Advanced Programming with R

Dries Debeer & Benjamin Becker

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Zurich University

Introduction

Introduction

Who are we?

Dries Debeer

Senior Researcher at itec (imec research group at KU Leuven) scDIFtest, permimp, eatATA, mstDIF

dries.debeer@kuleuven.be

Benjamin Becker

Researcher at IQB (Statistics Department)
eatGADS, eatDB, eatATA,
pisaRT

b.becker@iqb.hu-berlin.de

Introduction

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?

What do we expect from you?

You ...

- are a frequent R user (e.g. for data wrangling/analyses)
- have a rough understanding of R as a programming language
- have already written some R functions yourself
- are interested in learning more about the intricacies of R

Goal of this workshop

A deeper dive into R as a Programming language

- Better understanding of how R works as a programming language
- Better understanding of how larger programming projects can/should be structured
- Practical Git skills
- Practical R package building skills

Agenda

- Scoping & Environments
- Functionals & Split-Apply Paradigm

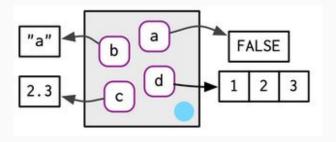
Lunch Break

- Object Orientation (S3)
- Packages & Version Controlling

Scoping & Environments

Environments

Like boxes, containing objects.



A bit simplified: If a function is called, its own environment is created with its parent being the environment from which it was called.

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Environments

```
simple_fun <- function(){</pre>
  a <- 1
  b <- "a"
  environment()
a <- simple_fun()
rlang::env_print(a)
# <environment: 000000013C6E640>
# parent: <environment: global>
 bindings:
# * b: <chr>
# * a: <dbl>
```

Scoping

Where does R find things?

- Argument matching (name, place...)
- Current environment
- Parent environment

Programming advice

Keep it simple, this can create chaos!

Scoping

```
add_things2 <- function(x) {
 x + 10 + y
add_things2(2)
# Error in add_things2(2): object 'y' not found
y <- 100
add_things2(2)
```

[1] 112

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
- ..

apply-family

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

apply-family

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

- lapply vector / list → list
- sapply vector / list → vector (matrix)
- ullet apply matrix / array / data.frame o vector (matrix)
- tapply, by
- mapply, Map
- rapply, eapply, vapply

app1y-family

A popular alternative from the tidy-verse: purrr

- map vector / list \rightarrow list
- ullet map2 multiple vectors / lists o vector (matrix)
- ..

apply-family

Our focus: lapply and Map

Why?

- Consistent output
- Fast
- No dependencies
- Understanding R basics

lapply takes mainly two arguments

X the input list/vector

FUN the function that should be repeatedly applied

```
example_list \leftarrow 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
```

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

```
example_list \leftarrow 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
```

We can use our own functions as input.

```
dropNAs <- function(x) {</pre>
  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
```

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"
```

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.

Map

Works very similar to lapply, with a few differences:

- Multiple input lists/vectors
- The list input should be named explicitly
- The order of the function and the list-input is switched

```
list1 <- list(mtcars[1:2, 1:3], iris[1:2, c(1, 2, 5)])
list2 <- list(mtcars[3:4, 1:3], iris[3:4, c(1, 2, 5)])
Map(rbind, x = list1, y = list2)</pre>
```

Map

```
[[1]]
#
                 mpg cyl disp
  Mazda RX4
                21.0
                       6 160
 Mazda RX4 Wag 21.0
                       6 160
                22.8 4 108
  Datsun 710
  Hornet 4 Drive 21.4
                       6
                          258
#
  [[2]]
#
    Sepal.Length Sepal.Width Species
# 1
             5.1
                        3.5
                             setosa
# 2
            4.9
                        3.0
                             setosa
# 3
            4.7
                        3.2
                             setosa
# 4
            4.6
                        3.1
                              setosa
```

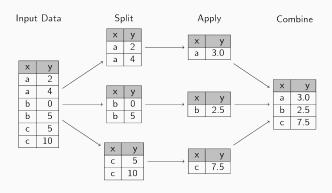
Again, anonymous functions can be supplied as input:

```
list1 <- list(mtcars[1:2, 1:3], iris[1:2, c(1, 2, 5)])
list2 <- list(mtcars[3:4, 1:3], iris[3:4, c(1, 2, 5)])

