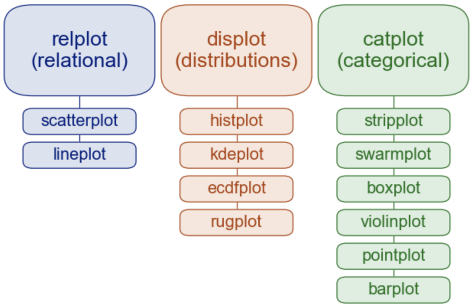
Homework 10



This lab features a gallery of several canonical plot types made in `ggplot2`. Your task is to recreate them using `seaborn` and `matplotlib`. As you work, I recommend using as a reference seaborns excellent documentation.

- You're welcome to use the atomic `seaborn` plot functions (`scatterplot()`, `boxplot()`, etc.) or their wrapper equivalents (`relplot()`, `displot()`, and `catplot()`).
- In terms of aesthetics, do try to match the main elements of the ggplot: the plot type, line types, the colors, the labels, and the title. Don't worry about getting the sizes identical or all of the axis tick marks to match up.
- Your code for these plots might involve bits of `pandas`, `seaborn`, and `matplotlib`. You're at a good point now where you should be able to get your code *working* fairly easily, so pay some attention to getting your code simple, readable, and well-formatted.

As you begin this journey from `ggplot2` users to `seaborn` users, I encourage you to read a blog post of data scientist Emily Robinson, as she went on a similar journey.

You'll want to start by prepping your R session,

```r
library(tidyverse)
library(palmerpenguins)
data(penguins)
penguins <- drop_na(penguins)
```

as well as your Python session.

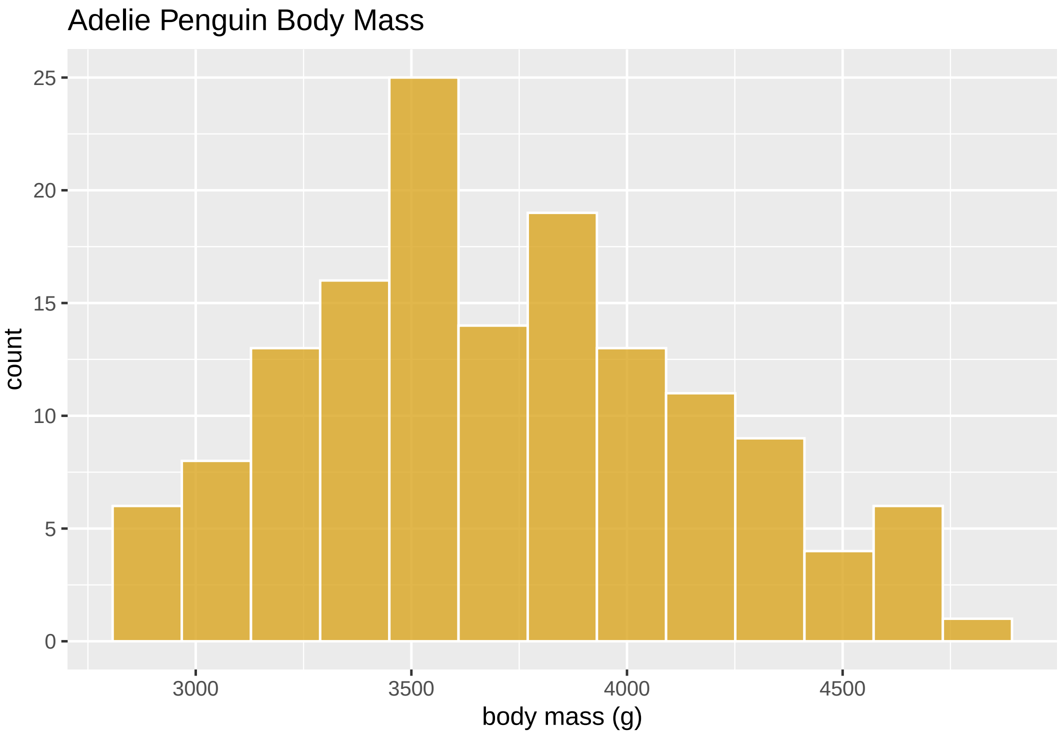
```python
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
# penguins = pd.read_csv("https://raw.githubusercontent.com/andrewpbray/python-for-r-users/maste
# plt.style.available
```

```
plt.style.use('ggplot')
```

