Getting to program in **R**

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Programming with **R**

My first function

The best way:

```
my_function <- function(input1, input2) {
  output <- input1 + input2
  return(output)
}

my_function(input1 = 1, input2 = 3)
```

```
## [1] 4
```

My first function

The best way:

```
my_function <- function(input1, input2) {
  output <- input1 + input2
  return(output)
}

my_function(input1 = 1, input2 = 3)
```

```
## [1] 4
```

If no `return()`, then it returns the last row:

```
my_function <- function(input1, input2) {
  input1 + input2
}

my_function(input1 = 1, input2 = 3)
```

```
## [1] 4
```

My first function

The best way:

```
my_function <- function(input1, input2) {
  output <- input1 + input2
  return(output)
}

my_function(input1 = 1, input2 = 3)
```

```
## [1] 4
```

If no `return()`, then it returns the last row:

```
my_function <- function(input1, input2) {
  input1 + input2
}

my_function(input1 = 1, input2 = 3)
```

```
## [1] 4
```

Inline shortcut (useful in `*apply()`):

```
my_function <- function(input1, input2) input1 + input2

my_function(input1 = 1, input2 = 3)
```

```
## [1] 4
```

My first function

You can set defaults for your inputs:

```
my_function <- function(input1, input2 = 10) {
  output <- input1 + input2
  return(output)
}

my_function(input1 = 1)

## [1] 11

my_function(input1 = 1, input2 = 0)

## [1] 1

my_function(input2 = 1)

## Error in my_function(input2 = 1):  argument "input1" is missing, with no default
```

My first function

You can pass optional arguments to another function via "...":

```
my_function <- function(input1, ...) {
  output <- mean(input1, ...)
  return(output)
}

x <- c(1, 2, 3, 4, 5, NA)
my_function(input1 = x)
```

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

```
my_function(input1 = x, na.rm = TRUE)
```

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

Note: this is particularly useful when designing plotting functions!

My first function

You can print things while the function runs:

```
my_function <- function() {
  print("This function will output 2")
  return(2)
}

my_function()
```

```
## [1] "This function will output 2"
## [1] 2
```

Note: observe also that it is possible to create functions that do not consider any input!

My first function

You can return only a single object; so if you need several outputs, you must combine them:

```
my_function <- function(input1, ...) {
  output1 <- min(input1, ...)
  output2 <- max(input1, ...)
  output <- list(output1 = output1, output2 = output2)
  return(output)
}

x <- c(1, 2, 3, 4, 5, NA)
my_function(input1 = x, na.rm = TRUE)
```

```
## $output1
## [1] 1
##
## $output2
## [1] 5
```

Note: you can also use a vector, a matrix, a data frame...

My first function

You can return the output "invisibly":

```
my_function <- function(input1) {
  output <- min(input1)
  return(invisible(output))
}

my_function(input1 = c(1, 2, 3, -4))
```

My first function

You can return the output "invisibly":

```
my_function <- function(input1) {
  output <- min(input1)
  return(invisible(output))
}

my_function(input1 = c(1, 2, 3, -4))
```

```
foo <- my_function(input1 = c(1, 2, 3, -4))
foo
```

```
## [1] -4
```

My first function

You don't have to return something:

```
my_function <- function(input1) {
  the_min <- min(input1)
  print(paste("The minimum is:", the_min))
  return(invisible(NULL))
}

my_function(input1 = c(1, 2, 3, -4))
```

```
## [1] "The minimum is: -4"
```

My first function

You don't have to return something:

```
my_function <- function(input1) {
  the_min <- min(input1)
  print(paste("The minimum is:", the_min))
  return(invisible(NULL))
}

my_function(input1 = c(1, 2, 3, -4))
## [1] "The minimum is: -4"
```

```
foo <- my_function(input1 = c(1, 2, 3, -4))
## [1] "The minimum is: -4"
foo
## NULL
```

Programming with **R**

Why writing your own **R** functions?

Using your own functions makes your scripts

- easier to understand
- safer to (re)use
- shorter to write (often)

What do you prefer?

```
d <- data.frame(proba = c(0.1, 0.5, 0.4), group = factor(c("A", "B", "C")))
```

```
with(data = d, (proba[group == "B"] / (1 - proba[group == "B"])) / (proba[group == "A"] / (1 - proba[group == "A"])))
## [1] 9
with(data = d, (proba[group == "C"] / (1 - proba[group == "C"])) / (proba[group == "A"] / (1 - proba[group == "A"])))
## [1] 6
with(data = d, (proba[group == "B"] / (1 - proba[group == "B"])) / (proba[group == "C"] / (1 - proba[group == "C"])))
## [1] 1.5
```

What do you prefer?

```
d <- data.frame(proba = c(0.1, 0.5, 0.4), group = factor(c("A", "B", "C")))
```

```
with(data = d, (proba[group == "B"] / (1 - proba[group == "B"])) / (proba[group == "A"] / (1 - proba[group == "A"])))
## [1] 9
with(data = d, (proba[group == "C"] / (1 - proba[group == "C"])) / (proba[group == "A"] / (1 - proba[group == "A"])))
## [1] 6
with(data = d, (proba[group == "B"] / (1 - proba[group == "B"])) / (proba[group == "C"] / (1 - proba[group == "C"])))
## [1] 1.5
```

Or

```
odds_ratio <- function(group1, group2){
  with(data = d, (proba[group == group1] / (1 - proba[group == group1])) / (proba[group == group2] / (1 - proba[group == group2])))
}

odds_ratio(group1 = "B", group2 = "A")
## [1] 9
odds_ratio(group1 = "C", group2 = "A")
## [1] 6
odds_ratio(group1 = "B", group2 = "C")
## [1] 1.5
```

What do you prefer?

