

Visualising data with ggplot2

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Q&A

ggplot vs ggformula?

ggformula is nice and concise. But more stats-y. And less common outside Calvin.

What's alpha?

0 = fully transparent. 1 = fully opaque

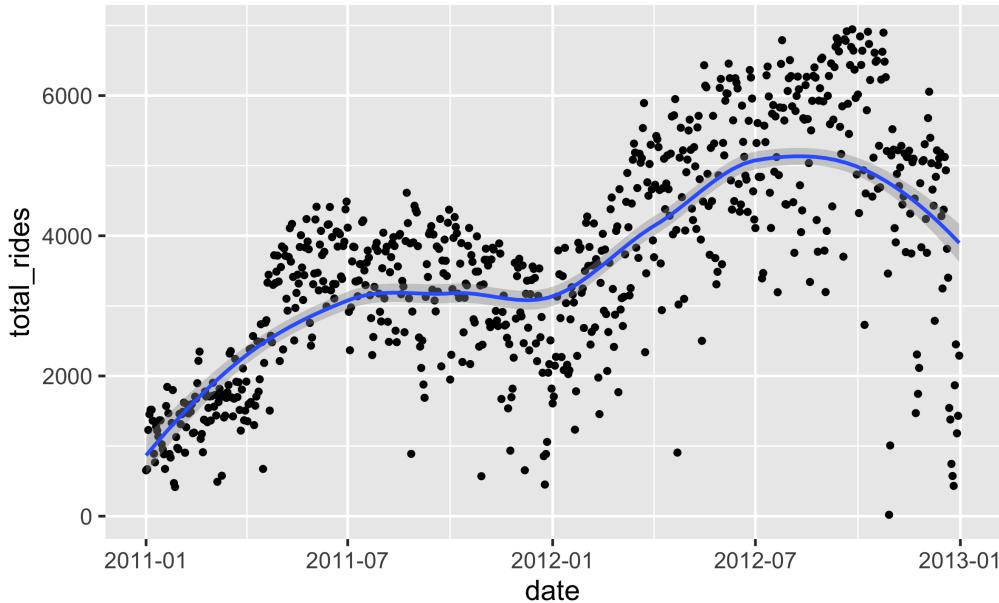
Where to get help?

Piazza, RStudio docs (cheatsheets!), StackOverflow (but be wise), [R Graph Gallery](#)

read_csv

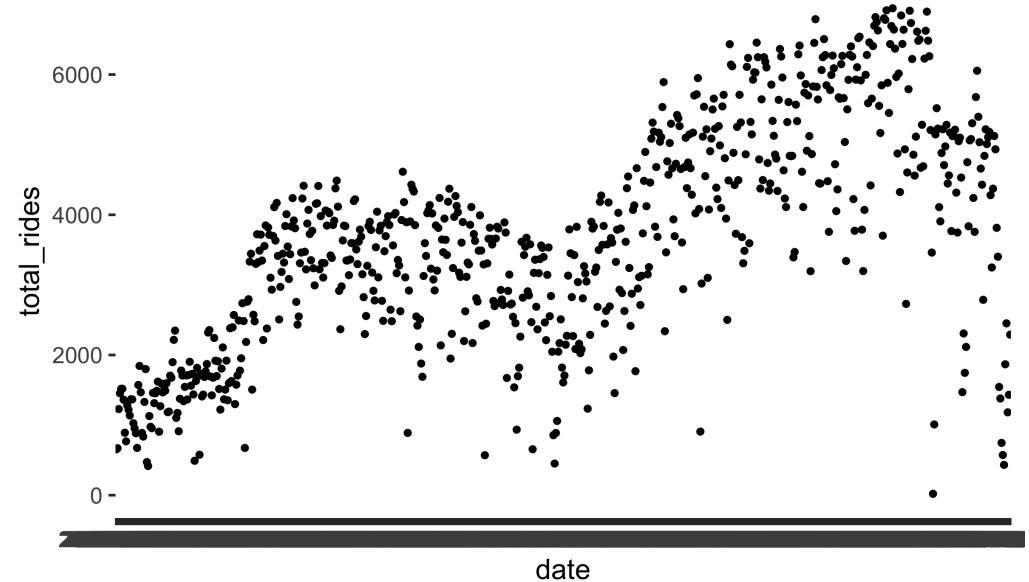
```
daily_rides <- read_csv(filename)  
class(daily_rides$date)
```

```
## [1] "Date"
```

