The Surgical Informatics Cookbook

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2019-09-27

Contents

Chapter 1

Introduction

1.1 How to contribute

(Steps 1. to 5. only need to be done once - to set-up.)

1. Connect your RStudio and GitHub using these instructions, only up to "Create new project" is necessary here (the repository/project already exists): https://www.datasurg.net/2015/07/13/rstudio-and-github/

2. Get your GitHub account added to the surgicalinformatics organisation on GitHub (ask Riinu/Ewen): https://github.com/SurgicalInformatics

3. Open the terminal on argonaut, go to your home folder (just `cd` will default to taking you home). If the prompt says `username@argonaut:~$` that means you're home - `~` means user's home.

4. In the terminal, do `git clone https://github.com/SurgicalInformatics/cookbook.git`

5. Look at the Files tab - a new folder called `cookbook` should have appeared at the bottom. Click on it and open the cookbook.Rproj file.

6. Add your thing by editing the appropriate .Rmd file - there's one for each chapter. **click on More - Clean All** (if you don't do this you may be able to compile the book with code that won't work at a subsequent clean build which can be trickier to debug). Use the Build tab to Build your changes into a book.

7. If anyone has pushed since you cloned/last pulled (hopefully they've not been working on the exact same chapter): Make sure you **click on More - Clean All** (as above). Then Pull from the Git tab. This only cleans the output files - html and PDF, it will not touch the changes you've made in the .Rmd file.

8. Then Build Book again - this will include the new changes you pulled as well as your changes.

9. Git tab - commit everything, Push quickly before anyone else does or you'll have to go back to step 7. You can check for new pushed commits here: https://github.com/SurgicalInformatics/cookbook/commits/master Alternatively there's no harm in clicking the Pull button again - it should then say "Already up-to-date".

   Pro tip: instead of clicking on every single file in the Git tab, go to the terminal, `cd cookbook` to go to the project folder if still home, and do `git add -A` which is the same thing. Still need to Commit though!

10. Have fun!

1.2 Rules of posting

Rules of how to post here.

1.3 Indexing

1.3.1 Index

Bold index headings:
`\index{linear regression@\textbf{linear regression}}` (ticks in .Rmd file are excluded when actually using)

Sub-entries of bold headings:
`\index{linear regression@\textbf{linear regression}!diagnostics}`

Stand-alone entries:
`\index{linear regression}`

1.3.2 Chapter and section references

You can label chapter and section titles using `{#label}` after them, e.g., we can reference Chapter `\@ref(intro)` (ticks in .Rmd are excluded when actually using). If you do not manually label them, there will be automatic labels anyway, e.g., Chapter `\@ref(methods)`.

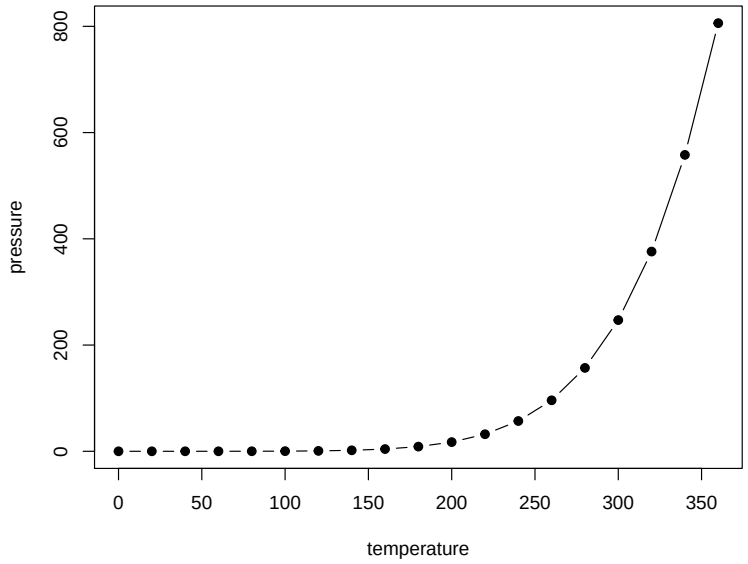


Figure 1.1: Here is a nice figure!