Still not convinced? Let's compute all pairwise comparisons:

```
with(data = d, (proba[group == "A"] / (1 - proba[group == "A"])) / (proba[group == "A"] / (1 - proba[group == "A"])))
## [1] 1
with(data = d, (proba[group == "B"] / (1 - proba[group == "B"])) / (proba[group == "A"] / (1 - proba[group == "A"])))
## [1] 9
with(data = d, (proba[group == "C"] / (1 - proba[group == "C"])) / (proba[group == "A"] / (1 - proba[group == "A"])))
## [1] 6
with(data = d, (proba[group == "A"] / (1 - proba[group == "A"])) / (proba[group == "B"] / (1 - proba[group == "B"])))
## [1] 0.1111111
with(data = d, (proba[group == "B"] / (1 - proba[group == "B"])) / (proba[group == "B"] / (1 - proba[group == "B"])))
## [1] 1
with(data = d, (proba[group == "C"] / (1 - proba[group == "C"])) / (proba[group == "B"] / (1 - proba[group == "B"])))
## [1] 0.6666667
with(data = d, (proba[group == "A"] / (1 - proba[group == "A"])) / (proba[group == "C"] / (1 - proba[group == "C"])))
## [1] 0.1666667
with(data = d, (proba[group == "B"] / (1 - proba[group == "B"])) / (proba[group == "C"] / (1 - proba[group == "C"])))
## [1] 1.5
with(data = d, (proba[group == "C"] / (1 - proba[group == "C"])) / (proba[group == "C"] / (1 - proba[group == "C"])))
## [1] 1
```

What do you prefer?

Still not convinced? Let's compute all pairwise comparisons:

```
for (group2 in d$group) {
  for (group1 in d$group) {
    print(paste(group1, group2, odds_ratio(group1 = group1, group2 = group2)))
  }
}
```

```
## [1] "A A 1"
## [1] "B A 9"
## [1] "C A 6"
## [1] "A B 0.111111111111111"
## [1] "B B 1"
## [1] "C B 0.666666666666667"
## [1] "A C 0.166666666666667"
## [1] "B C 1.5"
## [1] "C C 1"
```

Note: this is bad code, we will come back on this!

When to write your own functions?

Don't Repeat Yourself

Programming with **R**

Control structures: if()

```
i <- 1
a <- 2

if (i == 1) {
  a <- 1
}

a
```

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

Control structures: if()

```
i <- 1
a <- 2

if (i == 1) {
  a <- 1
}

a
```

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

```
i <- 5
a <- 2

if (i == 1) {
  a <- 1
} else {
  a <- 2
}

a
```

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

Note: for help, check `?"if"`.

Control structures: loops using for() & while()

```
for (i in 1:5) {
  print(i)
  }
```

```
## [1] 1
## [1] 2
## [1] 3
## [1] 4
## [1] 5
```

```
i <- 1

while (i < 5) {
  print(i)
  i <- i + 1
  }
```

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

Note: for help, check `?"for"`.

Random number generators

```
runif(5)
```

```
## [1] 0.109726050 0.007791146 0.553019024 0.976357527
## [5] 0.907579653
```

```
runif(5)
```

```
## [1] 0.6417671 0.7165911 0.7960540 0.7406247 0.6255349
```

Random number generators

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runif(5)
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```
## [1] 0.109726050 0.007791146 0.553019024 0.976357527
## [5] 0.907579653
```

```
runif(5)
```

```
## [1] 0.6417671 0.7165911 0.7960540 0.7406247 0.6255349
```

You can have reproducible results by setting a seed:

```
set.seed(10132)
runif(5)
```

```
## [1] 0.7258731 0.3086039 0.4393603 0.7952702 0.5325773
```

```
set.seed(10132)
runif(5)
```

```
## [1] 0.7258731 0.3086039 0.4393603 0.7952702 0.5325773
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Random number generators

```
runif(5)
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```
## [1] 0.109726050 0.007791146 0.553019024 0.976357527
## [5] 0.907579653
```

```
runif(5)
```

```
## [1] 0.6417671 0.7165911 0.7960540 0.7406247 0.6255349
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You can have reproducible results by setting a seed:

```
set.seed(10132)
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```
## [1] 0.7258731 0.3086039 0.4393603 0.7952702 0.5325773
```

```
set.seed(10132)
runif(5)
```

```
## [1] 0.7258731 0.3086039 0.4393603 0.7952702 0.5325773
```

Note: check `?Distributions` for more distributions.

Errors and Warnings

```
process_factor <- function(x) {
  if (!is.factor(x) & !is.character(x)) {
    stop("Your input for factor should be of class character or factor")
  }
  if (!is.factor(x) & is.character(x)) {
    x <- as.factor(x)
    warning("Your input has been converted to factor")
  }
  return(x)
}
```

Errors and Warnings

```
process_factor <- function(x) {
  if (!is.factor(x) & !is.character(x)) {
    stop("Your input for factor should be of class character or factor")
  }
  if (!is.factor(x) & is.character(x)) {
    x <- as.factor(x)
    warning("Your input has been converted to factor")
  }
  return(x)
}
```

```
process_factor(x = factor(c("A", "B")))
```

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

Errors and Warnings

```
process_factor <- function(x) {
  if (!is.factor(x) & !is.character(x)) {
    stop("Your input for factor should be of class character or factor")
  }
  if (!is.factor(x) & is.character(x)) {
    x <- as.factor(x)
    warning("Your input has been converted to factor")
  }
  return(x)
}
```

```
process_factor(x = factor(c("A", "B")))
```

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

```
process_factor(x = c("A", "B"))
```

```
## Warning in process_factor(x = c("A", "B")): Your input has been converted to factor
## [1] A B
## Levels: A B
```

Errors and Warnings

```
process_factor <- function(x) {
  if (!is.factor(x) & !is.character(x)) {
    stop("Your input for factor should be of class character or factor")
  }
  if (!is.factor(x) & is.character(x)) {
    x <- as.factor(x)
    warning("Your input has been converted to factor")
  }
  return(x)
}
```

```
process_factor(x = factor(c("A", "B")))
```

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

```
process_factor(x = c("A", "B"))
```

```
## Warning in process_factor(x = c("A", "B")): Your input has been converted to factor
## [1] A B
## Levels: A B
```

```
process_factor(x = c(2, 3))
```

```
## Error in process_factor(x = c(2, 3)): Your input for factor should be of class character or factor
```

Boolean logic in **R**

```
!TRUE
## [1] FALSE
!FALSE
## [1] TRUE
TRUE == 1
## [1] TRUE
TRUE & TRUE
## [1] TRUE
TRUE & FALSE
## [1] FALSE
FALSE & FALSE
## [1] FALSE
c(TRUE, TRUE) & c(TRUE, FALSE)
## [1]  TRUE FALSE
FALSE && "foo"
## [1] FALSE
FALSE & "foo"
## Error in FALSE & "foo":  operations are possible only for numeric,
logical or complex types
TRUE && "foo"
## Error in TRUE && "foo":  invalid 'y' type in 'x && y'
c(TRUE, TRUE) && c(TRUE, FALSE) ## dangerous
## [1] TRUE
```

