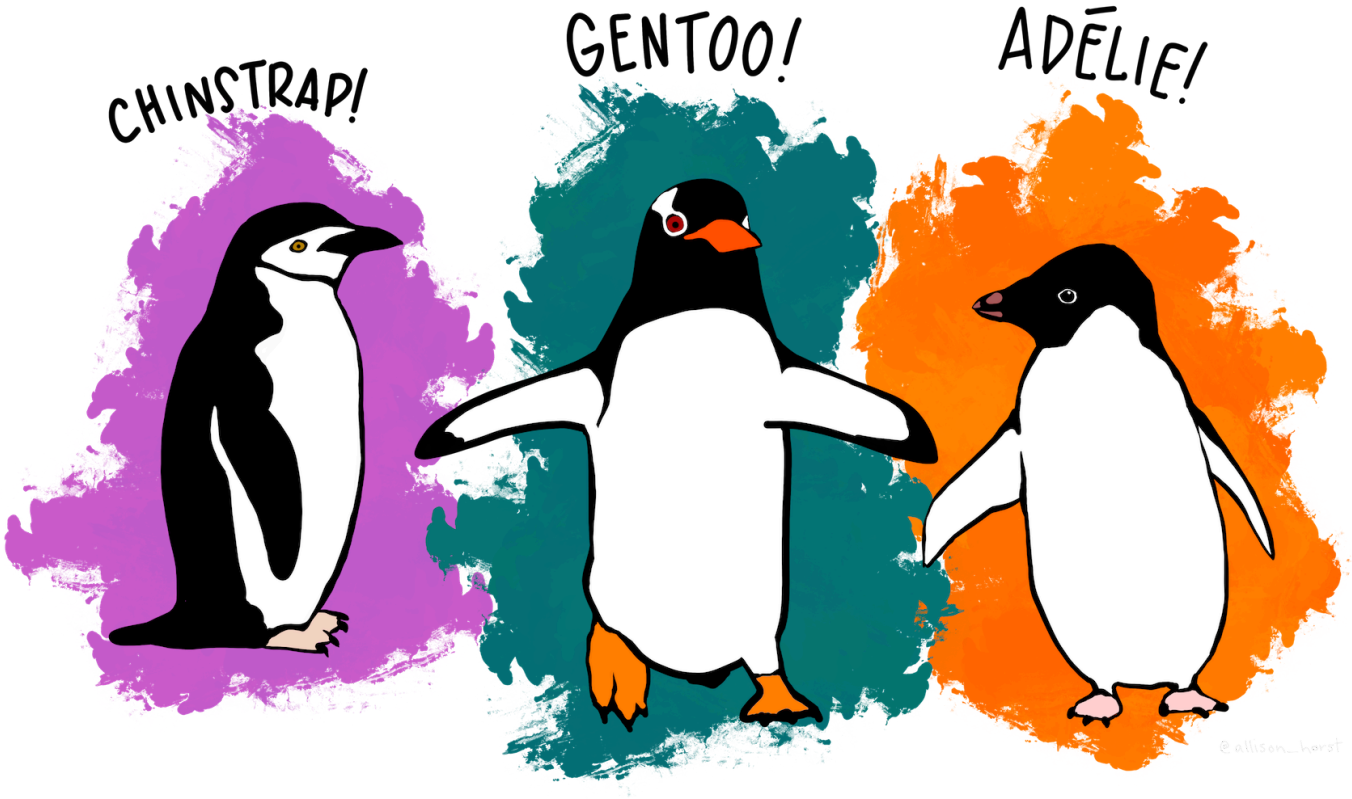
Visualization Lesson with Palmer Penguins

Introduction

Welcome to Day 2 of our data visualization journey! Today, we'll dive deeper into the world of visualizing data using the **Palmer Penguins dataset**. This dataset provides insights into penguins in the Palmer Archipelago, and it's a perfect opportunity for us to practice and hone our visualization skills.

- This session is an opportunity to:
  - Independently code visualizations.
  - Learn how to troubleshoot issues that arise.
  - Explore data in a hands-on manner.
- We will also teach several new data visualization tricks:
  - Changing shapes of points.
  - Customizing figure legends.
  - Using `facet_grid` for comparing many aspects of data simultaneously.
  - Other advanced plotting tricks.
- Approach this session with curiosity and an adventurous spirit:
  - Experiment with different plot types.
  - Play with colors and styles.
  - Let creativity guide your visual storytelling.
- Questions are welcome:
  - Learning together is key.
  - Your inquiries are a vital part of the process.
- Let's embark on this journey and enjoy the exploration of data visualization!



The Palmer Archipelago penguins. Artwork by @allison_horst.

Dataset Overview

First we load necessary packages. If the palmerpenguins package is not installed, we can install it by uncommenting “install.packages” below.

> **Tip – Suppress Package Startup Messages**
>
> The `suppressPackageStartupMessages()` function in R is used to prevent the display of startup messages when loading packages. This can make your R script output cleaner and more readable, especially when loading multiple packages.

```
suppressPackageStartupMessages(library(tidyverse))
#install.packages('palmerpenguins')
library(palmerpenguins)
```

The dataset includes measurements of penguin species: Adélie, Chinstrap, and Gentoo. The palmerpenguins pacakge automatically loads the data into an object called penguins.

First we check the data class of penguins with class(), and take a look at the first few rows using the head() command.

```
#what class is our data
class(penguins)
```

```
[1] "tbl_df"     "tbl"        "data.frame"
```

```
head(penguins)
```

```
# A tibble: 6 × 8
  species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
  <fct>   <fct>              <dbl>         <dbl>             <int>       <int>
1 Adelie  Torgersen           39.1          18.7               181        3750
2 Adelie  Torgersen           39.5          17.4               186        3800
3 Adelie  Torgersen           40.3          18                 195        3250
4 Adelie  Torgersen           NA            NA                  NA          NA
5 Adelie  Torgersen           36.7          19.3               193        3450
6 Adelie  Torgersen           39.3          20.6               190        3650
  sex     year
  <fct>  <int>
1 male    2007
2 female  2007
3 female  2007
4 <NA>    2007
5 female  2007
6 male    2007
```

As we can see, the dataset, which is a tibble/dataframe, contains many numerical (lengths, dephths, and masses), and categorical (species, island, and sex) variables. It also contains a variable that could be categorical or numerical (year).

Exploratory Questions

In this section, we will take some time to ask questions about the Palmer Penguins dataset. Asking questions is a fundamental part of data analysis, as it guides our exploration and helps us uncover interesting patterns and insights.

As you look at the dataset, consider the different types of questions you might ask. What different kinds of questions can we ask using different data types, and what kind of plots might we use to answer them?

Some example questions

If you are having trouble of thinking of questions on your own, here are some example questions related to different combinations of numerical or categorical variables:

Questions leading to numerical by numerical plots

Questions leading to categorical by numerical plot

Questions related to one numerical variable

Questions related to multiple categorical variables

Making plots!

Warm up: numerical by numerical plots

To compare two numerical variables, a scatterplot is often the simplest and most effective plotting method. Here, we will compare the flipper length and body mass of our penguins. Remember, the inputs to a scatterplot are the columns of our tibble, which should be numeric, integer, or double vectors. Lets take a look at our data with head() and confirm the datatype with class().

```
        head(penguins$flipper_length_mm)
```