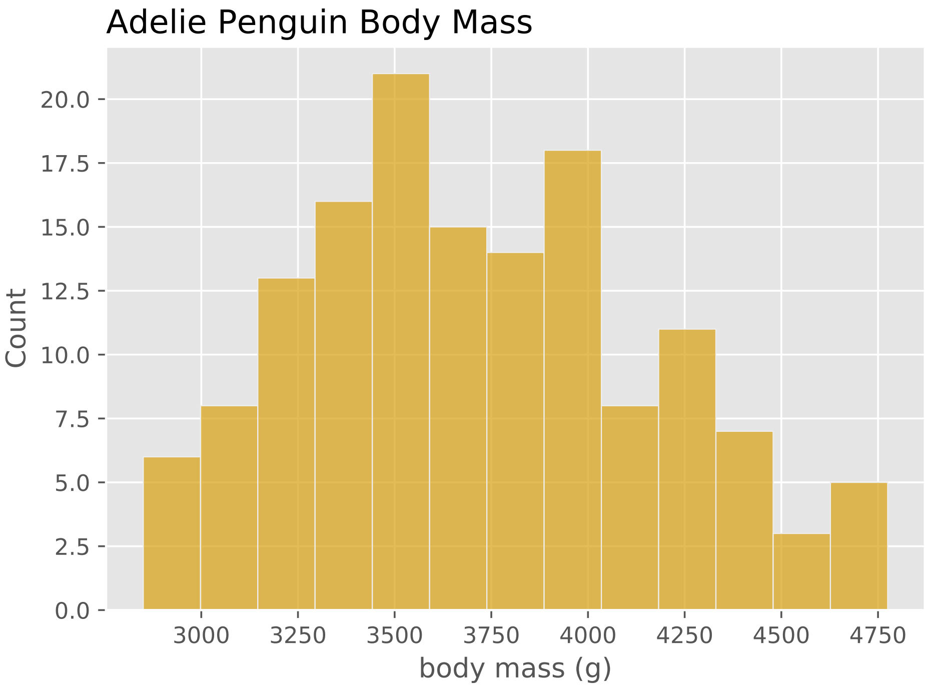
You may want to set up a parallel notebook to allow you to iterate on your seaborn plots a little more easily. If you do that, it will be easiest to read in the penguinds data from the csv file. Importantly: currently Berkeley's DataHub is using an older version of `seaborn` and there have been several important updates for current version `0.11.0`. To use the current version in your notebook, add a cell at the top with `!pip install seaborn==0.11.*`.

Example: Single histogram Below is the `ggplot2` code to generate a histogram and an analog using `seaborn`. You'll note that even though they both have 13 bins, the plots end up slightly different from one another, despite the fact that they're using the same data. The difference is that they use two different rules for determining when to start the first and last bins after the first and last observations, respectively. You may come across similar slight differences in the course of this homework; don't worry about ironing them out perfectly.

```
penguins %>%
  slice(-1) %>%
  filter(species == "Adelie") %>%
  ggplot(aes(x = body_mass_g)) +
  geom_histogram(bins = 13,
                 color = "white",
                 fill = "goldenrod",
                 alpha = .8) +
  xlab("body mass (g)") +
  ggtitle("Adelie Penguin Body Mass")
```