```
TRUE | TRUE
## [1] TRUE
TRUE | FALSE
## [1] TRUE
FALSE | FALSE
## [1] FALSE
c(TRUE, TRUE) | c(TRUE, FALSE)
## [1] TRUE TRUE
FALSE || "foo"
## Error in FALSE || "foo":  invalid 'y' type in 'x || y'
TRUE || "foo"
## [1] TRUE
any(c(FALSE, FALSE, FALSE, TRUE))
## [1] TRUE
```

Note: help available at ?"&".

Scope

Every object in **R** belongs to an environment:

```
i <- 1
i <- i + 1
i
```

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

```
e1 <- environment()
e1
```

```
## <environment: R_GlobalEnv>
```

```
get("i", envir = e1)
```

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

Scope

As a rule, anything created inside a function stays inside the function:

```
i <- 1

f <- function(i) {
  i <- i + 1
  return(i)
  }

f(i)
```

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

```
i
```

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

Scope

This is because the functions have their own environments:

```
i <- 1

f <- function(i) {
  i <- i + 1
  e <- environment()
  return(list(env = e, i = i))
  }

res <- f(i)
res$i
```

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

```
res$env
```

```
## <environment: 0x556a932f6e38>
```

Scope

This is because the functions have their own environments:

```
i <- 1

f <- function(i) {
  i <- i + 1
  e <- environment()
  return(list(env = e, i = i))
  }

res <- f(i)
res$i
```

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

```
res$env
```

```
## <environment: 0x556a932f6e38>
```

```
get("i", envir = globalenv()) ## globalenv() provides the address of the global environment
```

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

```
get("i", envir = res$env)
```

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

Scope

This is because the functions have their own environments:

```
i <- 1

f <- function(i) {
  i <- i + 1
  e <- environment()
  return(list(env = e, i = i))
  }

res <- f(i)
res$i
```

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

```
res$env
```

```
## <environment: 0x556a932f6e38>
```

```
get("i", envir = globalenv()) ## globalenv() provides the address of the global environment
```

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

```
get("i", envir = res$env)
```

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

Challenge: check whether the environment remains the same at each function call or not!

Scope

Environments can be hacked, but it is usually source of troubles:

```
i <- 1

f <- function(i) {
  i <<- i + 1
  return(i)
  }

f(i)
```

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

```
i
```

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

Scope

Environments can be defined, but it is usually not necessary:

```
i <- 1

f <- function(i) {
  i <- i + 1
  assign("i", i, envir = globalenv())
  return(i)
  }

f(i)
```

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

```
i
```

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

Scope

The best is to use a functional approach:

```
i <- 1

f <- function(i) {
  i <- i + 1
  return(i)
  }

i <- f(i)
i
```

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

Scope

There are a few scoping exceptions:

```
i <- 1

for (j in 1:10) {
  i <- i + 1
}

i
```

```
## [1] 11
```

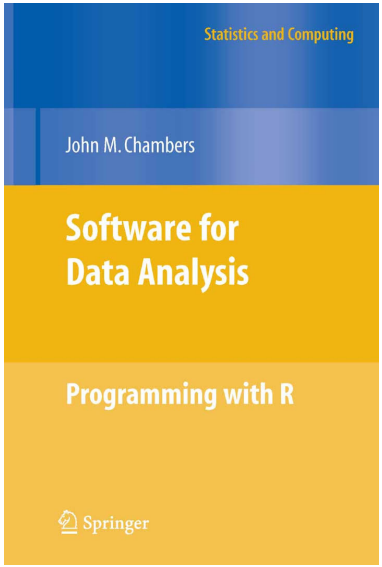
And yet, `for` is actually a function:

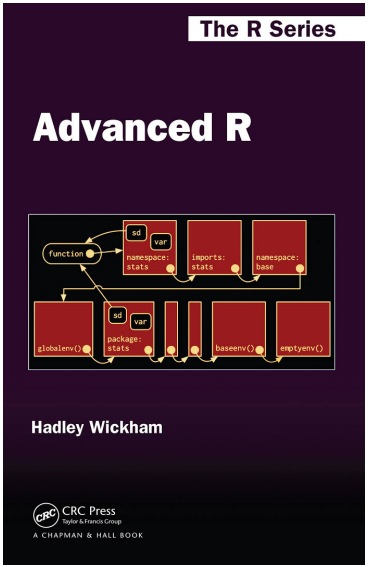
```
i <- 1

`for`(j, 1:10, i <- i + 1)
i
```

```
## [1] 11
```

Scope

For more info:





R has the same numerical issues as most programming languages

```
x <- 0.7 - 0.4 - 0.3
x == 0
```

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

R has the same numerical issues as most programming languages

```
x <- 0.7 - 0.4 - 0.3
x == 0
```

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

```
print(x, digits = 22)
```

```
## [1] -5.5511151231257827021181e-17
```

R has the same numerical issues as most programming languages

```
x <- 0.7 - 0.4 - 0.3
x == 0
```

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

```
print(x, digits = 22)
```

```
## [1] -5.5511151231257827021118e-17
```

```
print(seq(0, 1, 0.1), digits = 22)
```

```
##  [1] 0.0000000000000000000000 0.1000000000000000055511
##  [3] 0.2000000000000000111022 0.3000000000000000444089
##  [5] 0.4000000000000000222045 0.5000000000000000000000
##  [7] 0.6000000000000000888178 0.7000000000000000666134
##  [9] 0.8000000000000000444089 0.9000000000000000222045
## [11] 1.0000000000000000000000
```

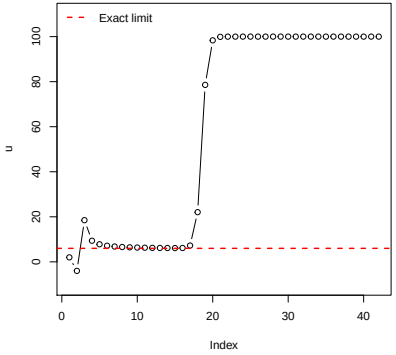
Note 1: same kind of thing can happen in Excel too (`https://support.microsoft.com/en-us/kb/214118`).
Note 2: this kind of problem sometimes kills people (`http://www-users.math.umn.edu/~arnold/disasters/Patriot-dharan-skeel-siam.pdf`).

R has the same numerical issues as most programming languages

The errors sometimes add up:

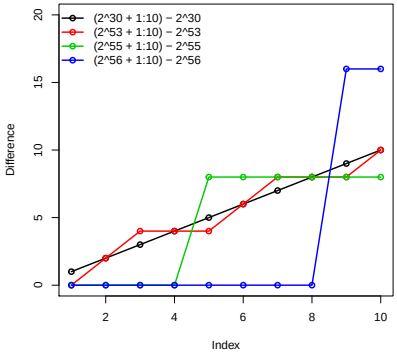
Example of the J.M Muller's Serie
$u_0 = 2$; $u_1 = -4$; $u_{n+1} = 111 - \frac{1130}{u_n} + \frac{3000}{u_n * u_{n-1}}$