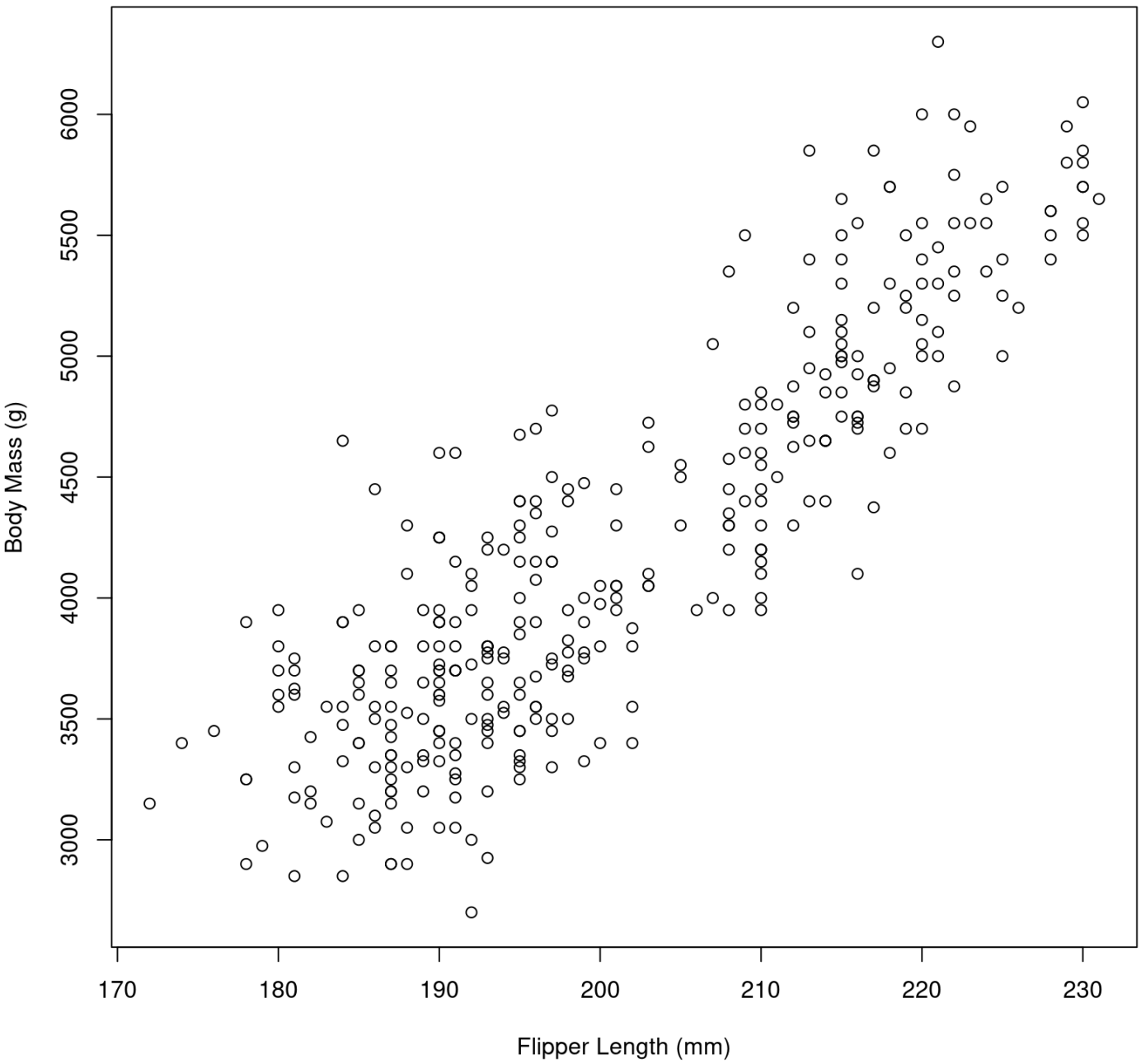
```
[1] 181 186 195  NA 193 190
```

```
        class(penguins$flipper_length_mm)
```

```
[1] "integer"
```

First we create a simple scatterplot with x and y labels in base r.

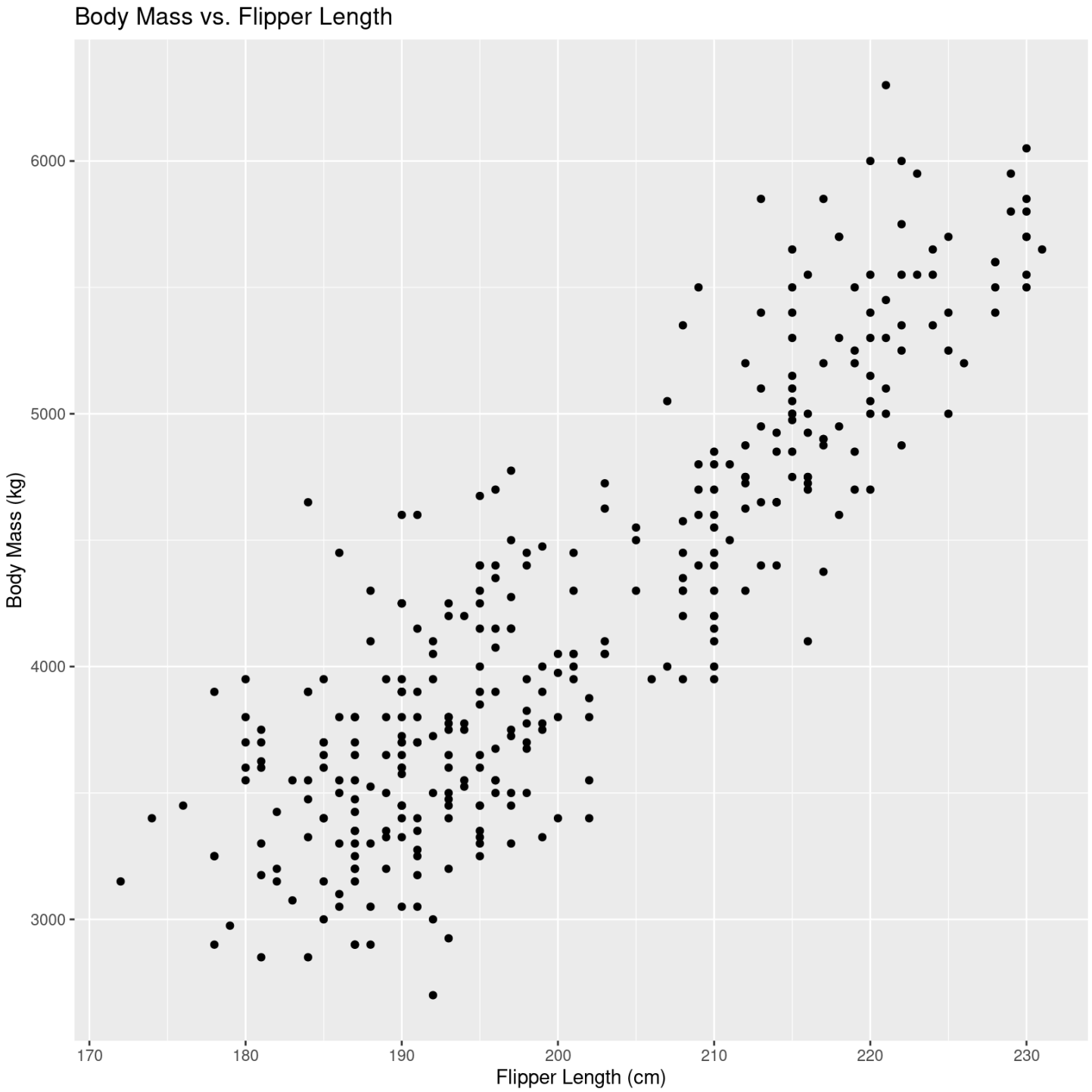
```
        #simple base r plot with x and y axis labeled
        plot(penguins$flipper_length_mm, penguins$body_mass_g,
             xlab = "Flipper Length (mm)", ylab = "Body Mass (g)")
```



Now we recreate the same plot using ggplot2.

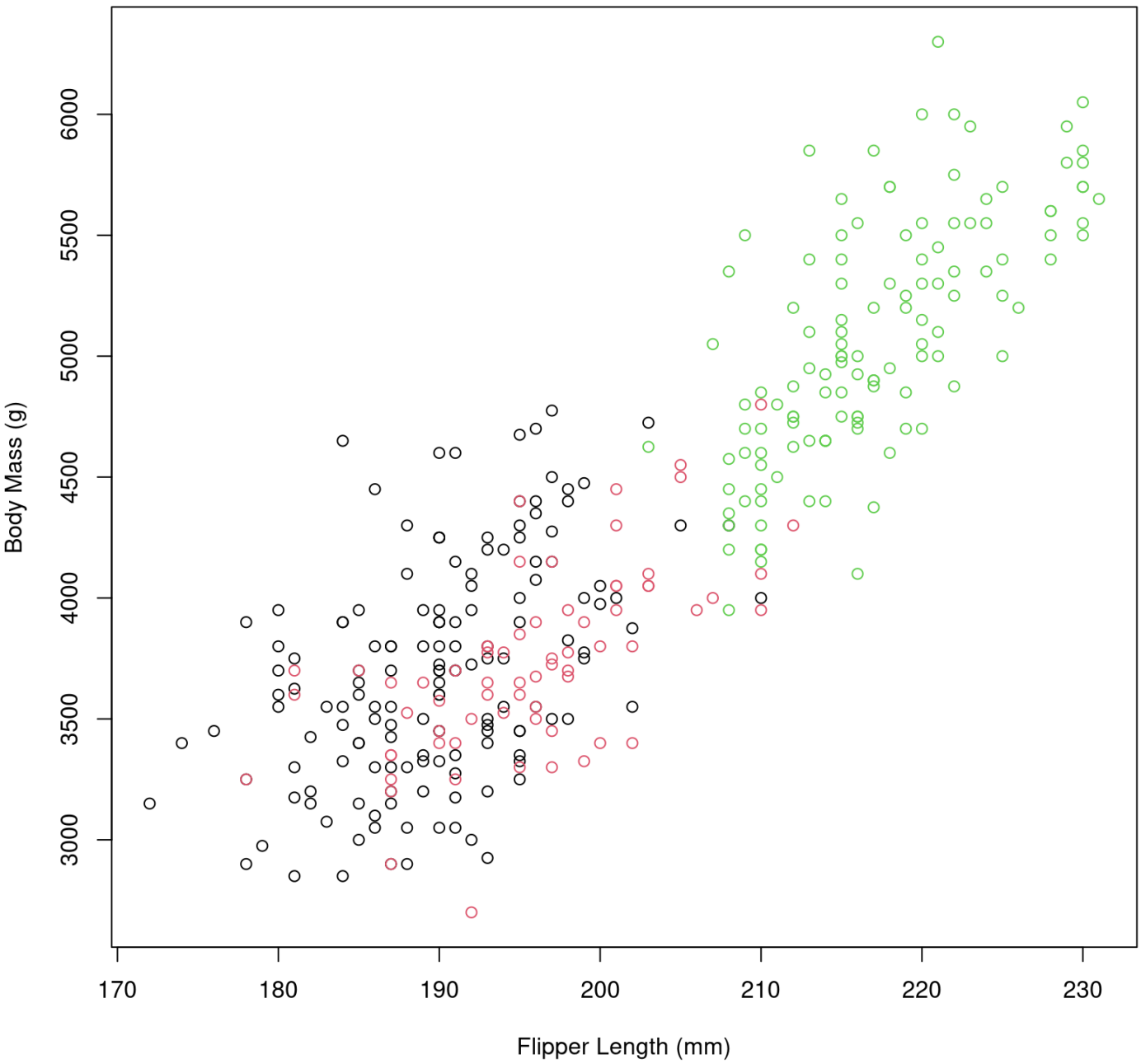
```
# same plot in tidyverse
ggplot(penguins, aes(x = flipper_length_mm, y = body_mass_g,)) +
  geom_point() +
  labs(x = "Flipper Length (cm)", y = "Body Mass (kg)",
       title = "Body Mass vs. Flipper Length")
```

```
Warning: Removed 2 rows containing missing values (`geom_point()`).
```



