Practice Solutions to Intro to R and Rstudio for EDA - Part 2

Jessica Minnier, PhD & Meike Niederhausen, PhD

OCTRI Biostatistics, Epidemiology, Research & Design (BERD) Workshop

2020/09/17

Practice 3

- 1. Continue adding code chunks to your Rmd (or, start a new one! But remember to load the libraries and data at the top.)
- 2. How many different years are in the data? (Hint: use tabyl() or n_distinct())
- 3. Count the number of penguins measured each year.
- 4. Calculate the median body mass by each species and sex subgroup. Use summarize() and group_by() to do this.
- 5. Create a 2x2 table of number of penguins measured in each year by each island.

Practice 3 Answers

2. How many different years are in the data? (Hint: use tabyl() or n_distinct())

Option 1:

```
penguins %>%
  summarize(n_distinct(year))
```

Option 2:

```
penguins %>% tabyl(year)
```

```
year n percent
2007 109 0.3187135
2008 114 0.3333333
2009 119 0.3479532
```

penguins %>% tabyl(year) %>% nrow

[1] 3

3. Count the number of penguins measured each year.

Option 1:

```
penguins %>% count(year)

# A tibble: 3 x 2
   year   n
   <dbl> <int>
1 2007 109
2 2008 114
3 2009 119
```

Option 2:

```
penguins %>% tabyl(year)
```

```
year n percent
2007 109 0.3187135
2008 114 0.3333333
2009 119 0.3479532
```

4. Calculate the median body mass by each species and sex subgroup. Use summarize() and group_by() to do this.

```
penguins %>%
 group_by(species, sex) %>%
  summarize(median(body_mass_g))
# A tibble: 8 x 3
# Groups: species [3]
 species sex
               `median(body mass g)`
 <chr> <chr>
                                  <dbl>
1 Adelie female
                                  3400
2 Adelie
        male
                                  4000
3 Adelie
           <NA>
                                  3475
4 Chinstrap female
                                  3550
5 Chinstrap male
                                  3950
          female
6 Gentoo
                                  4700
          male
7 Gentoo
                                  5500
8 Gentoo
           <NA>
                                  4688.
```

5. Create a 2x2 table of number of penguins measured in each year by each island.

```
penguins %>% tabyl(island, year)

island 2007 2008 2009

Biscoe 44 64 59

Dream 46 34 44

Torgersen 19 16 16
```

Practice 4

Create a new Rmd or continue in your current Rmd.

- 1. Create a dataset for just the Torgersen island penguins that are female.
- 2. Restrict the data to just Torgersen female penguins that weigh more than 3500 g.
- 3. Restrict the dataset from the previous step to just the columns with the original body measurements.
- 4. Add a column for the difference in the flipper and bill lengths, and call it flipper_bill_diff.
- 5. How many rows and columns does your final dataset have?

Practice 4 Answers

#1 Create a dataset for just the Torgersen island penguins that are female.

```
Torg_female <- penguins %>%
  filter(island == "Torgersen" & sex == "female")
```

#2 Restrict the data to just Torgersen female penguins that weigh more than 3500 g.

```
Torg_female2 <- Torg_female %>%
  filter(body_mass_g > 3500)
```

#3 Restrict the dataset from the previous step to include just the columns with the original body measurements.

```
Torg_female3 <- Torg_female2 %>%
  select(bill_length_mm:body_mass_g)
```

#4 Add a column for the difference in the flipper and bill lengths, and call it flipper_bill_diff.

```
Torg_female4 <- Torg_female3 %>%
  mutate(flipper_bill_diff = flipper_length_mm - bill_length_mm)
```

#5 How many rows and columns does your final dataset have?

```
dim(Torg_female4)
```

```
[1] 9 5
```

9 rows and 5 columns.

