

Programming with R/Advanced R

Dries Debeer & Benjamin Becker

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Agenda

Day 1

- Recap & Clean Code
- Functions (Introduction)
- Functions (Advanced)

Day 2

- Flow & Iteration
- Object oriented programming: S3
- Version Controlling

Open questions from day 1?

Functions II

Functions I

- Good functions?
- dot dot dot
- `on.exit()`
- Accessing the call
- Debugging

What makes a good function?

Pure functions!

- no side effects
- the only output is returned
- no dependency on global environment
- only input via arguments

Results in easier understanding and higher portability.

How can functions receive flexible numbers of inputs?

Examples:

- `sum()`
- `save()`
- ...

...

via dot dot dot (...)

```
add_all_things2 <- function(...) {  
  l <- list(...)  
  do.call(sum, l)  
}  
add_all_things2(2, 3, 5, 10)
```

[1] 20

on.exit()

Performing an action when the function terminates

```
add_things <- function(x, y) {  
  on.exit(cat("Sum of", x, "and", y))  
  x <- x + 20  
  x + y  
}  
out <- add_things(1, 2)
```

Sum of 21 and 2

```
out
```

```
[1] 23
```

Accessing the function call

Accessing the function call

```
showArgs <- function(x, y) {  
  match.call()  
}  
showArgs(1, 2)
```

```
showArgs(x = 1, y = 2)
```

Debugging

- `browser()`
- `traceback()`
- `options(error = recover)`
- `options(warn = 2)`

Also:

- `trace()` & `untrace()`
- `debug()` & `undebug()`, `debugonce()`

browser()

Inspecting a function interactively

```
some_function <- function(x, y) {  
  z <- x + y  
  browser()  
  z  
}  
some_function(x = 1, y = 5)
```

browser()

```
> some_function <- function(x, y) {  
+   z <- x + y  
+   browser()  
+   z  
+ }  
> some_function(x = 1, y = 5)  
Called from: some_function(x = 1, y = 5)  
Browse[1]> |
```

browser()

Navigating within a browser:

ls() Show existing objects in the current environment

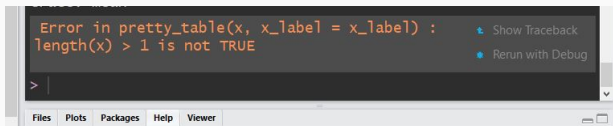
c Exit the browser and continue execution

Q Exit the browser, return to top level

where Show call stack

traceback()

Understanding the call stack:



traceback()

Understanding the call stack:

```
Error in pretty_table(x, x_label = x_label) :  
length(x) > 1 is not TRUE  
13. stop(simpleError(msg, call = if (p <- sys.parent(1L)) sys.c  
    all(p)))  
12. stopifnot(length(x) > 1)  
11. pretty_table(x, x_label = x_label)  
10. pretty_statistics(sub_dat$cy1, x_label = "cy1")  
9. FUN(data[x, , drop = FALSE], ...)  
8. FUN(X[[i]], ...)  
7. lapply(X = ans[index], FUN = FUN, ...)  
6. tapply(seq_len(32L), list('mtcars$carb' = c(4, 4, 1, 1, 2,  
    1,  
    4, 2, 2, 4, 4, 3, 3, 3, 4, 4, 4, 1, 2, 1, 1, 2, 2, 4, 2, 1,  
    2,  
    2, 4, 6, 8, 2)), function (x)  
    FUN(data[x, , drop = FALSE], ...), simplify = TRUE)  
5. eval(substitute(tapply(seq_len(nd), IND, FUNx, simplify = s  
    implify)),  
    data)  
4. eval(substitute(tapply(seq_len(nd), IND, FUNx, simplify = s  
    implify)),  
    data)  
3. structure(eval(substitute(tapply(seq_len(nd), IND, FUNx, si  
    mply = simplify)),  
    data), call = match.call(), class = "by")  
2. by.data.frame(mtcars, mtcars$carb, function(sub_dat) {  
    pretty_statistics(sub_dat$cy1, x_label = "cy1")  
  })  
1. by(mtcars, mtcars$carb, function(sub_dat) {  
    pretty_statistics(sub_dat$cy1, x_label = "cy1")  
  })  
> |
```


Being able to chose an environment from the call stack:

```
# on
options(error = recover)

# off
options(error = NULL)
```

