

Programming in R

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Introduction

Who are we?

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Who are you?

1. Occupation, employer?
2. Previous knowledge and experience
 - with R?
 - with other statistical software?
 - with other programming languages?
3. Specific interest/motivation for this workshop?

Why care about R coding?

1. Increase efficiency!
 - Save time and nerves
 - Avoid errors and bugs
 - High transfer effect to other projects (with data analysis)
2. Successful collaborations (including with your future self!)
3. Code as deliverable (i.e., part of research paper)

The Sunday Telegraph Sunday 17 May 2020

Coronavirus

Selling behind lockdown was a reliable buggsy mess, claim experts

Data that predicted 500,000 could die in UK unless extreme measures were taken are impossible to replicate, say scientific teams

Science

By Hannah Ireland and Peter Dinkworth
THE Covid-19 modelling that went into the lockdown, making the economy and leaving millions out of work has been criticised by experts.

Prof Nick Ferguson's Imperial College computer coding was derided as "totally unreliable" by leading experts, who warned it was "wonderful you wouldn't state your job title".

The model, credited with forcing the Government to close bars and introduce a nationwide lockdown, is a "buggy mess, which looks more like a bowl of angel hair pasta than a finely tuned piece of programming", said David Foray, the co-founder of British data technology company Wavelength.

"In our commercial reality, we would not agree for developers to use this and any business that relied on it to produce software for sale would likely go bust."

The comments are likely to relegate a row over whether the UK was right to go into lockdown, with conflicting models suggesting people may have already acquired substantial herd immunity and Covid-19 may have hit Britain earlier than first thought.

Scientists have also been split on the likely rate of Covid-19 which has resulted in vastly different models.

To add to the confusion, several models have been attacked by Imperial itself, which placed the fatality rate higher than others and predicted 500,000 in the UK could die without a lockdown.

It was said to have prompted a dramatic change in government policy causing businesses, schools and restaurants to be shut immediately in March. The bank of England has predicted that the economy could take a year to return to normal, after its worst recession in more than 80 years.

The Imperial model works by using data to simulate transport links, population size, social networks and health care provision, to predict how coronavirus would spread. However, questions have emerged over whether the model is accurate, after researchers released its code, which in its original form was "dozens of lines" dense and over more than 10 years.

In its initial form the code was untestable, developers claimed, with some parts looking "like they were ma-

'In our commercial reality, we would fire anyone for developing code like this'

'Any business that relied on it to produce software for sale would likely go bust'

'It looks more like a bowl of angel hair pasta than a finely tuned piece of programming'

'The early 2000s were yet another confirmation that their modelling approach was flawed to the core'

chine translated from Fortran", an old coding language, according to John Carroll, a US developer, who helped clean the code before it was published.

Yet, the problems appear to go much deeper than messy coding. Many have claimed that it is almost impossible to replicate the same results from the same data, using the same code.

Scientists from the University of Edinburgh said they got different results when they used different ma-

chine, and even in some cases using the same machines. "There appears to be a bug in either the compiler or in use of the network file. If we attempt two completely identical runs, only varying in that the second should use the network file produced by the first, the results are quite different", the Edinburgh researchers wrote on the GitHub website.

After a discussion with a GitHub developer, it was provided. It is said to be one of a number of bugs discovered within the system. GitHub developers said that the model was "dozens of lines" of code and "would give you different results depending on how many different code snippets you used before making policy decisions."

Writing for the Telegraph online, Prof Sir Nigel Meade, the principal of the Open Life Institute, which is co-funded with World Wide Web Innovator Sir Tim Berners-Lee, said: "Having a diverse variety of models, particularly those that make policy decisions to

explore predictions under different assumptions, and with different interventions, is incredibly powerful."

Like the Imperial code, a rival model by Prof Imperial's Gupta at the University of Oxford works on a so-called "SIR approach" in which the population is divided into those that are susceptible, infected and recovered. However, while Prof Gupta assumed that 0.1 per cent of infected people would die, Prof Ferguson worked on a 10 per cent. That led to a dramatic reversal in government policy from attempting to "lock" herd immunity to a full-on lockdown.

Concrete over Prof Ferguson's model have been raised, with Sir Kenneth Bracken, the UK's architect at Wavelength, saying his track record did not inspire confidence. In the early 2000s, Prof Ferguson's models incorrectly predicted up to 100,000 road core disease deaths, according from both his and a close team member.

"The facts from the early 2000s are not just another confirmation that their modelling approach was flawed to the core," says Sir Kenneth. "We don't know for sure if the same model/code was used, but we clearly see their methodology wasn't rigorous then and surely hasn't improved now."

A spokesman for Imperial's Covid-19 team said: "The Government has never relied on a single disease model to inform decisions making. As has been previously stated, decision making during lockdown was based on a consensus view of the scientific evidence, including several modelling studies by different academic groups."