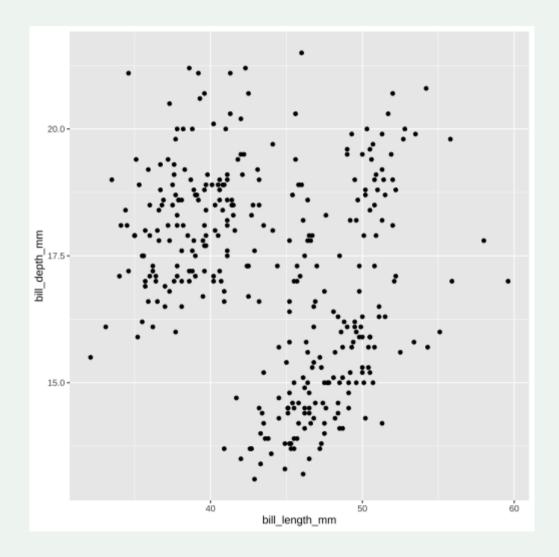
Note: Steps 1-4 could have been done with consecutive pipes:

```
Torg_female5 <- penguins %>%
  filter(island == "Torgersen" & sex == "female" & body_mass_g > 3500) %>%
  select(bill_length_mm:body_mass_g) %>%
  mutate(flipper_bill_diff = flipper_length_mm - bill_length_mm)
dim(Torg_female5)
```

Practice 5

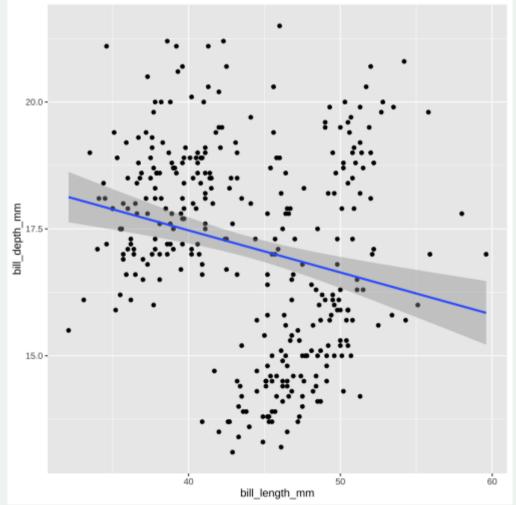
- 1. Continue adding code chunks to your Rmd (or, start a new one! But remember to load the libraries and data at the top.)
- 2. Make a scatter plot of bill depth vs bill length.
- 3. Add + geom_smooth(method="lm") to the plot. What is this saying about the association between bill depth and length?
- 4. Now add **color** = **species** to the aesthetic **aes()**. Keep **geom_smooth**. How do the associations look now?

2. Make a scatter plot of bill depth vs bill length.



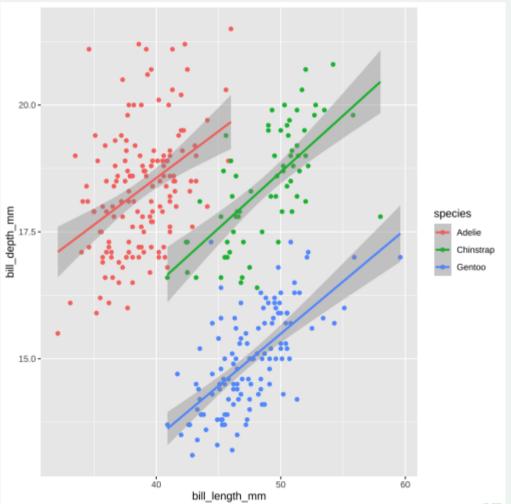
3. Add + geom_smooth(method="lm") to the plot. What is this saying about the association between bill depth and length?

It looks like as bill length increases, bill depth decreases. This is a negative association. But there is a wide variation and a lot of noise.



4. Now add color = species to the aesthetic aes(). Keep geom_smooth. How do the associations look now?

The association reverses, when we look inside species. As bill length increases, bill depth increases. This is an example of Simpson's paradox!



13 / 14

Here's a prettier version:

```
ggplot(data = penguins,
       aes(x = bill_length_mm,
           y = bill_depth_mm,
           color = species)) +
  geom_point()+
  geom_smooth(method="lm")+
  labs(
    title = "Flipper vs bill length",
    subtitle = "Palmer Station LTER",
    x = "Flipper length(mm)",
    y = "Bill length(mm)") +
  scale_color_viridis_d(
    name = "Species") +
  theme(legend.position = "bottom")+
  theme_bw()
```

