Getting to use data in **R**

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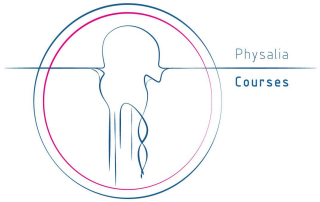

Getting started with **R**

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

Handling data in **R**

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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!

Note: if you don't master at least vectors and data frames, you will never get very far using **R**.

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
- lists
  - each element can have its own length
  - each element can have its own type
- data frames (and tibbles)
  - all rows & columns have same length
  - each column can have its own type

Getting started with **R**

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
```

Getting started with **R**

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)]  ## useful 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)]  ## useful 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

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```
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
```

```
foo[2] + foo[1]
```

```
## colin
##     3
```

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
```

```
foo[2] + foo[1]
```

```
## colin
##     3
```

Double squared brackets can also be used for subsetting of single elements; they drop names (and other attributes):

```
foo[[1]] + foo[[2]]
```

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

```
foo[["alex"]] + foo[["colin"]]
```

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

Vector: general properties

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

```
foo <- c(alex = 1, colin = 2)
attributes(foo)
```

```
## $names
## [1] "alex"  "colin"
```

Vector: general properties

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

```
foo <- c(alex = 1, colin = 2)
attributes(foo)
```

```
## $names
## [1] "alex"  "colin"
```

```
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(alex = 1, colin = 2)
attributes(foo)
```

```
## $names
## [1] "alex"  "colin"
```

```
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(alex = 1, colin = 2)
attributes(foo)
```

```
## $names
## [1] "alex"  "colin"
```

```
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`).

Getting started with **R**

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

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```
(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

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- logicals

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

- 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))
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```

- 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** automatically detects the type of input and creates the right type of vector for you!

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 really help to understand many 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: coercion

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: coercion

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: coercion

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

Vector: coercion

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
```

Vector: coercion

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: coercion

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
```

Vector: coercion

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
```

Getting started with **R**

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"
```

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
```

```
class(x = sex)
```

```
## [1] "factor"
```

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
```

```
class(x = sex)
```

```
## [1] "factor"
```

Better code:

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

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
```

```
class(x = sex)
```

```
## [1] "factor"
```

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(x = c("a", "b"))
foo
```

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

```
bar <- factor(x = 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(x = c("a", "b"))
foo
```

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

```
bar <- factor(x = c("b", "c"))
bar
```

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

Problem:

```
foo_bar <- c(foo, bar)
foo_bar
```

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

```
class(x = foo_bar)
```

```
## [1] "integer"
```

Combining vectors with different levels

We want to merge the two following vectors:

```
foo <- factor(x = c("a", "b"))
foo
```

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

```
bar <- factor(x = c("b", "c"))
bar
```

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

Problem:

```
foo_bar <- c(foo, bar)
foo_bar
```

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

```
class(x = foo_bar)
```

```
## [1] "integer"
```

Solution:

```
foo_bar <- factor(x =  c(as.character(x = foo), as.character(x = bar)))
foo_bar
```

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

```
class(x = foo_bar)
```

```
## [1] "factor"
```

Dropping unused levels

By default **R** keeps unused levels:

```
foo <- factor(x = 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(x = 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(x = 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:

```
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:

```
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
```

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

Getting started with **R**

Some simple functions for vectors

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

```r
any(is.na(x = foo))
```

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

```r
unique(x = foo)
```

```
## [1] "bla" "bli"
```

```r
length(x = foo)
```

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

```r
str(object = foo)
```

```
##  chr [1:3] "bla" "bla" "bli"
```

```r
summary(object = foo)
```

```
##    Length     Class      Mode
##         3 character character
```

Some simple functions for vectors

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

```r
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
```

```r
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`.

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.

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

Getting started with **R**

Matrices & arrays

The matrices and arrays are direct extentions 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 extentions 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.

Getting started with **R**

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 dimensions defined as an attribute:

```
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 dimensions defined as an attribute:

```
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"
```

Thus, you can also subset a matrix considering it is a vector:

```
my_matrix[5] == my_matrix[2, 2]
```

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

Matrices: general properties

In the background, a matrix is a vector with dimensions defined as an attribute:

```
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"
```