Multiple groups using different models concluded that the pandemic would overwhelm the NHS and cause an unacceptable high mortality in the absence of effective social distancing measures. Within the Imperial team, we use several models of differing levels of complexity, all of which produce consistent results. We are working with legitimate academic groups and technology companies to develop and further document the simulation code. In the future, we will release the partisan reviews of a few clearly identified model-based assumptions."

"Epistemology is not a branch of computer science and the continuous arrival of lockdowns rely not on any mathematical model but on the scientific consensus that Covid-19 is highly transmissible with an infection fatality ratio exceeding 0.1 per cent in the UK."



Goal of this workshop

An introduction to R as a Programming language

- Better practical R skills
- Better understanding of R (and programming)
- Different framing: R as a programming language

Agenda

- RStudio setup
- Flow & conditional programming
- Loops & iteration
- Functions (part I)
- Functions (part II)
- Functionals & split-apply-combine
- Good programming practices

RStudio setup

RStudio setup

1. Save the course content to a directory on your machine
2. Open RStudio
3. Choose File < New Project ...
4. Choose Existing Directory
5. Browse to the directory on your machine where you saved the course content and select the “[R-programming](#)” folder as the Project working directory
6. Click Open in new session
7. Click Create Project

RStudio setup - optional

1. Choose Tools < Global options
2. Under General
 - DON'T Restore .RData into workspace at startup
 - NEVER Save workspace to .Rdata on exit:
 - Save the code instead!
 - Use `saveRDS()` and `readRDS()` for objects that require a long time to compute
3. Further personalize RStudio

Flow & conditional programming

Flow & conditional programming

R has specific tools (functions) that help organize the flow of computations.

You can make computations conditional on other objects (“conditional computation”)

The most commonly used tools are:

- `if (+ else)`
- `ifelse`

Conditional Computation - if

if statements have the basic form

```
if(test){  
    some_computations  
}
```

- test should be either TRUE or FALSE (or code that results in one of both).
- If test == TRUE, than some_computations is executed, if test == FALSE, than not.
- **Important:** test should have length 1. If not, only the first element is considered.

Conditional Computation - if

else can be added, but it is optional

```
if(test){  
    some_computations  
} else if (test_2){  
    other_computations  
} else {  
    more_computations  
}
```

Typical test functions

Vectorized, elementwise	
<code>==</code>	equal to
<code>!=</code>	NOT equal to
<code>>, <</code>	is greater, less than
<code>>=, <=</code>	is greater, less than or equal to
<code>&</code>	AND operator
<code> </code>	OR operator
<code>xor</code>	exclusive OR

Typical test functions

Not Vectorized	
<code>identical()</code>	identical to
<code>any()</code>	at least one TRUE
<code>all()</code>	all TRUE
<code>&&</code>	AND operator
<code> </code>	OR operator
<code>is.character()</code> , <code>is.data.frame()</code> , ...	

Typical test functions

Compare:

```
c(TRUE, TRUE) & c(FALSE, TRUE)
```

```
> [1] FALSE TRUE
```

```
c(TRUE, TRUE) && c(FALSE, FALSE)
```

```
> [1] FALSE
```

Conditional Computation - if

The test should have length 1!

```
# only the first element is evaluated
age <- c(8, 17, 39, 55)
if (age >= 18) {
  "can vote"
} else {
  "too young"
}
```

```
> Warning in if (age >= 18) {: Bedingung hat Länge > 1 und nur
das erste Element wird benutzt
```

```
> [1] "too young"
```

Conditional Computation - if

Typical uses

```
if(any(is.na(x))){
  stop("computation impossible due to NA values")
}

if(!is.integer(vector)){
  warning("'vector' is automatically converted to integer.
          This may affect the results")
  vector <- as.integer(vector)
}

if(is.null(argument)){
  # default computations
} else if (argument == specific_value) {
  # other computations
}
```

Conditional Computation - if

Programming advice

- *if* is almost always used inside of functions or loops
- If possible, avoid using *else*
- Use meaningful initialization, early `return()`, `stop()`, etc. instead

Conditional Computation - if

Solution using *if* and *else*

```
age <- 17
if (age >= 18) {
  vote <- "can vote"
} else {
  vote <- "too young"
}
vote

> [1] "too young"
```

Conditional Computation - ifelse

A vectorized version is `ifelse()`.

```
# all elements are evaluated
```

```
age <- c(8, 17, 39, 55)
```

```
ifelse(age >= 18,  
       yes = "can vote",  
       no  = "too young")
```

```
> [1] "too young" "too young" "can vote"  "can vote"
```

Conditional Computation - ifelse

Go-to tool for conditional recoding

```
age_estimated <- c(10, 20, 35, 60)
age_self_rep <- c(NA, 17, 39, NA)

# Use available information, prioritize self report
ifelse(!is.na(age_self_rep),
      yes = age_self_rep,
      no = age_estimated)

> [1] 10 17 39 60
```


Exercises



Loops & Iteration

Loops & iteration

R has specific tools (functions) that help organize the flow of computations.