Map(function(x, y) {
   rbind(x, y)
   },
   x = list1, y = list2)</pre>
```

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 (?sapply, ?do.call)



```
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
                                      1.4
                         3.6
                                                   0.2 setosa
                                       1.7
# 6
             5.4
                         3.9
                                                   0.4 setosa
table(iris$Species)
#
#
      setosa versicolor virginica
#
          50
                     50
                                 50
```

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</pre>
```

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)
})</pre>
```

```
out_list[["virginica"]]
# Intercept Slope r2
# 3.907 0.902 0.209
```

Combine the results

Exercises



Object Oriented Programming

(S3)

Object Oriented Programming

Why?

- User-friendly: same function for different objects (summary())
- Coder-friendly: implementation can depends on object
- Coder-friendly: easier to maintain, extend

Object Oriented Programming

Basics

- a *class* is a definition
- an object is an *instance* of a class.
- a method is a procedure that behaves differently depending of the class it is applied to.
- *inheritance*: classes are organized in hierarchy. "is-a-type-of"-relation.

Object Oriented Programming in R

- S3
- S4
- RC
- R6
- ..

Compromise between interactive use, functional programming and object-oriented programming.

- "naming conventions"
- used in base R
- flexible: new classes, new methods

- class-attribute
- generics and methods
- inheritance and dispatch

A new class is made by adding an arbitrary class attribute to an object.

```
object <- 1:10
class(object) <- "myClass"
attributes(object)

# $class
# [1] "myClass"</pre>
```

Very flexible! Use it wisely!

```
class(iris)
# [1] "data.frame"
iris[1:4, 1:3]
#
  Sepal.Length Sepal.Width Petal.Length
# 1
               3.5
         5.1
                            1.4
# 2
         4.9 3.0 1.4
# 3
         4.7
                3.2
                          1.3
         4.6
                3.1
                          1.5
# 4
```

Changing the class changes the behavior!

```
class(iris) <- "no data.frame"
class(iris)

# [1] "no data.frame"

iris[1:4, 1:3]

# Error in iris[1:4, 1:3]: incorrect number of dimensions</pre>
```

Good practice: constructor function

- defines the structure of the class
- should be used to create objects of that class

Write a separate validation-function for computationally intensive validation.

- methods for a class belong to generics
- when a generic is called for a specific class, the corresponing method for that class will be used. common generics are: print(), plot(), summary(), anova()
- same function, but different computation depending on object-class

```
body(print)
# UseMethod("print")
```

Creating a new method (for an existing generic):

```
print.myClass <- function(x, ...){</pre>
  cat("This is a myClass-print:\n")
  cat(round(c(nValues = length(x),
                 mean = mean(x),
                 SD = sd(x), 3, ...)
my_object <- 1:5
class(my_object) <- "myClass"</pre>
print(my_object)
# This is a myClass-print:
# 5 3 1.581
```

Good practices (enforced for packages on CRAN):

- A method must have all the arguments of the generic, including . . . if the generic does.
- A method must have arguments in exactly the same order as the generic.
- If the generic specifies defaults, all methods should use the same defaults.

Inspect the generic!

```
formalArgs(print)
# [1] "x" "..."

formalArgs(summary)
# [1] "object" "..."
```

Creating a new generic:

```
center <- function(x, ...)</pre>
  UseMethod("center")
center.myClass <- function(x, ...){</pre>
  print("centering myClass:\n")
  return(x - mean(x))
center(my_object)
# [1] "centering myClass:\n"
# This is a myClass-print:
# 5 0 1.581
```

S3 - Inheritance and Dispatch

Objects can have more than one class

```
my_model <- glm(as.factor(books) ~ pared, data = pisa,
                family = "binomial")
class(my_model)
# [1] "glm" "lm"
class(my_model) == "lm"
# [1] FALSE TRUE
inherits(my_model, "lm")
# [1] TRUE
```

Good practice: hierachical inheritance (subclass and superclass)

S3 - Inheritance and Dispatch

When a method is not available for a (sub)class, the next available method (i.e., for the supperclass) will be used.