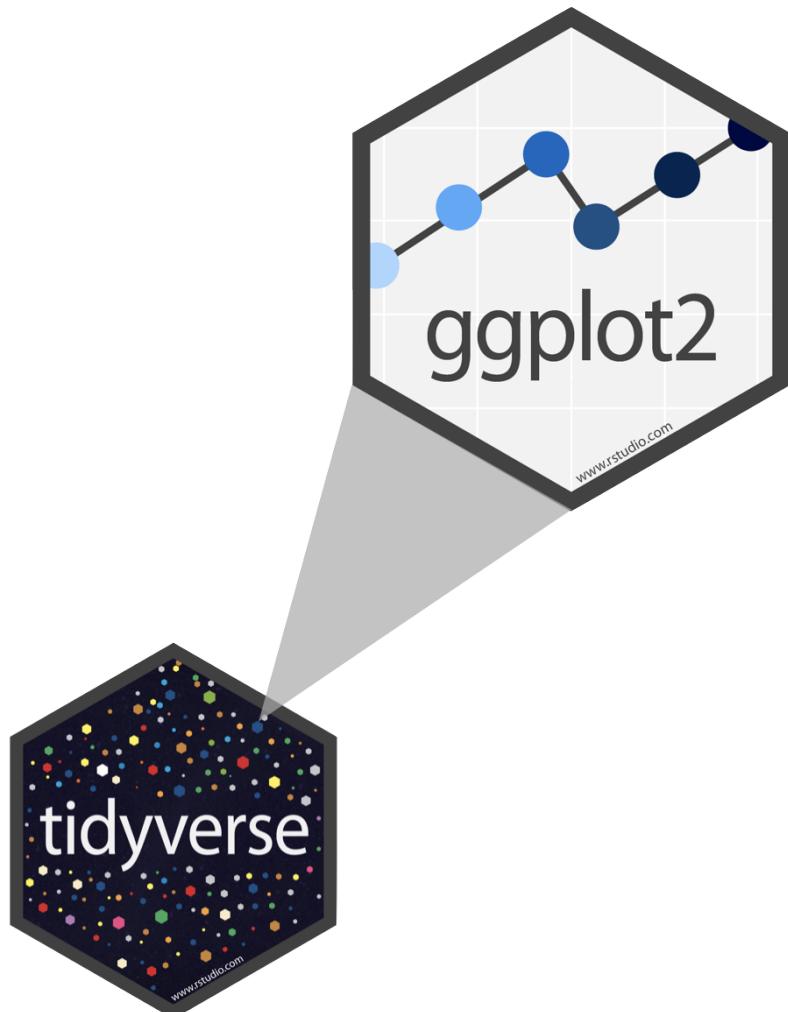


```
daily_rides <- read.csv(filename)  
class(daily_rides$date)
```

```
## [1] "character"
```



ggplot2 ∈ tidyverse



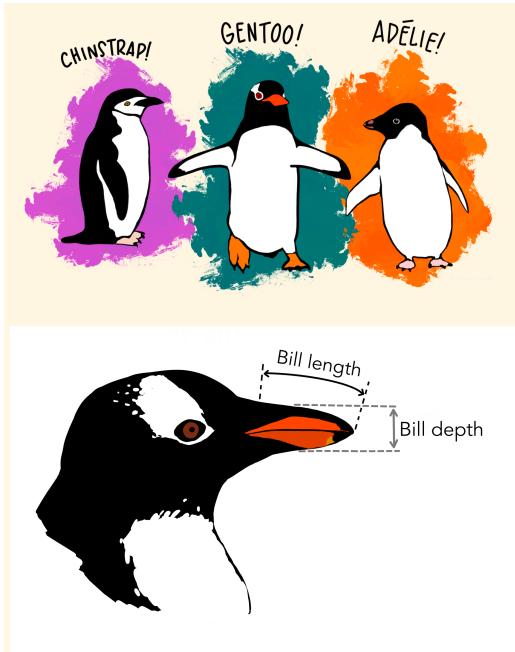
- **ggplot2** is tidyverse's data visualization package
- Structure of the code for plots:

```
ggplot(data = [dataset],  
       mapping = aes(x = [x-variable],  
                     y = [y-variable])) +  
  geom_xxx() +  
  other layers and options
```

ggplot2 ❤️ 🐧

Data: Palmer Penguins

Measurements for penguin species, island in Palmer Archipelago, size (flipper length, body mass, bill dimensions), and sex.

