Getting to use data in ${\bf R}$

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Getting started with \boldsymbol{R}

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

Handling data in \boldsymbol{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 ${\bf R}$

- 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 \mathbf{R} ; it is a sequence of data elements of the same kind.

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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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
```

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
```

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] 178 175 175 175
```

height_girls[2] ## returns element 2

[1] 175

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

```
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] 178 178 175 175 175 175
```

```
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
```

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</pre>
```

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</pre>
```

But names behave sometimes somewhat unexpectedly:

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

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"</pre>
```

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"</pre>
```

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"</pre>
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 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"</pre>
```

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"</pre>
```

integers

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

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"</pre>
```

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"
```

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"</pre>
```

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"</pre>
```

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"</pre>
```

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"</pre>
```

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

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"</pre>
```

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"</pre>
```

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

There are more classes than types:

factors

```
(foo <- factor(c("bla", "bli", "blo")))</pre>
## [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</pre>
table(foo)
## foo
## bla bli blo blu
## 1 1 1 0
```

There are more classes than types:

factors

```
(foo <- factor(c("bla", "bli", "blo")))</pre>
## [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</pre>
table(foo)
## foo
## bla bli blo blu
## 1 1 1 0
```

dates

There are more classes than types:

factors

```
(foo <- factor(c("bla", "bli", "blo")))</pre>
## [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

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

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

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

Vectors must contain elements of the same class (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
```

foo <- 1

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

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

foo + 1
## [1] 2
foo bar[1] + 1</pre>
```

Challenges:

• find out why the previous call produces an error.

Error in foo_bar[1] + 1: non-numeric argument to binary operator

- 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?

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 \leftarrow 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"
```

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 \leftarrow as.Date(x = "20180618", format = "%Y%m%d")
as.integer(x = foo)
```

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

[1] 17700

[1] 20180618

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Factors

You can create them after in two steps:

```
sex <- c("girl", "girl", "girl", "girl", "girl", "girl",</pre>
"boy", "boy", "boy", "boy")
class(x = sex)
## [1] "character"
sex <- factor(x = sex)</pre>
sex
## [1] girl girl girl girl girl boy boy boy
## Levels: boy girl
```

Factors

You can create them after in two steps:

```
sex <- c("girl", "girl", "girl", "girl", "girl", "girl",</pre>
"boy", "boy", "boy", "boy")
class(x = sex)
## [1] "character"
sex <- factor(x = sex)
sex
## [1] girl girl girl girl girl boy boy boy
## Levels: boy girl
```

Better code:

```
sex \leftarrow 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)),</pre>
                    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"))</pre>
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"))</pre>
foo
## [1] a b
## Levels: a b
bar <- factor(c("b", "c"))</pre>
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

## [2] b c</pre>
```

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"</pre>
```

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 \leftarrow 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)</pre>
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:

You want:

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

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)])</pre>
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)])</pre>
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")</pre>
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:

```
mv factor2 <- factor(x = mv factor1, levels = levels(mv 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")</pre>
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:

You want:

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

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!</pre>
my_factor2
## [1] A A A A D
## Levels: A D
```

Changing the levels of a factor

You have:

You want:

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

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!</pre>
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")</pre>
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!</pre>
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")</pre>
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
```

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 sily 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</pre>
```

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

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 sily 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
## [2.]
        1 1.2 3.141593
## [3.]
       1 1.2 3.141593
                           NΑ
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!

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 sily 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
## [2.]
        1 1.2 3.141593
## [3,] 1 1.2 3.141593
                           NΑ
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.

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 sily 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
## [2.]
        1 1.2 3.141593
## [3.]
       1 1.2 3.141593
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 extentions of vectors when there is more than one dimension (1 or 2 dimensions for matrices, any for arrays).

Example of a matrix:

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"</pre>
```

Note 1: since there are a kind of vectors, the same restrictions apply: all elements must have the same class! Note 2: useful for bulding 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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They can be combined:

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

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

They can be combined:

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

They can be combined:

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

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
```

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")</pre>
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
```

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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
```

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
## 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 \leftarrow 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"</pre>
```

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))</pre>
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</pre>
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
## $bovs
## [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)</pre>
dataframe_ht
      Height Sex
## 1
         181 girl
## 2
        189 girl
## 3
        174 girl
        177 girl
## 5
         178 girl
        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
        177 girl
## 4
## 5
         178 girl
## 6
        175 girl
## 7
        159 boy
## 8
         164 boy
## 9
         183 bov
## 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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They borough from both matrices and lists:

As for matrices:

They borough from both matrices and lists:

As for matrices:

```
(dataframe ht double <- cbind(dataframe ht, newcol = 1:10))
     Height Sex newcol
        181 girl
        189 girl
        174 girl
## 3
        177 girl
## 5
        178 girl
## 6
        175 girl
## 7
        159 boy
        164 boy
## 8
## 9
        183 bov
## 10
        192 bov
                    10
dataframe_ht[, "Sex"]
## [1] girl girl girl girl girl boy boy boy
## Levels: boy girl
dataframe_ht[2, 2]
## [1] girl
## Levels: boy girl
```