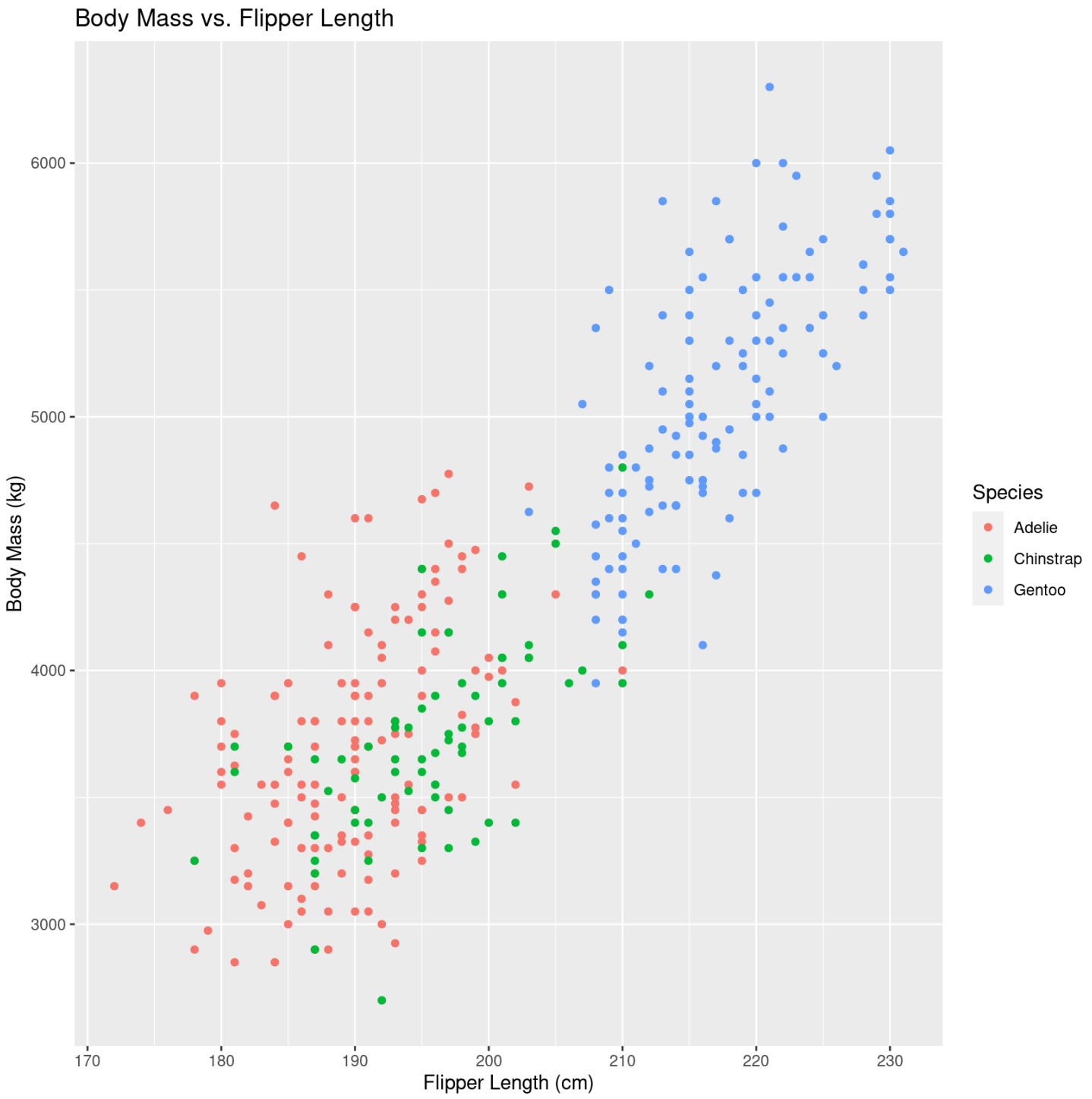
Can we compare different species in these plots? Let's color our points based on the species.

```
# color dots by species
plot(penguins$flipper_length_mm, penguins$body_mass_g,
     xlab = "Flipper Length (mm)", ylab = "Body Mass (g)",
     col = penguins$species)
```




```
ggplot(penguins, aes(x = flipper_length_mm, y = body_mass_g, color = species)) +
  geom_point() +
  labs(x = "Flipper Length (cm)", y = "Body Mass (kg)",
       title = "Body Mass vs. Flipper Length",
       color = "Species")
```

```
Warning: Removed 2 rows containing missing values (`geom_point()`).
```



Why are colors specified differently in base R and ggplot?

- In base R plotting, the color for each point is specified directly within the plot() function using the col argument. This argument can take a vector of colors, which will be applied to the points in the plot. In this example, we are passing the species information directly to the col argument to color the points based on the species.
- In ggplot2, the aesthetics (aes) of the plot are defined within the aes() function. The color aesthetic is specified inside the aes() function to map the species variable to the colors of the points. This approach follows the grammar of graphics philosophy, where data properties are mapped to visual properties in a structured way.

- Both methods allow us to compare different species in the plots by coloring the points based on the species. However, the ggplot2 approach is generally more flexible and powerful for creating complex visualizations.