```
u <- c(2, -4)
new.u <- function(u) 111 - 1130/u[length(u)] + 3000/(u[length(u)]*u[length(u) - 1])
for (i in 1:40) u <- c(u, new.u(u))
```



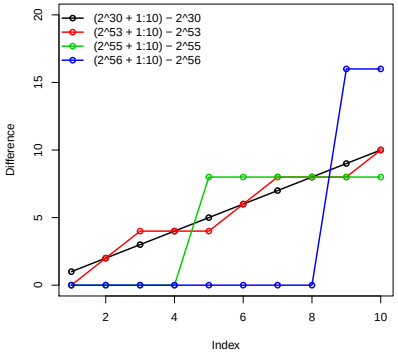
R has the same numerical issues as most programming languages

And it is not just about fractions:



R has the same numerical issues as most programming languages

And it is not just about fractions:




```
as.integer(2^31 - 1)  ## upper limit in 32 bits coding
## [1] 2147483647
as.integer(2^31)
## Warning:  NAs introduced by coercion to integer range
## [1] NA
```

R has the same numerical issues as most programming languages

Solution: beware of floats and use adequate functions, not boolean tests, when performing comparisons!

```
??"equality"
```

```
Help pages:
base::all.equal               Test if Two Objects are (Nearly) Equal
base::identical               Test Objects for Exact Equality
data.table::all.equal         Equality Test Between Two Data Tables
datasets::airquality          New York Air Quality Measurements
dplyr::all_equal              Flexible equality comparison for data frames
```

```
all.equal(target = 0, current = x)
```

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

Programming with **R**

Some key advices

- everything you use in the body must pass through the inputs
- everything you output must pass through the return
- try to write functions that you could reuse in other situations

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- everything you use in the body must pass through the inputs
- everything you output must pass through the return
- try to write functions that you could reuse in other situations

Bad:

```
d <- data.frame(proba = c(0.1, 0.5, 0.4), group = factor(c("A", "B", "C")))

odds_ratio <- function(group1, group2){
  with(data = d, (proba[group == group1] / (1 - proba[group == group1])) / (proba[group == group2] / (1 - proba[group == group2])))
}

for (group2 in d$group) {
  for (group1 in d$group) {
    print(paste(group1, group2, odds_ratio(group1 = group1, group2 = group2)))
  }
}
```

Why is this bad?

A better implementation of functions to compute odd ratios

Better because it is general and based on functions (example 1):

```
odds_ratio <- function(p1, p2){
  OR <- (p1/(1 - p1)) / (p2/(1 - p2))
  return(OR)
}

all_pairwise <- function(proba, groups){
  groups_id <- unique(groups)

  results <- matrix(NA, ncol = length(groups_id), nrow = length(groups_id))
  colnames(results) <- groups_id
  rownames(results) <- groups_id

  for (group1 in groups_id) {
    for (group2 in groups_id) {
      results[group1, group2] <- odds_ratio(p1 = proba[groups == group1], p2 = proba[groups == group2])
    }
  }

  return(results)
}

all_pairwise(proba = d$proba, groups = d$group)
```

```
##   A         B         C
## A 1 0.1111111 0.1666667
## B 9 1.0000000 1.5000000
## C 6 0.6666667 1.0000000
```

A better implementation of functions to compute odd ratios

Better because it is very general and based on functions (example 2):

```
odds_ratio <- function(p1, p2){
  OR <- (p1/(1 - p1)) / (p2/(1 - p2))
  return(OR)
}

all_pairwise2 <- function(proba, groups){
  groups_id <- unique(groups)
  to_do <- expand.grid(groups_id, groups_id)

  OR <- apply(to_do, 1, function(gr) { ## define anonymous function
    odds_ratio(p1 = proba[groups == gr[1]], p2 = proba[groups == gr[2]])
    })

  return(data.frame(group1 = to_do[, 1],
                    group2 = to_do[, 2],
                    OR = OR))
}

all_pairwise2(proba = d$proba, groups = d$group)
```

```
##   group1 group2        OR
## 1      A      A 1.0000000
## 2      B      A 9.0000000
## 3      C      A 6.0000000
## 4      A      B 0.1111111
## 5      B      B 1.0000000
## 6      C      B 0.6666667
## 7      A      C 0.1666667
## 8      B      C 1.5000000
## 9      C      C 1.0000000
```

Some key advices

- everything you use in the body must pass through the inputs
- everything you output must pass through the return
- try to write functions that you could reuse in other situations
- there are many ways to reach the same outcome; experiment a bit to find something you like/understand

Programming with **R**

Challenge

The t-test and the Mann-Whitney U tests are two tests aiming at comparing 2 groups. We want to compare the risk of false positives and true positives of these two tests in the following conditions:

- assuming that height of males is gaussian with mean 180 cm and SD 6 cm and that the height of females is gaussian with mean 170 cm and SD 5 cm, how many individuals (sex-ratio = 1) do I need to get a power of 80% (risk of false negative = 20%)?
- assuming that the null hyptohesis is true and that you have sampled 20 males and 20 females, what is the probability of false positives for the threshold alpha = 0.05? (And for any threshold between 0 and 1%?)

Programming with **R**

Learning by mimicking

Looking at code writen by others will teach you

- how their functions work
- how to code
- new functions or packages that could be useful for you

How to get the code behind a function?

Start by simply typing the function name (without brackets):

```
mosaic::oddsRatio
```

```
## function (x, conf.level = 0.95, verbose = !quiet, quiet = TRUE,
##     digits = 3)
## {
##     orrr(x, conf.level = conf.level, verbose = verbose, digits = digits,
##         relrisk = FALSE)
## }
## <bytecode: 0x556a93a13938>
## <environment: namespace:mosaic>
```

How to get the code behind a function?

Then, follows the successive calls:

```
mosaic::orrr
```

```
## function (x, conf.level = 0.95, verbose = !quiet, quiet = TRUE,
##     digits = 3, relrisk = FALSE)
## {
##     if (any(dim(x) != c(2, 2))) {
##         stop("expecting something 2 x 2")
##     }
##     names(x) <- NULL
##     row.names(x) <- NULL
##     colnames(x) <- NULL
##     rowsums <- rowSums(x)
##     p1 <- x[1, 1]/rowsums[1]
##     p2 <- x[2, 1]/rowsums[2]
##     o1 <- p1/(1 - p1)
##     o2 <- p2/(1 - p2)
##     RR <- p2/p1
##     OR <- o2/o1
##     crit <- qnorm((1 - conf.level)/2, lower.tail = FALSE)
##     names(RR) <- "RR"
##     log.RR <- log(RR)
##     SE.log.RR <- sqrt(sum(x[, 2]/x[, 1]/rowsums))
##     log.lower.RR <- log.RR - crit * SE.log.RR
##     log.upper.RR <- log.RR + crit * SE.log.RR
##     lower.RR <- exp(log.lower.RR)
##     upper.RR <- exp(log.upper.RR)
##     names(OR) <- "OR"
##     log.OR <- log(OR)
##     SE.log.OR <- sqrt(sum(1/x))
##     log.lower.OR <- log.OR - crit * SE.log.OR
##     log.upper.OR <- log.OR + crit * SE.log.OR
##     lower.OR <- exp(log.lower.OR)
##     upper.OR <- exp(log.upper.OR)
```

How to get the code behind a function?

Sometimes, the code is not directly displayed. . . e.g. **R** methods (S3):

```
residuals
```

```
## function (object, ...)
## UseMethod("residuals")
## <bytecode: 0x556a946d7908>
## <environment: namespace:stats>
```

`residuals()` is a *generic* function which rely on class specific *methods*:

```
methods(residuals)
```

```
##  [1] residuals.default*       residuals.glm
##  [3] residuals.gls*           residuals.glsStruct*
##  [5] residuals.gnls*          residuals.gnlsStruct*
##  [7] residuals.HoltWinters*   residuals.isoreg*
##  [9] residuals.lm             residuals.lme*
## [11] residuals.lmeStruct*     residuals.lmList*
## [13] residuals.loglm*         residuals.nlmeStruct*
## [15] residuals.nls*           residuals.psych*
## [17] residuals.smooth.spline* residuals.tukeyline*
## see '?methods' for accessing help and source code
```

The methods with a $*$ are not exported from their package namespace!

How to get the code behind a function?

Add the `class` at the end of the function name to get the code for exported **R** (S3) methods:

```
residuals.lm
## function (object, type = c("working", "response", "deviance",
##     "pearson", "partial"), ...)
## {
##     type <- match.arg(type)
##     r <- object$residuals
##     res <- switch(type, working = , response = r, deviance = ,
##         pearson = if (is.null(object$weights)) r else r * sqrt(object$weights),
##         partial = r)
##     res <- naresid(object$na.action, res)
##     if (type == "partial")
##         res <- res + predict(object, type = "terms")
##     res
## }
## <bytecode: 0x556a9b2904a0>
## <environment: namespace:stats>
```

Note: this requires to know the `class` of the object you work with!
You can use `class()` on your input to figure this out.

How to get the code behind a function?

It is also possible to get the code of non-exported **R** methods (S3):

```
residuals.nls
```

```
## Error in eval(expr, envir, enclos):  object 'residuals.nls' not found
```

```
getAnywhere("residuals.nls") # or getS3method("residuals", "nls")
```

```
## A single object matching 'residuals.nls' was found
## It was found in the following places
##   registered S3 method for residuals from namespace stats
##   namespace:stats
## with value
##
## function (object, type = c("response", "pearson"), ...)
## {
##     type <- match.arg(type)
##     if (type == "pearson") {
##         val <- as.vector(object$m$resid())
##         std <- sqrt(sum(val^2)/(length(val) - length(coef(object))))
##         val <- val/std
##         if (!is.null(object$na.action))
##             val <- naresid(object$na.action, val)
##         attr(val, "label") <- "Standardized residuals"
##     }
##     else {
##         val <- as.vector(object$m$lhs() - object$m$fitted())
##         if (!is.null(object$na.action))
##             val <- naresid(object$na.action, val)
##         lab <- "Residuals"
##         if (!is.null(aux <- attr(object, "units")$y))
##             lab <- paste(lab, aux)
##         attr(val, "label") <- lab
##     }
##     val
```

Challenge

Which function actually computes the numbers behind `boxplot()`?

Challenge

What is the code behind `t.test()`?

How to get the code behind a function?

Some functions – the interfaces – call functions that are written in other languages.
The source code of these latter functions is not directly visible (spotted as `.C()`, `.Fortran()`, `.Call()`, `.Primitive()`, `.Internal()`, `.External()`).

```
dnorm
```

```
## function (x, mean = 0, sd = 1, log = FALSE)
## .Call(C_dnorm, x, mean, sd, log)
## <bytecode: 0x556a9d6eed58>
## <environment: namespace:stats>
```

In these cases, the easiest is to use the read-only mirror for **R** (`https://github.com/wch/r-source`) or the relevant package on Github! (here, the answer lies in r-source/src/nmath/dnorm.c)

Challenge

What is the code really estimating coefficients behind `lm()`?

Programming with **R**

Debugging a faulty function

```
pythagora <- function(x, y) {
  x2 <- x^2
  y2 <- y^2
  hyp <- (x^2 + y^2)^1/2
  return(hyp)
}

pythagora(x = 2, y = 2)
## [1] 4
```

Debugging a faulty function

```
pythagora <- function(x, y) {
  x2 <- x^2
  y2 <- y^2
  hyp <- (x^2 + y^2)^1/2
  return(hyp)
}

pythagora(x = 2, y = 2)
## [1] 4
```

```
pythagora <- function(x, y) {
  x2 <- x^2
  y2 <- y^2
  browser()
  hyp <- (x^2 + y^2)^1/2
  return(hyp)
}

pythagora(x = 2, y = 2)
```

Note: this is very useful but you need to have access to the code!

Debugging a faulty function

```
pythagora <- function(x, y) {
  x2 <- x^2
  y2 <- y^2
  hyp <- (x^2 + y^2)^1/2
  return(hyp)
}

pythagora(x = 2, y = 2)
## [1] 4
```

```
debug(pythagora)

pythagora(x = 2, y = 2)

undebug(pythagora) ## when you are done, or use debugonce() above, or reload the function
```

Note: this can work on any function without having to mess with the code!

Debugging a faulty function

There are plenty more debugging possibilities out there!

Check:

- the nice possibilities with RStudio:
  `https://support.rstudio.com/hc/en-us/articles/205612627-Debugging-with-RStudio`
- `?option` and look at `error`
- `?traceback`
- `?trace`

Programming with **R**

Remember

"*premature optimization is the root of all evil* "

Donald Knuth, Computing Surveys, Vol 6, No 4, December 1974

When to optimize?

- optimize only when the code really works
- optimize only if needed

Profilling

You can time functions:

```
library(spaMM)

data("Loaloa")

system.time({
  fullfit <- fitme(maxNDVI ~ 1 + Matern(1|latitude+longitude), data = Loaloa)
})
##    user  system elapsed
##   9.173   0.033   9.237
```

Profilling

You can time functions:

```
library(spaMM)

data("Loaloa")

system.time({
  fullfit <- fitme(maxNDVI ~ 1 + Matern(1|latitude+longitude), data = Loaloa)
})
```

```
##    user  system elapsed
##   9.173   0.033   9.237
```

You can profile the code very precisely using `profvis`:

```
library(profvis)

profvis({
  fullfit <- fitme(maxNDVI ~ 1 + Matern(1|latitude+longitude), data = Loaloa)
})
```

Note: try it out!

General tips to improve speed

- limit to number of function calls as much as possible!

```
system.time({
  replicate(1e6, runif(1))
  })
```

```
##    user  system elapsed
##   3.136   0.020   3.168
```

```
system.time({
  runif(1e6)
  })
```

```
##    user  system elapsed
##   0.027   0.000   0.028
```

Note: it is always best to design functions that can work on vectors and not just on single values.

General tips to improve speed

- limit to number of function calls as much as possible!
- compare alternative implementations

```
d <- data.frame(proba = runif(500), group = factor(1:500))

system.time({
  all_pairwise(proba = d$proba, groups = d$group)
  })
##    user  system elapsed
##   5.639   0.000   5.648
```

```
system.time({
  all_pairwise2(proba = d$proba, groups = d$group)
  })
##    user  system elapsed
##   5.949   0.000   5.959
```

General tips to improve speed

- limit to number of function calls as much as possible!
- compare alternative implementations
- code bottlenecks in another language and rely on interfaces (advanced)

Programming with **R**

What is an **R** package

An **R** package is only a way to organise one's data, scripts and documentation!

Benefits:

- easy distribution
- thorough check of the code
- incentive to write up some documentation and examples

Note: it is good practice to write a research project as a package!

How to create an **R** package

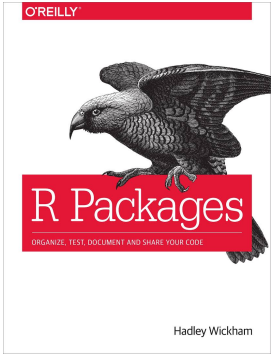
- you can simply use the function `package.skeleton()` (see help for example)
- you can use the combo RStudio + the **R** package `devtools`

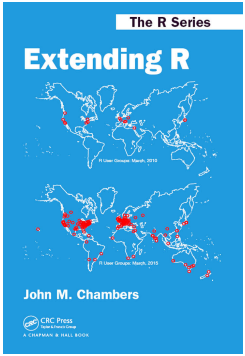
How to create an **R** package

- you can simply use the function `package.skeleton()` (see help for example)
- you can use the combo RStudio + the **R** package `devtools`

For more info:
`https://cran.r-project.org/doc/manuals/r-release/R-exts.html`

Or:





Programming with **R**

Working on the language

Crude:

```
set.seed(1)
d <- data.frame(foo = runif(10), bar = runif(10))

my_wilcox <- function(var1, var2, data) {
  w <- wilcox.test(x = data[, var1], y = data[, var2])  ## data$var1 would not work!
  return(w)
}

my_wilcox(var1 = "foo", var2 = "bar", data = d)
```

```
##
##  Wilcoxon rank sum test
##
## data:  data[, var1] and data[, var2]
## W = 47, p-value = 0.8534
## alternative hypothesis: true location shift is not equal to 0
```

Working on the language

Better:

```
set.seed(1)
d <- data.frame(foo = runif(10), bar = runif(10))

my_wilcox <- function(var1, var2, data) {
  w <- eval(substitute(wilcox.test(x = data$var1, y = data$var2)))
  return(w)
}

my_wilcox(var1 = "foo", var2 = "bar", data = d)
##
##  Wilcoxon rank sum test
##
## data:  d$foo and d$bar
## W = 47, p-value = 0.8534
## alternative hypothesis: true location shift is not equal to 0
```

Working on the language

`quote` & `substitute` generate unevaluated pieces of code.
`eval` can be used to evaluate the piece of code.

```
saved_code <- quote(a + b)
saved_code
```

```
## a + b
```

```
a <- 2
b <- 3

eval(saved_code)
```

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

```
eval_example <- function(){
  a <- 5
  b <- 5
  print(eval(saved_code))
  print(eval(saved_code, envir = .GlobalEnv))
}

eval_example()
```

```
## [1] 10
## [1] 5
```

Note: the difference between `quote` & `substitute` is that `substitute` allows for substitution before the evaluation (useful to play with variable names).

Working on the language

A few examples:

```
foo <- 1
getNameFromObject <- function(i) paste(substitute(i))
getNameFromObject(foo)
```

```
## [1] "foo"
```

```
getValueFromName <- function(i) get(i)
getValueFromName("foo")
```

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

```
setObjectFromName <- function(i, x) assign(i, x, envir = globalenv())
setObjectFromName("bar", 2)
bar
```

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

Note: there are plenty more possibilities for working on the language in **R**, but it would require to dive quite deeper into how **R** works.

Recursions

The Fibonacci example:

```
fibonacci <- function(x) {
  if (x == 0) return(0)
  if (x == 1) return(1)
  return(fibonacci(x - 1) + fibonacci(x - 2))
}
```

```
system.time(foo <- fibonacci(35))
```

```
##    user  system elapsed
##   9.088   0.020   9.121
```

```
foo
```

```
## [1] 9227465
```

Note: if you plan to rename functions, you can use "`Recall()`"!

Using C++ code within functions

The package Rcpp allows to run C++ code inside **R** on the fly!

