```
as.character(x = foo)
```

```
## [1] "10" "11" "12" "13" "14" "15" "16" "17" "18" "19" "20"
```

But not all:

```
as.numeric(x = foo)
```

```
## [1] 1 2 3 4 5 6 7 8 9 10 11
```

```
as.numeric(as.character(x = foo))
```

```
## [1] 10 11 12 13 14 15 16 17 18 19 20
```

```
foo <- as.Date(x = "20180618", format = "%Y%m%d")
```

```
as.integer(x = foo)
```

```
## [1] 17700
```

```
as.integer(x = gsub(pattern = "-", replacement = "", x = as.character(foo)))
```

```
## [1] 20180618
```

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# Factors

You can create them after in two steps:

```
sex <- c("girl","girl","girl","girl","girl", "girl",  
"boy","boy","boy","boy")  
class(x = sex)  
## [1] "character"
```

```
sex <- factor(x = sex)  
sex  
## [1] girl girl girl girl girl girl boy boy boy boy  
## Levels: boy girl
```

# Factors

You can create them after in two steps:

```
sex <- c("girl","girl","girl","girl","girl", "girl",
"boy","boy","boy","boy")
class(x = sex)
## [1] "character"
```

```
sex <- factor(x = sex)
sex
## [1] girl girl girl girl girl girl boy  boy  boy  boy
## Levels: boy girl
```

Better code:

```
sex <- factor(x = c(rep(x = "girl", times = 6),
                     rep(x = "boy", times = 4)))
```

Even better code:

```
sex <- factor(x = c(rep(x = "girl", times = length(x = height_girls)),
                    rep(x = "boy", times = length(x = height_boys)))))
```

Note: more on programming style later!

## Combining vectors with different levels

We want to merge the two following vectors:

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

```
bar <- factor(c("b", "c"))  
bar  
## [1] b c  
## Levels: b c
```

# Combining vectors with different levels

We want to merge the two following vectors:

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

```
bar <- factor(c("b", "c"))
bar
## [1] b c
## Levels: b c
```

## Problem:

```
foo_bar <- c(foo, bar)
foo_bar
## [1] 1 2 1 2
class(foo_bar)
## [1] "integer"
```

# Combining vectors with different levels

We want to merge the two following vectors:

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

```
bar <- factor(c("b", "c"))
bar
## [1] b c
## Levels: b c
```

## Problem:

```
foo_bar <- c(foo, bar)
foo_bar
## [1] 1 2 1 2
class(foo_bar)
## [1] "integer"
```

## Solution:

```
foo_bar <- factor(c(as.character(foo), as.character(bar)))
foo_bar
## [1] a b b c
## Levels: a b c
class(foo_bar)
## [1] "factor"
```

# Dropping unused levels

By default **R** keeps unused levels:

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

```
table(foo)
## foo
## a b c
## 2 1 1
```

```
bar <- foo[-4]
table(bar)
## bar
## a b c
## 2 1 0
```

# Dropping unused levels

By default **R** keeps unused levels:

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

```
table(foo)
## foo
## a b c
## 2 1 1
```

```
bar <- foo[-4]
table(bar)
## bar
## a b c
## 2 1 0
```

If you want to update the levels you need to use the function `droplevels`:

```
new_bar <- droplevels(bar)
table(new_bar)
## new_bar
## a b
## 2 1
```

Or use the argument `drop`:

```
bar <- foo[-4, drop = TRUE]
table(bar)
## bar
## a b
## 2 1
```

# Changing the order of levels of a factor

You have:

```
my_factor1  
## [1] A A B B C  
## Levels: A B C
```

You want:

```
my_factor2  
## [1] A A B B C  
## Levels: C B A
```



# Changing the order of levels of a factor

You have:

```
my_factor1  
## [1] A A B B C  
## Levels: A B C
```

You want:

```
my_factor2  
## [1] A A B B C  
## Levels: C B A
```

You do:

```
my_factor2 <- factor(x = my_factor1, levels = levels(my_factor1)[c(3, 2, 1)])  
my_factor2  
## [1] A A B B C  
## Levels: C B A
```

# Changing the order of levels of a factor

You have:

```
my_factor1
## [1] A A B B C
## Levels: A B C
```

You want:

```
my_factor2
## [1] A A B B C
## Levels: C B A
```

You do:

```
my_factor2 <- factor(x = my_factor1, levels = levels(my_factor1)[c(3, 2, 1)])
my_factor2
## [1] A A B B C
## Levels: C B A
```

Or if you only care about the first level:

```
my_factor3 <- relevel(x = my_factor1, ref = "C")
my_factor3
## [1] A A B B C
## Levels: C A B
```

# Changing the order of levels of a factor

You have:

```
my_factor1
## [1] A A B B C
## Levels: A B C
```

You want:

```
my_factor2
## [1] A A B B C
## Levels: C B A
```

You do:

```
my_factor2 <- factor(x = my_factor1, levels = levels(my_factor1)[c(3, 2, 1)])
my_factor2
## [1] A A B B C
## Levels: C B A
```

Or if you only care about the first level:

```
my_factor3 <- relevel(x = my_factor1, ref = "C")
my_factor3
## [1] A A B B C
## Levels: C A B
```

Note: the order of levels influences the meaning of parameter estimates in linear models and some plotting functions (e.g. order in the legend of a ggplot) ...

# Changing the levels of a factor

You have:

```
my_factor1  
## [1] A A B B C  
## Levels: A B C
```

You want:

```
my_factor2  
## [1] A A A A D  
## Levels: A D
```

# Changing the levels of a factor

You have:

```
my_factor1
## [1] A A B B C
## Levels: A B C
```

You want:

```
my_factor2
## [1] A A A A D
## Levels: A D
```

You do:

```
## Using base:
levels(x = my_factor1)
## [1] "A" "B" "C"

my_factor2 <- my_factor1
levels(x = my_factor2) <- c("A", "A", "D") ## in same order!
my_factor2
## [1] A A A A D
## Levels: A D
```

# Changing the levels of a factor

You have:

```
my_factor1
## [1] A A B B C
## Levels: A B C
```

You want:

```
my_factor2
## [1] A A A A D
## Levels: A D
```

You do:

```
## Using base:
levels(x = my_factor1)
## [1] "A" "B" "C"

my_factor2 <- my_factor1
levels(x = my_factor2) <- c("A", "A", "D") ## in same order!
my_factor2
## [1] A A A A D
## Levels: A D
```

```
## Using dplyr:
library(dplyr)
my_factor2 <- recode(.x = my_factor1, A = "A", B = "A", C = "D")
my_factor2
## [1] A A A A D
## Levels: A D
```

# Changing the levels of a factor

You have:

```
my_factor1
## [1] A A B B C
## Levels: A B C
```

You want:

```
my_factor2
## [1] A A A A D
## Levels: A D
```

You do:

```
## Using base:
levels(x = my_factor1)
## [1] "A" "B" "C"

my_factor2 <- my_factor1
levels(x = my_factor2) <- c("A", "A", "D") ## in same order!
my_factor2
## [1] A A A A D
## Levels: A D
```

```
## Using dplyr:
library(dplyr)
my_factor2 <- recode(.x = my_factor1, A = "A", B = "A", C = "D")
my_factor2
## [1] A A A A D
## Levels: A D
```

Note: if you want more modern functions to manipulate factors, look at the package `forcats` from `tidyverse`.