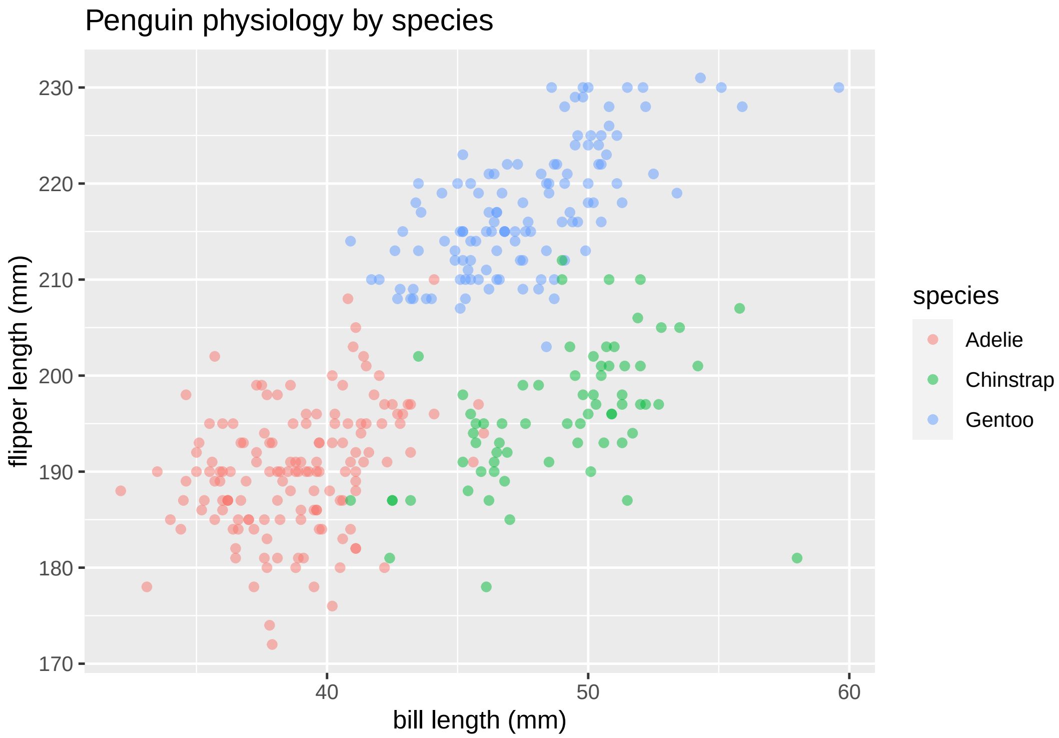


```
p = sns.histplot(x = "body_mass_g",
                 data = r.penguins[r.penguins["species"] == "Adelie"].iloc[1:, :],
                 bins = 13,
                 color = "goldenrod")
p.set_xlabel("body mass (g)")
p.set_title("Adelie Penguin Body Mass", loc = "left")
```



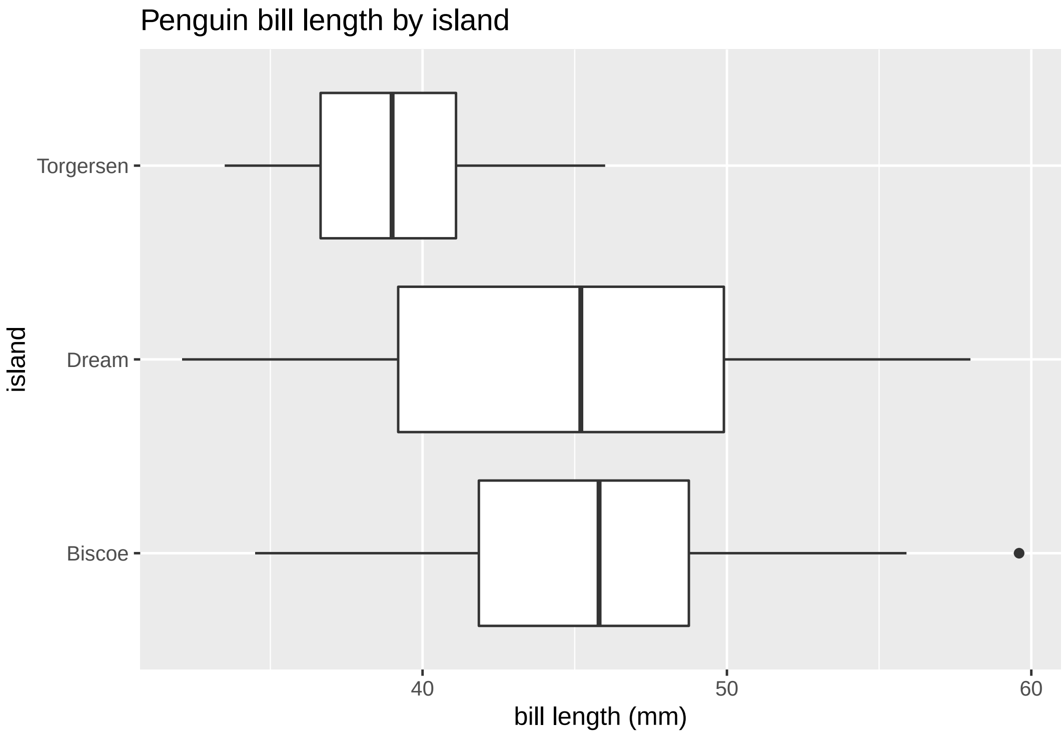
1.

```
penguins %>%
  ggplot(aes(x = bill_length_mm,
             y = flipper_length_mm,
             color = species)) +
  geom_point(size = 1.5, alpha = .5) +
  labs(x = "bill length (mm)",
       y = "flipper length (mm)",
       title = "Penguin physiology by species")
```