Another way to change the colors in a ggplot–local aesthetics

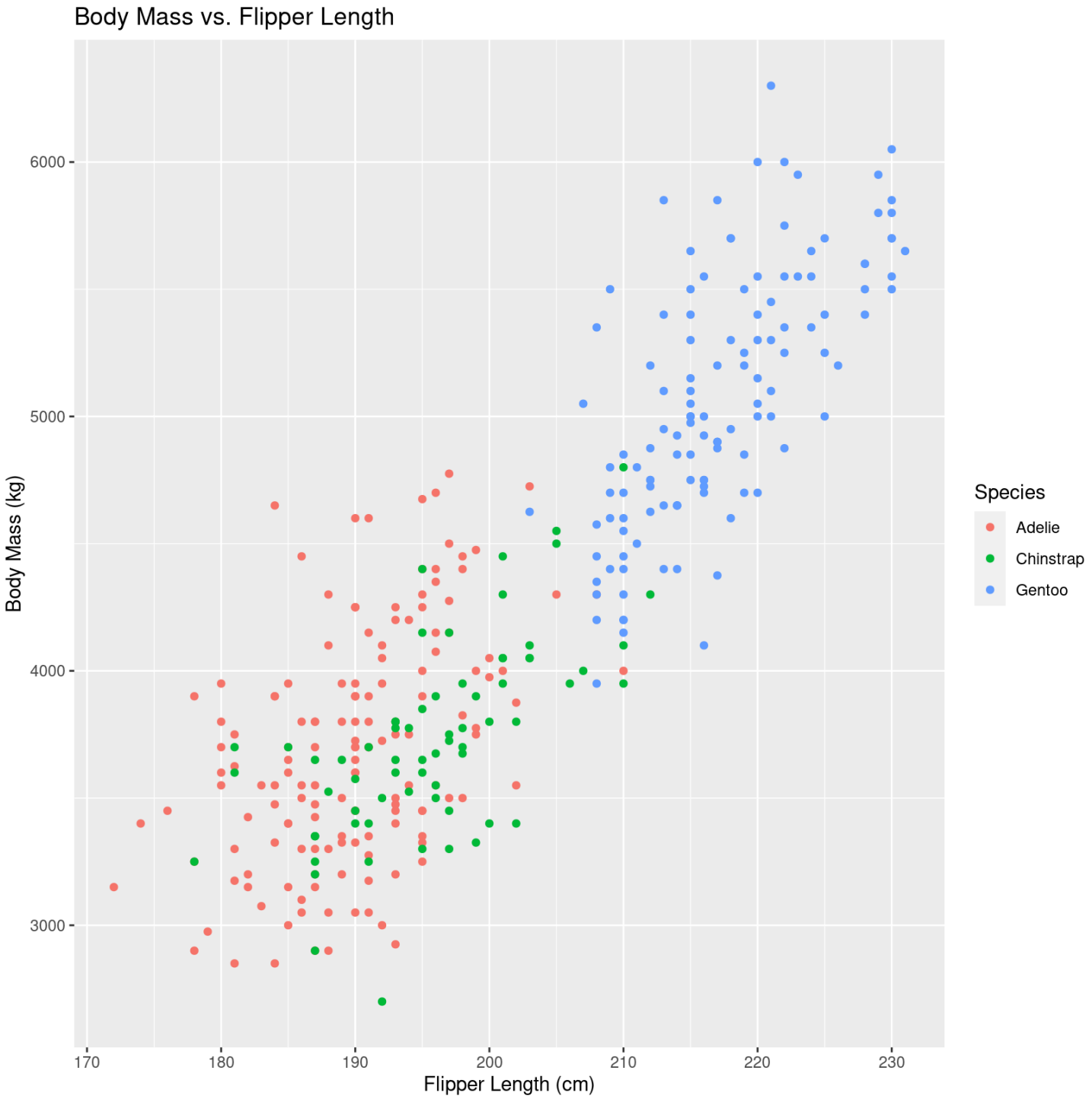
In `ggplot2`, the `aes()` function is used to map data variables to visual properties (aesthetics) of the plot. The placement of the `color` specification can vary based on whether it is applied globally or locally.

- Global aesthetics apply to all geoms in the plot, and are added in the initial ggplot() call (or in a stand-alone aes() layer).
- Local aesthetics apply only to the geom to which they are added.

This first plot produces the same output as our orignal plot.

```
        ggplot(penguins, aes(x = flipper_length_mm, y = body_mass_g)) +
          geom_point(aes(color = species)) +
          labs(x = "Flipper Length (cm)", y = "Body Mass (kg)",
               title = "Body Mass vs. Flipper Length",
               color = "Species")
```

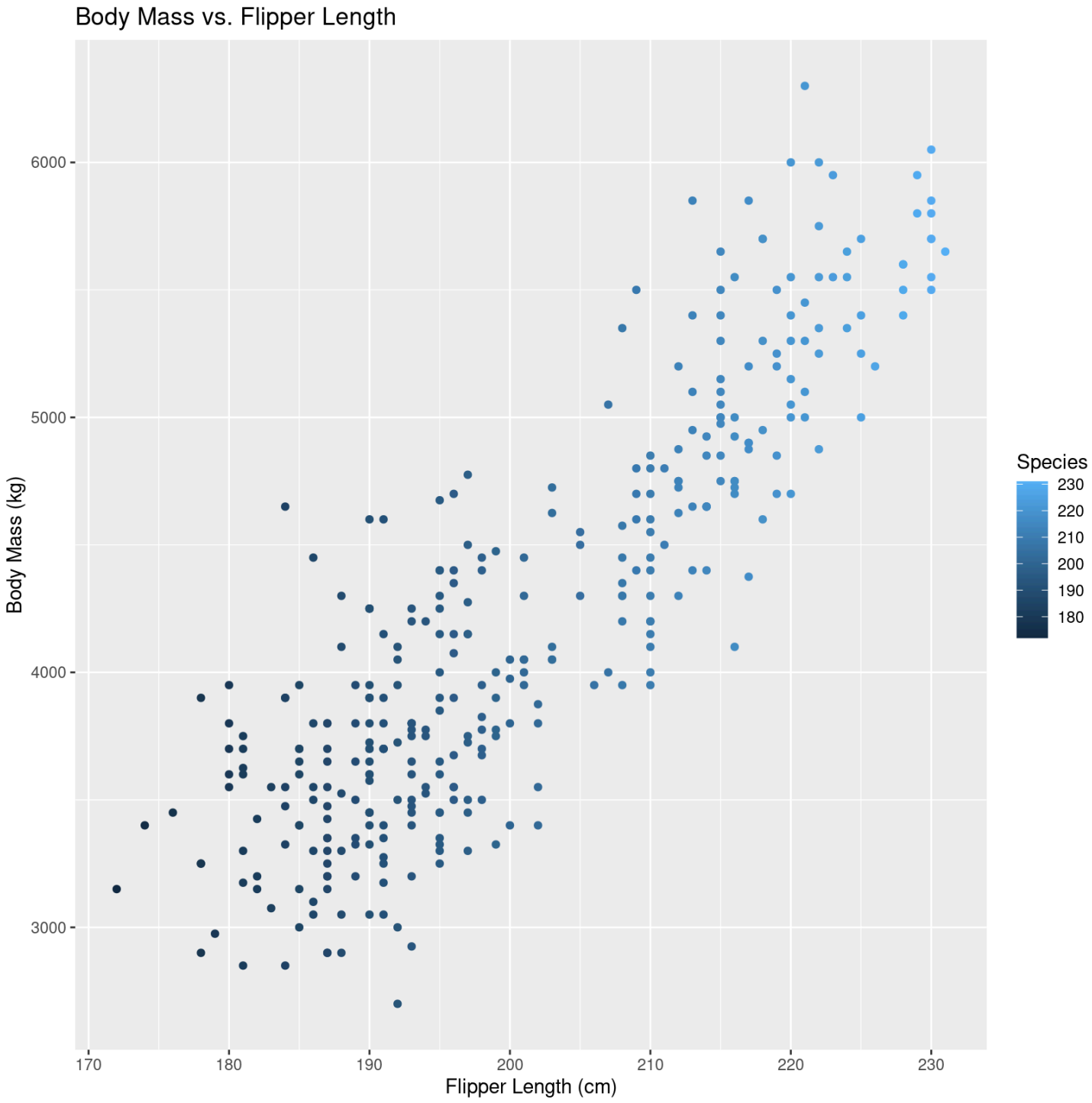
```
Warning: Removed 2 rows containing missing values (`geom_point()`).
```



In this second plot, the local aesthetic overrides the global one.

```
ggplot(penguins, aes(x = flipper_length_mm, y = body_mass_g, color = species)) +
  geom_point(aes(color = flipper_length_mm)) +
  labs(x = "Flipper Length (cm)", y = "Body Mass (kg)",
       title = "Body Mass vs. Flipper Length",
       color = "Species")
```

```
Warning: Removed 2 rows containing missing values (`geom_point()`).
```



Challenge plot: Let's customize these plots some more! Here we show you could change the shapes of the points for each species, add a customized legend in the position of the plot we want, and change the size of the points.

Take 5-10 minutes to try to figure out one or more of the changes we made to the plot: - Change the shape of the points based on species. - Change the position of the legend. - Add custom colors for the species. - Add a subtitle to the figure.