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# Some simple functions for vectors

```
foo <- c("bla", "bla", "bli")  
bar <- c(1, 1.2, pi, NA)
```

```
any(is.na(x = foo))  
## [1] FALSE  
  
unique(x = foo)  
## [1] "bla" "bli"  
  
length(x = foo)  
## [1] 3  
  
str(object = foo)  
## chr [1:3] "bla" "bla" "bli"  
  
summary(object = foo)  
##      Length      Class      Mode  
##          3 character character
```

# Some simple functions for vectors

```
foo <- c("bla", "bla", "bli")
bar <- c(1, 1.2, pi, NA)
```

```
any(is.na(x = foo))
## [1] FALSE

unique(x = foo)
## [1] "bla" "bli"

length(x = foo)
## [1] 3

str(object = foo)
## chr [1:3] "bla" "bla" "bli"

summary(object = foo)
##      Length      Class      Mode
##          3 character character
```

```
any(is.na(x = bar))
## [1] TRUE

unique(x = bar)
## [1] 1.000000 1.200000 3.141593      NA

length(x = bar)
## [1] 4

str(object = bar)
## num [1:4] 1 1.2 3.14 NA

summary(object = bar)
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##      1.000   1.100   1.200   1.781   2.171   3.142     1
```

## A more complex function: `sapply()`

`sapply()` is a function to apply a function on each element of a vector:

```
triple <- function(x) c(x, x, x) ## let us create a silly function
triple(x = "a")
## [1] "a" "a" "a"
```

```
sapply(X = bar, FUN = triple) ## here returns a matrix (automatic choice)
##      [,1] [,2]      [,3] [,4]
## [1,]  1  1.2 3.141593    NA
## [2,]  1  1.2 3.141593    NA
## [3,]  1  1.2 3.141593    NA
```

## A more complex function: `sapply()`

`sapply()` is a function to apply a function on each element of a vector:

```
triple <- function(x) c(x, x, x) ## let us create a silly function
triple(x = "a")
## [1] "a" "a" "a"
```

```
sapply(X = bar, FUN = triple) ## here returns a matrix (automatic choice)
##      [,1] [,2]      [,3] [,4]
## [1,]    1  1.2 3.141593    NA
## [2,]    1  1.2 3.141593    NA
## [3,]    1  1.2 3.141593    NA
```

```
sapply(X = bar, FUN = triple, simplify = FALSE) ## same but always returns a list
## [[1]]
## [1] 1 1 1
##
## [[2]]
## [1] 1.2 1.2 1.2
##
## [[3]]
## [1] 3.141593 3.141593 3.141593
##
## [[4]]
## [1] NA NA NA
```

## A more complex function: `sapply()`

`sapply()` is a function to apply a function on each element of a vector:

```
triple <- function(x) c(x, x, x) ## let us create a silly function
triple(x = "a")
## [1] "a" "a" "a"
```

```
sapply(X = bar, FUN = triple) ## here returns a matrix (automatic choice)
##      [,1] [,2]      [,3] [,4]
## [1,]    1  1.2 3.141593    NA
## [2,]    1  1.2 3.141593    NA
## [3,]    1  1.2 3.141593    NA
```

```
sapply(X = bar, FUN = triple, simplify = FALSE) ## same but always returns a list
## [[1]]
## [1] 1 1 1
##
## [[2]]
## [1] 1.2 1.2 1.2
##
## [[3]]
## [1] 3.141593 3.141593 3.141593
##
## [[4]]
## [1] NA NA NA
```

Note 1: this is useful when the function cannot work on vector and when the return is more than one element. For example, the input could be a vector of file names and the output one dataset per file!

## A more complex function: `sapply()`

`sapply()` is a function to apply a function on each element of a vector:

```
triple <- function(x) c(x, x, x) ## let us create a silly function
triple(x = "a")
## [1] "a" "a" "a"
```

```
sapply(X = bar, FUN = triple) ## here returns a matrix (automatic choice)
##      [,1] [,2]      [,3] [,4]
## [1,]    1  1.2 3.141593    NA
## [2,]    1  1.2 3.141593    NA
## [3,]    1  1.2 3.141593    NA
```

```
sapply(X = bar, FUN = triple, simplify = FALSE) ## same but always returns a list
## [[1]]
## [1] 1 1 1
##
## [[2]]
## [1] 1.2 1.2 1.2
##
## [[3]]
## [1] 3.141593 3.141593 3.141593
##
## [[4]]
## [1] NA NA NA
```

Note 1: this is useful when the function cannot work on vector and when the return is more than one element. For example, the input could be a vector of file names and the output one dataset per file!

Note 2: if you want more modern functions more consistent than the `*apply()` ones, look at the package `purrr` from `tidyverse`.

## A more complex function: `sapply()`

`sapply()` is a function to apply a function on each element of a vector:

```
triple <- function(x) c(x, x, x) ## let us create a silly function
triple(x = "a")
## [1] "a" "a" "a"
```

```
sapply(X = bar, FUN = triple) ## here returns a matrix (automatic choice)
##      [,1] [,2]      [,3] [,4]
## [1,]    1  1.2 3.141593    NA
## [2,]    1  1.2 3.141593    NA
## [3,]    1  1.2 3.141593    NA
```

```
sapply(X = bar, FUN = triple, simplify = FALSE) ## same but always returns a list
## [[1]]
## [1] 1 1 1
##
## [[2]]
## [1] 1.2 1.2 1.2
##
## [[3]]
## [1] 3.141593 3.141593 3.141593
##
## [[4]]
## [1] NA NA NA
```

Note 1: this is useful when the function cannot work on vector and when the return is more than one element. For example, the input could be a vector of file names and the output one dataset per file!

Note 2: if you want more modern functions more consistent than the `*apply()` ones, look at the package `purrr` from `tidyverse`.

Challenge: can you think of an alternative to do that without using `sapply()`?

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# Matrices & arrays

The matrices and arrays are direct extensions of vectors when there is more than one dimension (1 or 2 dimensions for matrices, any for arrays).

## Example of a matrix:

```
my_matrix <- matrix(data = 1:12, ncol = 4, nrow = 3)
my_matrix
##      [,1] [,2] [,3] [,4]
## [1,]   1   4   7  10
## [2,]   2   5   8  11
## [3,]   3   6   9  12
class(x = my_matrix)
## [1] "matrix"
typeof(x = my_matrix) ## behind the curtain, matrices are stored as vectors!
## [1] "integer"
```

# Matrices & arrays

The matrices and arrays are direct extensions of vectors when there is more than one dimension (1 or 2 dimensions for matrices, any for arrays).

## Example of a matrix:

```
my_matrix <- matrix(data = 1:12, ncol = 4, nrow = 3)
my_matrix
##      [,1] [,2] [,3] [,4]
## [1,]   1   4   7  10
## [2,]   2   5   8  11
## [3,]   3   6   9  12
class(x = my_matrix)
## [1] "matrix"
typeof(x = my_matrix) ## behind the curtain, matrices are stored as vectors!
## [1] "integer"
```

Note 1: since there are a kind of vectors, the same restrictions apply: all elements must have the same class!

Note 2: useful for building the input of some statistical tests (e.g. chi-square), for linear algebra (e.g. computation behind linear models), for handling GIS information & for understanding data frames.

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# Matrices: general properties

They can be combined:

```
(my_2nd_matrix <- matrix(data = 13:18, ncol = 2, nrow = 3))  
##      [,1] [,2]  
## [1,]  13  16  
## [2,]  14  17  
## [3,]  15  18  
  
(my_3rd_matrix <- matrix(data = 1:4, nrow = 1))  
##      [,1] [,2] [,3] [,4]  
## [1,]    1    2    3    4
```

# Matrices: general properties

They can be combined:

```
(my_2nd_matrix <- matrix(data = 13:18, ncol = 2, nrow = 3))
```

```
##      [,1] [,2]  
## [1,]   13  16  
## [2,]   14  17  
## [3,]   15  18
```

```
(my_3rd_matrix <- matrix(data = 1:4, nrow = 1))
```

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

```
cbind(my_matrix, my_2nd_matrix) ## bind columns
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6]  
## [1,]    1    4    7   10   13   16  
## [2,]    2    5    8   11   14   17  
## [3,]    3    6    9   12   15   18
```

# Matrices: general properties

They can be combined:

```
(my_2nd_matrix <- matrix(data = 13:18, ncol = 2, nrow = 3))  
##      [,1] [,2]  
## [1,]  13  16  
## [2,]  14  17  
## [3,]  15  18  
  
(my_3rd_matrix <- matrix(data = 1:4, nrow = 1))  
##      [,1] [,2] [,3] [,4]  
## [1,]    1    2    3    4
```

```
cbind(my_matrix, my_2nd_matrix) ## bind columns  
##      [,1] [,2] [,3] [,4] [,5] [,6]  
## [1,]    1    4    7   10   13   16  
## [2,]    2    5    8   11   14   17  
## [3,]    3    6    9   12   15   18
```

```
rbind(my_matrix, my_3rd_matrix) ## bind rows  
##      [,1] [,2] [,3] [,4]  
## [1,]    1    4    7   10  
## [2,]    2    5    8   11  
## [3,]    3    6    9   12  
## [4,]    1    2    3    4
```

# Matrices: general properties

Subsets can be made (with indexes, booleans or names):

```
my_matrix[2, ]  
## [1] 2 5 8 11  
my_matrix[, 1]  
## [1] 1 2 3  
my_matrix[3, , drop = FALSE] ## to keep a matrix  
##      [,1] [,2] [,3] [,4]  
## [1,]    3    6    9   12  
my_matrix[2, 1]  
## [1] 2  
my_matrix[c(1:2), c(1:2)]  
##      [,1] [,2]  
## [1,]    1    4  
## [2,]    2    5
```