Thus, you can also subset a matrix considering it is a vector:

```
my_matrix[5] == my_matrix[2, 2]
```

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

Note: by default, a matrix is always filled column by column (top → bottom then left → right):

```
(my_matrix4 <- matrix(data = 1:4, ncol = 2, nrow = 2)) ## but you can use the option byrow = TRUE to do fill matrices row by row instead!
```

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

Getting started with **R**

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
```

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.

Getting started with **R**

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 necessary because no function can output more than one object in **R**!

Getting started with **R**

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
```

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
```

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
```

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
```

Getting started with **R**

Some simple functions for lists

```
length(x = list_full) ## number of elements
```

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

```
str(object = list_full)  ## using str() on a list is really useful to understand the output of complex functions
```

```
## 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
```

Getting started with **R**

Data frames

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

Example:

```
height <- c(172, 178, 182, 162, 175, 168)
sex    <- factor(c("female", "male", "male", "female", "male", "male"))

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

```
##   Height    Sex
## 1    172 female
## 2    178   male
## 3    182   male
## 4    162 female
## 5    175   male
## 6    168   male
```

```
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:

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height <- c(172, 178, 182, 162, 175, 168)
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dataframe_ht <- data.frame(Height = height, Sex = sex)
dataframe_ht
```

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## 1    172 female
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```

```
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!

Getting started with **R**

Data frames: general properties

The usage borrows from both matrices and lists:

As for matrices:

```
(dataframe_ht2 <- cbind(dataframe_ht,
                        newcol = 1:nrow(dataframe_ht)))
```

```
##   Height    Sex newcol
## 1    172 female      1
## 2    178   male      2
## 3    182   male      3
## 4    162 female      4
## 5    175   male      5
## 6    168   male      6
```

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##   Height    Sex newcol
## 1    172 female      1
## 2    178   male      2
## 3    182   male      3
## 4    162 female      4
## 5    175   male      5
## 6    168   male      6
```

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

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

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

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

Data frames: general properties

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As for matrices:

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(dataframe_ht2 <- cbind(dataframe_ht,
                        newcol = 1:nrow(dataframe_ht)))
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## 5    175   male      5
## 6    168   male      6
```

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

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

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

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

As for lists:

```
dataframe_ht$Height
```

```
## [1] 172 178 182 162 175 168
```

```
str(dataframe_ht)
```

```
## 'data.frame': 6 obs. of  2 variables:
##  $ Height: num  172 178 182 162 175 168
##  $ Sex   : Factor w/ 2 levels "female","male": 1 2 2 1 2 2
```

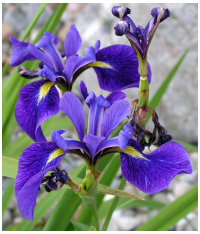
Getting started with **R**

Data frames: challenge

The `iris` 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 but here we display only the first 2
```

```
##   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`):

Iris setosa

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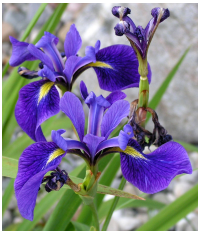

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```
head(x = iris, n = 2L) ## this function displays by default the first 6 rows but here we display only the first 2
```

```
##   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] 172
```

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] 172
```

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

```
##   Height    Sex linenumber
## 1    172 female          1
## 2    178   male          2
## 3    182   male          3
## 4    162 female          4
## 5    175   male          5
## 6    168   male          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] 172
```

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

```
##   Height    Sex linenumber
## 1    172 female          1
## 2    178   male          2
## 3    182   male          3
## 4    162 female          4
## 5    175   male          5
## 6    168   male          6
```

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

```
##   Height    Sex
## 1    172 female
## 2    178   male
## 3    182   male
## 4    162 female
## 5    175   male
## 6    168   male
```

Getting started with **R**

Some simple functions for data frames

```r
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
```

```r
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
```

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

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

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

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

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

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

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

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

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

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

```r
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()`

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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:

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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()`.

Getting started with **R**

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

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Example:

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

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

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

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save(my_iris, file = "my_iris.rda") ## check the help for compression
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```
rm(list = ls()) ## removes everything!
head(x = my_iris)
```

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

```
load(file = "my_iris.rda")
head(x = 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(x = my_iris, file = "my_iris.csv", row.names = FALSE)
```

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Writing a data set:

```
write.csv(x = 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(file = "my_iris.csv") ## or read.table() with adequate options!
head(x = my_iris)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
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## 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**.