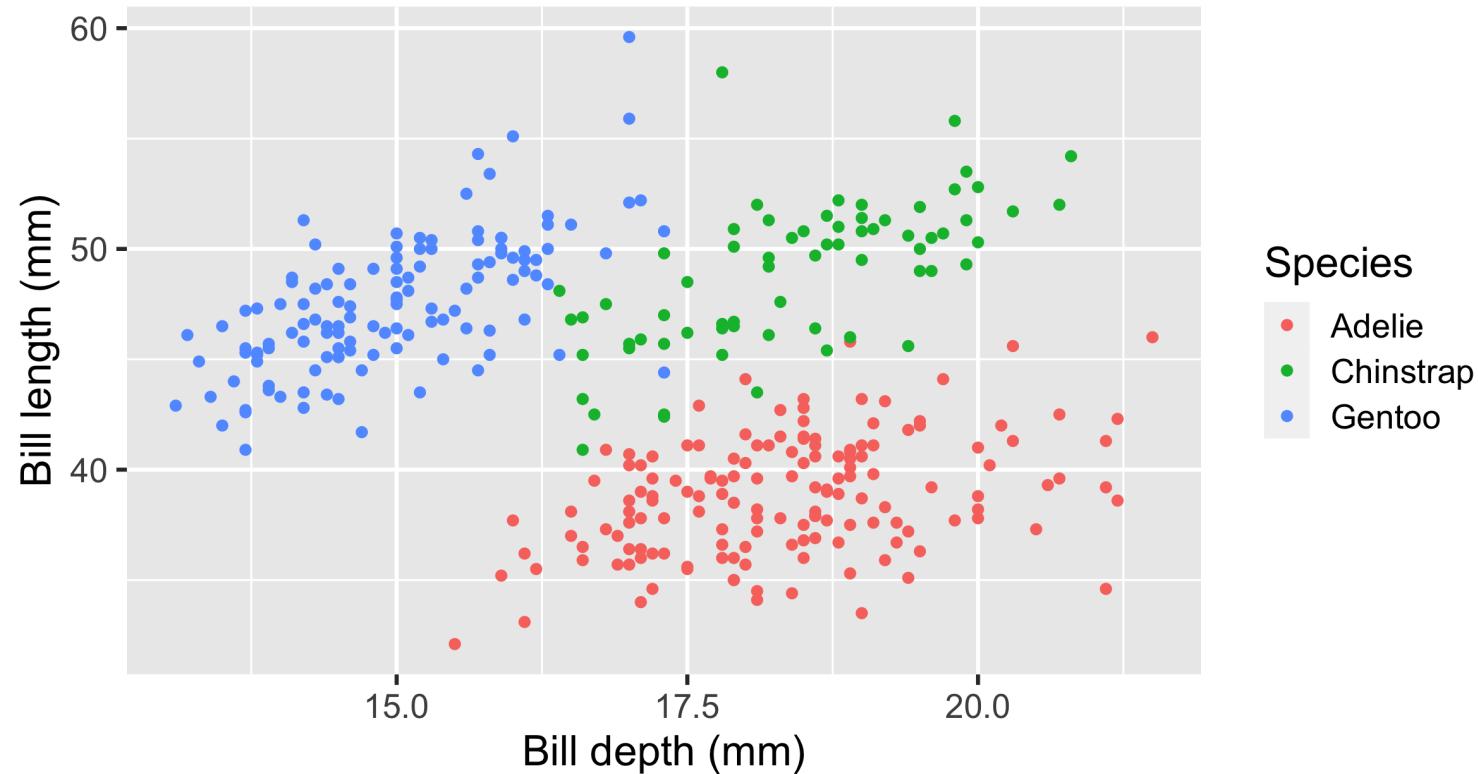


```
library(palmerpenguins)  
glimpse(penguins)
```

```
## Rows: 344  
## Columns: 8  
## $ species          <fct> Adelie, Adelie, Adelie, Adelie,  
## $ island            <fct> Torgersen, Torgersen, Torgersen, Torg  
## $ bill_length_mm    <dbl> 39.1, 39.5, 40.3, NA, 36.7, 39.3, 38.  
## $ bill_depth_mm     <dbl> 18.7, 17.4, 18.0, NA, 19.3, 20.6, 17.  
## $ flipper_length_mm <int> 181, 186, 195, NA, 193, 190, 181, 195  
## $ body_mass_g        <int> 3750, 3800, 3250, NA, 3450, 3650, 362  
## $ sex                <fct> male, female, female, NA, female, mal  
## $ year               <int> 2007, 2007, 2007, 2007, 2007, 2007, 2
```