1.3.3 Figure and table references

Figures and tables with captions will be placed in `figure` and `table` environments, respectively.

```
par(mar = c(4, 4, .1, .1))
plot(pressure, type = 'b', pch = 19)
```

Reference a figure by its code chunk label with the `fig:` prefix, e.g., see Figure `\@ref(fig:nice-fig)`. Similarly, you can reference tables generated from `knitr::kable()`, e.g., see Table `\@ref(tab:nice-tab)`.

```
knitr::kable(
  head(iris, 20), caption = 'Here is a nice table!',
  booktabs = TRUE
)
```

1.3.4 Citations

You can write citations, too. For example, we are using the **bookdown** package (Xie, 2019) in this sample book, which was built on top of R Markdown and **knitr** (Xie, 2015).

Table 1.1: Here is a nice table!

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa
4.6	3.4	1.4	0.3	setosa
5.0	3.4	1.5	0.2	setosa
4.4	2.9	1.4	0.2	setosa
4.9	3.1	1.5	0.1	setosa
5.4	3.7	1.5	0.2	setosa
4.8	3.4	1.6	0.2	setosa
4.8	3.0	1.4	0.1	setosa
4.3	3.0	1.1	0.1	setosa
5.8	4.0	1.2	0.2	setosa
5.7	4.4	1.5	0.4	setosa
5.4	3.9	1.3	0.4	setosa
5.1	3.5	1.4	0.3	setosa
5.7	3.8	1.7	0.3	setosa
5.1	3.8	1.5	0.3	setosa

Chapter 2

Snippets

Random useful snippets that do not fit anywhere else.

2.1 Creating Reproducible R Examples to Share in the Group (binder, holepunch and docker)

When asking for help with R code having a reproducible example is crucial (some mock data that others can use along with your code to reproduce your error). Often this can be done easily with creation of a small tibble and posting of the code on slack but sometimes it requires more complex data or the error is due to something in the Linux system in which RStudio server is hosted. For example if the `cairo` package for Linux isn't installed then plots don't work. The `holepunch` package helps to reproduce examples like these (not suitable for projects with confidential data).

2.1.1 Create Basic Reproducible Examples

The three main parts of the reproducible example (reprex) in Surgical Informatics are 1. packages, 2. small dataset and 3. code. Other things like R version and Linux version can be assumed as we all use one of only a few servers.

If you have a small (and confidential) set of data in a tibble or data frame called `my_data` and want it to be easily copied run: `dput(droplevels(my_data))`. This will print out code in the console that can be copy-pasted to reproduce the data frame. Alternatively use the `tibble` or `tribble` functions to create it from scratch (this is preferable for simple datasets). Then copy in the packages

and finally the code (ideally the least amount possible to generate the error) and share with the group e.g.:

```
library(tidyverse)

# Output generated from dput(droplevels(my_data))
data = structure(list(a = c(1, 2, 3), b = c("a", "b", "c"), c = 10:12), .Names = c("a"
"b", "c"), row.names = c(NA, -3L), class = c("tbl_df", "tbl",
"data.frame"))

data %>%
  mutate(newvar = a /b)
```

```
## Error in a/b: non-numeric argument to binary operator
```

2.1.2 `holepunch` - Complex Reproducible Examples

From your project with data you are happy to make public make sure you are backed up to `git` and `GitHub`. See the relevant chapter on how to do this. Then run the following:

```
# Holepunch testing

remotes::install_github("karthik/holepunch")

library(holepunch)
write_compendium_description(package = "Title of my project",
                             description = "Rough description of project or issue")

write_dockerfile(maintainer = "SurgicalInformatics")

generate_badge()

build_binder()
```

The file will generate some text to copy into the top of a `README.md` file. It will look like:

```
<!-- badges: start -->
[![Launch Rstudio Binder](http://mybinder.org/badge_logo.svg)](https://mybinder.org/v2/
<!-- badges: end -->
```

Now, whenever somebody clicks on the badge in the `README` on `GitHub` they will be taken to an RStudio server instance with all your files (excluding files listed in `.gitignore`), all the current versions of your package, all the current Linux packages and the current R version. They can then test your code in an near-identical environment to help identify the source of the error, their session

will time out after 10 minutes of inactivity or 12 hours since starting and will not save anything so should only be used for bug-testing or quick examples.

As this is a free version of RStudio server there is a limit to what is supported and it shouldn't be used for computationally-intensive processes.