They borough from both matrices and lists:

As for matrices:

```
(dataframe ht double <- cbind(dataframe ht, newcol = 1:10))
     Height Sex newcol
        181 girl
        189 girl
        174 girl
        177 girl
## 5
        178 girl
## 6
        175 girl
## 7
        159 bov
        164 boy
## 8
        183 bov
## 9
        192 boy
                    10
## 10
dataframe_ht[, "Sex"]
## [1] girl girl girl girl girl 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 2 1 1 1 1
```

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Data frames: challenge

The iris data set:

```
head(iris) ## this function displays the first 6 rows
    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
              5.1
                         3.5
## 1
                                       1.4
                                                   0.2 setosa
              4.9
                         3.0
## 2
                                       1.4
                                                        setosa
              4.7
                         3.2
                                       1.3
                                                   0.2 setosa
              4.6
                         3.1
                                       1.5
                                                   0.2 setosa
## 5
              5.0
                         3.6
                                       1.4
                                                        setosa
              5.4
                                       1.7
## 6
                         3.9
                                                   0.4 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 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</pre>
```

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
       189 girl
## 3
       174 girl
## 4
       177 girl
                         4
## 5
       178 girl
                          5
## 6
       175 girl
                          6
```

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$linenumber <- 1:nrow(x = dataframe_ht) # add column
head(x = dataframe_ht)
    Height Sex linenumber
## 1
       181 girl
       189 girl
## 3
      174 girl
## 4
      177 girl
                         4
## 5
      178 girl
                         5
## 6
      175 girl
                         6
dataframe ht$linenumber <- NULL # remove column
head(x = dataframe_ht)
    Height Sex
       181 girl
## 2
      189 girl
## 3
      174 girl
## 4
      177 girl
## 5
       178 girl
```

6

175 girl

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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
             4.9
                         3.0
                                      1.4
                                                       setosa
## 3
             4.7
                         3.2
                                      1.3
                                                  0.2 setosa
## 4
             4.6
                         3.1
                                      1.5
                                                  0.2 setosa
             5.0
                         3.6
                                      1.4
                                                  0.2 setosa
             5.4
                         3.9
                                      1.7
## 6
                                                  0.4 setosa
summary(object = iris)
     Sepal.Length
                    Sepal.Width
                                    Petal.Length
   Min. :4.300
                          :2.000
                                         :1.000
                   Min.
                                   Min.
    1st Qu.:5.100
                   1st Qu.:2.800
                                   1st Qu.:1.600
    Median :5.800
                   Median :3.000
                                   Median :4.350
    Mean
         :5.843
                   Mean :3.057
                                   Mean
                                         :3.758
    3rd Qu.:6.400
                   3rd Qu.:3.300
                                   3rd Qu.:5.100
    Max
         .7 900
                   Max. :4.400
                                          .6.900
                                   Max.
    Petal.Width
                         Species
   Min. :0.100
                    setosa
                             :50
    1st Qu.:0.300
                   versicolor:50
   Median :1.300
                   virginica:50
    Mean :1.199
   3rd Qu.:1.800
   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"
## [4] "Petal.Width" "Species"
```

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:

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

The dyplr alternative to tapply()

The same operation in dyplr looks very different:

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

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



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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) $+ \sim 70$ full time employees + tons of volunteers
- free + commercial

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R core team

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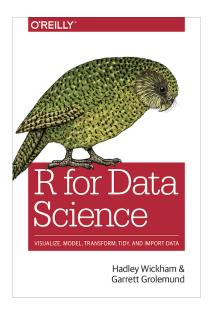
Note 1: that has led to two quite distinct **R** dialects

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

Note 3: we will see a bit of both dialects

RStudio

- build RStudio IDE, tidyverse and more
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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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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

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
       181 girl 1
## 2
      189 girl 2
      174 girl 3
## 3
```

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
       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
```

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
```

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
       181 girl 1
## 1
## 2
      189 girl 2
## 3
      174 girl 3
```

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
      159 boy 7
      164 boy 8
## 2
      174 girl 3
## 3
```

Around dplyr verbs

These main dplr 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:

you want:

```
## 'data.frame': 150 obs. of 5 variables: ## '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.Length: chr "5.1" "4.9" "4.7" "4.6" ... ## $ Sepal.Width : num 3.5 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ... ## $ Sepal.Width : chr "3.5" "33" "3.2" "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.Length: chr "1.4" "1.3" "1.5" ... ## $ Petal.Width : num 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 .. ## $ Petal.Width : chr "0.2" "0.2" "0.2" "0.2" ... ## $ Species : Factor w/ 3 levels "setosa", "versicolor",..: 1 1 ## $ Species : Factor w/ 3 levels "setosa", "versicolor",..: 1
```

you do:

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

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

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ullet mutate() or transmute() o one value per observation

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

It is very powerful when combined to:

summarize() → one value per group

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

ullet slice() o 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
     bov
               174.5
                             173.5 4
                             177.5 6
## 2 girl
               179.0
```

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
        181 girl 1
                          179.0
                                        177.5 6
## 1
        189 girl 2
## 2
                          179.0
                                        177.5 6
## 3
        174 girl 3
                          179.0
                                       177.5 6
        177 girl 4
                          179.0
                                       177.5 6
## 4
## 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
        183 boy 9
                          174.5
                                       173.5 4
## 9
        192 boy 10
                          174.5
                                        173.5 4
## 10
```

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 irices:

```
iris %>%
 group_by(Species) %>%
 slice(1:2) %>%
  as.data.frame()
    Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1
             5.1
                        3.5
                                     1.4
                                                 0.2
## 2
             4.9
                        3.0
                                     1.4
                                                0.2
            7.0
                        3.2
                                     4.7
                                                1.4
           6.4
                     3.2
                                     4.5
                                                1.5
         6.3
                        3.3
                                     6.0
                                                 2.5
## 6
             5.8
                        2.7
                                     5.1
                                                1.9
       Species
## 1
        setosa
## 2
        setosa
## 3 versicolor
## 4 versicolor
    virginica
## 6 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)
mv_df1[4, 1] <- NA
my_df1
    Sepal.Length Petal.Length Species
             5.1
                         1.4 setosa
## 2
             4.9
                        1.4 setosa
             4.7
                        1.3 setosa
## 3
## 4
              NA
                        1.5 setosa
```

Data frame #2:

```
my_df2 <- iris %>%
  filter(Species == "virginica") %>%
  select(Sepal.Length, Petal.Width, Species) %>%
  slice(1:4)
mv_df2[3, 2] <- NA
my_df2
    Sepal.Length Petal.Width
                               Species
             6.3
## 1
                         2.5 virginica
## 2
             5.8
                        1.9 virginica
## 3
             7.1
                        NA virginica
             6.3
                         1.8 virginica
## 4
```

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
                              setosa
                                                NA
## 2
             4.9
                          1.4 setosa
                                                NΑ
             4.7
                          1.3 setosa
## 3
                                                NA
             NΑ
                          1.5
                              setosa
                                                NΑ
## 4
## 5
             6.3
                           NA virginica
                                               2.5
             5.8
                           NA virginica
## 6
                                               1.9
            7.1
                           NA virginica
                                               NA
## 7
             6.3
                           NA virginica
                                               1.8
## 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:

- all individuals
- individuals below 15 yrs only

Getting started with R

- Introduction
- Vectors
 - general properties
 - types & classes
 - factors
 - functions
- Matrices and arrays
 - general properties
 - functions
- List
 - general properties
 - functions
- Data frames and tibbles
 - general properties
 - challenge
 - functions
 - dplyr
 - tidyr
 - Importing & exporting data

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:

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

Unfortunatelly, 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
```

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)
```

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
## 1 1 girl 81 156 171 181
dim(my_df1)
## [1] 1 6
```

From long to wide

you have:

```
head(my_df2)
## ID Sex Age Height
## 1 1 girl age1
## 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
## 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
## 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
## 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
## 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
## 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
## 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 \boldsymbol{R}

- Introduction
- 2 Vectors
- Matrices and arrays
- 4 List
- 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] "/home/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"
## [3] "usingdata.pdf.asis" "usingdata.Rnw"
## [5] "usingdata.snm" "usingdata.tex"
## [7] "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 ${\bf R}$ binary format

 ${f R}$ 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</pre>
```

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</pre>
```

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
            4.7
                    3.2
                                    1.3
## 3
                                                0.2 setosa
            4.6
                       3.1
                                                0.2 setosa
## 4
                                    1.5
             5.0
                        3.6
                                    1.4
                                                0.2 setosa
## 5
             5.4
                        3.9
                                    1.7
                                                0.4 setosa
## 6
```

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")</pre>
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
             4.7
                         3.2
                                     1.3
                                                 0.2 setosa
             4.6
                         3.1
                                     1.5
                                                 0.2 setosa
## 5
             5.0
                         3.6
                                      1.4
                                                  0.2 setosa
             5.4
                         3.9
                                      1.7
                                                  0.4 setosa
## 6
```

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)
```

Reading a data set:

```
rm(my_iris) ## delete the object my iris
mv iris <- read.csv("mv iris.csv")</pre>
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
              4.7
                          3.2
                                       1.3
                                                   0.2 setosa
              4.6
                          3.1
                                       1.5
                                                    0.2 setosa
              5.0
                          3.6
                                       1.4
                                                    0.2 setosa
## 5
              5.4
                                       1.7
## 6
                          3.9
                                                    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 \mathbf{R} .