# Matrices: general properties

Subsets can be made (with indexes, booleans or names):

```
my_matrix[2, ]
## [1]  2  5  8 11
my_matrix[, 1]
## [1] 1 2 3
my_matrix[3, , drop = FALSE] ## to keep a matrix
##      [,1] [,2] [,3] [,4]
## [1,]    3    6    9   12
my_matrix[2, 1]
## [1] 2
my_matrix[c(1:2), c(1:2)]
##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
```

```
colnames(x = my_matrix) <- c("A", "B", "C", "D")
rownames(x = my_matrix) <- c("a", "b", "c")
my_matrix
##   A B C D
## a 1 4 7 10
## b 2 5 8 11
## c 3 6 9 12
my_matrix["b", ]
##   A B C D
##  2 5 8 11
```



# Matrices: general properties

In the background, a matrix is a vector with dimension attributes (i.e. number of columns and rows).

```
attributes(my_matrix)
## $dim
## [1] 3 4
##
## $dimnames
## $dimnames[[1]]
## [1] "a" "b" "c"
##
## $dimnames[[2]]
## [1] "A" "B" "C" "D"

str(my_matrix)
## int [1:3, 1:4] 1 2 3 4 5 6 7 8 9 10 ...
## - attr(*, "dimnames")=List of 2
## ..$ : chr [1:3] "a" "b" "c"
## ..$ : chr [1:4] "A" "B" "C" "D"
```

# Matrices: general properties

In the background, a matrix is a vector with dimension attributes (i.e. number of columns and rows).

```
attributes(my_matrix)
## $dim
## [1] 3 4
##
## $dimnames
## $dimnames[[1]]
## [1] "a" "b" "c"
##
## $dimnames[[2]]
## [1] "A" "B" "C" "D"

str(my_matrix)
## int [1:3, 1:4] 1 2 3 4 5 6 7 8 9 10 ...
## - attr(*, "dimnames")=List of 2
## ..$ : chr [1:3] "a" "b" "c"
## ..$ : chr [1:4] "A" "B" "C" "D"
```

You can subset the data using this dimension attributes or not:

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

my_matrix[2, 2]
## [1] 5
```

## Matrices: general properties

In the background, a matrix is a vector with dimension attributes (i.e. number of columns and rows).

```
attributes(my_matrix)
## $dim
## [1] 3 4
##
## $dimnames
## $dimnames[[1]]
## [1] "a" "b" "c"
##
## $dimnames[[2]]
## [1] "A" "B" "C" "D"

str(my_matrix)
## int [1:3, 1:4] 1 2 3 4 5 6 7 8 9 10 ...
## - attr(*, "dimnames")=List of 2
## ..$ : chr [1:3] "a" "b" "c"
## ..$ : chr [1:4] "A" "B" "C" "D"
```

You can subset the data using this dimension attributes or not:

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

my_matrix[2, 2]
## [1] 5
```

A matrix will be filled from top - bottom, left - right:

```
(my_matrix4 <- matrix(data = 1:4, ncol = 2, nrow = 2)) ## but try byrow = TRUE

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

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# Some simple functions for matrices

## Dimensions:

```
dim(x = my_matrix)
## [1] 3 4

ncol(x = my_matrix)
## [1] 4

nrow(x = my_matrix)
## [1] 3

length(x = my_matrix)
## [1] 12
```

## Names:

```
colnames(x = my_matrix)
## [1] "A" "B" "C" "D"

rownames(x = my_matrix)
## [1] "a" "b" "c"
```

## Linear algebra:

```
t(x = my_matrix) ## transpose

##   a b c
## A 1 2 3
## B 4 5 6
## C 7 8 9
## D 10 11 12

my_matrix %*% c(1:4) ## matrix multiplication

##   [,1]
## a    70
## b    80
## c    90

diag(x = my_matrix) ## extract diagonal
## [1] 1 5 9
```

## A more complex function: `apply()`

`apply()` is a function to apply a function on each row or column of a matrix:

```
apply(X = my_matrix, MARGIN = 1, FUN = mean) ## row means
```

```
##   a   b   c
```

```
## 5.5 6.5 7.5
```

```
apply(X = my_matrix, MARGIN = 2, FUN = sd) ## column SDs
```

```
## A B C D
```

```
## 1 1 1 1
```

# Arrays?

Arrays are very similar to matrices but allow for more dimensions:

```
foo <- array(data = 1:8, dim = c(2, 2, 2))
foo
## , , 1
##
##      [,1] [,2]
## [1,]    1    3
## [2,]    2    4
##
## , , 2
##
##      [,1] [,2]
## [1,]    5    7
## [2,]    6    8
```

```
foo[1, 2, 2]
## [1] 7
apply(X = foo, MARGIN = 3, FUN = sum)
## [1] 10 26
```

Note: only useful in some very specific situations.

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# Lists

Lists allow the organisation of any set of entities into a single **R** object.

## Example of a list:

```
list_height <- list(height_girls, height_boys)
list_height

## [[1]]
## [1] 178 175 159 164 183 192
##
## [[2]]
## [1] 181 189 174 177
class(x = list_height)
## [1] "list"
typeof(x = list_height)
## [1] "list"
```

Note 1: list elements can be anything!

Note 2: lists are very important because no function can output more than one object!

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## Lists: general properties

They can be combined:

```
list_full <- c(list_height, list(my_matrix))
list_full
## [[1]]
## [1] 178 175 159 164 183 192
##
## [[2]]
## [1] 181 189 174 177
##
## [[3]]
##   A B C D
## a 1 4 7 10
## b 2 5 8 11
## c 3 6 9 12
```

## Lists: general properties

Subsets can be made (with indexes, booleans or names):

```
list_height <- list(girls = height_girls, boys = height_boys) ## create a list with names
list_height
## $girls
## [1] 178 175 159 164 183 192
##
## $boys
## [1] 181 189 174 177
```

```
list_height$girls
## [1] 178 175 159 164 183 192
```

```
list_height["boys"] ## still a list
## $boys
## [1] 181 189 174 177
```

```
list_height[["boys"]] ## vector
## [1] 181 189 174 177
```

```
list_height[[2]][3]
## [1] 174
```

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## Some simple functions for lists

```
length(x = list_full) ## number of elements
## [1] 3
```

```
str(object = list_full) ## this function is really useful!

## List of 3
## $ : num [1:6] 178 175 159 164 183 192
## $ : num [1:4] 181 189 174 177
## $ : int [1:3, 1:4] 1 2 3 4 5 6 7 8 9 10 ...
## ..- attr(*, "dimnames")=List of 2
## .. ..$ : chr [1:3] "a" "b" "c"
## .. ..$ : chr [1:4] "A" "B" "C" "D"
```

Challenge: run the examples from `lm()` and explore the list `lm.D9`.

## A more complex function: `lapply()`

`lapply()` is a function to apply a function on each element of a list:

```
lapply(X = list_full, FUN = mean)
## [[1]]
## [1] 175.1667
##
## [[2]]
## [1] 180.25
##
## [[3]]
## [1] 6.5
```

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# Data frames

Data frames allow the organisation of vectors of the same length as a matrix-like structure:

## Example:

```
dataframe_ht <- data.frame(Height = height, Sex = sex)
dataframe_ht

##      Height Sex
## 1      181 girl
## 2      189 girl
## 3      174 girl
## 4      177 girl
## 5      178 girl
## 6      175 girl
## 7      159 boy
## 8      164 boy
## 9      183 boy
## 10     192 boy

class(dataframe_ht)
## [1] "data.frame"

typeof(dataframe_ht)
## [1] "list"
```

# Data frames

Data frames allow the organisation of vectors of the same length as a matrix-like structure:

## Example:

```
dataframe_ht <- data.frame(Height = height, Sex = sex)
dataframe_ht

##      Height Sex
## 1      181 girl
## 2      189 girl
## 3      174 girl
## 4      177 girl
## 5      178 girl
## 6      175 girl
## 7      159  boy
## 8      164  boy
## 9      183  boy
## 10     192  boy

class(dataframe_ht)
## [1] "data.frame"

typeof(dataframe_ht)
## [1] "list"
```

Note 1: this is the best choice of representation for datasets!

Note 2: it is safer to work on data frames than on floating vectors!

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# Data frames: general properties

They borrow from both matrices and lists:

As for matrices:

```
(dataframe_ht_double <- cbind(dataframe_ht, newcol = 1:10))
```

##	Height	Sex	newcol
## 1	181	girl	1
## 2	189	girl	2
## 3	174	girl	3
## 4	177	girl	4
## 5	178	girl	5
## 6	175	girl	6
## 7	159	boy	7
## 8	164	boy	8
## 9	183	boy	9
## 10	192	boy	10

# Data frames: general properties

They borrow from both matrices and lists:

As for matrices:

```
(dataframe_ht_double <- cbind(dataframe_ht, newcol = 1:10))
```

```
##      Height Sex newcol
## 1      181 girl      1
## 2      189 girl      2
## 3      174 girl      3
## 4      177 girl      4
## 5      178 girl      5
## 6      175 girl      6
## 7      159 boy       7
## 8      164 boy       8
## 9      183 boy       9
## 10     192 boy      10
```

```
dataframe_ht[, "Sex"]
```

```
## [1] girl girl girl girl girl boy boy boy boy
## Levels: boy girl
```

```
dataframe_ht[2, 2]
```

```
## [1] girl
## Levels: boy girl
```

# Data frames: general properties

They borrow from both matrices and lists:

As for matrices:

```
(dataframe_ht_double <- cbind(dataframe_ht, newcol = 1:10))

##      Height Sex newcol
## 1      181 girl      1
## 2      189 girl      2
## 3      174 girl      3
## 4      177 girl      4
## 5      178 girl      5
## 6      175 girl      6
## 7      159 boy       7
## 8      164 boy       8
## 9      183 boy       9
## 10     192 boy      10
```

```
dataframe_ht[, "Sex"]
## [1] girl girl girl girl girl boy  boy  boy  boy
## Levels: boy girl

dataframe_ht[2, 2]
## [1] girl
## Levels: boy girl
```

As for lists:

```
dataframe_ht$Height
## [1] 181 189 174 177 178 175 159 164 183 192

str(dataframe_ht)
## 'data.frame': 10 obs. of  2 variables:
## $ Height: num  181 189 174 177 178 175 159 164 183 192
## $ Sex : Factor w/ 2 levels "boy","girl": 2 2 2 2 2 1 1 1 1 1
```

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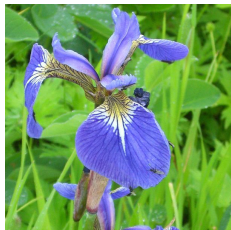
## 5 Data frames and tibbles

- general properties
- **challenge**
- functions
- dplyr
- tidyr
- tibbles

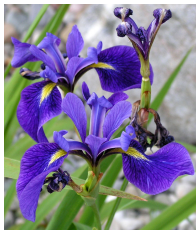
## 6 Importing & exporting data

# Data frames: challenge

The iris data set ([https://en.wikipedia.org/wiki/Iris\\_flower\\_data\\_set](https://en.wikipedia.org/wiki/Iris_flower_data_set)):



*Iris setosa*  
©Miya.m



*Iris versicolor*  
©D.G.E. Robertson



*Iris virginica*  
©F. Mayfield

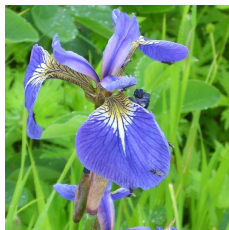
```
head(x = iris, n = 2L) ## this function displays by default the first 6 rows
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
## 2         4.9         3.0         1.4         0.2   setosa
```

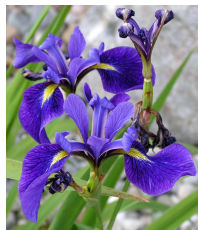


# Data frames: challenge

The iris data set ([https://en.wikipedia.org/wiki/Iris\\_flower\\_data\\_set](https://en.wikipedia.org/wiki/Iris_flower_data_set)):



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*Iris virginica*  
©F. Mayfield

```
head(x = iris, n = 2L) ## this function displays by default the first 6 rows
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
## 2         4.9         3.0         1.4         0.2   setosa
```

Using the `iris` data frame, find out:

- what is the average sepal length across all flowers?
- what is the median sepal length across *Iris versicolor*?

# Data frames: general properties

Data frames can easily be edited:

```
backup <- dataframe_ht[1, 1]
dataframe_ht[1, 1] <- 171.3
dataframe_ht[1, 1]

## [1] 171.3

dataframe_ht[1, 1] <- backup
dataframe_ht[1, 1]

## [1] 181
```

# Data frames: general properties

Data frames can easily be edited:

```
backup <- dataframe_ht[1, 1]
dataframe_ht[1, 1] <- 171.3
dataframe_ht[1, 1]
```

```
## [1] 171.3
```

```
dataframe_ht[1, 1] <- backup
dataframe_ht[1, 1]
```

```
## [1] 181
```

```
dataframe_ht$linenumber <- 1:nrow(x = dataframe_ht) # add column
head(x = dataframe_ht)
```

```
##   Height Sex linenumber
## 1    181 girl          1
## 2    189 girl          2
## 3    174 girl          3
## 4    177 girl          4
## 5    178 girl          5
## 6    175 girl          6
```

# Data frames: general properties

## Data frames can easily be edited:

```
backup <- dataframe_ht[1, 1]
dataframe_ht[1, 1] <- 171.3
dataframe_ht[1, 1]

## [1] 171.3

dataframe_ht[1, 1] <- backup
dataframe_ht[1, 1]

## [1] 181
```

```
dataframe_ht$linenumber <- 1:nrow(x = dataframe_ht) # add column
head(x = dataframe_ht)

##   Height Sex linenumber
## 1    181 girl          1
## 2    189 girl          2
## 3    174 girl          3
## 4    177 girl          4
## 5    178 girl          5
## 6    175 girl          6
```

```
dataframe_ht$linenumber <- NULL # remove column
head(x = dataframe_ht)

##   Height Sex
## 1    181 girl
## 2    189 girl
## 3    174 girl
## 4    177 girl
## 5    178 girl
## 6    175 girl
```

# Getting started with R

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- general properties
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## 4 List

- general properties
- functions

## 5 Data frames and tibbles

- general properties
- challenge
- **functions**
- dplyr
- tidyr
- tibbles

## 6 Importing & exporting data

# Some simple functions for data frames

```
head(x = iris) ## try also tail()
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
## 2         4.9         3.0         1.4         0.2   setosa
## 3         4.7         3.2         1.3         0.2   setosa
## 4         4.6         3.1         1.5         0.2   setosa
## 5         5.0         3.6         1.4         0.2   setosa
## 6         5.4         3.9         1.7         0.4   setosa
```

```
summary(object = 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
```

```
dim(x = iris)
```

```
## [1] 150  5
```

```
ncol(x = iris)
```

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

```
nrow(x = iris)
```

```
## [1] 150
```

```
length(x = iris) ## not as in matrix!!
```

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

```
rownames(x = iris)[1:10]
```

```
## [1] "1" "2" "3" "4" "5" "6" "7" "8" "9" "10"
```

```
colnames(x = iris)
```

```
## [1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "
```

## A more complex function: `tapply()`

`tapply()` is a function to apply a function on subsets of a given column from the data frame:

```
tapply(X = iris$Sepal.Length, INDEX = iris$Species, FUN = mean)
```

```
##      setosa versicolor  virginica  
##      5.006      5.936      6.588
```

## A more complex function: `tapply()`

`tapply()` is a function to apply a function on subsets of a given column from the data frame:

```
tapply(X = iris$Sepal.Length, INDEX = iris$Species, FUN = mean)
##      setosa versicolor  virginica
##      5.006      5.936      6.588
```

Or similarly:

```
with(data = iris, tapply(X = Sepal.Length, INDEX = Species, FUN = mean))
##      setosa versicolor  virginica
##      5.006      5.936      6.588
```



## A more complex function: `tapply()`

`tapply()` is a function to apply a function on subsets of a given column from the data frame:

```
tapply(X = iris$Sepal.Length, INDEX = iris$Species, FUN = mean)
##      setosa versicolor  virginica
##      5.006      5.936      6.588
```

Or similarly:

```
with(data = iris, tapply(X = Sepal.Length, INDEX = Species, FUN = mean))
##      setosa versicolor  virginica
##      5.006      5.936      6.588
```

Or similarly:

```
by(data = iris, INDICES = iris$Species, FUN = function(x) mean(x$Sepal.Length))
## iris$Species: setosa
## [1] 5.006
## -----
## iris$Species: versicolor
## [1] 5.936
## -----
## iris$Species: virginica
## [1] 6.588
```

Note: `by()` is more powerful but more complex than `tapply()`.

## The dplyr alternative to tapply()

The same operation in dplyr looks very different:

```
iris %>%  
  group_by(Species) %>%  
  summarize(mean_sepal_length = mean(Sepal.Length),  
            mean_sepal_width = mean(Sepal.Width)) %>%  
  as.data.frame() ## optional but otherwise tibble and not data frame  
  