Getting started with **R**

Meeting the tidyverse world

Two different ways to solve the problem: *what is the average length and width for each iris species?*

Standard **R** approach:

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

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

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

```
##     setosa versicolor  virginica
##      3.428      2.770      2.974
```

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##     setosa versicolor  virginica
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```

The same operation using the package `dplyr` from `tidyverse`:

```
library(tidyverse)  ## or just load dplyr

iris %>%
  group_by(Species) %>%
  summarize(mean_sepal_length = mean(Sepal.Length), mean_sepal_width = mean(Sepal.Width))
```

```
## # A tibble: 3 x 3
##   Species    mean_sepal_length mean_sepal_width
##   <fct>                  <dbl>            <dbl>
## 1 setosa                  5.01             3.43
## 2 versicolor              5.94             2.77
## 3 virginica               6.59             2.97
```

Meeting the tidyverse world

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```
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iris %>%
  group_by(Species) %>%
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```

```
## # A tibble: 3 x 3
##   Species    mean_sepal_length mean_sepal_width
##   <fct>                  <dbl>            <dbl>
## 1 setosa                  5.01             3.43
## 2 versicolor              5.94             2.77
## 3 virginica               6.59             2.97
```

Note: which one do you prefer?

Getting started with **R**

Some words about the tidyverse

The tidyverse packages (https://www.tidyverse.org/) are developped by RStudio:

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The tidyverse packages (https://www.tidyverse.org/) are developped by RStudio:

R is from the R core team who

- 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?)

tidyverse is from the RStudio people who

- build RStudio IDE, tidyverse and more
- tidyverse philosophy: 1 function = 1 action
- backward compatibility is not the priority
- $\sim$ 80 employees + tons of volunteers
- free + commercial

Some words about the tidyverse

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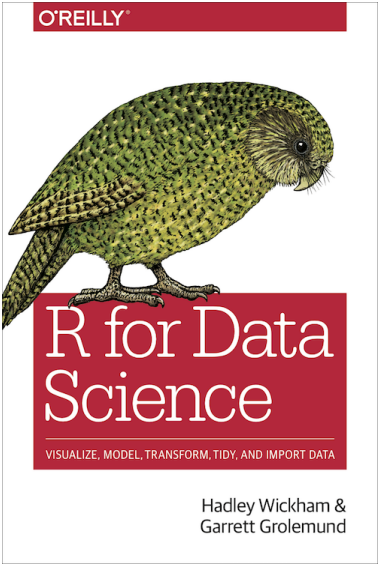
- build RStudio IDE, tidyverse and more
- tidyverse philosophy: 1 function = 1 action
- backward compatibility is not the priority
- $\sim$ 80 employees + tons of volunteers
- free + commercial

Note 1: that has led to two quite distinct **R** dialects.
Note 2: more and more users rely on tidyverse and many recent packages use the tidyverse grammar.
Note 3: we will see a bit of both dialects.

Getting started with tidyverse



Note: there are also multiple tutorials on the web (e.g. `https://www.r-bloggers.com/lesser-known-dplyr-tricks/`).

Key tidyverse principles

- one verb = one action = one function
- 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 (exception: `ggplot2` that uses "+" instead)
- the outcome of a given function is always of the same `class`

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Pros

- clear code
- consistent
- powerful
- fast
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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. help not looked at)
- wider gap between users and developers

Getting started with **R**

dplyr verbs

Useful dplyr functions:

- add column with mutate()

```
iris %>%
  mutate(double_SL = 2*Sepal.Length) %>%
  head(n = 3)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species double_SL
## 1          5.1         3.5          1.4         0.2  setosa      10.2
## 2          4.9         3.0          1.4         0.2  setosa       9.8
## 3          4.7         3.2          1.3         0.2  setosa       9.4
```

dplyr verbs

Useful `dplyr` functions:

- add column with `mutate()`

```
iris %>%
  mutate(double_SL = 2*Sepal.Length) %>%
  head(n = 3)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species double_SL
## 1          5.1         3.5          1.4         0.2  setosa      10.2
## 2          4.9         3.0          1.4         0.2  setosa       9.8
## 3          4.7         3.2          1.3         0.2  setosa       9.4
```