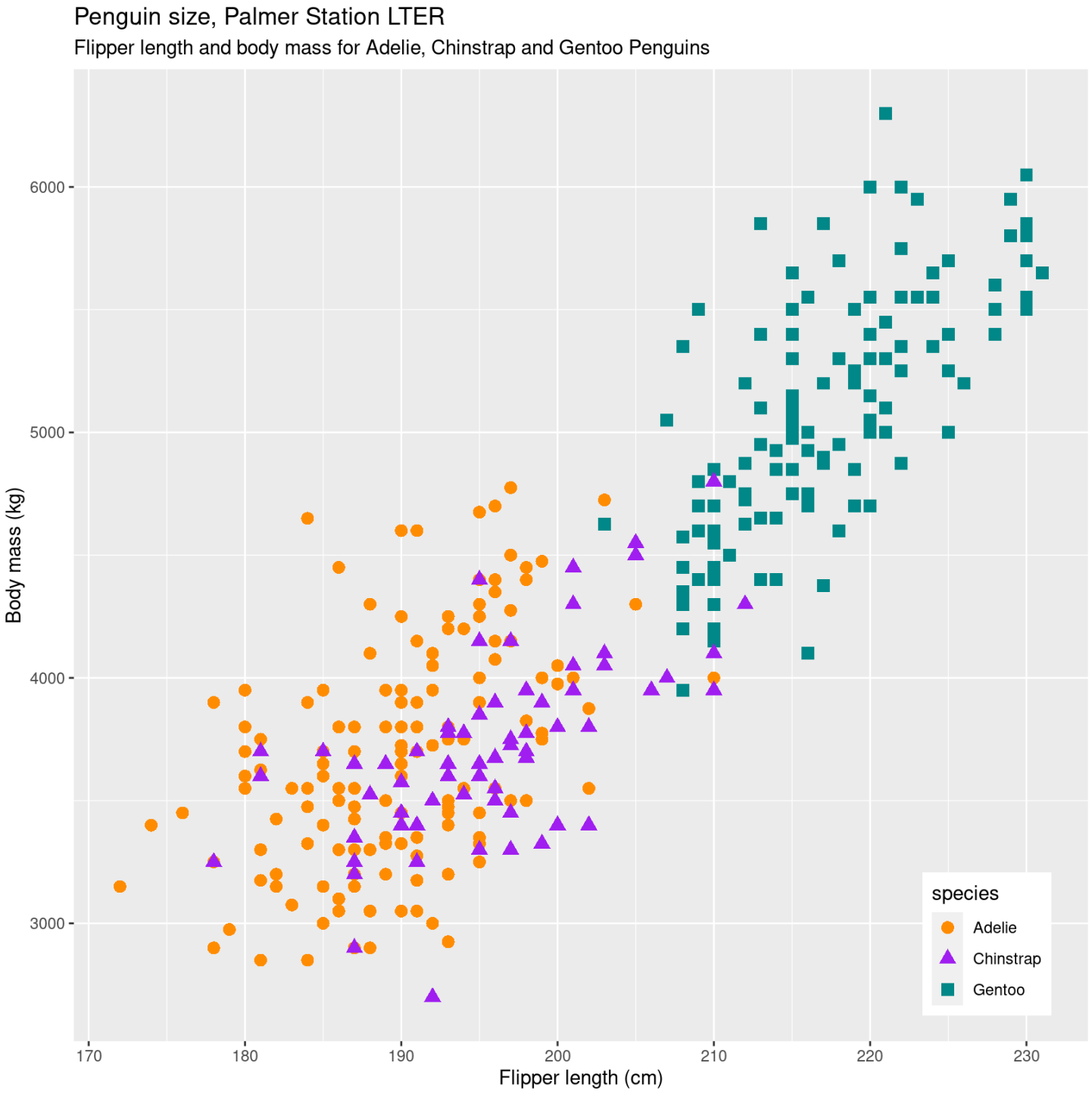
Feel free to try ggplot or base R, depending on your preference. Practice finding this information using:

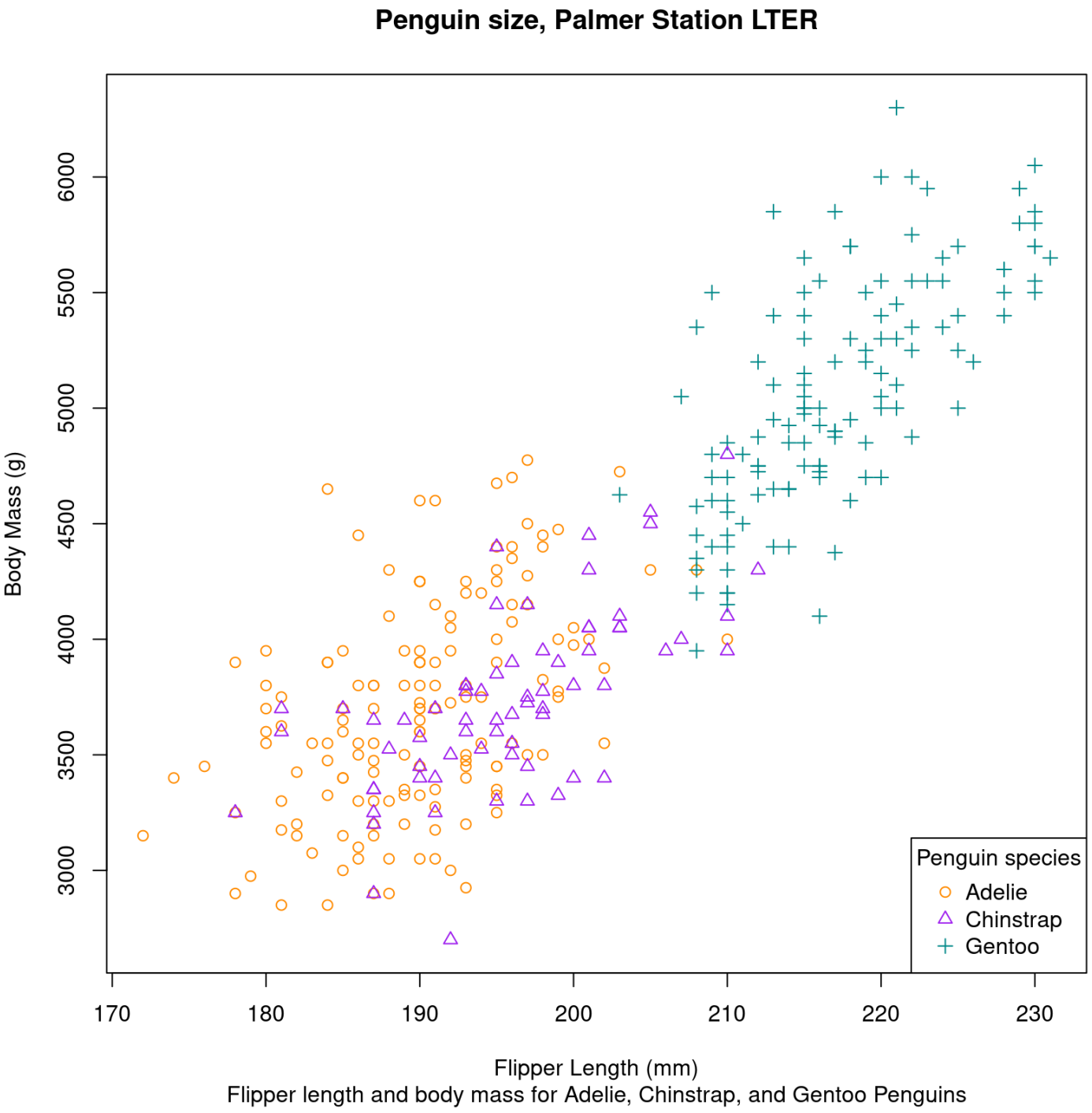
- The base r docs for the plot() function or ggplot2 docs
- Use google to find informative articles online like this

- Ask a friend or instructor for help if you get stuck.

Feel free to add your own touches to the figure, and experiment with changing the numbers and variables in the figure!

```
Warning: Removed 2 rows containing missing values (`geom_point()`).
```





Code used to make the plot–try on your own first!

Time to practice! Independent plot making.

In this section, you'll have the chance to make more plots on your own. We'll display different plots with several new features to try, and you can use your plotting and researching skills to recreate them. This is a great opportunity to experiment, be creative, and see what you can come up with! Remember, questions are always welcome.

