

# The Surgical Informatics Cookbook

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# Chapter 1

## Introduction

### 1.1 Rules of posting

Rules of how to post here.

### 1.2 Indexing

#### 1.2.1 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}`

#### 1.2.2 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)`.

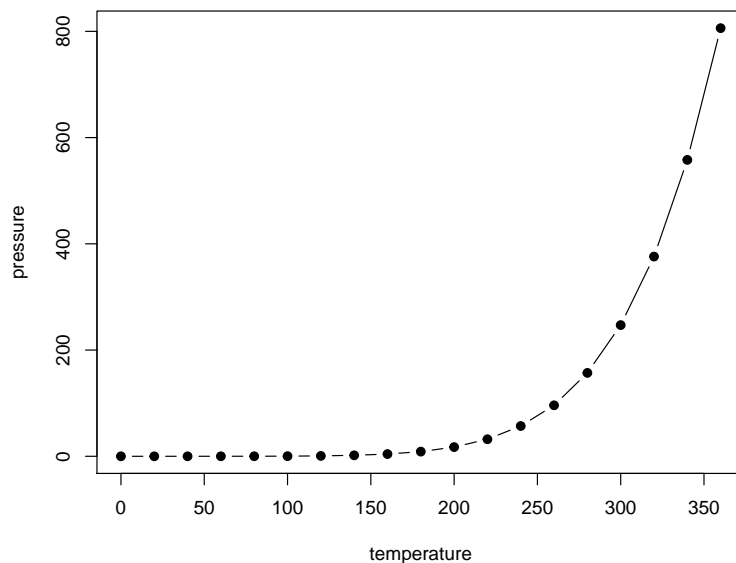


Figure 1.1: Here is a nice figure!

### 1.2.3 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
)
```

### 1.2.4 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 Extract dob and gender from chi

```
library(tidyverse)
library(lubridate)
x = tibble(
  chi = c("1009761234", "1009762345")
)

x %>%
  mutate(
    dob = str_extract(chi, ".{6}") %>%
      dmy(),
    gender = str_sub(chi, 9, 9) %>%
      as.numeric() %>%
      {ifelse(. %% 2 == 0, "Female", "Male")}
  )

## # A tibble: 2 x 3
##   chi      dob      gender
##   <chr>    <date>    <chr>
## 1 1009761234 1976-09-10 Male
## 2 1009762345 1976-09-10 Female
```



## 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 GGHhighlight Example

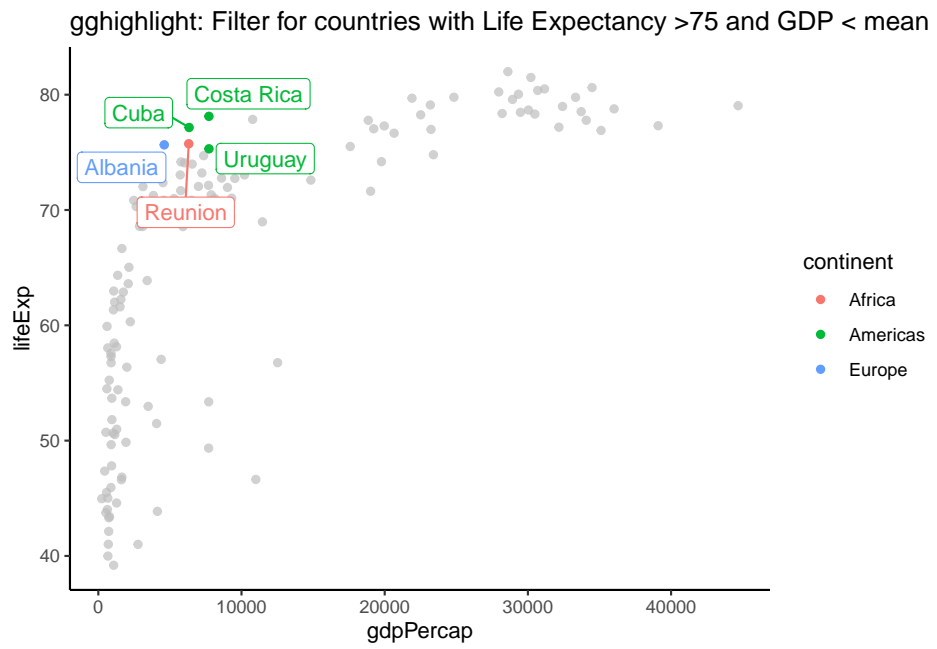
Plotting with gghighlight is pretty awesome allowing you to filter on any variable. It seems that gghighlight overwrites any 'colour' variable you put in the main aes. To get round this and have labels, save as a plot and add geom\_label\_repel separately.

```
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_d
```



# Bibliography

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.