You can repeat a similar computation multiple times typically with changing options (“iteration”). The most commonly used tools are:

- loops
 - for
 - while
 - repeat
- apply - family

Loops & Iteration - for

for statements have the basic form

```
for (element in vector) {  
    computation  
}
```

For each element in the vector, the computation is executed.
Often, the computation depends on the element in that iteration.

Loops & Iteration - for

```
# iterate over a numeric vector
for (index in 1:3){
  cat(" computation -")
}

> computation - computation - computation -

# iterate over a character vector
for (name in c("Alice", "Bob", "Casey")){
  if(name == "Bob") cat(" This was Bob -")
  else cat(" Not Bob -")
}

> Not Bob - This was Bob - Not Bob -
```

Loops & Iteration - while

while statements have the basic form

```
while (condition){  
    computation  
}
```

As long as the condition is TRUE, the computation is executed. Often, the computation depends on something that is related to the condition.

Loops & Iteration - repeat

repeat statements have the basic form

```
repeat {  
    computation  
}
```

Without a `break` the computation is repeated infinite times

Loops & Iteration - next break

- `next` starts next iteration
- `break` ends iteration (of the innermost loop)

```
index <- 0
repeat {
  index <- index + 1
  if (index %in% c(3, 5)) next
  if (index > 6) break
  print(index)
}
```

```
> [1] 1
> [1] 2
> [1] 4
> [1] 6
```


Loops & Iteration - next break

- `next` starts next iteration
- `break` ends iteration (of the innermost loop)

Same idea, now with `for` loop

```
for(index in 1:6) {  
  if (index %in% c(3, 5)) next  
  print(index)  
}
```

```
> [1] 1  
> [1] 2  
> [1] 4  
> [1] 6
```

Loops & Iteration - nested loops

Nested loops (over the rows and columns of a matrix)

```
matrix <- matrix(NA, nrow = 2, ncol = 3)
for (rowNr in 1:2){
  for (colNr in 1:3){
    matrix[rowNr, colNr] <- rowNr * 10 + colNr
  }
}
matrix
```

```
>      [,1] [,2] [,3]
> [1,]   11   12   13
> [2,]   21   22   23
```

Iteration - Good practice

Programming advice

Use `seq()`, `seq_len()`, or `seq_along()`.

```
x <- numeric()
for (index in 1:length(x)){
  print(index)
}

> [1] 1
> [1] 0

for (index in seq_along(x)){
  print(index)
}
```

Loops & Iteration - Good practice

Programming advice

Don't grow, replace.

```
x <- letters
result1 <- numeric()           # grow
result2 <- numeric(length(x)) # replace
for (index in seq_along(x)){
  result1 <- c(result1, paste(index, x[index])) # grow
  result2[index] <- paste(index, x[index])      # replace
}
```

Loops & Iteration - apply

`apply` lets you iterate over rows or columns of a matrix or `data.frame`. You can *apply* a function to all rows/columns

```
apply(matrix,  
      MARGIN = 1,      # 1 = iterate over rows  
                        # 2 = iterate over columns  
      FUN = function)  # function to apply to rows/columns
```

apply

- for objects with dimensions (matrix, array, data.frame)
- apply over (a) chosen dimension(s)

```
my_matrix <- matrix(1:6, nrow = 2)
apply(my_matrix, 1, max)      # apply per row

> [1] 5 6

apply(my_matrix, 2, max)      # apply per column

> [1] 2 4 6
```

apply

```
my_array <- array(1, dim = c(2, 3, 4))
apply(my_array, c(1, 2), sum) # per row and column

>      [,1] [,2] [,3]
> [1,]    4    4    4
> [2,]    4    4    4

apply(my_array, 3, sum)      # per "third dimension"

> [1] 6 6 6 6
```

Exercises



Functions I

“To understand computations in R, two slogans are helpful: Everything that exists is an object. Everything that happens is a function call.”

— John Chambers

Function Calls

Computing in R happens through function calls. A function is applied to one or more objects, and returns an object after the computation.



Figure 1: A function call.

The typical use is:

```
function(object1, argument = object2)
```

Function Calls

- Computations that seem not to be done using function calls are actually also function calls. Try ``<` (a, 5)` or ``>` (5, 2)`
- most functions that seem not to return an object, return it invisibly. Check `(a <- 5)`.

Building Blocks

Functions are the building blocks of R code. Writing functions allows you to organize and optimize the computations that you want to do.

Functions should:

- have a clear purpose
- be well documented
- be portable

Central stepping stone for R users:

Move from solely using functions written by others to writing your own functions.

Function definition

- Name
- Arguments/Formals (input)
- Body (what happens inside, R-code with the computations)
- Output

Function definition

```
countNA <- function(x) {  
  out <- sum(is.na(x))  
  out  
}
```

Name
Arguments/Formals
Body
Output

Function Names

Every function needs a (meaningful) name!