- create and keep only new columns with `transmute()`

```
iris %>%
  transmute(double_SL = 2*Sepal.Length) %>%
  head(n = 3)
```

```
##   double_SL
## 1      10.2
## 2       9.8
## 3       9.4
```

dplyr verbs

Useful dplyr functions:

- select columns with select()

```
iris %>%
  select(Sepal.Length) %>%
  head(n = 3)
```

```
##   Sepal.Length
## 1          5.1
## 2          4.9
## 3          4.7
```

dplyr verbs

Useful `dplyr` functions:

- select columns with `select()`

```
iris %>%
  select(Sepal.Length) %>%
  head(n = 3)
```

```
##   Sepal.Length
## 1          5.1
## 2          4.9
## 3          4.7
```

- select rows with `filter()`

```
iris %>%
  filter(Species == "virginica") %>%
  head(n = 3)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
## 1          6.3         3.3          6.0         2.5 virginica
## 2          5.8         2.7          5.1         1.9 virginica
## 3          7.1         3.0          5.9         2.1 virginica
```

dplyr verbs

Useful `dplyr` functions:

- select columns with `select()`

```
iris %>%
  select(Sepal.Length) %>%
  head(n = 3)
```

```
##   Sepal.Length
## 1          5.1
## 2          4.9
## 3          4.7
```

- select rows with `filter()`

```
iris %>%
  filter(Species == "virginica") %>%
  head(n = 3)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
## 1          6.3         3.3          6.0         2.5 virginica
## 2          5.8         2.7          5.1         1.9 virginica
## 3          7.1         3.0          5.9         2.1 virginica
```

- sort rows with `arrange()`

```
iris %>%
  arrange(Petal.Length) %>% ## arrange(desc(Petal.Length)) for the other direction
  head(n = 3)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          4.6         3.6          1.0         0.2  setosa
## 2          4.3         3.0          1.1         0.1  setosa
## 3          5.8         4.0          1.2         0.2  setosa
```

Getting started with **R**

What are tibbles?

Tibbles are modified data frames that can be used and (sometimes automatically) produced by `tidyverse` packages:

```
iris %>%
  group_by(Species) %>%
  mutate(Sepal.Length.meam = mean(Sepal.Length)) -> iris_tbl ## note the inverted arrow!
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(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(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(data.frame(iris_tbl))  ## no need for head() when using tibbles!
```

```
## # 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(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(data.frame(iris_tbl))  ## no need for head() when using tibbles!
```

```
## # 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
```

Reseting setting:

```
options(old_opt)
x
```

```
## # A tibble: 1 x 1
##       pi
##    <dbl>
## 1  3.14
```

Getting started with **R**

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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- mutate() or transmute() → one value per observation

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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()

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"
- `do()` → for applying custom functions on each "group"
  (but advanced and perhaps soon deprecated)

group_by() with summarize()

Example: for each species you want the mean petal length, the sd and the number of observations:

```
iris %>%
  group_by(Species) %>%
  summarize(mean_PL = mean(Petal.Length),
            sd_PL = sd(Petal.Length),
            n = n())
```

```
## # A tibble: 3 x 4
##   Species    mean_PL sd_PL     n
##   <fct>        <dbl> <dbl> <int>
## 1 setosa        1.46 0.174    50
## 2 versicolor    4.26 0.470    50
## 3 virginica     5.55 0.552    50
```

group_by() with mutate()

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

```
iris %>%
  group_by(Species) %>%
  mutate(mean_PL = mean(Petal.Length),
            sd_PL = sd(Petal.Length),
            n = n())
```

```
## # A tibble: 150 x 8
## # Groups:   Species [3]
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species mean_PL sd_PL     n
##           <dbl>       <dbl>        <dbl>       <dbl> <fct>     <dbl> <dbl> <int>
##  1          5.1         3.5          1.4         0.2 setosa     1.46 0.174    50
##  2          4.9         3            1.4         0.2 setosa     1.46 0.174    50
##  3          4.7         3.2          1.3         0.2 setosa     1.46 0.174    50
##  4          4.6         3.1          1.5         0.2 setosa     1.46 0.174    50
##  5          5           3.6          1.4         0.2 setosa     1.46 0.174    50
##  6          5.4         3.9          1.7         0.4 setosa     1.46 0.174    50
##  7          4.6         3.4          1.4         0.3 setosa     1.46 0.174    50
##  8          5           3.4          1.5         0.2 setosa     1.46 0.174    50
##  9          4.4         2.9          1.4         0.2 setosa     1.46 0.174    50
## 10          4.9         3.1          1.5         0.1 setosa     1.46 0.174    50
## # ... with 140 more rows
```

