Advanced Programming with R

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15. October 2021

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Introduction

Introduction

Who are we?

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Introduction

Who are you?

1. Occupation, employer?
2. Previous knowledge and experience
    - with R?
    - 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/plots)
- have a rough understanding of R as a programming language
  $\rightarrow$ e.g. you 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

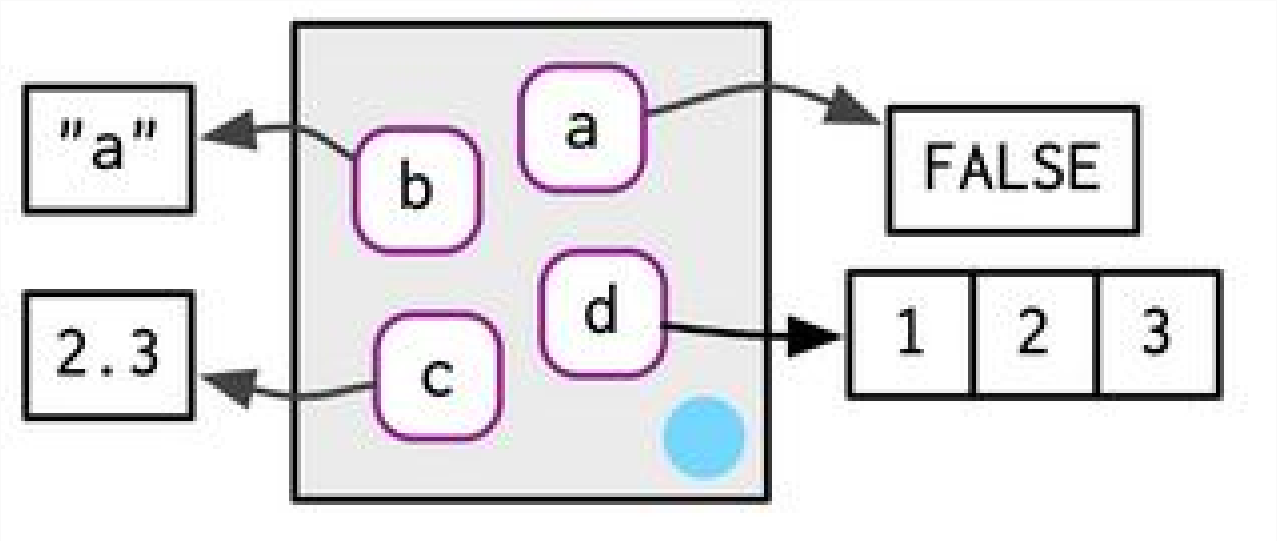
- *Lunch Break* -

- 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.

Environments

```
simple_fun <- function(){
  a <- 1
  b <- "a"
  environment()
}
a <- simple_fun()
rlang::env_print(a)

# <environment: 00000000185DBA58>
# 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 $\rightarrow$ list
- `sapply` vector / list $\rightarrow$ vector (matrix)
- `apply` matrix / array / data.frame $\rightarrow$ vector (matrix)
- `tapply`, `by`
- `mapply`, `Map`
- `rapply`, `eapply`, `vapply`

`apply`-family

A popular alternative from the tidyverse: `purrr`

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

`apply`-family

Our focus: `lapply` and `Map`

Why?

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

lapply

`lapply` takes mainly two 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
```

lapply

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"
```

lapply

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)
```

Map

```
# [[1]]
#                   mpg cyl disp
# Mazda RX4         21.0   6  160
# Mazda RX4 Wag     21.0   6  160
# Datsun 710        22.8   4  108
# 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
```

Map

Again, anonymous functions can be supplied as input:

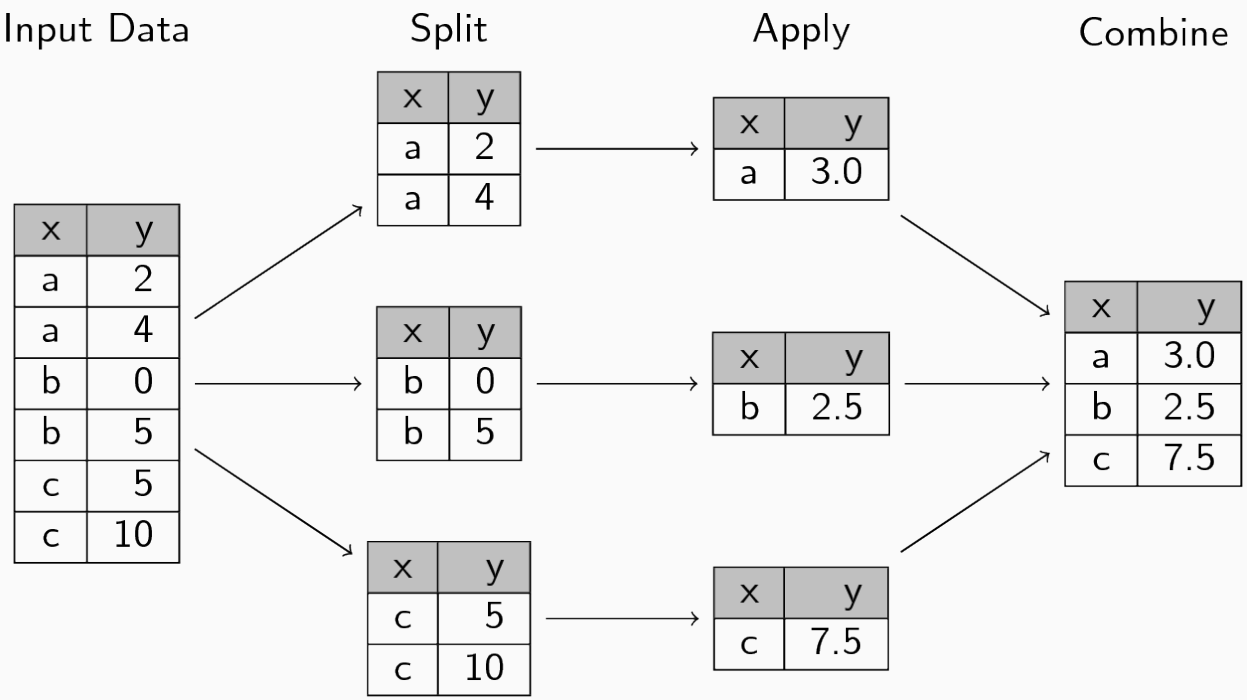
```
list1 <- list(mtcars[1:2, 1:3], iris[1:2, c(1, 2, 5)])
list2 <- list(mtcars[3:4, 1:3], iris[3:4, c(1, 2, 5)])

Map(function(x, y) {
  rbind(x, y)
  },
  x = list1, y = list2)
```

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 (`?sapply`, `?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

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
- ...

S3

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

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

S3

- `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
```

S3 - class

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
```

S3 - class

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 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")
```

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
```