- Usually a **verb** (what does the function do?)
- Avoid existing names
- Better longer than unclear
- CamelCase vs snake_case

Function Names

Good

- `computeAIC()`
- `removeNAs()`
- `drop_NA_rows()`
- `factor_to_dummies()`

Bad

- `myFun()`
- `foo()`
- `statistics()`
- `data_preparation()`

Arguments

Most functions take one or multiple inputs.

These are usually:

- One or two data arguments
- Additional Options

Functions with zero arguments

- `getwd()`
- `Sys.time()`
- ...

Functions with one argument

- `dim()`
- `names()`
- ...

Functions with multiple arguments

- `mean()`
- `median()`
- `lm()`
- ...

Arguments

Programming advice

Less arguments = better!

Arguments

Often arguments have to be objects of a specific type.

```
sum(c("a", "b", "c")) # gives an error
```

```
> Error in sum(c("a", "b", "c")): ungültiger 'type' (character)  
des Argumentes
```

The documentation typically gives (or should give) information about what objects the arguments should be. Check `?sum`

Default arguments

What happens if the user omits an argument?

```
countNA <- function(x, percent) {  
  out <- sum(is.na(x))  
  if(percent) out/length(x)  
  out  
}  
x <- c(1, 5, NA, 3)  
countNA(x = x)
```

```
> Error in countNA(x = x): Argument "percent" fehlt (ohne  
Standardwert)
```

Default arguments

Default arguments are made for such instances!

```
countNA <- function(x, percent = FALSE) {  
  out <- sum(is.na(x))  
  if(percent) out/length(x)  
  out  
}  
x <- c(1, 5, NA, 3)  
countNA(x = x)  
  
> [1] 1
```

Default arguments

Additional arguments give (the user) flexibility. Default arguments keep the function easy to use.

Try ?lm

Programming advice

- Think which arguments to include, and which should (not) have defaults
- Choose sensible defaults

Single return object

Pure functions return a single object.

- (Standard) The last evaluated object
- Object defined by return()



Figure 2: A pure function.

Return object

`return()` stops the computation, and returns the object.

```
return_early <- function(x, early) {  
  x2 <- x*2  
  if(early) (return(x2))  
  out <- x + x2 # not executed  
  out  
}  
return_early(2, early = TRUE)  
  
> [1] 4  
  
return_early(2, early = FALSE)  
  
> [1] 6
```

Return object

Multiple return objects can be combined in a list!

```
do_this <- function(vector, other_vector) {  
  # many computations  
  return(list(output1 = this,  
              output2 = that))  
}
```

Name
Arguments
Body
Output

Return Object

The return object is a list with multiple objects.

```
get_info <- function(x){  
  mean_x <- mean(x)  
  median_x <- median(x)  
  n_obs_x <- length(x)  
  range_x <- range(x)  
  return(list(mean = mean_x, median = median_x,  
              n_obs = n_obs_x, range = range_x))  
}  
str(get_info(airquality$Wind))
```

```
> List of 4  
> $ mean : num 9.96  
> $ median: num 9.7  
> $ n_obs : int 153  
> $ range : num [1:2] 1.7 20.7
```

Exercises



Functions II

Why write functions?

- They make code ...
 - shorter (less repetition)
 - easier to read and understand
- They help avoid copy-paste errors
- They make it easier to change your code
- They increase transfer
 - other use cases
 - other projects
 - other persons
- They keep your work space clean

Writing a function:

```
RMSE <- get_RMSE(predictions, observations)
```

Not writing a function:

```
diff <- observations - predictions  
sq_diff <- diff^2  
m_sq_diff <- mean(diff)  
RMSE <- sqrt(m_sq_diff)
```

Side Effects

Functions can have “side effects”:

- console output
- plots
- write/save on drive
- ...

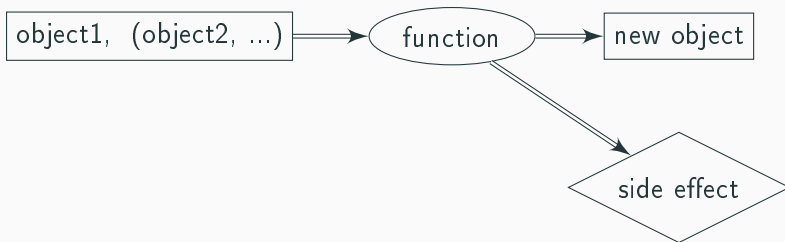


Figure 3: A function with side effect.