Bill depth and length

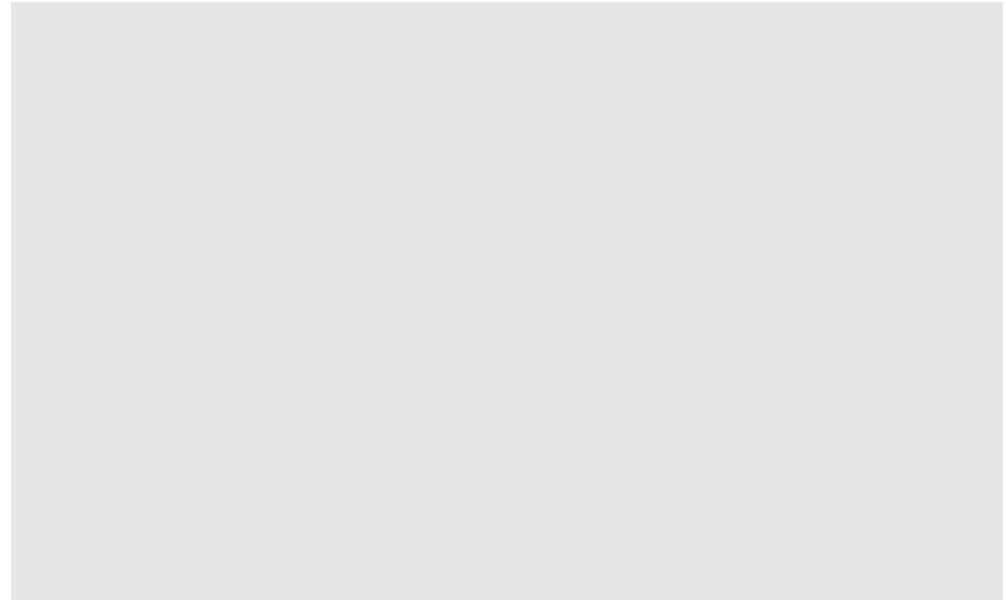
Dimensions for Adelie, Chinstrap, and Gentoo Penguins