And, as mentioned: **No confidential data.**

2.2 Working with CHIs

Here are 4 functions for CHIs that could even be put in a small package. The Community Health Index (CHI) is a population register, which is used in Scotland for health care purposes. The CHI number uniquely identifies a person on the index.

2.2.1 `chi_dob()` - Extract date of birth from CHI

Note `cutoff_2000`. As CHI has only a two digit year, need to decide whether year is 1900s or 2000s. I don't think there is a formal way of determining this.

```
library(dplyr)
chi = c("1009701234", "1811431232", "1304496368")
# These CHIs are not real.
# The first is invalid, two and three are valid.

# Cut-off any thing before that number is considered 2000s
# i.e. at cutoff_2000 = 20, "18" is considered 2018, rather than 1918.
chi_dob = function(.data, cutoff_2000 = 20){
  .data %>%
    stringr::str_extract(".{6}") %>%
    lubridate::parse_date_time2("dmy", cutoff_2000 = cutoff_2000) %>%
    lubridate::as_date() # Make Date object, rather than POSIXct
}

chi_dob(chi)
```

```
## [1] "1970-09-10" "1943-11-18" "1949-04-13"
```

```
# From tibble
tibble(chi = chi) %>%
  mutate(
    dob = chi_dob(chi)
  )
```

```
## # A tibble: 3 x 2
##   chi        dob
```

```
##   <chr>      <date>
## 1 1009701234 1970-09-10
## 2 1811431232 1943-11-18
## 3 1304496368 1949-04-13
```

2.2.2 `chi_gender()` - Extract gender from CHI

Ninth digit is odd for men and even for women. A test for even is `x modulus 2 == 0`.

```
chi_gender = function(.data){
  .data %>%
    stringr::str_sub(9, 9) %>%
    as.numeric() %>%
    {ifelse(. %% 2 == 0, "Female", "Male")}
}

chi_gender(chi)
```

```
## [1] "Male"   "Male"   "Female"
```

```
# From tibble
tibble(chi = chi) %>%
  mutate(
    dob = chi_dob(chi),
    gender = chi_gender(chi)
  )
```

```
## # A tibble: 3 x 3
##   chi        dob        gender
##   <chr>      <date>     <chr>
## 1 1009701234 1970-09-10 Male
## 2 1811431232 1943-11-18 Male
## 3 1304496368 1949-04-13 Female
```

2.2.3 `chi_age()` - Extract age from CHI

Works for a single date or a vector of dates.

```
chi_age = function(.data, ref_date, cutoff_2000 = 20){
  dob = chi_dob(.data, cutoff_2000 = cutoff_2000)
  lubridate::interval(dob, ref_date) %>%
    as.numeric("years") %>%
    floor()
}
```

```
# Today
chi_age(chi, Sys.time())
```

```
## [1] 49 75 70
```

```
# Single date
library(lubridate)
chi_age(chi, dmy("11/09/2018"))
```

```
## [1] 48 74 69
```

```
# Vector
dates = dmy("11/09/2018",
            "09/05/2015",
            "10/03/2014")
chi_age(chi, dates)
```

```
## [1] 48 71 64
```

```
# From tibble
tibble(chi = chi) %>%
  mutate(
    dob = chi_dob(chi),
    gender = chi_gender(chi),
    age = chi_age(chi, Sys.time())
  )
```

```
## # A tibble: 3 x 4
##   chi        dob        gender   age
##   <chr>      <date>     <chr>  <dbl>
## 1 1009701234 1970-09-10 Male      49
## 2 1811431232 1943-11-18 Male      75
## 3 1304496368 1949-04-13 Female    70
```

2.2.4 `chi_valid()` - Logical test for valid CHI

The final digit of the CHI can be used to test that the number is correct via the modulus 11 algorithm.

```
chi_valid = function(.data){
  .data %>%
    stringr::str_split("", simplify = TRUE) %>%
    .[, -10] %>%              # Working with matrices hence brackets
    apply(1, as.numeric) %>%  # Convert from string
    {seq(10, 2) %*% .} %>%    # Multiply and sum step
    {. %% 11} %>%             # Modulus 11
    {11 - .} %>%              # Substract from 11
```

```
    dplyr::near(              # Compare result with 10th digit.
      {stringr::str_sub(chi, 10) %>% as.numeric()}
    ) %>%
    as.vector()
}

chi_valid(chi)
```