Console output: ?cat and ?print

```
print_info <- function(x){  
  info <- get_info(x)  
  cat("There are ", info$n_obs,  
      " observed values. \nThe mean is ",  
      round(info$mean, 2), ". \nThe median is ",  
      round(info$median, 2), ". \n", sep = "")  
}  
print_info(airquality$Wind)
```

```
> There are 153 observed values.  
> The mean is 9.96.  
> The median is 9.7.
```

Programming advice

- Write pure functions (no-side effects)
- Write separate functions for side effects
- Plotting functions should return NULL or the plot as an object

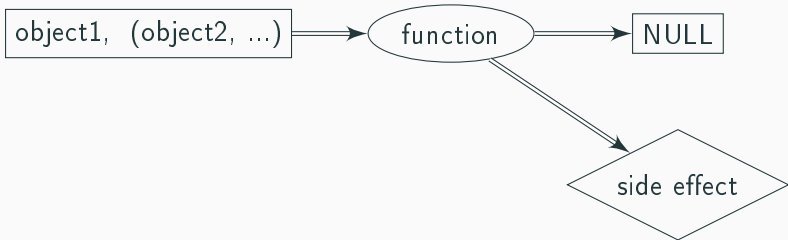


Figure 4: A side effect function.

Error, warning, & message

Error: computation is interrupted without return object!

?stop

```
get_log_xtox <- function(x) {  
  if(!is.numeric(x)) stop("This does not work!")  
  x_x <- x^x  
  return(log(x_x))  
}  
get_log_xtox("a")  
  
> Error in get_log_xtox("a"): This does not work!
```

Error, warning, & message

Error: computation is interrupted without return object!

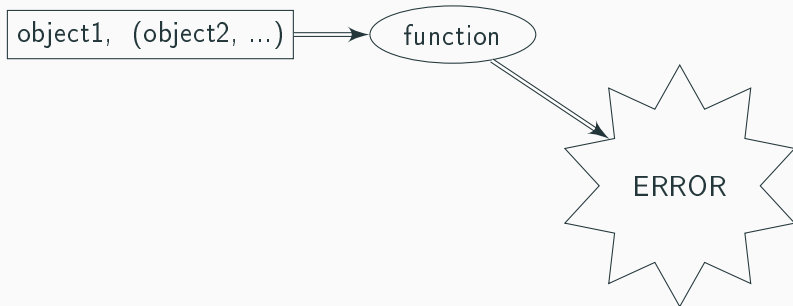


Figure 5: Computation with Error.

Error, warning, & message

?stopifnot is an abbreviation for if(!test) stop():

```
get_log_xtox <- function(x) {  
  stopifnot(is.numeric(x))  
  x_x <- x^x  
  return(log(x_x))  
}  
get_log_xtox("a")
```

```
> Error in get_log_xtox("a"):  is.numeric(x) ist nicht TRUE
```

Error, warning, & message

Message: To inform the user about something.

?message

```
get_log_xtox <- function(x) {  
  x_x <- x^x  
  message("Thank you for using this function!")  
  return(log(x_x))  
}  
get_log_xtox(2)  
  
> Thank you for using this function!  
  
> [1] 1.386294
```

Error, warning, & message

Warning: Warn the user that something may be fishy.

?warning

```
get_log_xtox <- function(x) {  
  if(x < 0 && (x %% 2 == 0))  
    warning("Not sure you can trust the result.",  
           call. = FALSE)  
  x_x <- x^x  
  return(log(x_x))  
}  
get_log_xtox(-2)
```

```
> Warning: Not sure you can trust the result.
```

```
> [1] -1.386294
```

Error, warning, & message

Message & warning: computation is NOT interrupted!

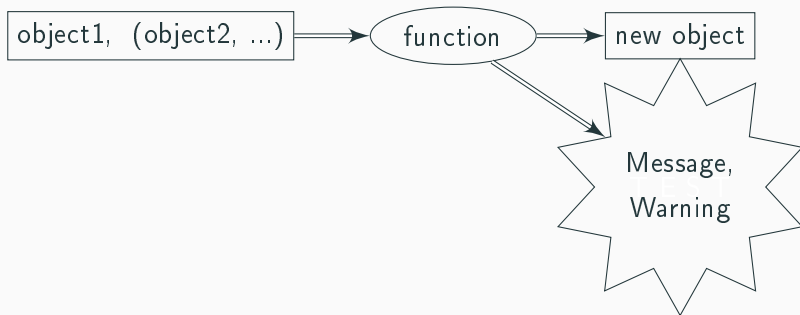


Figure 6: A message or warning.

Programming advice

- Choose carefully when something warrants a message, warning or error
- Write clear and helpful warnings, errors, messages

Where does a function find objects?

R uses specific rules to find objects, which lead to the following:

```
a <- 55
add_a <- function(x){
  return(x + a)
}
add_a(5)

> [1] 60
```

When a function is called, the computations in the body are run line by line. When R cannot find an object inside the function, it looks outside the function.

Where does a function find objects?

Name masking!

Objects inside the function mask objects outside the function with the same name.

```
a <- 55
add_a <- function(x){
  a <- 5
  return(x + a)
}
add_a(5)

> [1] 10
```

... dot-dot-dot

R has a special argument (in the definition of the function):

... (dot-dot-dot)

Useful when you don't know how many arguments there will be.

Examples:

- ?sum
- ?save
- ?cbind
- ?paste
- ...