##      Species mean_sepal_length mean_sepal_width  
## 1   setosa          5.006          3.428  
## 2 versicolor        5.936          2.770  
## 3  virginica        6.588          2.974
```

Note: this replaces two tapply() calls and remains easy to read.

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- general properties
- challenge
- functions
- **dplyr**
- tidyr
- tibbles

## 6 Importing & exporting data

## Some words about dplyr & co.

dplyr is part of the growing tidyverse world (<https://www.tidyverse.org/>) developed by RStudio:



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dplyr is part of the growing tidyverse world (<https://www.tidyverse.org/>) developed by RStudio:



### R core team

- build the core of **R** and the original **R** GUI
- maintain CRAN
- backward compatibility is the priority
- limited man power (20 selected volunteers)
- not commercial (but Microsoft may creep in?)

### RStudio

- build RStudio IDE, tidyverse and more
- tidyverse philosophy: 1 function = 1 action
- backward compatibility is not the priority
- 1 leader (Hadley Wickham) + ~ 70 full time employees + tons of volunteers
- free + commercial

## Some words about dplyr & co.

dplyr is part of the growing tidyverse world (<https://www.tidyverse.org/>) developed by RStudio:



### R core team

- build the core of **R** and the original **R** GUI
- maintain CRAN
- backward compatibility is the priority
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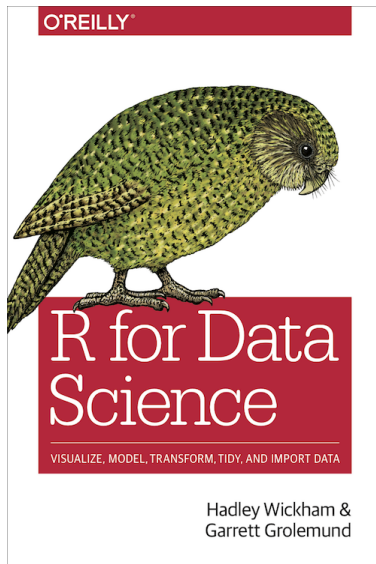
- build RStudio IDE, tidyverse and more
- tidyverse philosophy: 1 function = 1 action
- backward compatibility is not the priority
- 1 leader (Hadley Wickham) + ~ 70 full time employees + tons of volunteers
- free + commercial

Note 1: that has led to two quite distinct **R** dialects

Note 2: more and more users rely on tidyverse...

Note 3: we will see a bit of both dialects

## Some words about dplyr & co.



# dplyr

- in dplyr one verb = one action = one function (tidyverse philosophy)
- operations can be chained with the pipe operator `%>%` (from package `magrittr`), which considers the output from one function as the input of the next function



# dplyr

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- operations can be chained with the pipe operator `%>%` (from package `magrittr`), which considers the output from one function as the input of the next function

## Pros

- clear code
- consistent
- powerful
- fast
- many tutorials

# dplyr

- in dplyr one verb = one action = one function (tidyverse philosophy)
- operations can be chained with the pipe operator `%>%` (from package `magrittr`), which considers the output from one function as the input of the next function

## Pros

- clear code
- consistent
- powerful
- fast
- many tutorials

## Cons

- different & redundant
- buggy (but less & less so)
- poor traditional documentation
- lead to bad habits (e.g. arguments not named, help not looked at)
- broaden the gap between users and programmers

# dplyr verbs

Useful dplyr functions:

- add column with `mutate()`

```
dataframe_ht <- dataframe_ht %>% mutate(ID = 1:nrow(dataframe_ht))  
head(x = dataframe_ht, n = 3)
```

```
##   Height Sex ID  
## 1    181 girl 1  
## 2    189 girl 2  
## 3    174 girl 3
```

# dplyr verbs

Useful dplyr functions:

- add column with `mutate()`

```
dataframe_ht <- dataframe_ht %>% mutate(ID = 1:nrow(dataframe_ht))  
head(x = dataframe_ht, n = 3)
```

```
##   Height Sex ID  
## 1    181 girl 1  
## 2    189 girl 2  
## 3    174 girl 3
```

- change column with `transmute()`

```
dataframe_ht2 <- dataframe_ht %>% transmute(double_height = 2*height)  
head(x = dataframe_ht2, n = 3)
```

```
##   double_height  
## 1             362  
## 2             378  
## 3             348
```

# dplyr verbs

Useful dplyr functions:

- select columns with `select()`

```
dataframe_ht_sex <- dataframe_ht %>% select(Sex)
head(x = dataframe_ht_sex, n = 3)

##      Sex
## 1 girl
## 2 girl
## 3 girl
```

# dplyr verbs

Useful dplyr functions:

- select columns with `select()`

```
dataframe_ht_sex <- dataframe_ht %>% select(Sex)
head(x = dataframe_ht_sex, n = 3)

##      Sex
## 1 girl
## 2 girl
## 3 girl
```

- select rows with `filter()`

```
dataframe_ht_female <- dataframe_ht %>% filter(Sex == "girl")
head(dataframe_ht_female, n = 3)

##   Height Sex ID
## 1    181 girl  1
## 2    189 girl  2
## 3    174 girl  3
```

# dplyr verbs

Useful dplyr functions:

- select columns with `select()`

```
dataframe_ht_sex <- dataframe_ht %>% select(Sex)
head(x = dataframe_ht_sex, n = 3)

##      Sex
## 1 girl
## 2 girl
## 3 girl
```

- select rows with `filter()`

```
dataframe_ht_female <- dataframe_ht %>% filter(Sex == "girl")
head(dataframe_ht_female, n = 3)

##   Height Sex ID
## 1    181 girl  1
## 2    189 girl  2
## 3    174 girl  3
```

- sort rows with `arrange()`

```
dataframe_ht_sorted <- dataframe_ht %>% arrange(Height)  ## add arrange(desc(Height)) for the other direction
head(dataframe_ht_sorted, n = 3)

##   Height Sex ID
## 1    159 boy  7
## 2    164 boy  8
## 3    174 girl  3
```

## Around dplyr verbs

These main dplyr functions have derivatives and some of them can be useful:

e.g. `mutate_if` performs mutation if a condition is fulfilled, which could be useful for example if you want to change all numeric variables into character variables:

you have:

```
## 'data.frame': 150 obs. of  5 variables:
## $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
## $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
## $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ..
## $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ..
## $ Species      : Factor w/ 3 levels "setosa","versicolor",...: 1
```

you want:

```
## 'data.frame': 150 obs. of  5 variables:
## $ Sepal.Length: chr  "5.1" "4.9" "4.7" "4.6" ...
## $ Sepal.Width : chr  "3.5" "3" "3.2" "3.1" ...
## $ Petal.Length: chr  "1.4" "1.4" "1.3" "1.5" ...
## $ Petal.Width : chr  "0.2" "0.2" "0.2" "0.2" ...
## $ Species      : Factor w/ 3 levels "setosa","versicolor",...: 1 1
```

you do:

```
iris_numeric <- iris %>%
  mutate_if(is.numeric, ~ as.character(.))
```



## group\_by()

The `group_by()` function allows you to perform operation on grouped data.

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It is very powerful when combined to:

- `summarize()` → one value per group

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It is very powerful when combined to:

- `summarize()` → one value per group
- `mutate()` or `transmute()` → one value per observation

## group\_by()

The `group_by()` function allows you to perform operation on grouped data.

It is very powerful when combined to:

- `summarize()` → one value per group
- `mutate()` or `transmute()` → one value per observation
- `slice()` → select some rows for each "group"

## group\_by() with summarize()

Example: you want the mean height of males and females, the median height and the number in each group:

```
dataframe_ht %>%  
  group_by(Sex) %>%  
  summarize(mean_height = mean(Height),  
            median_height = median(Height),  
            n = n()) %>%  
  as.data.frame()  
  
##      Sex mean_height median_height n  
## 1  boy      174.5      173.5 4  
## 2 girl      179.0      177.5 6
```

## group\_by() with mutate()

Same as before, but we want to repeat the value for each individual:

```
dataframe_ht %>%
  group_by(Sex) %>%
  mutate(mean_height = mean(Height),
         median_height = median(Height),
         n = n()) %>%
  as.data.frame()
```

##	Height	Sex	ID	mean_height	median_height	n
## 1	181	girl	1	179.0	177.5	6
## 2	189	girl	2	179.0	177.5	6
## 3	174	girl	3	179.0	177.5	6
## 4	177	girl	4	179.0	177.5	6
## 5	178	girl	5	179.0	177.5	6
## 6	175	girl	6	179.0	177.5	6
## 7	159	boy	7	174.5	173.5	4
## 8	164	boy	8	174.5	173.5	4
## 9	183	boy	9	174.5	173.5	4
## 10	192	boy	10	174.5	173.5	4

Note: many other functions than `n()` can be used, see `?summarise` !

## group\_by() with slice()

Example: you want the first two rows of each species of irises:

```
iris %>%  
  group_by(Species) %>%  
  slice(1:2) %>%  
  as.data.frame()
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	5.1	3.5	1.4	0.2	setosa
## 2	4.9	3.0	1.4	0.2	setosa
## 3	7.0	3.2	4.7	1.4	versicolor
## 4	6.4	3.2	4.5	1.5	versicolor
## 5	6.3	3.3	6.0	2.5	virginica
## 6	5.8	2.7	5.1	1.9	virginica

# Challenge

Use the dataset called `population_UK` and compute the total population size for:

- 1915
- 2015
- all years in the dataset
- all years between 1915 and 2015

Use the dataset called `deaths_UK` and figure out:

- which were the top 3 detailed causes of death before 1930 for each of the 21 broader categories
- the death toll for all individuals below 15 yrs for each year



# Using dplyr to merge datasets

## Data frame #1:

```
my_df1 <- iris %>%  
  filter(Species == "setosa") %>%  
  select(Sepal.Length, Petal.Length, Species) %>%  
  slice(1:4)  
my_df1[4, 1] <- NA  
my_df1
```

##	Sepal.Length	Petal.Length	Species
## 1	5.1	1.4	setosa
## 2	4.9	1.4	setosa
## 3	4.7	1.3	setosa
## 4	NA	1.5	setosa

## Data frame #2:

```
my_df2 <- iris %>%  
  filter(Species == "virginica") %>%  
  select(Sepal.Length, Petal.Width, Species) %>%  
  slice(1:4)  
my_df2[3, 2] <- NA  
my_df2
```

##	Sepal.Length	Petal.Width	Species
## 1	6.3	2.5	virginica
## 2	5.8	1.9	virginica
## 3	7.1	NA	virginica
## 4	6.3	1.8	virginica

We will see how to merge these two data frames!

## Using dplyr to merge datasets

There are several options but `full_join()` is the most effective one: it keeps all the rows of the two data frames and adds NA when no data are present!

```
my_df3 <- full_join(my_df1, my_df2)
## Joining, by = c("Sepal.Length", "Species")
my_df3
##   Sepal.Length Petal.Length   Species Petal.Width
## 1         5.1         1.4    setosa         NA
## 2         4.9         1.4    setosa         NA
## 3         4.7         1.3    setosa         NA
## 4         NA         1.5    setosa         NA
## 5         6.3         NA virginica         2.5
## 6         5.8         NA virginica         1.9
## 7         7.1         NA virginica         NA
## 8         6.3         NA virginica         1.8
```

Note: you can also do that without `dplyr` but the outcome is a bit more messy:

```
merge(my_df1, my_df2, all = TRUE)
```

## Using dplyr to merge datasets

You can also use `left_join()` to keep all data from the first dataset and keep only the new data from the second data set that fit in:

```
(flower_quality <- data.frame(Species = c("setosa", "versicolor", "virginica"),  
                             Quality = c("High", "Medium", "Low")))
```

```
##      Species Quality  
## 1    setosa    High  
## 2 versicolor Medium  
## 3  virginica    Low
```

## Using dplyr to merge datasets

You can also use `left_join()` to keep all data from the first dataset and keep only the new data from the second data set that fit in:

```
(flower_quality <- data.frame(Species = c("setosa", "versicolor", "virginica"),  
                             Quality = c("High", "Medium", "Low")))
```

```
##      Species Quality  
## 1    setosa    High  
## 2 versicolor Medium  
## 3  virginica    Low
```

```
left_join(my_df3, flower_quality, by = "Species")
```

```
##   Sepal.Length Petal.Length   Species Petal.Width Quality  
## 1         5.1         1.4    setosa         NA     High  
## 2         4.9         1.4    setosa         NA     High  
## 3         4.7         1.3    setosa         NA     High  
## 4         NA         1.5    setosa         NA     High  
## 5         6.3         NA virginica         2.5     Low  
## 6         5.8         NA virginica         1.9     Low  
## 7         7.1         NA virginica         NA     Low  
## 8         6.3         NA virginica         1.8     Low
```

## Using dplyr to merge datasets

You can also use `left_join()` to keep all data from the first dataset and keep only the new data from the second data set that fit in:

```
(flower_quality <- data.frame(Species = c("setosa", "versicolor", "virginica"),
                             Quality = c("High", "Medium", "Low")))
```

```
##      Species Quality
## 1    setosa    High
## 2 versicolor Medium
## 3  virginica    Low
```

```
left_join(my_df3, flower_quality, by = "Species")
```

```
##   Sepal.Length Petal.Length   Species Petal.Width Quality
## 1         5.1         1.4    setosa         NA     High
## 2         4.9         1.4    setosa         NA     High
## 3         4.7         1.3    setosa         NA     High
## 4         NA         1.5    setosa         NA     High
## 5         6.3         NA virginica         2.5     Low
## 6         5.8         NA virginica         1.9     Low
## 7         7.1         NA virginica         NA     Low
## 8         6.3         NA virginica         1.8     Low
```

```
full_join(my_df3, flower_quality, by = "Species")
```

```
##   Sepal.Length Petal.Length   Species Petal.Width Quality
## 1         5.1         1.4    setosa         NA     High
## 2         4.9         1.4    setosa         NA     High
## 3         4.7         1.3    setosa         NA     High
## 4         NA         1.5    setosa         NA     High
## 5         6.3         NA virginica         2.5     Low
## 6         5.8         NA virginica         1.9     Low
## 7         7.1         NA virginica         NA     Low
## 8         6.3         NA virginica         1.8     Low
## 9         NA         NA  versicolor         NA   Medium
```

# Challenge

Use the datasets called `population_UK` and `deaths_UK` to compute yearly mortality rates for:

- all individuals
- individuals below 15 yrs only

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- general properties
- challenge
- functions
- dplyr
- **tidyr**
- tibbles

## 6 Importing & exporting data

## Reshaping data frame

For most data analyses, you need:

- one row = one observation
- one column = one variable

Unfortunately, it is often not the way people input data!



## Reshaping data frame

For most data analyses, you need:

- one row = one observation
- one column = one variable

Unfortunately, it is often not the way people input data!

The `tidyverse` package `tidyr` offers solutions:

- `gather()` turns wide data into long
- `spread()` turns long data into wide

# From wide to long

you have:

```
head(my_df1)
##   ID Sex age1 age2 age3 age4
## 1  1 girl  81  156  171  181

dim(my_df1)
## [1] 1 6
```

you want:

```
head(my_df2)
##   ID Sex Age Height
## 1  1 girl age1     81
## 2  1 girl age2    156
## 3  1 girl age3    171
## 4  1 girl age4    181

dim(my_df2)
## [1] 4 4
```

# From wide to long

you have:

```
head(my_df1)
##   ID Sex age1 age2 age3 age4
## 1  1 girl  81  156  171  181

dim(my_df1)
## [1] 1 6
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you want:

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head(my_df2)
##   ID Sex Age Height
## 1  1 girl age1     81
## 2  1 girl age2    156
## 3  1 girl age3    171
## 4  1 girl age4    181

dim(my_df2)
## [1] 4 4
```

you do:

```
library(tidyr)
my_df2 <- my_df1 %>%
  gather("Age", "Height", -Sex, -ID) %>%
  arrange(ID, Age)
```

# From wide to long

you have:

```
head(my_df1)
##   ID Sex age1 age2 age3 age4
## 1  1 girl  81  156  171  181

dim(my_df1)
## [1] 1 6
```

you want:

```
head(my_df2)
##   ID Sex Age Height
## 1  1 girl age1     81
## 2  1 girl age2    156
## 3  1 girl age3    171
## 4  1 girl age4    181

dim(my_df2)
## [1] 4 4
```

you do:

```
library(tidyr)
my_df2 <- my_df1 %>%
  gather("Age", "Height", -Sex, -ID) %>%
  arrange(ID, Age)
```

or:

```
my_df2 <- my_df1 %>%
  gather("Age", "Height", 3:ncol(my_df1)) %>%
  arrange(ID, Age)
```

# From long to wide

you have:

```
head(my_df2)
##   ID Sex Age Height
## 1  1 girl age1     81
## 2  1 girl age2    156
## 3  1 girl age3    171
## 4  1 girl age4    181
dim(my_df2)
## [1] 4 4
```

you want:

```
head(my_df1)
##   ID Sex age1 age2 age3 age4
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# From long to wide

you have:

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head(my_df2)
##   ID Sex Age Height
## 1  1 girl age1     81
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## 3  1 girl age3    171
## 4  1 girl age4    181
dim(my_df2)
## [1] 4 4
```

you want:

```
head(my_df1)
##   ID Sex age1 age2 age3 age4
## 1  1 girl   81  156  171  181
dim(my_df1)
## [1] 1 6
```

you do:

```
my_df2 %>%
  spread(-Sex, -ID)
##   ID Sex age1 age2 age3 age4
## 1  1 girl   81  156  171  181
```

Note: but why on Earth would you need that?!