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

group_by() with slice()

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

```
iris %>%
  group_by(Species) %>%
  slice(1:2)
```

```
## # A tibble: 6 x 5
## # Groups:   Species [3]
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##          <dbl>       <dbl>        <dbl>       <dbl> <fct>
## 1          5.1         3.5          1.4         0.2 setosa
## 2          4.9         3            1.4         0.2 setosa
## 3          7           3.2          4.7         1.4 versicolor
## 4          6.4         3.2          4.5         1.5 versicolor
## 5          6.3         3.3          6           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` (careful, quite large!) and figure out:

- the death toll for all individuals below 15 yrs for each year
- which were the top 3 detailed causes of death before 1930 for each of the 8 broader categories (most difficult)

Possible solution

Which were the top 3 detailed causes of death before 1930 for each of the 8 broader categories?

```
str(deaths_UK)
```

```
## 'data.frame': 1445659 obs. of  8 variables:
##  $ ICD         : chr  "0010" "0010" "0020" "0020" ...
##  $ Year        : num  1901 1901 1901 1901 1901 ...
##  $ Sex         : Factor w/ 2 levels "Males","Females": 1 2 1 2 1 2 1 2 1 2 ...
##  $ Deaths      : num  2 7 4 7 4 3 5 11 34 27 ...
##  $ Age_cat     : Factor w/ 6 levels "Infant (< 1 yr)",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ Desc        : Factor w/ 6673 levels "\"Pink\" disease",..: 5995 5995 5994 5994 5993 5993 1563 1563 1141 1141 ...
##  $ Cause       : Factor w/ 21 levels "Certain conditions originating in the perinatal period",..: 2 2 2 2 2 2 2 2 2 2 ...
##  $ Cause_simple: Factor w/ 8 levels "Infectious and parasitic diseases",..: 1 1 1 1 1 1 1 1 1 1 ...
```

Possible solution

Which were the top 3 detailed causes of death before 1930 for each of the 8 broader categories?

```
str(deaths_UK)
```

```
## 'data.frame': 1445659 obs. of  8 variables:
##  $ ICD         : chr  "0010" "0010" "0020" "0020" ...
##  $ Year        : num  1901 1901 1901 1901 1901 ...
##  $ Sex         : Factor w/ 2 levels "Males","Females": 1 2 1 2 1 2 1 2 1 2 ...
##  $ Deaths      : num  2 7 4 7 4 3 5 11 34 27 ...
##  $ Age_cat     : Factor w/ 6 levels "Infant (< 1 yr)",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ Desc        : Factor w/ 6673 levels "\"Pink\" disease",..: 5995 5995 5994 5994 5993 5993 1563 1563 1141 1141 ...
##  $ Cause       : Factor w/ 21 levels "Certain conditions originating in the perinatal period",..: 2 2 2 2 2 2 2 2 2 2 ...
##  $ Cause_simple: Factor w/ 8 levels "Infectious and parasitic diseases",..: 1 1 1 1 1 1 1 1 1 1 ...
```

```
deaths_UK %>%
  filter(Year <= 1930) %>%
  group_by(Cause_simple, Desc) %>%
  summarize(tot_deaths = sum(Deaths)) %>%
  arrange(Cause_simple, desc(tot_deaths)) %>%
  slice(1:3) %>%
  View() ## for nice display as a spreadsheet
```

Possible solution

Which were the top 3 detailed causes of death before 1930 for each of the 8 broader categories?