... dot-dot-dot

A function that checks for multiple objects if they are character vectors. (A wrapper around `(?is.character)`)

```
is_character <- function(...){  
  input <- list(...)  
  out <- logical(length(input))  
  for(ell_nr in seq_along(input)){  
    out[ell_nr] <- is.character(input[[ell_nr]])  
  }  
  names(out) <- names(input)  
  out  
}  
is_character(a = "Awesome", b = 5, new = "YES")  
  
>      a      b    new  
> TRUE FALSE  TRUE
```

... dot-dot-dot

... can take *any* number of additional arguments.

Useful for passing arguments to other functions like:

- apply-family
- plot-family
- ...

... dot-dot-dot

apply example:

```
get_quantiles <- function(x, ...){  
  if(is.null(dim(x))) return(quantile(x, ...))  
  apply(x, 2, quantile, ...)  
}  
get_quantiles(airquality, na.rm = TRUE,  
              probs = c(.2, .8))
```

```
>      Ozone Solar.R  Wind Temp Month Day  
> 20%    14      92  6.90   69   5.4   7  
> 80%    73     266 12.96   86   8.0  25
```

WARNING!

Watch out with spelling mistakes, arguments can get lost!

```
get_quantiles <- function(x, ...){  
  if(is.null(dim(x))) return(quantile(x, ...))  
  apply(x, 2, quantile, ...)  
}  
get_quantiles(airquality, na.rm = TRUE,  
              probs = c(.2, .8))
```

```
>      Ozone Solar.R Wind Temp Month Day  
> 0%      1.00      7.00  1.7   56     5   1  
> 25%     18.00    115.75  7.4   72     6   8  
> 50%     31.50    205.00  9.7   79     7  16  
> 75%     63.25    258.75 11.5   85     8  23  
> 100%    168.00    334.00 20.7   97     9  31
```

Writing Functions

Before creating a function

- What should my function do?
- Which input objects (Arguments)?
- which additional options (Arguments)?
- What should the output object be?

After creating a function

- Test it
- Add input validation
- Document

Exercises



Functionals

Higher Order Functions

Higher order functions are functions that either **take functions as input** or **return functions as output**.

Functionals

As defined by Hadley Wickham: A **functional** is a function that takes another function as an input. Common argument names are `FUN` or `f`.

Examples

- `apply-family`
- `Reduce, Filter`
- `nlm`
- `optimize`
- ...

The apply-family *applies* a function repeatedly. This can be seen as an abstraction of a for loop, with the following advantages:

- requires less code to write
- can be easier to read / understand
- does not store intermediate results
- no need to replace / grow

The members of the apply-family in Base R are:

- `lapply` vector / list \rightarrow list
- `sapply` vector / list \rightarrow vector (matrix)
- `apply` matrix / array / data.frame \rightarrow vector (matrix)
- `tapply`, `by`
- `mapply`, `Map`
- `rapply`, `eapply`, `vapply`

A popular alternative from the tidyverse: `purrr`-package

- `map` vector / list \rightarrow list
- `map2` multiple vectors / lists \rightarrow list
- ...

Our focus: `lapply`

Why?

- Consistent output
- Fast
- No dependencies
- We want to understand R basics

lapply

`lapply` has two main arguments

`X` the input list/vector

`FUN` the function that should be repeatedly applied

```
example_list <- list(vec1 = c(1, 3, 4),  
                     vec2 = c(4, 2, 10),  
                     vec3 = c(2, NA, 1))  
lapply(example_list, FUN = mean)
```

```
> $vec1  
> [1] 2.666667  
>  
> $vec2  
> [1] 5.333333  
>  
> $vec3  
> [1] NA
```

lapply

Other arguments can be passed through `lapply` via `'...'`.

```
example_list <- list(vec1 = c(1, 3, 4),  
                     vec2 = c(4, 2, 10),  
                     vec3 = c(2, NA, 1))  
lapply(example_list, FUN = mean, na.rm = TRUE)
```

```
> $vec1  
> [1] 2.666667  
>  
> $vec2  
> [1] 5.333333  
>  
> $vec3  
> [1] 1.5
```

lapply

We can use our own functions as input.

```
dropNAs <- function(x) {  
  x[!is.na(x)]  
}  
lapply(example_list, FUN = dropNAs)  
  
> $vec1  
> [1] 1 3 4  
>  
> $vec2  
> [1] 4 2 10  
>  
> $vec3  
> [1] 2 1
```