```
library(Rcpp)
fibRcpp <- cppFunction('
int fibonacci(const int x) {
   if (x == 0) return(0);
   if (x == 1) return(1);
   return (fibonacci(x - 1) + fibonacci(x - 2));
}
')
system.time(foo <- fibRcpp(35))  ## beware: memory issue if x is too large!
```

```
##    user  system elapsed
##   0.036   0.000   0.036
```

```
foo
```

```
## [1] 9227465
```

Programming with **R**

Definitions

What is an object?
An instance of a class.

What is a class?
A data structure for which specific methods can be defined.

What is a method?
A function that is designed to work with all objects of a given class.

R is an object-based system

Rule #1:
Everything that exists in **R** is an object

(John M. Chambers)

Example

```
res <- 1
```

```
res
```

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

```
class(res)
```

```
## [1] "numeric"
```

```
methods(class = "numeric")
```

```
##  [1] [             [<-           all.equal     Arith
##  [5] as.data.frame as.Date       as.POSIXct    as.POSIXlt
##  [9] as.raster     cbind2        coerce        Compare
## [13] confint       Logic         Ops           rbind2
## see '?methods' for accessing help and source code
```

```
`<-`
```

```
## .Primitive("<-")
```

```
class(`<-`)
```

```
## [1] "function"
```

```
methods(class = "function")
```

```
## [1] as.data.frame as.list       coef          coerce
## [5] coerce<-      head          plot          print
## [9] tail
## see '?methods' for accessing help and source code
```

Objects are accessed or modified using references

Reference = a name + an environment:

```
ls()
```

```
##  [1] "a"                  "all_pairwise"
##  [3] "all_pairwise2"      "b"
##  [5] "bar"                "d"
##  [7] "do_slow"            "e1"
##  [9] "eval_example"       "f"
## [11] "fibonacci"          "fibRcpp"
## [13] "foo"                "fullfit"
## [15] "getNameFromObject" "getValueFromName"
## [17] "group1"             "group2"
## [19] "i"                  "j"
## [21] "Loaloa"             "my_function"
## [23] "my_wilcox"          "new.u"
## [25] "odds_ratio"         "process_factor"
## [27] "pythagora"          "res"
## [29] "saved_code"         "setObjectFromName"
## [31] "u"                  "x"
```

```
environmentName(pryr::where("res"))
```

```
## [1] "R_GlobalEnv"
```

Note: remember, we discussed environments earlier on!

Objects are accessed or modified using references

Behind one reference there is one memory address:

```
pryr::address(res)
```

```
## [1] "0x556a9e7e3320"
```

Behind one memory address there can be several references:

```
res2 <- res
pryr::address(res2)
```

```
## [1] "0x556a9e7e3320"
```

Note: as we will see, the address behind a reference can change during computation.

There are different systems for defining and using objects in **R**

Native class systems:

- S3 (legacy from S version 3, in *base*)
- S4 (legacy from S version 4, in core package *methods*)
- Reference Class (sometimes referred to as R5, in *methods*)

There are different systems for defining and using objects in **R**

Native class systems:

- S3 (legacy from S version 3, in *base*)
- S4 (legacy from S version 4, in core package *methods*)
- Reference Class (sometimes referred to as R5, in *methods*)

Additional class systems:

- R6 (in the package *R6*, one of the most downloaded package on CRAN!)
- ggproto (in the package *ggplot2*)
- others (proto, . . .)

Note: the objects created with one system can contain objects created with another.

The 2 main object-based programming paradigms

Functional (Object Oriented) Programming

- suitable for analytical workflows
- S3, S4
- methods defined outside the objects
- objects are not mutable
- $a \xrightarrow{fn} b \xrightarrow{fn} c \xrightarrow{fn} \ldots$

The 2 main object-based programming paradigms

Functional (Object Oriented) Programming

- suitable for analytical workflows
- S3, S4
- methods defined outside the objects
- objects are not mutable
- $a \xrightarrow{fn} b \xrightarrow{fn} c \xrightarrow{fn} \ldots$

Encapsulated Object Oriented Programming (aka OOP)

- suitable for data that evolve over time (modularity and reusability)
- RC, R6
- methods defined inside the objects
- objects are mutable
- $a \xrightarrow{fn} b \;\&\; a \xrightarrow{fn} \varnothing$

Note: actual programming can borrow from multiple paradigms (pure form is difficult).

A simple example using S3

```
addone <- function(x) res + 1
res <- 1
addone(res)
```

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

A simple example using S4

```
setClass(Class = "S4_obj", slots = list(value = "numeric"))
setGeneric(name = "addone", def = function(object) stop("only for S4_obj")) ## set generic with default behaviour
```

```
## [1] "addone"
```

```
setMethod(f = "addone", signature = "S4_obj", definition = function(object) {
  object@value <- object@value + 1
  return(object)
  }
  )
```

```
resS4 <- new("S4_obj", value = 1)
addone(resS4)
```

```
## An object of class "S4_obj"
## Slot "value":
## [1] 2
```

A simple example using RC

```
RC_obj <- setRefClass(Class   = "RC_obj",
                      fields  = list(value = "numeric"),
                      methods = list(
                        addone = function() value <<- value + 1)
                      )
```

```
resRC <- RC_obj$new(value = 1)
resRC$addone()
resRC
```

```
## Reference class object of class "RC_obj"
## Field "value":
## [1] 2
```

A simple example using R6

```
library(R6)
R6_obj <- R6Class(
  public  = list(
    value = NA,
    initialize = function(value) self$value <- value,
    addone = function() self$value <- self$value + 1
  )
)
```

```
resR6 <- R6_obj$new(value = 1)
resR6$addone()
resR6$value
```

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

```
resR6$value <- 1
replicate(10, resR6$addone())
```

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

```
resR6$value
```

```
## [1] 11
```

Encapsulated OOP requires mutability

S3 objects are (generally) not mutable (same for S4):

```
a <- 1:3
a
## [1] 1 2 3
pryr::address(a)
## [1] "0x556aa3ee5098"
```

```
a[2] <- 10
a
## [1]  1 10  3
pryr::address(a)
## [1] "0x556aa7dae948"
```

```
b <- a
b
## [1]  1 10  3
pryr::address(b)
## [1] "0x556aa7dae948"
```

```
b[2] <- 11
pryr::address(b)
## [1] "0x556aa88f4fc8"
pryr::address(a)
## [1] "0x556aa7dae948"
```

```
a
## [1]  1 10  3
```

Encapsulated OOP requires mutability

R6 objects are mutable (same for RC):

```
resR6$value
## [1] 11
pryr::address(resR6)
## [1] "0x556aa32dda98"
```

```
resR6$value <- 3
resR6$value
## [1] 3
pryr::address(resR6)
## [1] "0x556aa32dda98"
```