Coding out loud

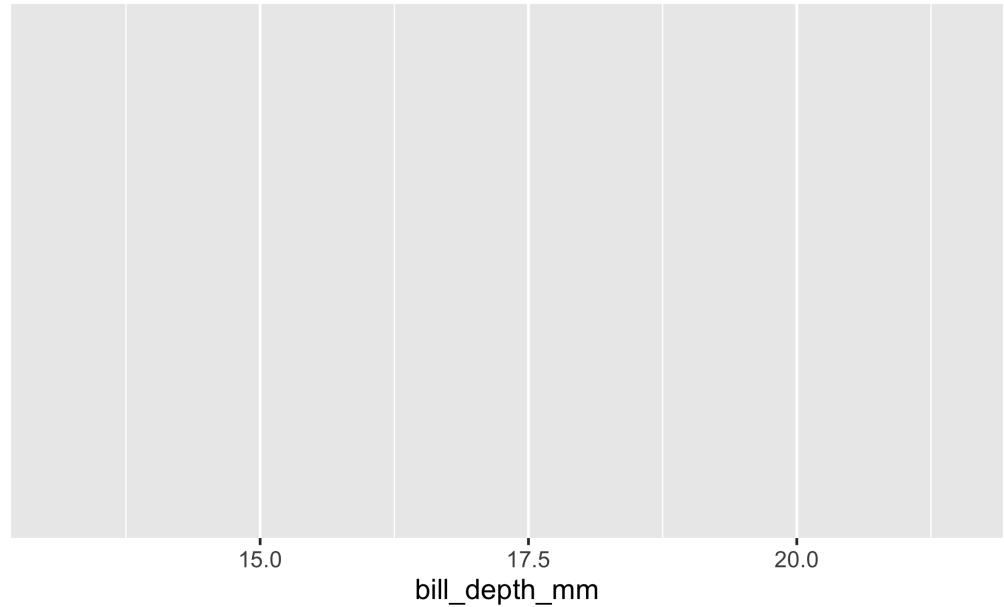
| Start with the penguins **data frame**

```
ggplot(data = penguins)
```



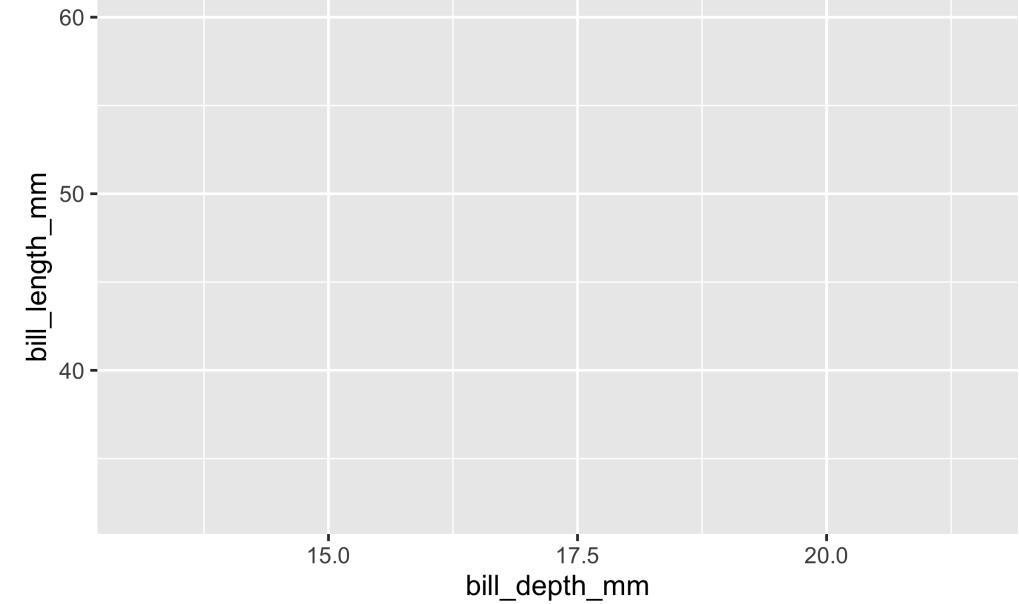
| Start with the penguins data frame, **map bill depth to the x-axis**

```
ggplot(data = penguins,  
       mapping = aes(x = bill_depth_mm))
```