S3 - Generics and Methods

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: 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"
```

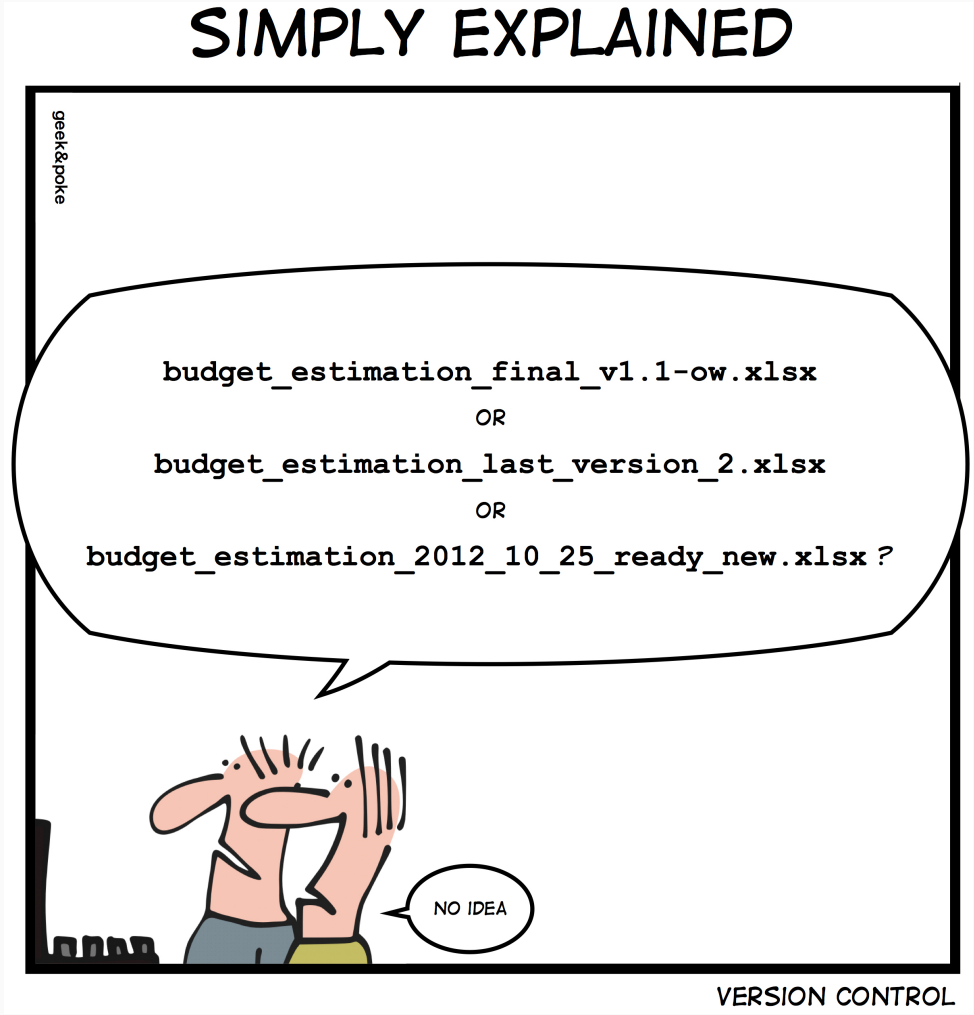
Exercises

Version Controlling (Git + Github)

Version Controlling

- Motivation
- Setup
- Work flow
- Recommendations
- Resources

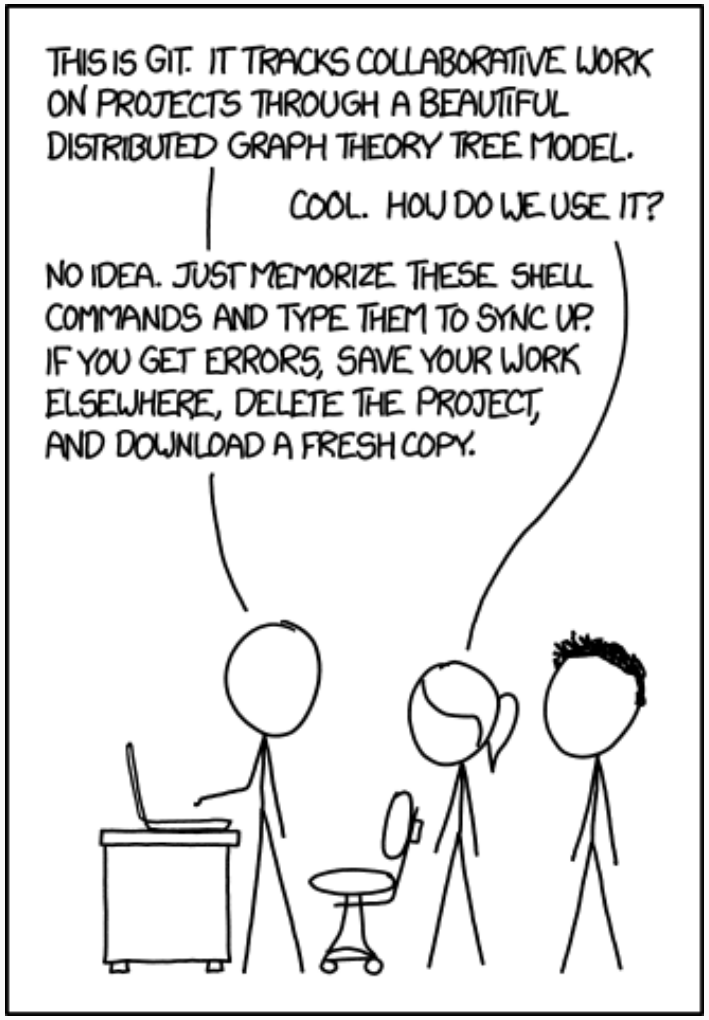
Motivation


SIMPLY EXPLAINED
geek&poke
budget_estimation_final_v1.1-ow.xlsx
OR
budget_estimation_last_version_2.xlsx
OR
budget_estimation_2012_10_25_ready_new.xlsx ?
NO IDEA
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...


THIS IS GIT. IT TRACKS COLLABORATIVE WORK ON PROJECTS THROUGH A BEAUTIFUL DISTRIBUTED GRAPH THEORY TREE MODEL.
COOL. HOW DO WE USE IT?
NO IDEA. JUST MEMORIZE THESE SHELL COMMANDS AND TYPE THEM TO SYNC UP. IF YOU GET ERRORS, SAVE YOUR WORK ELSEWHERE, DELETE THE PROJECT, AND DOWNLOAD A FRESH COPY.

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

Excursion: 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**)
- Perform changes in your local repository
  $\rightarrow$ Create/modify/delete files
- **Stage** your changes
- **Commit** your changes (aka new version)
- **Push** your changes (online repository is updated)

Excursion: mergen

Conflicts between different updated versions

- Common when working collaborativley
- Discrepancies between your own different local repos $\rightarrow$ Git communicates these and indicates conflicts
- Select the desired changes
- Stage selection, commit and push

Excursion: 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
- **Note**: RStudio 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 your code easier accessible (for others and yourself)
- It provides a great framework for documenting your code
- It provides 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 regular Github Repository
- Clone the repository regularly
- Use `usethis::use_package(getwd())` to create the minimal package structure
- Use `usethis` if you want to add more specific architecture

R functions

Your actual code lives in the `R` folder.

- Write small functions which do one specific thing
- Organize your functions logically
- 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 as 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

- Writing R Extensions (`https://cloud.r-project.org/doc/manuals/r-release/R-exts.html`)
- R Packages (`https://r-pkgs.org/`)

Wrap Up

General Advice

- Try to always learn new things about R and / or programming
- Try to automate as much as possible
- If you are re-using code regularly, write a package!
- Learn from masters
- Rewrite important code - the first attempt is usually not the best approach

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!

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Questions? Remarks?