Anonymous functions can be used as input.

```
lapply(example_list, FUN = function(x) x[!is.na(x)])
```

```
> $vec1
```

```
> [1] 1 3 4
```

```
>
```

```
> $vec2
```

```
> [1] 4 2 10
```

```
>
```

```
> $vec3
```

```
> [1] 2 1
```

lapply

Data.frames are lists, too.

```
lapply(iris, FUN = class)
```

```
> $Sepal.Length
```

```
> [1] "numeric"
```

```
>
```

```
> $Sepal.Width
```

```
> [1] "numeric"
```

```
>
```

```
> $Petal.Length
```

```
> [1] "numeric"
```

```
>
```

```
> $Petal.Width
```

```
> [1] "numeric"
```

```
>
```

```
> $Species
```

```
> [1] "factor"
```

lapply

Atomic vectors can be used as input, but often vectorization could be used instead.

```
lapply(c(1, 2, 3), FUN = function(x) {  
  paste0("ID", x)  
})
```

```
> [[1]]  
> [1] "ID1"  
>  
> [[2]]  
> [1] "ID2"  
>  
> [[3]]  
> [1] "ID3"
```

Limitation of `lapply`:

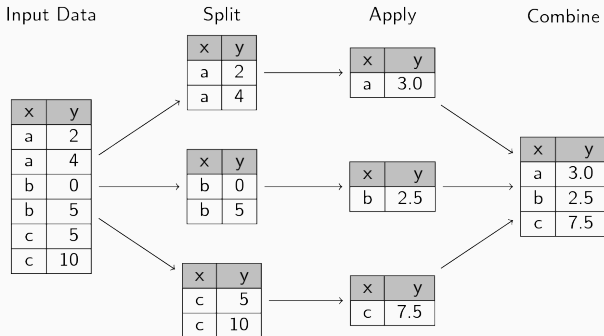
Only a single list/vector can be supplied as input. `Map` is a generalization of `lapply`! It is usually needed less often but a very powerful tool.

Split & Apply & Combine

A common use case for the apply-family is the **Split & Apply & Combine** paradigm. Here, we want to perform the same analyses for various subgroups in our data set:

- **split** a data.frame or vector (`?split`)
- **apply** computations on each split (`?lapply`)
- **combine** the results (`?do.call`)

Split & Apply & Combine



Split & Apply & Combine

```
head(iris)
```

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

```
table(iris$Species)
```

```
>
>   setosa versicolor virginica
>     50       50       50
```

Split & Apply & Combine

Splitting the data set via a single (or multiple) grouping variables

```
data_list <- split(iris, f = iris$Species)
class(data_list)

> [1] "list"

length(data_list)

> [1] 3
```


Split & Apply & Combine

Apply the same computation to all data sets

```
out_list <- lapply(data_list, function(subdat) {  
  mod <- lm(Sepal.Length ~ Sepal.Width, data = subdat)  
  sum_mod <- summary(mod)  
  out <- c(Intercept = coef(mod)[[1]],  
    Slope = coef(mod)[[2]],  
    r2 = sum_mod$r.squared)  
  round(out, 3)  
})
```

Split & Apply & Combine

```
out_list[["virginica"]]
```

```
> Intercept      Slope      r2  
>      3.907      0.902      0.209
```

Split & Apply & Combine

Combine the results

```
do.call(rbind, out_list)
```

```
>           Intercept Slope    r2  
> setosa          2.639 0.690 0.551  
> versicolor      3.540 0.865 0.277  
> virginica       3.907 0.902 0.209
```

Exercises



Good programming practices

“Write code for humans, not for machines!”

Invest time in writing readable R-code.

- It will make collaborations easier
- It will make debugging easier
- It will make your analyses more reproducible

There is a complete *tidyverse* style-guide

<https://style.tidyverse.org/>.

Go easy on your eyes

- with spaces before and after: `- + / * = <- < == >`
- always use `<-` for assignments
- only use `=` in function calls
- use indentation (largely automatic in RStudio)
- `CamelCaseNames` vs `snake_case_names`
- be consistent!
- wrap long lines at column 70-80 (Rstudio)

White space

```
new_var=(var1*var2/2)-5/(var3+var4)
```

```
# versus
```

```
new_var <- (var1 * var2 / 2) - 5 / (var3 + var4)
```

Indentation

```
for(name in names){formula=as.formula(paste0("y~.",name))
fit<-lm(formula,data=my_data)
coefs[["name"]]=coef(fit)
print(name)
print(summary(fit))}
```

versus

```
for(name in names){
  formula <- as.formula(paste0("y~.", name))
  fit <- lm(formula, data = my_data)
  coefs[["name"]] <- coef(fit)
  print(name)
  print(summary(fit))
}
```

Wrap long lines

```
final_results <- data.frame(first_variable =  
  sqrt(results$mean_squared_error), second_variable =  
  paste0(results$condition, results$class, sep = ":"),  
  third_variable = results$bias)
```

versus

```
final_results <- data.frame(  
  first_variable = sqrt(results$mean_squared_error),  
  second_variable = paste0(results$condition,  
                           results$class, sep = ":"),  
  third_variable = results$bias)
```

Go easy on your mind

- use meaningful names: “self-explainable”
- always write the formal arguments in function calls (except the first)
- benefit from autocompletion (`<tab>`) \Rightarrow embrace longer names
- use `TRUE` and `FALSE` not `T` and `F`
- comment, comment, comment
 - NOT what (should be clear from the code)
 - but why
 - explain the reasoning, not the code

Use meaningful names

```
V <- myFun(m1_B)
```

```
# versus
```

```
RMSE_age_gender <- get_RMSE(lm_age_gender)
```

Programming advice

Use verbs for functions and nouns for other objects.