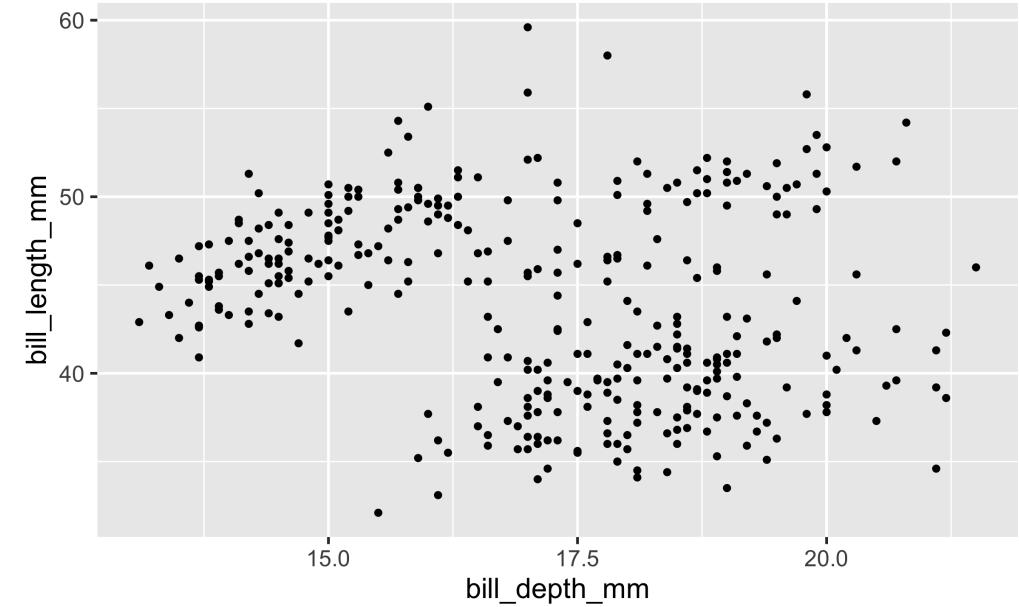
Start with the penguins data frame, map bill depth to the x-axis **and map bill length to the y-axis.**

```
ggplot(data = penguins,  
       mapping = aes(x = bill_depth_mm,  
                      y = bill_length_mm))
```



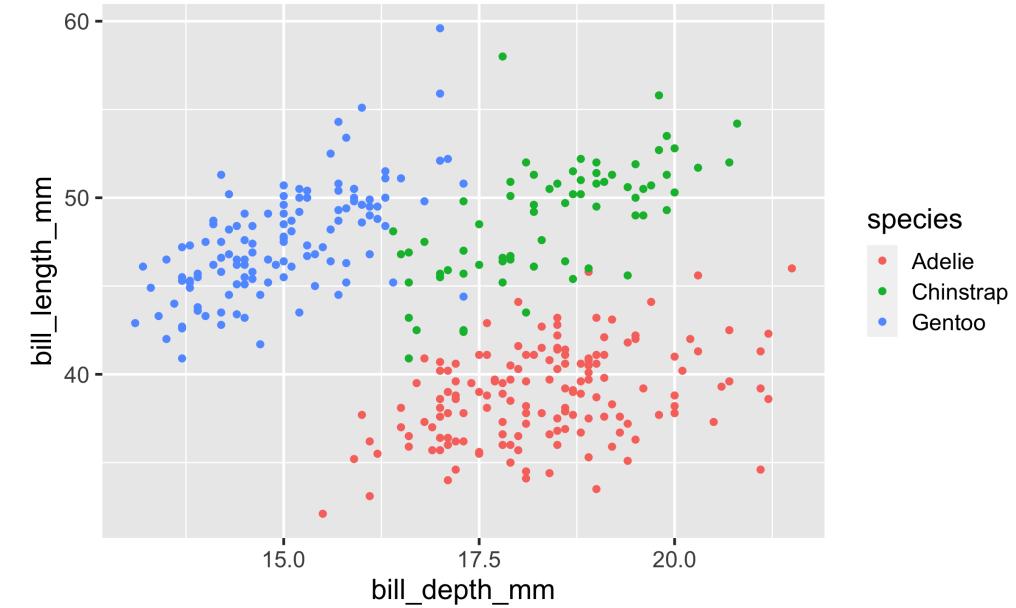
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis.
Represent each observation with a point

```
ggplot(data = penguins,  
       mapping = aes(x = bill_depth_mm,  
                      y = bill_length_mm))  
  geom_point()
```