```
str(deaths_UK)
```

```
## 'data.frame': 1445659 obs. of  8 variables:
##  $ ICD         : chr  "0010" "0010" "0020" "0020" ...
##  $ Year        : num  1901 1901 1901 1901 1901 ...
##  $ Sex         : Factor w/ 2 levels "Males","Females": 1 2 1 2 1 2 1 2 1 2 ...
##  $ Deaths      : num  2 7 4 7 4 3 5 11 34 27 ...
##  $ Age_cat     : Factor w/ 6 levels "Infant (< 1 yr)",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ Desc        : Factor w/ 6673 levels "\"Pink\" disease",..: 5995 5995 5994 5994 5993 5993 1563 1563 1141 1141 ...
##  $ Cause       : Factor w/ 21 levels "Certain conditions originating in the perinatal period",..: 2 2 2 2 2 2 2 2 2 2 ...
##  $ Cause_simple: Factor w/ 8 levels "Infectious and parasitic diseases",..: 1 1 1 1 1 1 1 1 1 1 ...
```

```
deaths_UK %>%
  filter(Year <= 1930) %>%
  group_by(Cause_simple, Desc) %>%
  summarize(tot_deaths = sum(Deaths)) %>%
  arrange(Cause_simple, desc(tot_deaths)) %>%
  slice(1:3) %>%
  View() ## for nice display as a spreadsheet
```

Note: to clearly understand, check the output after each step!

group_by() with do()

Advanced: you want to apply a function that returns several elements, such as the range of `Petal.Length` for each species of iris:

```
iris %>%
  group_by(Species) %>%
  do(tibble(range = range(.$Petal.Length))) ## must be turned into a tibble or data.frame to work
```

```
## # A tibble: 6 x 2
## # Groups:   Species [3]
##    Species    range
##   <fct>      <dbl>
## 1 setosa       1
## 2 setosa       1.9
## 3 versicolor   3
## 4 versicolor   5.1
## 5 virginica    4.5
## 6 virginica    6.9
```

group_by() with do()

Advanced: you want to apply a function that returns several elements, such as the range of `Petal.Length` for each species of iris:

```
iris %>%
  group_by(Species) %>%
  do(tibble(range = range(.$Petal.Length))) ## must be turned into a tibble or data.frame to work
```

```
## # A tibble: 6 x 2
## # Groups:   Species [3]
##    Species    range
##    <fct>      <dbl>
## 1 setosa       1
## 2 setosa       1.9
## 3 versicolor   3
## 4 versicolor   5.1
## 5 virginica    4.5
## 6 virginica    6.9
```

More sophisticated alternative (combining `tidyverse` and standard **R**):

```
Range <- function(x, ...) c(min = min(x, ...), max = max(x, ...)) ## same as range() but output a named vector!
iris %>%
  group_by(Species) %>%
  do(data.frame(as.list(Range(.$Petal.Length)))) ## for this specific example we could of course use summarize with min and max
```

```
## # A tibble: 3 x 3
## # Groups:   Species [3]
##    Species      min   max
##    <fct>      <dbl> <dbl>
## 1 setosa       1     1.9
## 2 versicolor   3     5.1
## 3 virginica    4.5   6.9
```

group_by() with do()

Advanced: you want to apply a function that returns several elements, such as the range of `Petal.Length` for each species of iris:

```
iris %>%
  group_by(Species) %>%
  do(tibble(range = range(.$Petal.Length))) ## must be turned into a tibble or data.frame to work
```

```
## # A tibble: 6 x 2
## # Groups:   Species [3]
##    Species    range
##    <fct>      <dbl>
## 1 setosa       1
## 2 setosa       1.9
## 3 versicolor   3
## 4 versicolor   5.1
## 5 virginica    4.5
## 6 virginica    6.9
```

More sophisticated alternative (combining `tidyverse` and standard **R**):

```
Range <- function(x, ...) c(min = min(x, ...), max = max(x, ...)) ## same as range() but output a named vector!
iris %>%
  group_by(Species) %>%
  do(data.frame(as.list(Range(.$Petal.Length)))) ## for this specific example we could of course use summarize with min and max
```

```
## # A tibble: 3 x 3
## # Groups:   Species [3]
##    Species      min   max
##    <fct>      <dbl> <dbl>
## 1 setosa       1     1.9
## 2 versicolor   3     5.1
## 3 virginica    4.5   6.9
```

Alternatively, stick to standard **R** and the function `tapply()`.

Using dplyr to merge datasets

Data frame #1:

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

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          4.6          1.5  setosa
```