## Some other useful functions from tidyr

`unite()` merges 2 columns of a data frame:

```
my_df3 <- my_df2 %>% unite(New_col, ID, Sex)
head(my_df3)
```

```
##   New_col Age Height
## 1  1_girl age1     81
## 2  1_girl age2    156
## 3  1_girl age3    171
## 4  1_girl age4    181
```

## Some other useful functions from tidyr

**unite()** merges 2 columns of a data frame:

```
my_df3 <- my_df2 %>% unite(New_col, ID, Sex)
```

```
head(my_df3)
```

```
##   New_col Age Height
## 1 1_girl age1     81
## 2 1_girl age2    156
## 3 1_girl age3    171
## 4 1_girl age4    181
```

**separate()** splits 2 columns of a data frame:

```
my_df3 %>% separate(New_col, c("ID", "Sex"))
```

```
##   ID Sex Age Height
## 1  1 girl age1     81
## 2  1 girl age2    156
## 3  1 girl age3    171
## 4  1 girl age4    181
```



## Some other useful functions from tidyr

`unite()` merges 2 columns of a data frame:

```
my_df3 <- my_df2 %>% unite(New_col, ID, Sex)
```

```
head(my_df3)
```

```
##   New_col Age Height
## 1 1_girl age1     81
## 2 1_girl age2    156
## 3 1_girl age3    171
## 4 1_girl age4    181
```

`separate()` splits 2 columns of a data frame:

```
my_df3 %>% separate(New_col, c("ID", "Sex"))
```

```
##   ID Sex Age Height
## 1  1 girl age1     81
## 2  1 girl age2    156
## 3  1 girl age3    171
## 4  1 girl age4    181
```

Note: the **R** base equivalent are `paste()` and `strsplit()` but they are a bit more tedious to use.

# Getting started with R

## 1 Introduction

## 2 Vectors

- general properties
- types & classes
- factors
- functions

## 3 Matrices and arrays

- general properties
- functions

## 4 List

- general properties
- functions

## 5 Data frames and tibbles

- general properties
- challenge
- functions
- dplyr
- tidyr
- **tibbles**

## 6 Importing & exporting data

# What are tibbles?

Tibbles are modified data frames that are automatically created by tidyverse packages:

```
iris_tbl <- iris %>%
  group_by(Species) %>%
  mutate(Sepal.Length.meam = mean(Sepal.Length))
iris_tbl
```

## # A tibble: 150 x 6

## # Groups: Species [3]

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	Sepal.Length.meam
##	<dbl>	<dbl>	<dbl>	<dbl>	<fct>	<dbl>
## 1	5.1	3.5	1.4	0.2	setosa	5.01
## 2	4.9	3	1.4	0.2	setosa	5.01
## 3	4.7	3.2	1.3	0.2	setosa	5.01
## 4	4.6	3.1	1.5	0.2	setosa	5.01
## 5	5	3.6	1.4	0.2	setosa	5.01
## 6	5.4	3.9	1.7	0.4	setosa	5.01
## 7	4.6	3.4	1.4	0.3	setosa	5.01
## 8	5	3.4	1.5	0.2	setosa	5.01
## 9	4.4	2.9	1.4	0.2	setosa	5.01
## 10	4.9	3.1	1.5	0.1	setosa	5.01

## # ... with 140 more rows

Note: most of what works on objects of class `data.frame` works on objects of class `tbl` (but not all as they don't consider row names).

# From tibbles to data frames and back

You can easily convert one into the other:

```
head(as.data.frame(iris_tbl))
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	Sepal.Length.meam
## 1	5.1	3.5	1.4	0.2	setosa	5.006
## 2	4.9	3.0	1.4	0.2	setosa	5.006
## 3	4.7	3.2	1.3	0.2	setosa	5.006
## 4	4.6	3.1	1.5	0.2	setosa	5.006
## 5	5.0	3.6	1.4	0.2	setosa	5.006
## 6	5.4	3.9	1.7	0.4	setosa	5.006

# From tibbles to data frames and back

You can easily convert one into the other:

```
head(as.data.frame(iris_tbl))
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Sepal.Length.meam
## 1         5.1         3.5         1.4         0.2   setosa         5.006
## 2         4.9         3.0         1.4         0.2   setosa         5.006
## 3         4.7         3.2         1.3         0.2   setosa         5.006
## 4         4.6         3.1         1.5         0.2   setosa         5.006
## 5         5.0         3.6         1.4         0.2   setosa         5.006
## 6         5.4         3.9         1.7         0.4   setosa         5.006
```

```
as_tibble(as.data.frame(iris_tbl)) ## no need for head as tibble!
```

```
## # A tibble: 150 x 6
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Sepal.Length.meam
##   <dbl>         <dbl>         <dbl>         <dbl> <fct>         <dbl>
## 1         5.1         3.5         1.4         0.2   setosa         5.01
## 2         4.9         3         1.4         0.2   setosa         5.01
## 3         4.7         3.2         1.3         0.2   setosa         5.01
## 4         4.6         3.1         1.5         0.2   setosa         5.01
## 5         5         3.6         1.4         0.2   setosa         5.01
## 6         5.4         3.9         1.7         0.4   setosa         5.01
## 7         4.6         3.4         1.4         0.3   setosa         5.01
## 8         5         3.4         1.5         0.2   setosa         5.01
## 9         4.4         2.9         1.4         0.2   setosa         5.01
## 10        4.9         3.1         1.5         0.1   setosa         5.01
## # ... with 140 more rows
```

# From tibbles to data frames and back

You can easily convert one into the other:

```
head(as.data.frame(iris_tbl))
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Sepal.Length.meam
## 1         5.1         3.5         1.4         0.2   setosa         5.006
## 2         4.9         3.0         1.4         0.2   setosa         5.006
## 3         4.7         3.2         1.3         0.2   setosa         5.006
## 4         4.6         3.1         1.5         0.2   setosa         5.006
## 5         5.0         3.6         1.4         0.2   setosa         5.006
## 6         5.4         3.9         1.7         0.4   setosa         5.006
```

```
as_tibble(as.data.frame(iris_tbl)) ## no need for head as tibble!
```

```
## # A tibble: 150 x 6
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Sepal.Length.meam
##   <dbl>         <dbl>         <dbl>         <dbl> <fct>         <dbl>
## 1         5.1         3.5         1.4         0.2   setosa         5.01
## 2         4.9         3         1.4         0.2   setosa         5.01
## 3         4.7         3.2         1.3         0.2   setosa         5.01
## 4         4.6         3.1         1.5         0.2   setosa         5.01
## 5         5         3.6         1.4         0.2   setosa         5.01
## 6         5.4         3.9         1.7         0.4   setosa         5.01
## 7         4.6         3.4         1.4         0.3   setosa         5.01
## 8         5         3.4         1.5         0.2   setosa         5.01
## 9         4.4         2.9         1.4         0.2   setosa         5.01
## 10        4.9         3.1         1.5         0.1   setosa         5.01
## # ... with 140 more rows
```

Note: for linear models, it is safer to convert everything into data frames!

# How to influence the display of tibbles?

You can change the number of rows being displayed:

```
print(iris_tbl, n = 2)

## # A tibble: 150 x 6
## # Groups:   Species [3]
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Sepal.Length.meam
##         <dbl>         <dbl>         <dbl>         <dbl> <fct>         <dbl>
## 1           5.1           3.5           1.4           0.2 setosa         5.01
## 2           4.9           3            1.4           0.2 setosa         5.01
## # ... with 148 more rows
```

```
print(iris_tbl, n = 8)