Write formal arguments

Benefit from auto completion using tab

```
m1_B <- lm(outcome ~ age*gender,  
            exp1, condition_1, freq)
```

versus

```
lm_age_gender <- lm(outcome ~ age * gender,  
                    data = exp1,  
                    subset = condition_1,  
                    weights = freq)
```

Comment, comment, comment

```
## Start every Rscript with a comment that explains
##  what the code in the script does, why it does
##  this, and to which project it belongs.
##  Your future self will be very thankful!
##
## Mention which packages you are using in this Rscript.

## Use sections to separate chunks -----

## Maybe even subsections =====

## Recode variables so that missings are coded as "NA"
dat[dat %in% c(99, 999)] <- NA # missings coded 99 or 999
```

Keep your code slim

Try to limit your *package-dependencies*.

Only load `library()` the packages that you absolutely need. If you are only using `dplyr`, it does not make sense to load the complete `tidyverse`.

Controversial: when possible, use the `::` operator (and consider not loading the package). `<package>::<function>`

- explicit dependencies
- less name conflicts

Never Attach

Forget about `attach()`!

Don't use it, unless you completely understand what happens (see `?attach`).

Use `with(data.frame, expression)` instead.

```
# using with()
n <- 2e+4
data <- data.frame(x = runif(n),
                   y = runif(n),
                   z = seq_len(n))
result <- with(data, exp(x) / log(z) + 5 * sqrt(y))
```

Writing code is error prone. Incorporate tests and checks in your workflow.

- minimal examples
- write tests and checks
- helpful packages: `testthat`, `RUnit`, `testit`, ...

Computing speed can become an issue. Avoid common pitfalls:

- don't grow, but replace
- vectorize where possible
- check the computing speed

?system.time, microbenchmark or profiling tools

```
n <- 2e+4  
data <- data.frame(x = runif(n),  
                  y = runif(n),  
                  z = seq_len(n))
```

Don't grow!

```
system.time({  
  new_data <- NULL  
  
  for(row_nr in seq_len(NROW(data))){  
    new_data <- cbind(  
      data[row_nr,],  
      result = exp(data$x[row_nr]) /  
        log(data$z[row_nr]) +  
        5 * sqrt(data$y[row_nr]))  
  }  
})
```

```
>      User      System verstrichen  
>      1.85      0.00      1.86
```

Replace!

```
system.time({  
  n_rows <- dim(data)[1]  
  data$result <- rep(NA, n_rows)  
  
  for(row_nr in seq_len(n_rows)){  
    data$result[row_nr] <- exp(data$x[row_nr]) /  
      log(data$z[row_nr]) +  
      5 * sqrt(data$y[row_nr])  
  }  
})
```

```
>      User      System verstrichen  
>      0.25      0.01      0.28
```

Vectorize!

```
system.time({  
  data$result <- exp(data$x) / log(data$z) +  
    5 * sqrt(data$y)  
})
```

```
>      User      System verstrichen  
>      0      0      0
```

Speed

Compare the speed of different implementations using:

`microbenchmark::microbenchmark`

```
get_mean1 <- function(x){  
  weight <- 1/length(x)  
  out <- 0  
  for(i in seq_along(x)){  
    out <- out + x[i] * weight  
  }  
  return(out)  
}
```

```
get_mean2 <- function(x){  
  sum(x)/length(x)  
}
```

Compare the speed of different implementations using:

```
microbenchmark::microbenchmark
```

```
x <- rnorm(500)
microbenchmark::microbenchmark(
  mean(x), get_mean1(x), get_mean2(x))
```

> Unit: nanoseconds

	expr	min	lq	mean	median	uq	max	neval
>	mean(x)	2100	2200	3004	2400	2500	16100	100
>	get_mean1(x)	13600	13800	38708	14000	15100	2422000	100
>	get_mean2(x)	600	700	10133	800	800	930000	100

Programming advice

Don't worry about speed before it becomes an issue.

Wrap Up

General Advice

- Investing time in learning R pays off
- It's a steady learning curve
- Learn from masters
- Rewrite important code - the first attempt is usually not the best approach

General R Advice

- Document well
- Use a consistent style
- Write functions
- Split long functions in smaller ones
- Write wrappers
- Use Iteration (don't copy paste)
- Use matrix operations and vectorized functions instead of loops
- Use git

R Resources

- Advanced R Ed. 1 (<http://adv-r.had.co.nz/>)
- Advanced R Ed. 2 (<https://adv-r.hadley.nz/>)
- R Inferno (https://www.burns-stat.com/pages/Tutor/R_inferno.pdf)
- R Packages (<https://r-pkgs.org/>)

Thank you for your attention!

Thank you for your attention!

Questions? Remarks?