Data frame #2:

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

my_df2
```

```
##   Sepal.Length Petal.Width   Species
## 1          6.3         2.5 virginica
## 2          5.8         1.9 virginica
## 3          7.1         2.1 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          4.6          1.5    setosa          NA
## 5          6.3           NA virginica         2.5
## 6          5.8           NA virginica         1.9
## 7          7.1           NA virginica         2.1
## 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)
```

Challenge

Use the datasets called `population_UK` and `deaths_UK` to compute yearly mortality rates for individuals below 15 yrs only.

Possible solution

```
deaths_UK %>%
  filter(Age_cat %in% levels(Age_cat)[1:3]) %>%
  group_by(Year) %>%
  summarize(tot_Deaths = sum(Deaths)) -> deaths_processed

population_UK %>%
  group_by(Year) %>%
  summarize(tot_Pop = sum(Pop)) -> pop_processed

full_join(deaths_processed, pop_processed) %>%
  mutate(rel_Deaths = 1000*tot_Deaths/tot_Pop)
```

```
## Joining, by = "Year"
## # A tibble: 116 x 4
##     Year tot_Deaths  tot_Pop rel_Deaths
##    <dbl>      <dbl>    <dbl>      <dbl>
##  1  1901     223738 32612100       6.86
##  2  1902     206866 32950800       6.28
##  3  1903     199771 33293400       6.00
##  4  1904     219726 33731300       6.51
##  5  1905     193913 33988900       5.71
##  6  1906     198937 34342000       5.79
##  7  1907     182930 34699000       5.27
##  8  1908     183493 35155400       5.22
##  9  1909     169945 35423700       4.80
## 10  1910     157712 35792000       4.41
## # ... with 106 more rows
```

Reshaping data frame

For most data analyses, you need:

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

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

Reshaping data frame

For most data analyses, you need:

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The `tidyverse` package `tidyr` offers solutions:

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

From wide to long

you have:

```
my_df1
```

```
##      Species day_1 day_2 day_3 day_4 day_5
## 1     setosa   5.1   4.9   4.7   4.6   5.0
## 2 versicolor   7.0   6.4   6.9   5.5   6.5
```

you want:

```
my_df2
```

```
##       Species day Sepal.Length
## 1      setosa   1          5.1
## 2      setosa   2          4.9
## 3      setosa   3          4.7
## 4      setosa   4          4.6
## 5      setosa   5          5.0
## 6  versicolor   1          7.0
## 7  versicolor   2          6.4
## 8  versicolor   3          6.9
## 9  versicolor   4          5.5
## 10 versicolor   5          6.5
```

From wide to long

you have:

```
my_df1
```

```
##      Species day_1 day_2 day_3 day_4 day_5
## 1     setosa   5.1   4.9   4.7   4.6   5.0
## 2 versicolor   7.0   6.4   6.9   5.5   6.5
```

you want:

```
my_df2
```

```
##       Species day Sepal.Length
## 1      setosa   1          5.1
## 2      setosa   2          4.9
## 3      setosa   3          4.7
## 4      setosa   4          4.6
## 5      setosa   5          5.0
## 6  versicolor   1          7.0
## 7  versicolor   2          6.4
## 8  versicolor   3          6.9
## 9  versicolor   4          5.5
## 10 versicolor   5          6.5
```

you do:

```
my_df1 %>%
   gather(key = "day", value = "Sepal.Length", -Species) %>% ## after, optional
   separate(day, c("obs", "day")) %>%
   select(-obs) %>%
   as_tibble() %>%
   mutate(day = as.numeric(day)) %>%
   arrange(Species, day)
```

```
## # A tibble: 10 x 3
##    Species      day Sepal.Length
##    <fct>      <dbl>        <dbl>
##  1 setosa         1          5.1
##  2 setosa         2          4.9
##  3 setosa         3          4.7
##  4 setosa         4          4.6
##  5 setosa         5          5
##  6 versicolor     1          7
##  7 versicolor     2          6.4
##  8 versicolor     3          6.9
##  9 versicolor     4          5.5
## 10 versicolor     5          6.5
```

Note: run the code step by step to understand everything that is happening!