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Departement Public Health

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Nursing Science

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Report center 501

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1 Einleitung

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2 Methode

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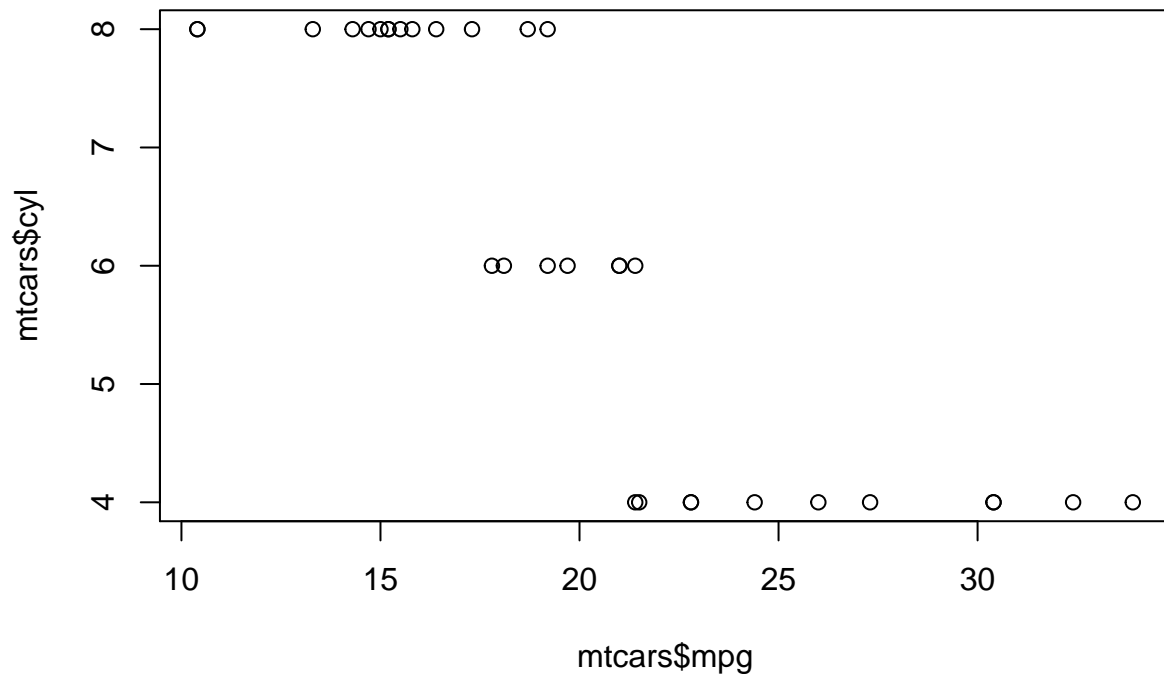my awesome project – logo