Being able to choose an environment from a call stack:

```
Error in pretty_table(x, x_label = x_label) : length(x) > 1 is not TRUE
Enter a frame number, or 0 to exit

1: by(mtcars, mtcars$carb, function(sub_dat) {
  pretty_statistics(sub_dat$cy1, x_label = "Cy1")
2: by.data.frame(mtcars, mtcars$carb, function(sub_dat) {
  pretty_statistics(sub_dat$cy1, x_label = "Cy1")
3: structure(eval(substitute(tapply(seq_len(nd), IND, FUNx, simplify = simplify))), data), call =
4: eval(substitute(tapply(seq_len(nd), IND, FUNx, simplify = simplify))), data)
5: eval(substitute(tapply(seq_len(nd), IND, FUNx, simplify = simplify))), data)
6: tapply(seq_len(32), list(mtcars$carb), c(4, 4, 1, 1, 2, 1, 4, 2, 2, 4, 4, 3, 3, 3, 4, 4, 4,
7: tapply(X = ans[index], FUN = FUN, ...)
8: FUN(X[[i]], ...)
9: FUN(data[x, , drop = FALSE], ...)
10: #2: pretty_statistics(sub_dat$cy1, x_label = "Cy1")
11: #3: pretty_table(x, x_label = x_label)
12: #2: stopifnot(length(x) > 1)

Selection: |
```

Warnings

Turning warnings into errors

```
# on
options(warn = 2)

# off
options(warn = 1)
```

Exercises



Functionals

A functional is a function that takes another function as an argument.

Focus on the `apply`-family. These functions *apply* a function repeatedly.

Can be seen as an abstraction of a `for` loop, with the following advantages

- requires less code to write
- does not store intermediate results
- no need to replace / grow

Functionals

The most commonly used functionals 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`

All of which have an argument that should be a function.

lapply

Data.frames are lists

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

```
# $Sepal.Length
```

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

```
#
```

```
# $Sepal.Width
```

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

```
#
```

```
# $Petal.Length
```

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

```
#
```

```
# $Petal.Width
```

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

```
#
```

```
# $Species
```

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

lapply

- an anonymous function can be used
- any type of element can be used
- other arguments can be passed through

```
lapply(c(min, median, max), FUN = function(fun, x) {  
  fun(x)  
}, x = 2:8)
```

```
# [[1]]  
# [1] 2  
#  
# [[2]]  
# [1] 5  
#  
# [[3]]  
# [1] 8
```


supply

- wrapper around lapply
- if possible, the output is combined into an atomic vector or matrix

```
supply(airquality, FUN = sd)
```

```
#      Ozone  Solar.R      Wind      Temp      Month      Day  
#         NA        NA 3.523001 9.465270 1.416522 8.864520
```

```
supply(airquality, FUN = quantile, prob = c(.1, .9),  
       na.rm = TRUE)
```

```
#      Ozone  Solar.R  Wind Temp Month Day  
# 10%      11     47.5  5.82 64.2     5   4  
# 90%      87    288.5 14.90 90.0     9  28
```

apply

- for objects with dimension (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_matrix <- matrix(1:6, nrow = 2)
apply(my_matrix, c(1, 2),
      function(value) value^2)    # apply per row and column
```

```
#      [,1] [,2] [,3]
# [1,]    1    9   25
# [2,]    4   16   36
```

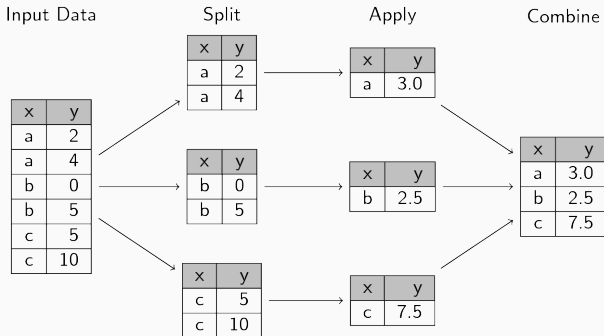
```
apply(airquality, 2, median)
```

```
#   Ozone Solar.R   Wind   Temp   Month   Day
#    NA      NA    9.7   79.0    7.0   16.0
```

Split & Apply & Combine

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

Split & Apply & Combine



Exercises



Object Oriented Programming (S3)

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.

- 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`

S3 - class

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"
```

Very flexible! Use it wisely!