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

```
# From tibble
tibble(chi = chi) %>%
  mutate(
    dob = chi_dob(chi),
    gender = chi_gender(chi),
    age = chi_age(chi, Sys.time()),
    chi_valid = chi_valid(chi)
  )
```

```
## # A tibble: 3 x 5
##   chi        dob        gender   age chi_valid
##   <chr>      <date>     <chr>  <dbl> <lgl>
## 1 1009701234 1970-09-10 Male      49 FALSE
## 2 1811431232 1943-11-18 Male      75 TRUE
## 3 1304496368 1949-04-13 Female    70 TRUE
```

2.3 Working with dates

2.3.1 Difference between two dates

I always forget how to do this neatly. I often want days as a numeric, not a lubridate type object.

```
library(lubridate)
date1 = dmy("12/03/2018", "14/05/2017")
date2 = dmy("11/09/2019", "11/04/2019")

interval(date1, date2) %>%
  as.numeric("days")
```

```
## [1] 548 697
```

2.3.2 Lags

This is useful for calculating, for instance, the period off medications. Lags are much better than long to wide solutions for this.

```
library(tidyverse)
library(lubridate)
id = c(2, 2, 2, 2, 3, 5)
medication = c("aspirin", "aspirin", "aspirin", "tylenol", "lipitor", "advil")
start.date = c("05/01/2017", "05/30/2017", "07/15/2017", "05/01/2017", "05/06/2017", "05/28/2017"
stop.date = c("05/04/2017", "06/10/2017", "07/27/2017", "05/15/2017", "05/12/2017", "06/13/2017")
df = tibble(id, medication, start.date, stop.date)
df
```

```
## # A tibble: 6 x 4
##      id medication start.date stop.date
##   <dbl> <chr>      <chr>      <chr>
## 1     2 aspirin    05/01/2017 05/04/2017
## 2     2 aspirin    05/30/2017 06/10/2017
## 3     2 aspirin    07/15/2017 07/27/2017
## 4     2 tylenol    05/01/2017 05/15/2017
## 5     3 lipitor    05/06/2017 05/12/2017
## 6     5 advil      05/28/2017 06/13/2017
```

```
df %>%
  mutate_at(c("start.date", "stop.date"), lubridate::mdy) %>% # make a date
  arrange(id, medication, start.date) %>%
  group_by(id, medication) %>%
  mutate(
    start_date_diff = start.date - lag(start.date),
    medication_period = stop.date-start.date
  )
```

```
## # A tibble: 6 x 6
## # Groups:   id, medication [4]
##    id medication start.date stop.date  start_date_diff medication_period
##   <dbl> <chr>      <date>     <date>     <drtn>          <drtn>
## 1     2 aspirin    2017-05-01 2017-05-04 NA days         3 days
## 2     2 aspirin    2017-05-30 2017-06-10 29 days        11 days
## 3     2 aspirin    2017-07-15 2017-07-27 46 days        12 days
## 4     2 tylenol    2017-05-01 2017-05-15 NA days        14 days
## 5     3 lipitor    2017-05-06 2017-05-12 NA days         6 days
## 6     5 advil      2017-05-28 2017-06-13 NA days        16 days
```

Chapter 3

Methods

We describe our methods in this chapter.

Chapter 4

Machine learning

4.1 Deep learning

4.1.1 Pulling images from REDCap directly to argodeep

4.1.1.1 Original file names

```
library(REDCapR)
uri = "https://redcap.cir.ed.ac.uk/api/"
token = "" # API token here
record_list = 1:318
field_list = c("photo", "photo_2", "photo_3", "photo_4")
event_list = c("wound_concerns_arm_2", "questionnaire_1_arm_2",
               "questionnaire_2_arm_2", "questionnaire_3_arm_2")
directory = "wound_raw" # destination directory must exist already


for(record in record_list){
  for(field in field_list){
    for(event in event_list){
      result =
        tryCatch({      # suppress breaking error when no image in slot
          redcap_download_file_oneshot(
            record        = record,
            field         = field,
            redcap_uri    = uri,
            token         = token,
            event         = event,
            overwrite     = TRUE,
```

```
            directory     = directory
          )
        }, error=function(e){})
    }
  }
}
```