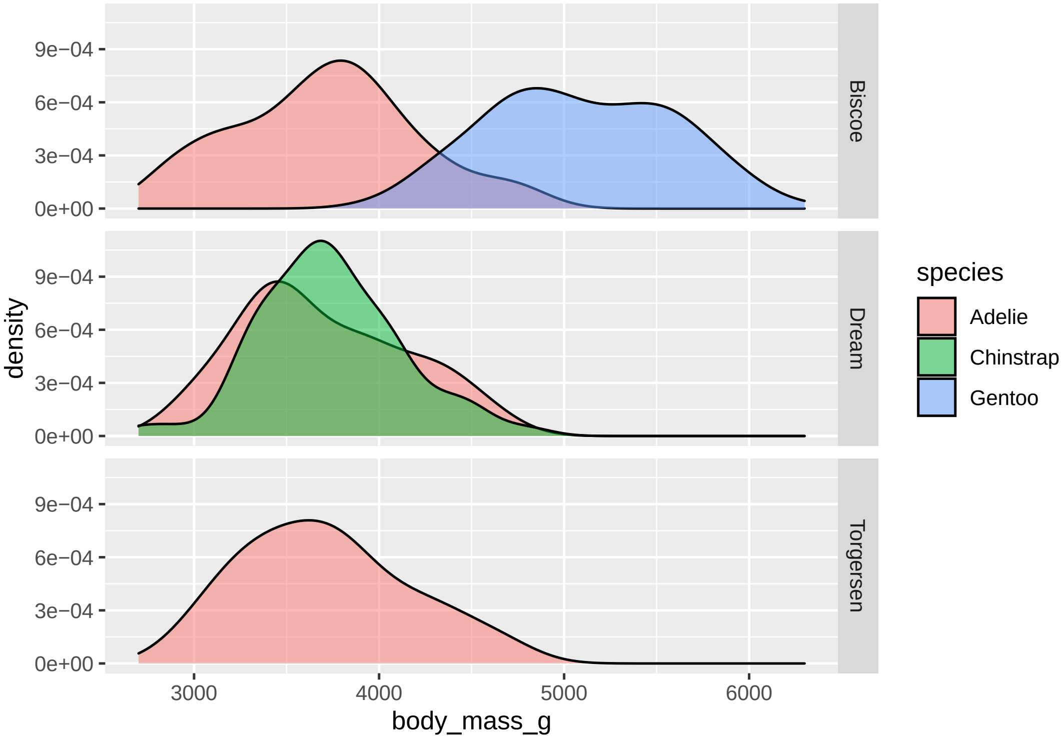
2.

```
penguins %>%
  ggplot(aes(x = island,
             y = bill_length_mm)) +
  geom_boxplot() +
  coord_flip() +
  labs(y = "bill length (mm)",
       x = "island",
       title = "Penguin bill length by island")
```



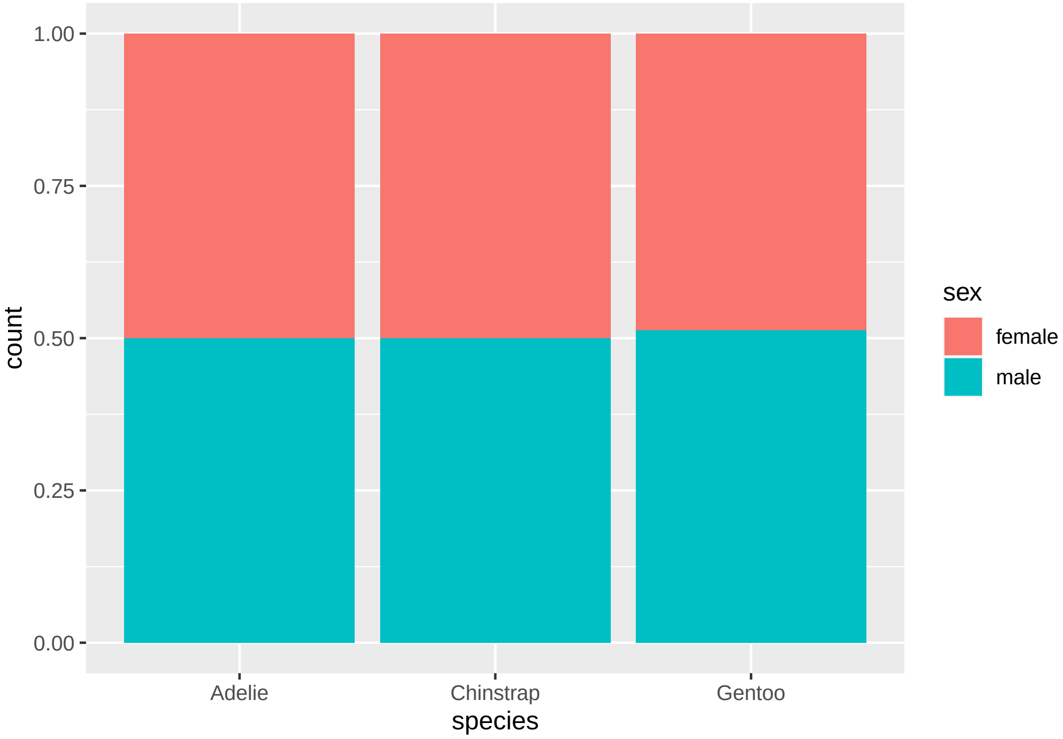
3.

```
penguins %>%
  ggplot(aes(x = body_mass_g,
             fill = species)) +
  geom_density(alpha = .5) +
  facet_grid(rows = vars(island))
```