3   Ergebnisse
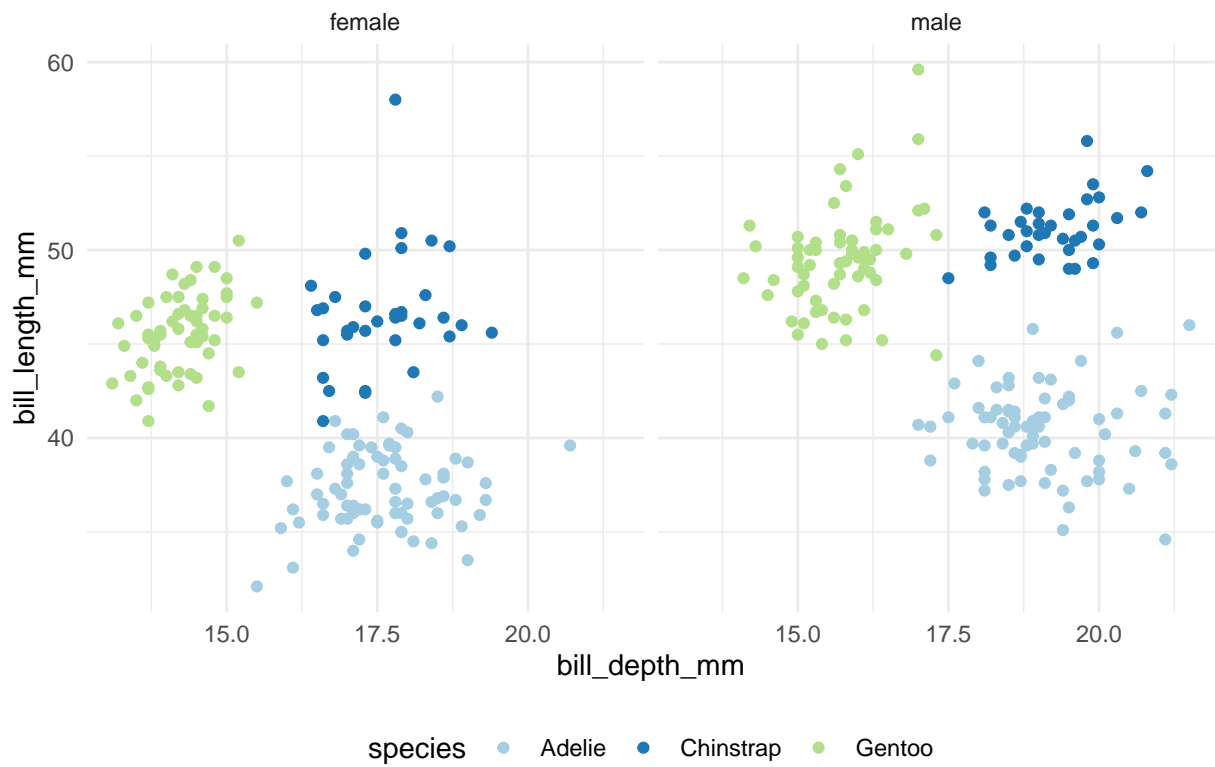
3.1   Bilder

Abbildung 1: a plot

some boring text

3.2   Tabellen

Tabelle 1: A table

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	1

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3.3   Mehr Grafiken

data source: palmerpenguins−package

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4 Appendix 1

```r
# the 'setup' chunk is the first chunk and allows you to set global options for
# later on - i.e. rules for all chunks

knitr::opts_chunk$set(eval = TRUE, echo = FALSE,
                      warning = FALSE, warnings = FALSE)



# second, you load all the packages you need
suppressPackageStartupMessages(library(tidyverse))
suppressPackageStartupMessages(library(kableExtra))

# third, you load your data and source the reporting vectors
source("R/00_import.R")
source("R/99_reporting_vectors.R")

# fourth, you source all the scripts you wrote to prepare your data and results
source("R/01_prepare.R")

# next, source the functions you need to use




# the 'select_chapters' chunk selects the files that will be stitched together
# via the next chunk i.e. if you want to omit/add chapters, you need to 1) create the chapter within
# the chapter/ directory, then add the filename in the c()-command below

chapter_files <- paste0("chapters/",
                        params$language,
                        c("-01_intro.Rmd",
                          "-02_methods.Rmd",
                          "-03_results.Rmd"))

# the stitch_chapters-chunk needs to be left empty - through the 'child' command
# it is specified, what files will be stitched together



plot(mtcars$mpg, mtcars$cyl)
kableExtra::kable(head(mtcars), caption = "A table") %>%
  kableExtra::kable_styling(latex_options = c("hold_position"))
#
# n_valid <- function(x) {sum(!is.na(x))}
#
# full1 <- as.list(sample_data[ , vec_leadership])
# filter1 <- as.list(filtered_data[ , vec_leadership])
#
# map2(full1, filter1, n_valid)

ggplot(drop_na(palmerpenguins::penguins),
       aes(x = bill_depth_mm, y = bill_length_mm, color = species)) +
```

```
geom_point() +
facet_wrap(~sex) +
scale_color_brewer(palette = 3, type = "qual") +
labs(caption = "data source: palmerpenguins-package") +
theme_minimal() +
theme(legend.position = "bottom")
```

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