4.1.1.2 Named from REDCap record ID and event

```
library(REDCapR)
uri = "https://redcap.cir.ed.ac.uk/api/"
token = "" # API token here
record_list = 1:318
field_list = c("photo", "photo_2", "photo_3", "photo_4")
event_list = c("wound_concerns_arm_2", "questionnaire_1_arm_2",
               "questionnaire_2_arm_2", "questionnaire_3_arm_2")
directory = "wound_named" # destination directory must exist already

for(record in record_list){
  for(field in field_list){
    for(event in event_list){
      file_name = paste0(record, "_", field, "_", event, ".jpg")
      result =
        tryCatch({
          redcap_download_file_oneshot(
            record        = record,
            field         = field,
            redcap_uri    = uri,
            token         = token,
            event         = event,
            overwrite     = TRUE,
            directory     = directory,
            file_name     = file_name
          )
        }, error=function(e){})
    }
  }
}
```

Chapter 5

Final Words

We have finished a nice book.

Chapter 6

Plotting

6.1 GGHighlight Example

Plotting with gghighlight is pretty awesome allowing you to filter on any variable. It seems that gghighlight overwrites any 'colour' variable you put in the main aes. To get round this and have labels, save as a plot and add geom_label_repel separately.

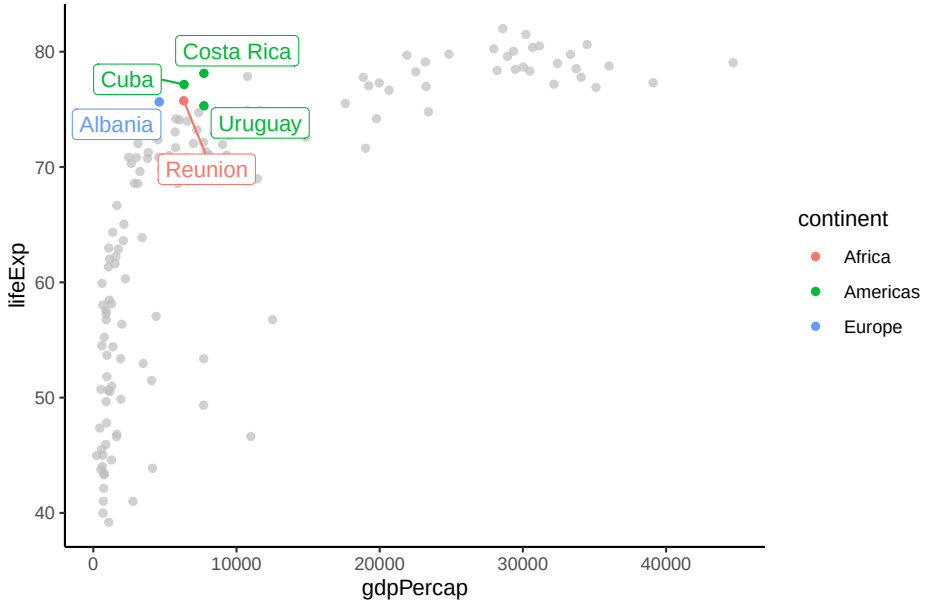
```
library(gghighlight)
library(ggrepel)

mydata=gapminder


plot = mydata %>%
  filter(year == "2002") %>%
  ggplot(aes(x = gdpPercap, y = lifeExp, colour=continent)) +
  geom_point()+
  gghighlight(lifeExp > 75 & gdpPercap < mean(gdpPercap), label_key = country, use_direct_label =
  theme_classic()+
  labs(title= "gghighlight: Filter for countries with Life Expectancy >75 and GDP < mean" )

plot + geom_label_repel(aes(label= country), show.legend = FALSE) #only needed if you use  use_di
```

gghighlight: Filter for countries with Life Expectancy >75 and GDP < mean



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Xie, Y. (2015). *Dynamic Documents with R and knitr*. Chapman and Hall/CRC, Boca Raton, Florida, 2nd edition. ISBN 978-1498716963.

Xie, Y. (2019). *bookdown: Authoring Books and Technical Documents with R Markdown*. R package version 0.12.