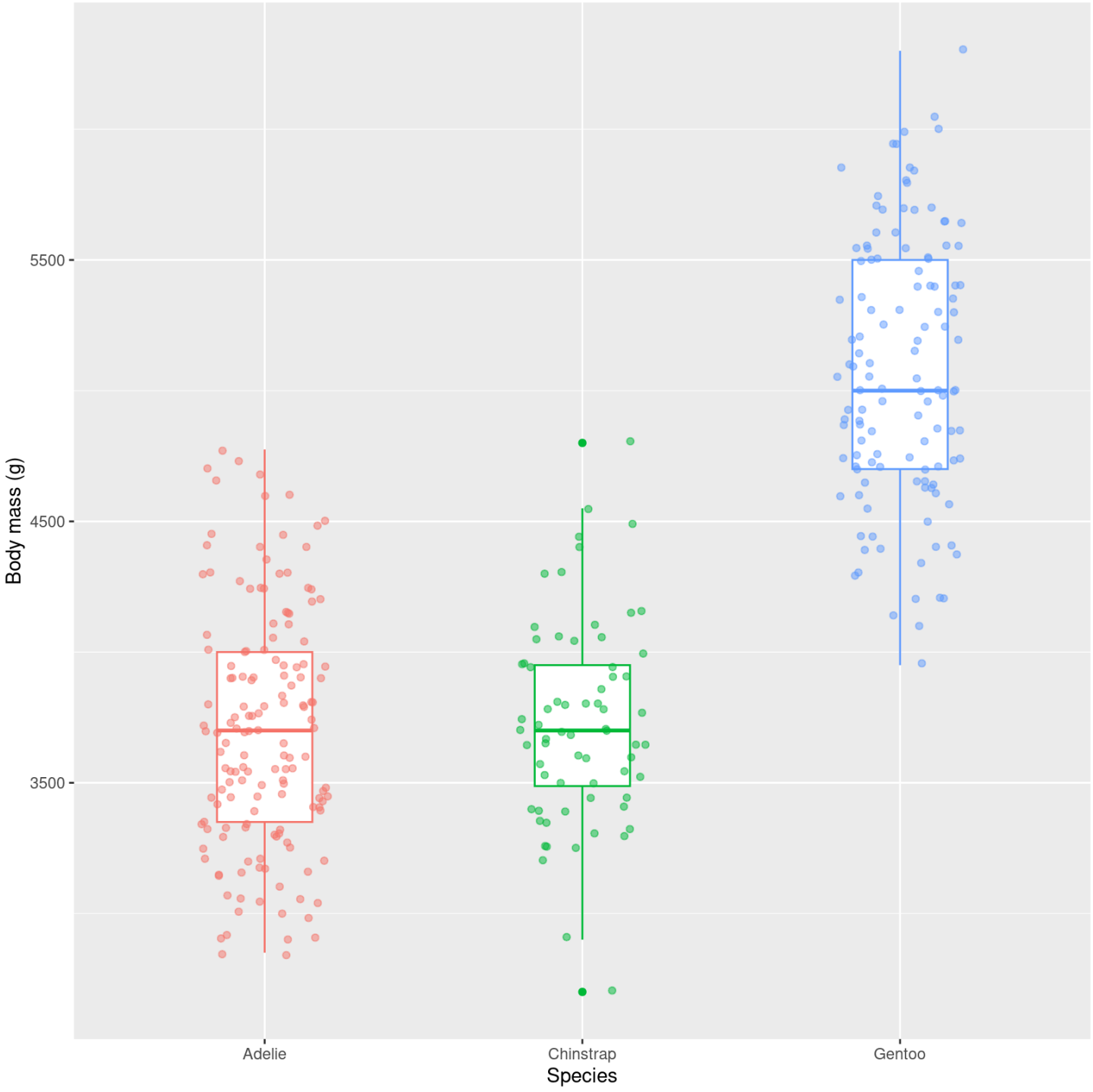
Numerical by categorical plots

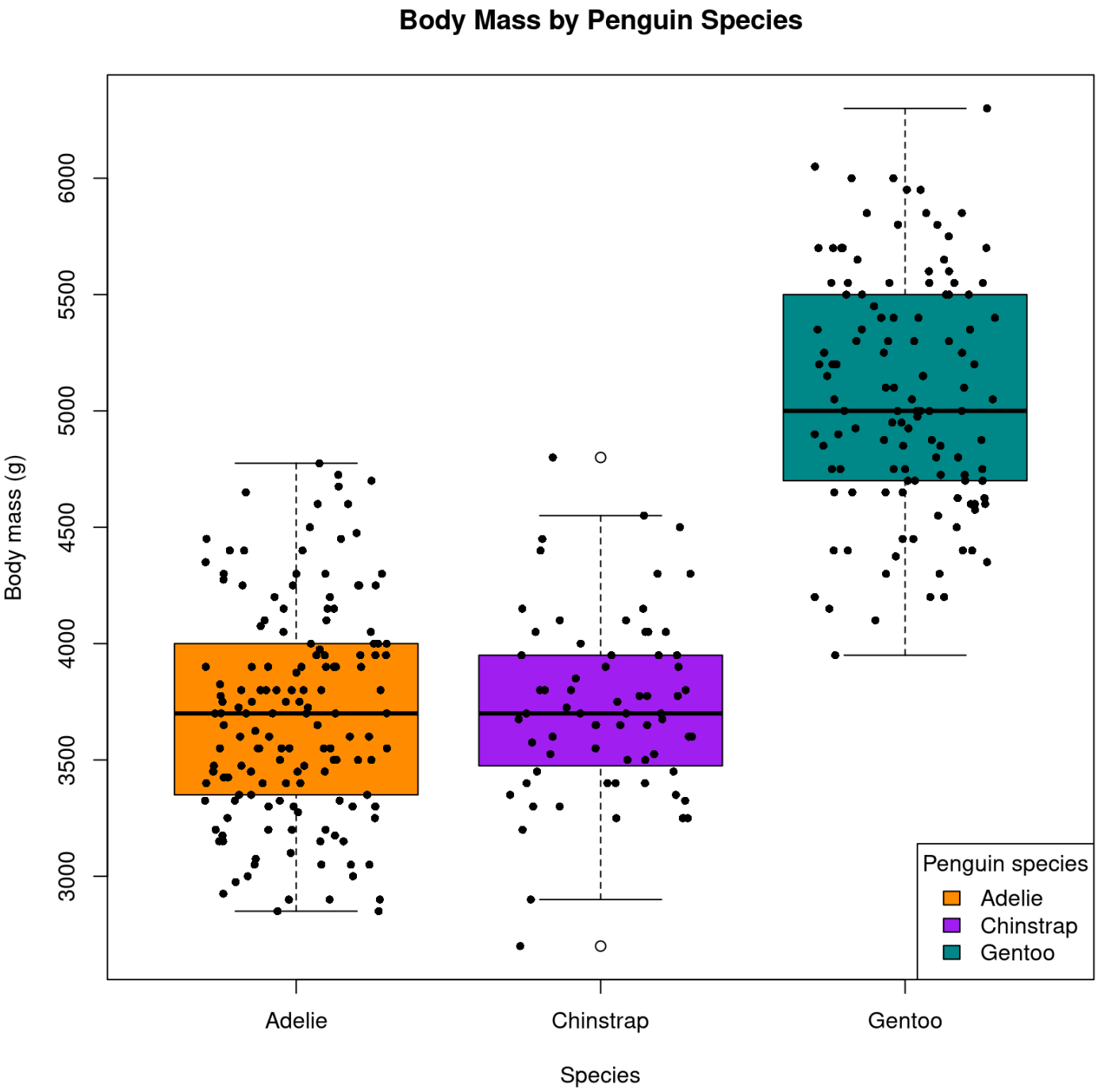
Try making some numerical by categorical plots on your own using this dataset! This example looks at body mass in each species, using jittered points. See if you can recreate this on your own!

> **Hint – a reminder of the basic syntax for boxplots**

```
Warning: Removed 2 rows containing non-finite values (`stat_boxplot()`).

Warning: Removed 2 rows containing missing values (`geom_point()`).
```