```
"variable.names.glm" %in% methods(class = "glm")
# [1] FALSE
"variable.names.lm" %in% methods(class = "lm")
# [1] TRUE
variable.names(my_model)
# [1] "(Intercept)" "pared"
```

Exercises



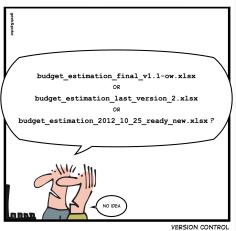
Version Controlling (Git + Github)

Version Controlling

- Motivation
- Setup
- Work flow
- Recommendations
- Resources

Motivation

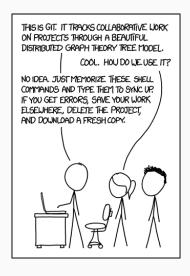
SIMPLY EXPLAINED



Motivation

- Implementation of long term change history
 - No ridiculous file names
 - No archive subfolder
 - Always perfect overview of file history and changes
- Collaborations
 - What has changed?
 - Who has changed it?
 - Documentation of changes
 - Parallel working possible (merging)

But...



Setup

See the workshop preparation materials

Work flow 1

Creating a repository

- Create an **online repository** (e.g. on Github)
 - Use an R specific .gitignore
 - Initialize with a short readme (.md)
- Clone the repository to your local machine
- An R-Project is added automatically to the existing repository

Exkurs: gitignore

- Plain text file
- Which files should not be tracked by git?
 - \rightarrow These then only exist locally in their current version!
- Options
 - Single files
 - Folder
 - Specific data types
 - Combinations of the above
- Use cases
 - Large files (Data, images, ...)
 - Auxiliary files (e.g. created during latex compilation)

Work flow 2

Working with an existing repository

- Before working: Synch your local repo (Pull or clone)
- ullet Perform changes in your local repository o Create/modify/delete files
- Stage your changes
- Commit your changes (aka new version)
- Push your changes (online repository is updated)

Exkurs: mergen

Conflicts between different updated versions

- Common when working collaborativley
- ullet Own discrepancies between different machines o Git communicates these and indicates conflicts
- Select the desired changes
- Stage selection, commit and push

Exkurs: Branches

Multiple parallel versions of a project within one repository

- e.g. one stable and one development branch
- Only certrain modifications should be made in the stable branch
- Careful: RStudion GUI has limited support for this

Recommendations

- Keep it simple!
 - If not necessary, no branches/forks/pull requests
- Have meaningful commits
- Keep it lean (no big files)

Resources

Git (+ R) Resources

- Small Intro (https://r-bio.github.io/intro-git-rstudio/)
- Happy Git with R (https://happygitwithr.com/)
- R Packages and Git (https://r-pkgs.org/git.html)
- Git Book (http://git-scm.com/book/en/v2)

R Packages

Motivation

- It is incredibly easy!
- It makes you code easier accessible (for others and yourself)
- It gives a great framework for documenting your code
- There are great tools for testing your code
- It is a form of scientific output (packages can be cited)

Setup

Use usethis and/or RStudio to set up everything.

- Create a Github Repository and clone it locally
- Create an R project (-> R package) in the existing repository
- Use usethis if you want to create more specific architecture

R functions

Your actual code lives in the R folder. Organize your functions logically and avoid very long scripts.

Using other packages

If you want to use another package in your source code, add it to the Imports-Field in your description file and use its functions using package::function.

Documentation

Use roxygen2 to document your code and to manage your namespace.

Testing

Use testthat for automated testing. This has multiple advantages:

- Good test coverage serves is a quality attribute of a good and stable package
- modifying existing code becomes much easier
- Your code becomes more robust
- It helps you sleep at night

Resources

Writing R packages

- Extending R
 (https://r-bio.github.io/intro-git-rstudio/)
- R Packages (https://r-pkgs.org/)

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

Literature Recommendations

R Resources

- Advanced R Ed. 1 (http://adv-r.had.co.nz/)
- Advanced R Ed. 2 (https://adv-r.hadley.nz/)
- Notes on Functionals (https://www.stat.umn.edu/geyer/ 8054/notes/functional.html)
- R language definition (https://cloud.r-project.org/doc/manuals/r-release/R-lang.html)
- R Inferno (https: //www.burns-stat.com/pages/Tutor/R_inferno.pdf)
- R Packages (https://r-pkgs.org/)
- Clean Code (https://enos.itcollege.ee/~jpoial/oop/ naited/Clean%20Code.pdf)



Thank you for your attention!

Questions? Remarks?