## # A tibble: 150 x 6
## # Groups:   Species [3]
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Sepal.Length.meam
##         <dbl>         <dbl>         <dbl>         <dbl> <fct>         <dbl>
## 1           5.1           3.5           1.4           0.2 setosa         5.01
## 2           4.9           3            1.4           0.2 setosa         5.01
## 3           4.7           3.2           1.3           0.2 setosa         5.01
## 4           4.6           3.1           1.5           0.2 setosa         5.01
## 5           5            3.6           1.4           0.2 setosa         5.01
## 6           5.4           3.9           1.7           0.4 setosa         5.01
## 7           4.6           3.4           1.4           0.3 setosa         5.01
## 8           5            3.4           1.5           0.2 setosa         5.01
## # ... with 142 more rows
```

# How to influence the display of tibbles?

You can change the number of rows being displayed:

```
print(iris_tbl, n = 2)

## # A tibble: 150 x 6
## # Groups:   Species [3]
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Sepal.Length.meam
##         <dbl>         <dbl>         <dbl>         <dbl> <fct>         <dbl>
## 1         5.1           3.5           1.4           0.2 setosa         5.01
## 2         4.9           3             1.4           0.2 setosa         5.01
## # ... with 148 more rows
```

```
print(iris_tbl, n = 8)

## # A tibble: 150 x 6
## # Groups:   Species [3]
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Sepal.Length.meam
##         <dbl>         <dbl>         <dbl>         <dbl> <fct>         <dbl>
## 1         5.1           3.5           1.4           0.2 setosa         5.01
## 2         4.9           3             1.4           0.2 setosa         5.01
## 3         4.7           3.2           1.3           0.2 setosa         5.01
## 4         4.6           3.1           1.5           0.2 setosa         5.01
## 5         5             3.6           1.4           0.2 setosa         5.01
## 6         5.4           3.9           1.7           0.4 setosa         5.01
## 7         4.6           3.4           1.4           0.3 setosa         5.01
## 8         5             3.4           1.5           0.2 setosa         5.01
## # ... with 142 more rows
```

Note: to always display all row you can set options(dplyr.print\_min = Inf).



# How to influence the display of tibbles?

You can change the number of digits being displayed:

Default:

```
x <- as_tibble(data.frame(pi = pi))
x
## # A tibble: 1 x 1
##       pi
##   <dbl>
## 1  3.14
```

# How to influence the display of tibbles?

You can change the number of digits being displayed:

Default:

```
x <- as_tibble(data.frame(pi = pi))
x
## # A tibble: 1 x 1
##       pi
##   <dbl>
## 1  3.14
```

Changing setting:

```
old_opt <- options(pillar.sigfig = 10)
x
## # A tibble: 1 x 1
##       pi
##   <dbl>
## 1 3.141592654
```

# How to influence the display of tibbles?

You can change the number of digits being displayed:

Default:

```
x <- as_tibble(data.frame(pi = pi))
x
## # A tibble: 1 x 1
##       pi
##   <dbl>
## 1  3.14
```

Changing setting:

```
old_opt <- options(pillar.sigfig = 10)
x
## # A tibble: 1 x 1
##       pi
##   <dbl>
## 1 3.141592654
```

Resetting setting:

```
options(old_opt)
x
## # A tibble: 1 x 1
##       pi
##   <dbl>
## 1  3.14
```

# How to influence the display of tibbles?

Sometimes the default is a little too dangerous!

```
foo <- c(178, 175, 159, 164, 183, 160, 181, 189, 174, 177)
level <- c(rep("A", 6), rep("B", 4))
```

```
d <- data.frame(foo, level)
d %>%
  group_by(level) %>%
  summarize(Mean = mean(foo))

## # A tibble: 2 x 2
##   level Mean
##   <fct> <dbl>
## 1 A      170.
## 2 B      180.
```

# How to influence the display of tibbles?

Sometimes the default is a little too dangerous!

```
foo <- c(178, 175, 159, 164, 183, 160, 181, 189, 174, 177)
level <- c(rep("A", 6), rep("B", 4))
```

```
d <- data.frame(foo, level)
d %>%
  group_by(level) %>%
  summarize(Mean = mean(foo))

## # A tibble: 2 x 2
##   level Mean
##   <fct> <dbl>
## 1 A     170.
## 2 B     180.
```

Compare to base R:

```
c(mean(foo[level == "A"]), mean(foo[level == "B"]))
## [1] 169.8333 180.2500
```

Note: but at least they have recently added the "." suggesting there are more number out there!

# Getting started with R

- 1 Introduction
- 2 Vectors
- 3 Matrices and arrays
- 4 List
- 5 Data frames and tibbles
- 6 Importing & exporting data**

## Working directory

Before anything, you must know where you read & write on your hard drive!

```
getwd() ## get the working directory, to change it use setwd()
## [1] "/Users/alex/Dropbox/Boulot/Mes_projets_de_recherche/R_packages/BeginR_project/BeginR/sources_vignettes/usingdata"

dir() ## list all files in the working directory
## [1] "usingdata.nav"      "usingdata.pdf"      "usingdata.pdf.asis" "usingdata.Rnw"      "usingdata.snm"
## [6] "usingdata.tex"      "usingdata.toc"      "usingdata.vrb"

dir(pattern = "*.csv") ## list all files with the extension csv
## character(0)
```

Note: you can also set this up with RStudio but it won't be saved unless you set up a project file.

## Exporting and importing data in the R binary format

R can write and read binary formats that take by convention the extensions `.rda` or `.RData`.

Example:

```
my_iris <- iris  
save(my_iris, file = "my_iris.rda") ## check the help for compression
```



## Exporting and importing data in the R binary format

R can write and read binary formats that take by convention the extensions `.rda` or `.RData`.

Example:

```
my_iris <- iris
save(my_iris, file = "my_iris.rda") ## check the help for compression
```

```
rm(list = ls()) ## removes everything!
head(my_iris)

## Error in head(my_iris): object 'my_iris' not found
```

## Exporting and importing data in the R binary format

R can write and read binary formats that take by convention the extensions `.rda` or `.RData`.

Example:

```
my_iris <- iris
save(my_iris, file = "my_iris.rda") ## check the help for compression
```

```
rm(list = ls()) ## removes everything!
head(my_iris)

## Error in head(my_iris): object 'my_iris' not found
```

```
load(file = "my_iris.rda")
head(my_iris)
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	5.1	3.5	1.4	0.2	setosa
## 2	4.9	3.0	1.4	0.2	setosa
## 3	4.7	3.2	1.3	0.2	setosa
## 4	4.6	3.1	1.5	0.2	setosa
## 5	5.0	3.6	1.4	0.2	setosa
## 6	5.4	3.9	1.7	0.4	setosa

Note: this is useful and best for R to R exchanges (but it is useless without R).

## Exporting and importing data sets in plain text

- **R** cannot read/write .xls(x) files out of the box
- Several packages can do that, but it is safer to use .csv or .txt files
- Excel can read and write .csv & .txt files!

Writing a data set:

```
write.csv(my_iris, file = "my_iris.csv", row.names = FALSE)
```

## Exporting and importing data sets in plain text

- **R** cannot read/write .xls(x) files out of the box
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### Writing a data set:

```
write.csv(my_iris, file = "my_iris.csv", row.names = FALSE)
```

### Reading a data set:

```
rm(my_iris) ## delete the object my_iris
my_iris <- read.csv("my_iris.csv") ## or read.table() with adequate options!
head(my_iris)
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	5.1	3.5	1.4	0.2	setosa
## 2	4.9	3.0	1.4	0.2	setosa
## 3	4.7	3.2	1.3	0.2	setosa
## 4	4.6	3.1	1.5	0.2	setosa
## 5	5.0	3.6	1.4	0.2	setosa
## 6	5.4	3.9	1.7	0.4	setosa

## Exporting and importing data sets in plain text

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### Writing a data set:

```
write.csv(my_iris, file = "my_iris.csv", row.names = FALSE)
```

### Reading a data set:

```
rm(my_iris) ## delete the object my_iris
my_iris <- read.csv("my_iris.csv") ## or read.table() with adequate options!
head(my_iris)
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1          3.5          1.4          0.2 setosa
## 2          4.9          3.0          1.4          0.2 setosa
## 3          4.7          3.2          1.3          0.2 setosa
## 4          4.6          3.1          1.5          0.2 setosa
## 5          5.0          3.6          1.4          0.2 setosa
## 6          5.4          3.9          1.7          0.4 setosa
```

Note 1: always check your file in a text editor before importing it or use RStudio "File/Import Datasets GUI".

Note 2: you will have often to change the arguments sep (and dec if you are german).

Note 3: setting stringsAsFactors = FALSE can avoid a lot of troubles!

# Challenge

Create a data frame using your favorite spreadsheet software (or choose an existing one) and import it in **R**.