S3 - class

```
class(iris)
```

```
# [1] "data.frame"
```

```
iris[1:4, 1:3]
```

```
#   Sepal.Length Sepal.Width Petal.Length
# 1           5.1           3.5           1.4
# 2           4.9           3.0           1.4
# 3           4.7           3.2           1.3
# 4           4.6           3.1           1.5
```

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
```

Good practice: *constructor function*

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

```
myClass <- function(element1, element2){  
  # validation of the elements  
  structure(list(element1),  
            attribute1 = element2,  
            class = "myClass")  
}
```

Write a separate validation-function for computationally intensive validation.

S3 - Generics and Methods

- *methods* for a class belong to *generics*
- when a generic is called for a specific class, the corresponding 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")
```

S3 - Generics and Methods

Creating a new method (for an existing generic):

```
print.myClass <- function(x, ...){  
  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"  
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.

S3 - Generics and Methods

Inspect the generic!

```
formalArgs(print)
```

```
# [1] "x"    "..."
```

```
formalArgs(summary)
```

```
# [1] "object" "..."
```

S3 - Generics and Methods

Creating a new generic:

```
center <- function(x, ...)  
  UseMethod("center")  
  
center.myClass <- function(x, ...){  
  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: hierarchical 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 superclass) 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"
```

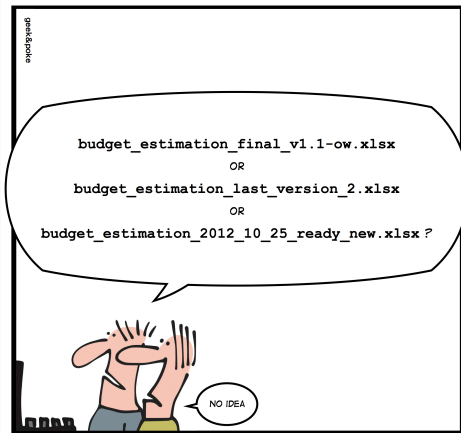
Exercises



Version Controlling (Git + Github)

- Motivation
- Setup
- Work flow
- Recommendations
- Resources

SIMPLY EXPLAINED



VERSION CONTROL

Motivation

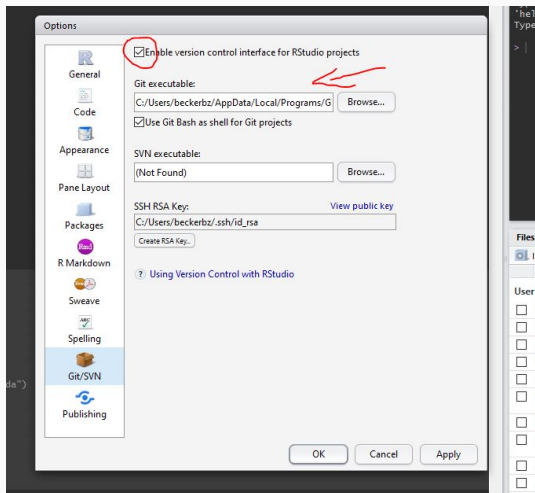
- Implementation of long term change history
 - No ridiculous file names
 - No archive subfolder
 - Always perfect overview of file history and changes
- Collaborations
 - What has changed?
 - Who has changed it?
 - Documentation of changes
 - Parallel working possible (merging)

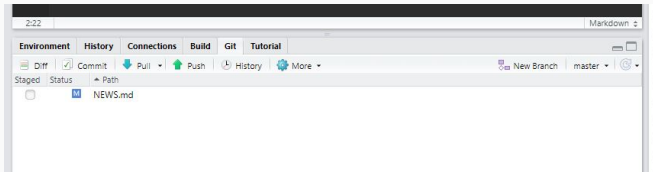
But...



Requirements

- Install git
- (optional) Install/Setup GUI for git (RStudio, Gitkraken, ...)
- Setup account for Github/Bitbucket/Gitlab/...
- Connect everything





Creating a repository

- Create an online repository (e.g. on Github)
 - Use an R specific .gitignore
 - Initialize with a short readme
- Clone the repository to your local machine
- (optional) Place an R project in the existing repository

Working with a repository

- Before working: Synch your local repo (**Pull**)
- Perform changes in your local repository
- **Stage** your changes
- **Commit** your changes (aka new version)
- **Push** your changes

Recommendations

- Keep it simple!
 - No branches/forks/pull requests
- Have meaningful commits
- Keep it lean (no big files)

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>)

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/>)
- Clean Code (<https://enos.itcollege.ee/~jpoial/oop/naited/Clean%20Code.pdf>)

Thank you for your attention!

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Questions? Remarks?