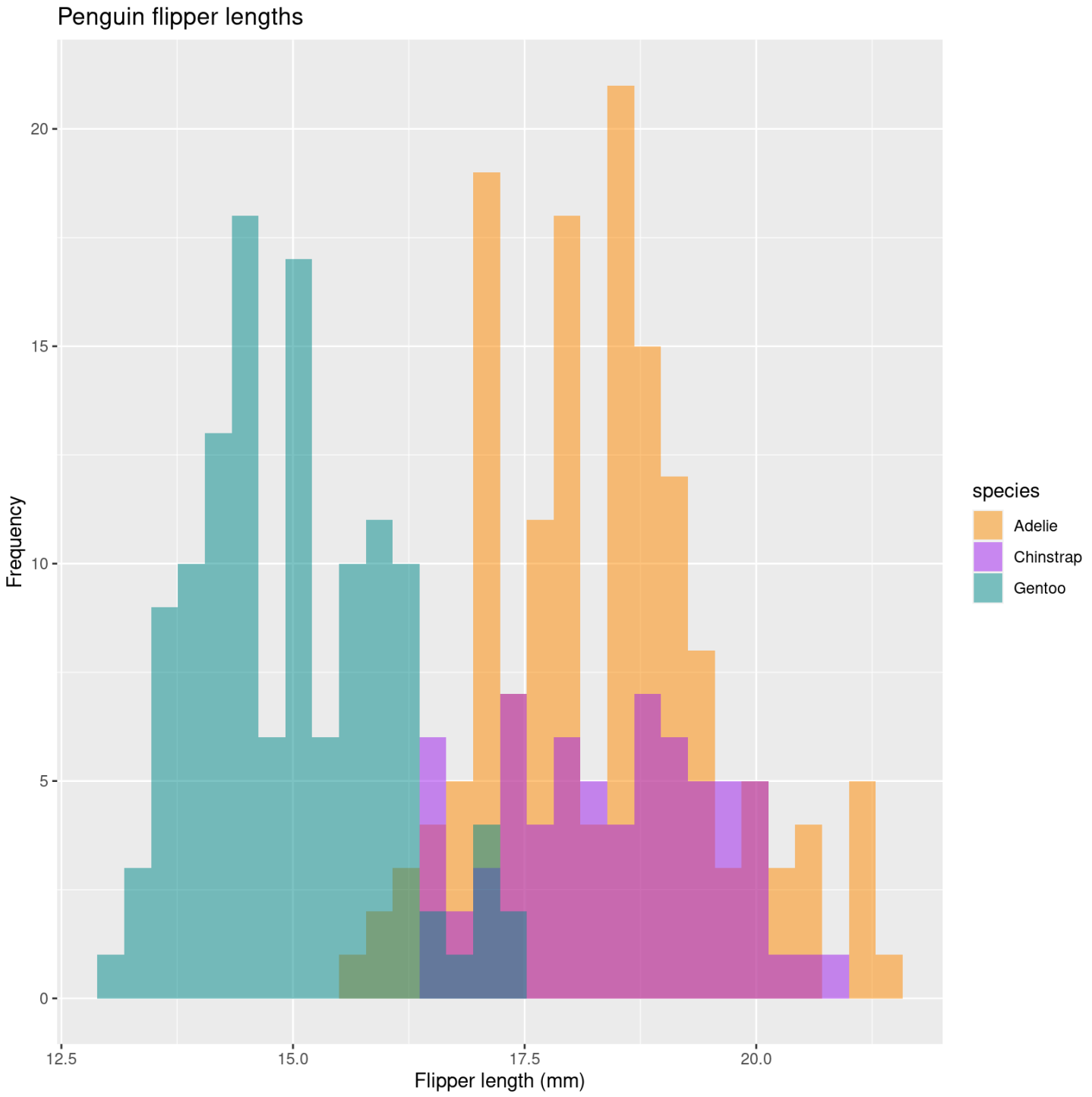
How to recreate this plot–try on your own first!

Example plot: distribution of a numerical variable

If we want to loot at the distribution of one numerical variable in detail, we could use a histogram. Here is an example of histograms that show us the distributions of each species, using new features like partially transparent colors and custom bar widths.

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
Warning: Removed 2 rows containing non-finite values (`stat_bin()`).
```



> **Hint – a reminder of the basic syntax for histograms**

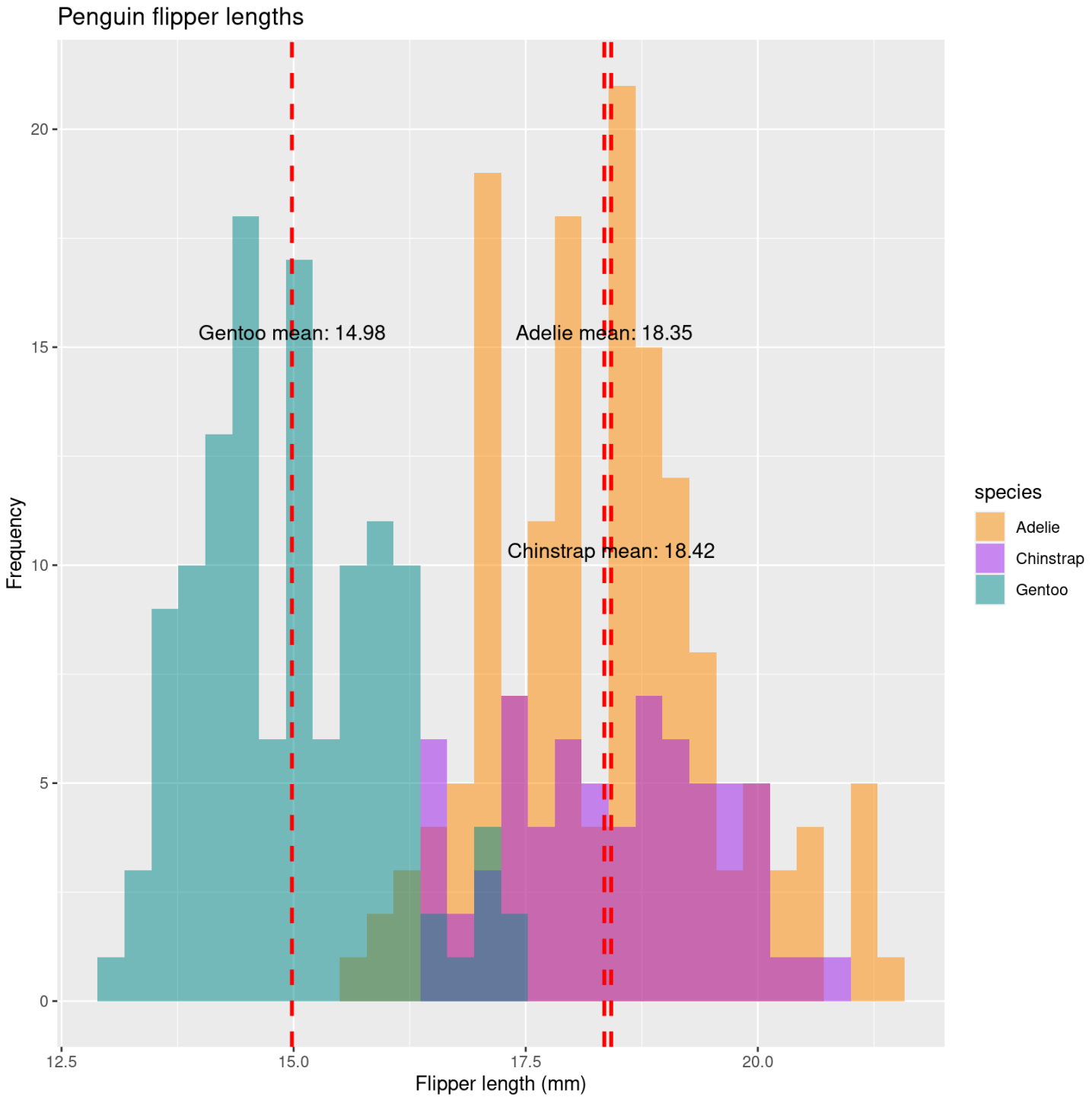
> **How do we change bin widths for histograms?**

Challenge: Can we find the means of these distributions, and plot the means on our histograms? Can we add text so the plot viewer can see what the mean is?

```
Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
ℹ Please use `linewidth` instead.
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
Warning: Removed 2 rows containing non-finite values (`stat_bin()`).
```



Code for this image

Mini-Lesson: Introduction to facet_grid in ggplot2

Background:

In data visualization, particularly when dealing with complex datasets, it's beneficial to compare subsets of data across different categories simultaneously. ggplot2 provides various functions for creating faceted

plots, with **facet_grid** being a prominent choice for creating grids that can help in exploring interactions between variables.

Faceting:

Faceting refers to the strategy of splitting one plot into multiple plots based on a factor (or factors) included in the dataset. Each plot represents a level of the factor(s) and shares the same axis scaling and grids, which makes them easy to compare.

The facet_grid function creates a matrix of panels defined by row and column faceting variables. The general syntax is:

```
facet_grid(rows ~ cols)
```

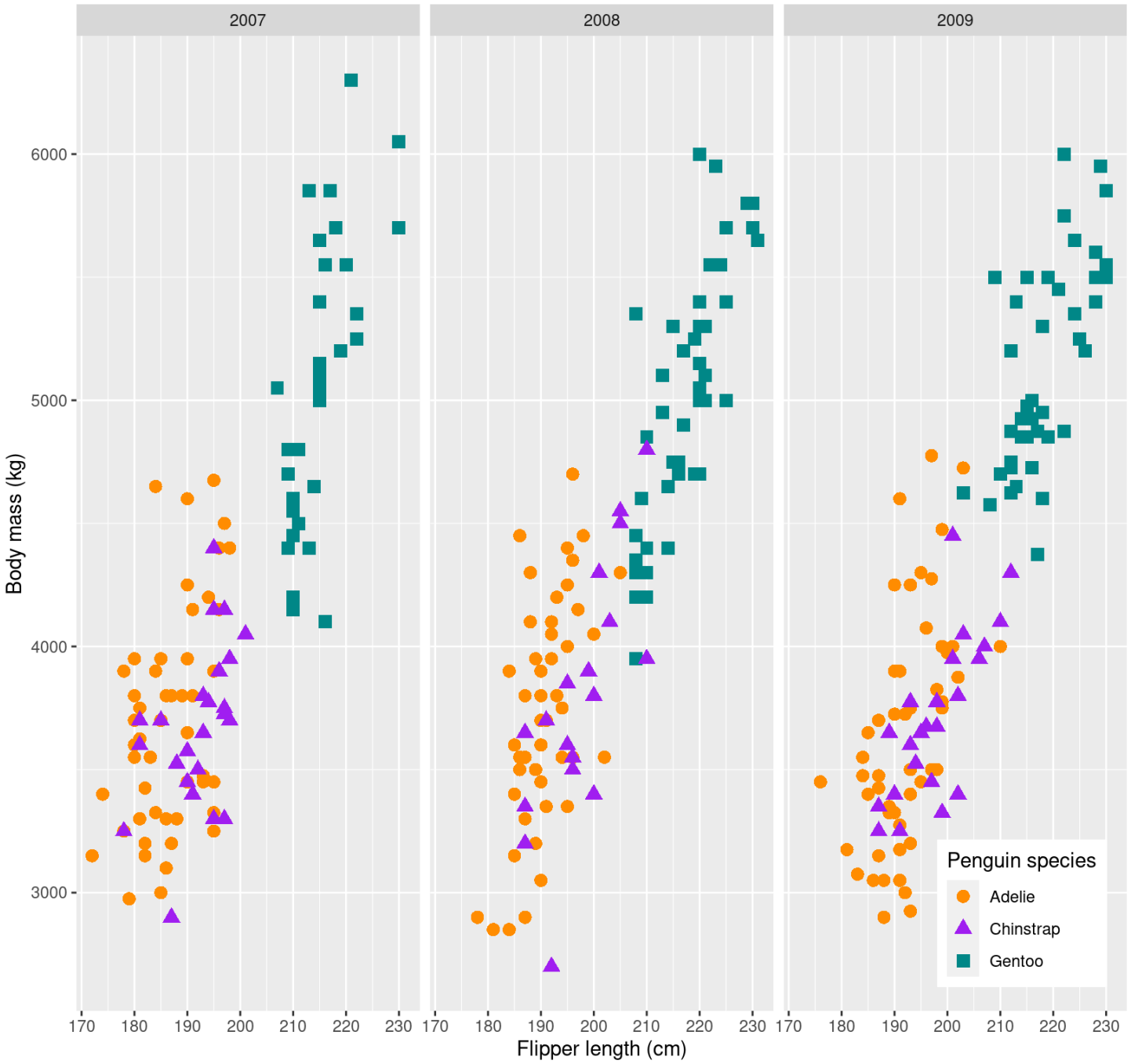
If we just want to facet by rows or just by columns, replace that spot with a ".".

```
#facet by rows
facet_grid(rows ~ .)
#facet by cols
facet_grid(. ~ cols)
```

Lets take some of the plots we made earlier and facet them by the categorical variable year! Note that in some situations it makes more sense to facet by columns, and others by rows.

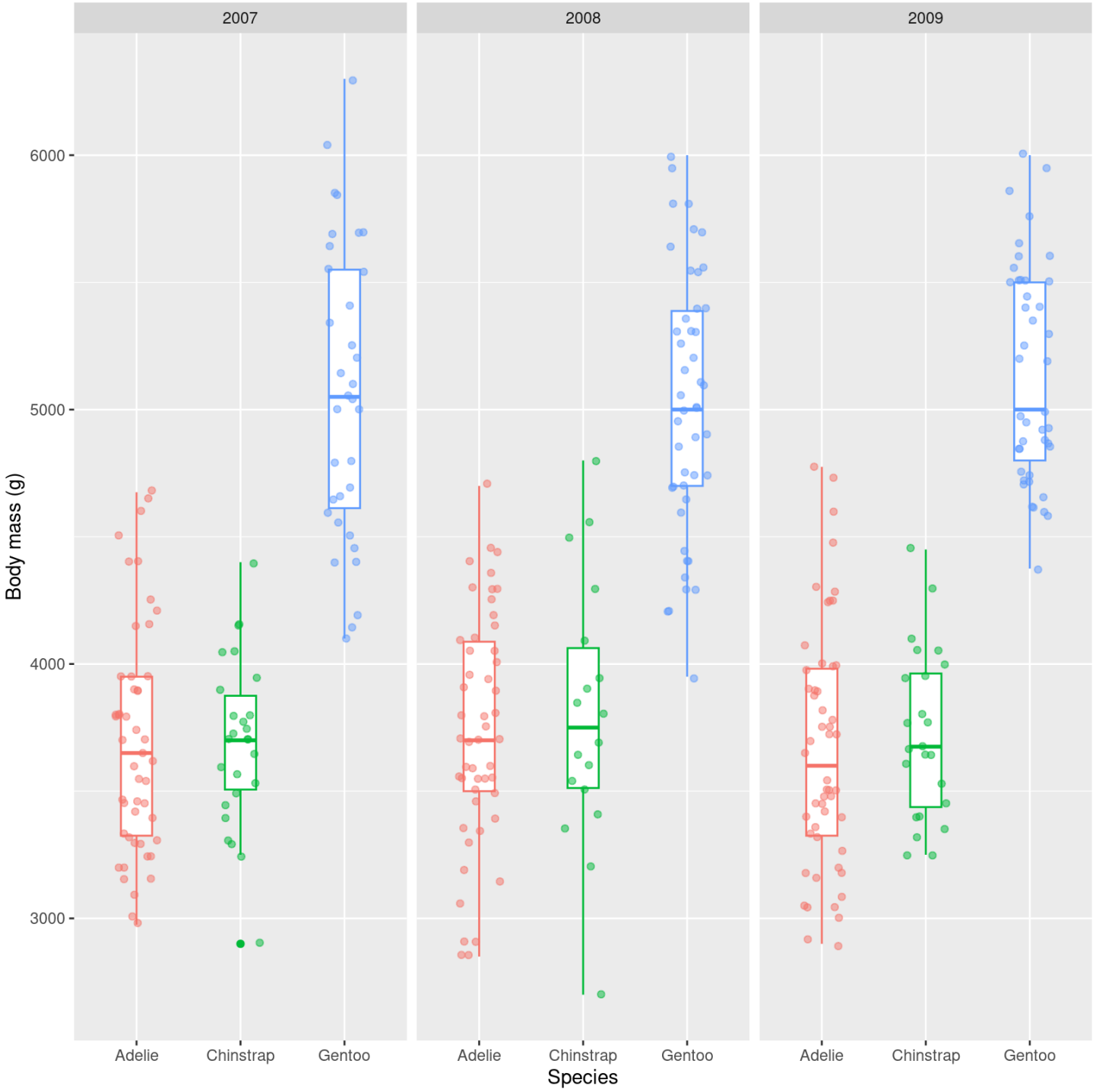
```
# Scatter plots with facet_grid
ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(aes(color = species, shape = species), size = 3) +
  scale_color_manual(values = c("darkorange","purple","cyan4")) +
  labs(title = "Penguin size, Palmer Station LTER",
       subtitle = "Flipper length and body mass for Adelie, Chinstrap and Gentoo Peng
       x = "Flipper length (cm)",
       y = "Body mass (kg)",
       color = "Penguin species",
       shape = "Penguin species") +
  theme(legend.position = c(0.9, 0.1), # x and y on a relative scale (0-1)
        plot.title.position = "plot",
        plot.caption = element_text(hjust = 0, face= "italic"),
        plot.caption.position = "plot") +
  facet_grid(. ~ year)
```

```
Warning: Removed 2 rows containing missing values (`geom_point()`).
```




```
#Boxplots with facet_grid
ggplot(data = penguins, aes(x = species, y = body_mass_g)) +
  geom_boxplot(aes(color = species), width = 0.3, show.legend = FALSE) +
  geom_jitter(aes(color = species), alpha = 0.5, show.legend = FALSE, position = posi
  labs(x = "Species",
       y = "Body mass (g)") +
  facet_grid(. ~ year)
```

```
Warning: Removed 2 rows containing non-finite values (`stat_boxplot()`).
Removed 2 rows containing missing values (`geom_point()`).
```




```
# Histograms with facet_grid for year
ggplot(penguins, aes(x = bill_depth_mm, fill = species)) +
  geom_histogram(aes(fill = species),
     alpha = 0.5,
     position = "identity",
     binwidth=0.5) +
  scale_fill_manual(values = c("darkorange","purple","cyan4")) +
  labs(x = "Flipper length (mm)",
     y = "Frequency",
     title = "Penguin flipper lengths")+
  geom_vline(data = mean_depth, aes(xintercept = mean_bill_depth),
     color = "red", linetype = "dashed", size = 1) +
```

```
          geom_text(data = mean_depth, aes(x = mean_bill_depth, y = c(10,7,5,10,7,5,10,7,5),
             label = paste(species, "mean:", round(mean_bill_depth, 2))),
             color = "black", vjust = -0.3, hjust = 0.5, size = 4) +
          facet_grid(year ~ .)
```

```
Warning: Removed 2 rows containing non-finite values (`stat_bin()`).
```