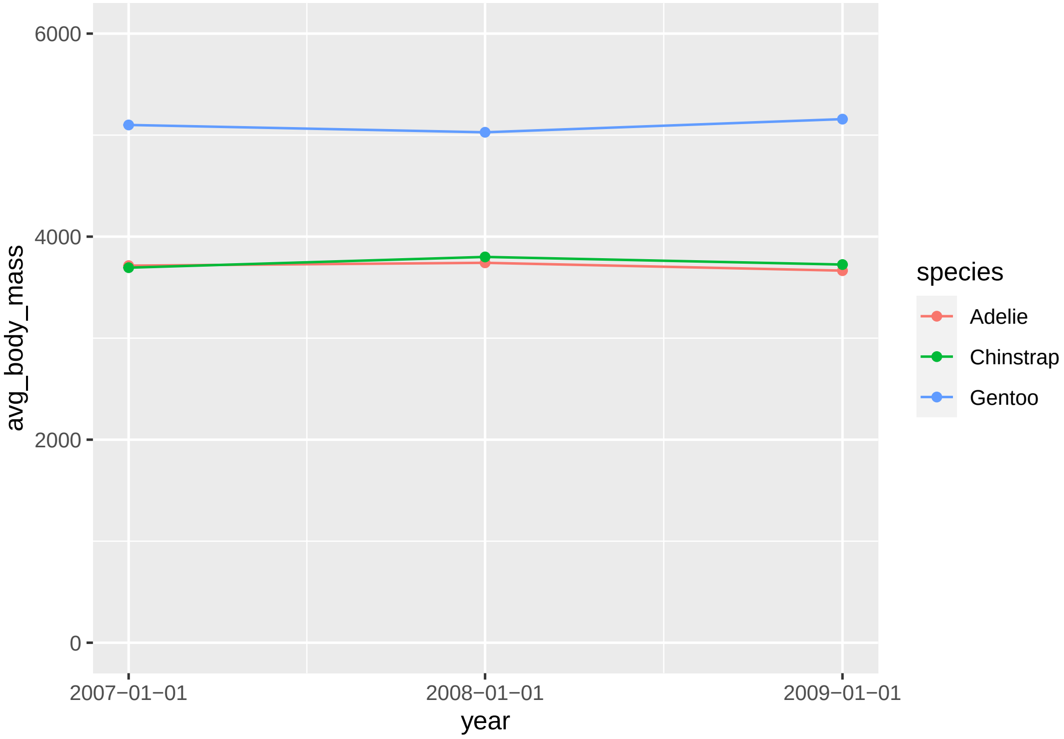
4.

```
penguins %>%
  ggplot(aes(x = species,
             fill = sex)) +
  geom_bar(position = "fill")
```



5.

```
library(lubridate)
penguins %>%
  mutate(year = ymd(year, truncated = 2L)) %>%
  group_by(species, year) %>%
  summarize(avg_body_mass = mean(body_mass_g)) %>%
  ggplot(aes(x = year,
             y = avg_body_mass,
             color = species)) +
  geom_line() +
  geom_point() +
  lims(y = c(0, 6000)) +
  scale_x_date(date_breaks = "1 year")
```


6000
4000
2000
0
avg_body_mass
2007−01−01
2008−01−01
2009−01−01
year
species
Adelie
Chinstrap
Gentoo