```
resR6_bis <- resR6
pryr::address(resR6_bis)
## [1] "0x556aa32dda98"
```

```
resR6_bis$value
## [1] 3
resR6_bis$value <- 4
resR6_bis$value
## [1] 4
```

```
resR6$value
## [1] 4
```

Note: mutability can be prevented if necessary.

Example: An simple Individual Based Models (IBM)

Setup:

- two age classes: children (0–14 yrs), adults (15+ yrs)
- children die at an average rate of 15 deaths per 1000 per year
- adults die at an average rate of 5 deaths per 1000 per year
- children do not reproduce
- adults reproduce at an average rate of 10 births per 1000 per year

Question:
Starting with 1000 individuals (with age following a uniform distribution between 0 and 40 yrs), what is the number of children and adults after 50 years?

Functional way using S3: functions

```
death <- function(pop) {
  death_children <- rbinom(n = length(pop), size = 1, prob = 15/1000)
  death_adults   <- rbinom(n = length(pop), size = 1, prob = 5/1000)
  alive <- rep(1, length(pop))
  alive[pop < 15] <- 1 - death_children[pop < 15]
  alive[pop > 14] <- 1 - death_adults[pop > 14]
  pop <- pop[alive == 1]
  return(pop)
}

birth <- function(pop) {
  adults <- pop[pop > 14]
  babies_nb <- sum(rbinom(n = length(adults), size = 1, prob = 10/1000))
  babies <- rep(0, babies_nb)
  pop <- c(pop, babies)
  return(pop)
}

age <- function(pop) pop <- pop + 1
```

Functional way using S3: run

```
pop <- round(runif(1000, min = 0, max = 40))

for (i in 1:50) {
  pop <- birth(pop)
  pop <- death(pop)
  pop <- age(pop)
}
table(pop > 14)
```

```
##
## FALSE  TRUE
##   111  1032
```

OOP way using R6: definition of the class `individual`

```
individual <- R6Class(
  public  = list(
    age = NA,
    alive = 1,
    initialize = function(age = 0) {self$age <- age},
    die = function() {
      if (self$age < 15 & self$alive) self$alive <- 1 - rbinom(n = 1, size = 1, prob = 15/1000)
      if (self$age > 14 & self$alive) self$alive <- 1 - rbinom(n = 1, size = 1, prob =  5/1000)
    },
    reproduce = function() {
      ifelse(self$alive == 1 & self$age > 14, rbinom(n = 1, size = 1,  prob = 10/1000), FALSE)
    },
    aging = function() {
      if (self$alive == 1) {self$age <- self$age + 1; self$die()}
    }
  )
)
```

OOP way using R6: test

You can test things before creating the population!

```
alex <- individual$new()
alex
```

```
## <R6>
##   Public:
##     age: 0
##     aging: function ()
##     alive: 1
##     clone: function (deep = FALSE)
##     die: function ()
##     initialize: function (age = 0)
##     reproduce: function ()
```

```
for (i in 1:200) alex$aging()
alex
```

```
## <R6>
##   Public:
##     age: 59
##     aging: function ()
##     alive: 0
##     clone: function (deep = FALSE)
##     die: function ()
##     initialize: function (age = 0)
##     reproduce: function ()
```

OOP way using R6: definition of the class `population`

```
population <- R6Class(
  public  = list(
    individuals = list(),
    initialize = function(N = 1000) {
        for (i in 1:N)
          self$individuals[[i]] <- individual$new(age = round(runif(n = 1, min = 0, max = 40)))
    },
    repro = function() {
      for (i in 1:length(self$individuals))
        if (self$individuals[[i]]$reproduce() == TRUE)
          self$individuals[[length(self$individuals) + 1]] <- individual$new()
      },
    death = function(){
      alive <- sapply(self$individuals, function(i) i[["alive"]])
      self$individuals[!alive] <- NULL
      },
    aging = function(){
      for (i in 1:length(self$individuals)) self$individuals[[i]]$aging()
      },
    year = function() {self$repro(); self$death(); self$aging()},
    count = function() table(sapply(self$individuals, function(i) i[["age"]]) > 14)
  )
)
```

OOP way using R6: run

```
pop <- population$new()
for (i in 1:50) pop$year()
pop$count()
```

```
##
## FALSE  TRUE
##   130   980
```

Note: I did not handle the possible population crash, so it may crash :-/

Our Individual Based Models (IBM): UPDATE

Setup:

- two age classes: children (0–14 yrs), adults (15+ yrs)
- children die at an average rate of 15 deaths per 1000 per year
- adults die at an average rate of 5 deaths per 1000 per year
- children do not reproduce
- adults reproduce at an average rate of 10 births per 1000 per year
- two sexes, females do not reproduce after 45 yrs (males do not reproduce)

Question:
Starting with 1000 individuals (with age following a uniform distribution between 0 and 40 yrs), what is the number of children and adults after 50 years?

OOP way using R6: re-definition of the class `individual`

```
individual <- R6Class(
  public  = list(
    age = NA,
    alive = 1,
    sex = NA,                                                    ##new
    initialize = function(age = 0) {
      self$age <- age
      self$sex <- ifelse(runif(1) < 0.5, "male", "female")       ##new
    },
    die = function() {
      if (self$age < 15 & self$alive) self$alive <- 1 - rbinom(n = 1, size = 1, prob = 15/1000)
      if (self$age > 14 & self$alive) self$alive <- 1 - rbinom(n = 1, size = 1, prob =  5/1000)
    },
    reproduce = function() {
      ifelse(self$alive == 1 &
               (self$age > 14 & self$age < 44 & self$sex == "female"),     ##new
             rbinom(n = 1, size = 1,  prob = 10/1000), FALSE)
    },
    aging = function() {
      if (self$alive == 1) {self$age <- self$age + 1; self$die()}
    }
  )
)
```

Note: there is no need to redefine the class `population`!

OOP way using R6: re-run

```
pop <- population$new()
for (i in 1:50) pop$year()
pop$count()
```

```
##
## FALSE  TRUE
##     3   846
```

Functional way using S3: re-defining functions

We would have to recode everything . . .

Pros and cons of R6 for IBM

Pros

- clearer structure (see butterfly example)
- easier to modify once existing
- easier to share classes between projects, packages...
- easier to translate to C++

Cons

- initially difficult for those knowing mostly S3
- much slower (cost can somewhat be reduced with some tweaks)
- additional issues to take care (e.g. side effects)

A more advanced simulation model using R6

```
?load_butterfly_example
```