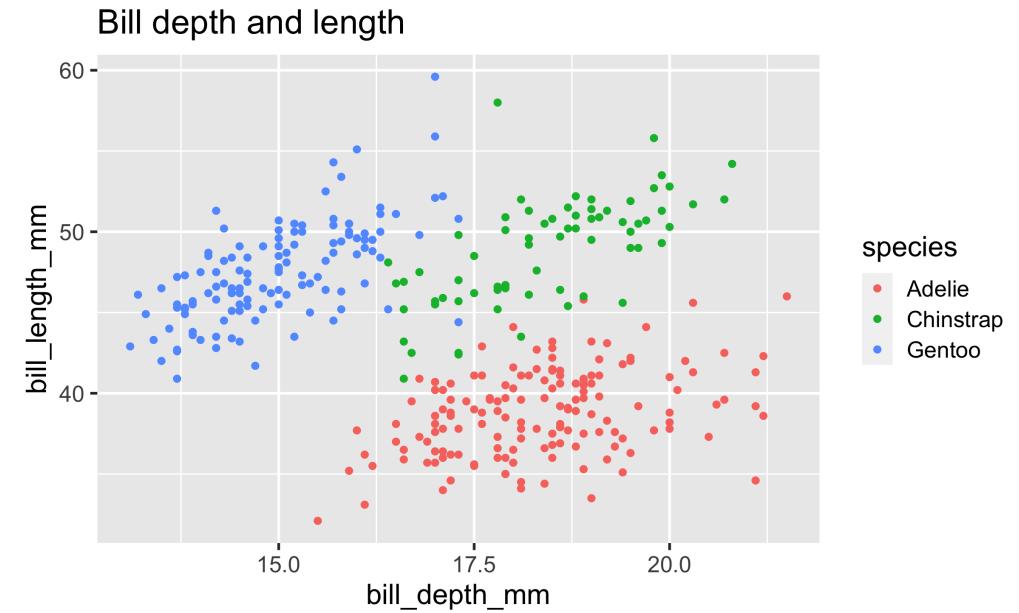
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point **and map species to the color of each point.**

```
ggplot(data = penguins,  
       mapping = aes(x = bill_depth_mm,  
                      y = bill_length_mm,  
                      color = species)) +  
  geom_point()
```



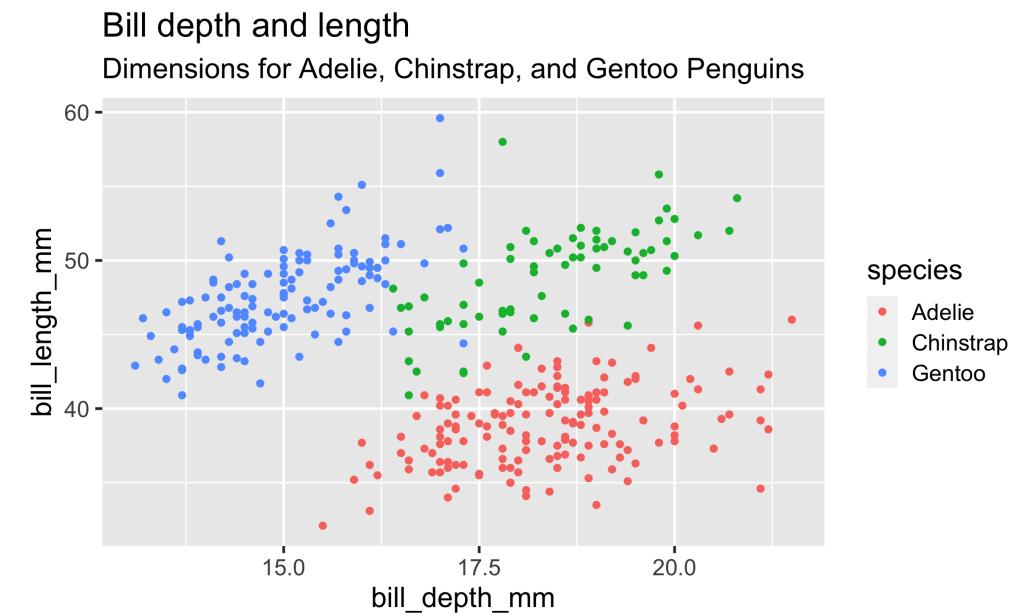
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. **Title the plot "Bill depth and length"**

```
ggplot(data = penguins,  
       mapping = aes(x = bill_depth_mm,  
                      y = bill_length_mm,  
                      color = species)) +  
  geom_point() +  
  labs(title = "Bill depth and length")
```



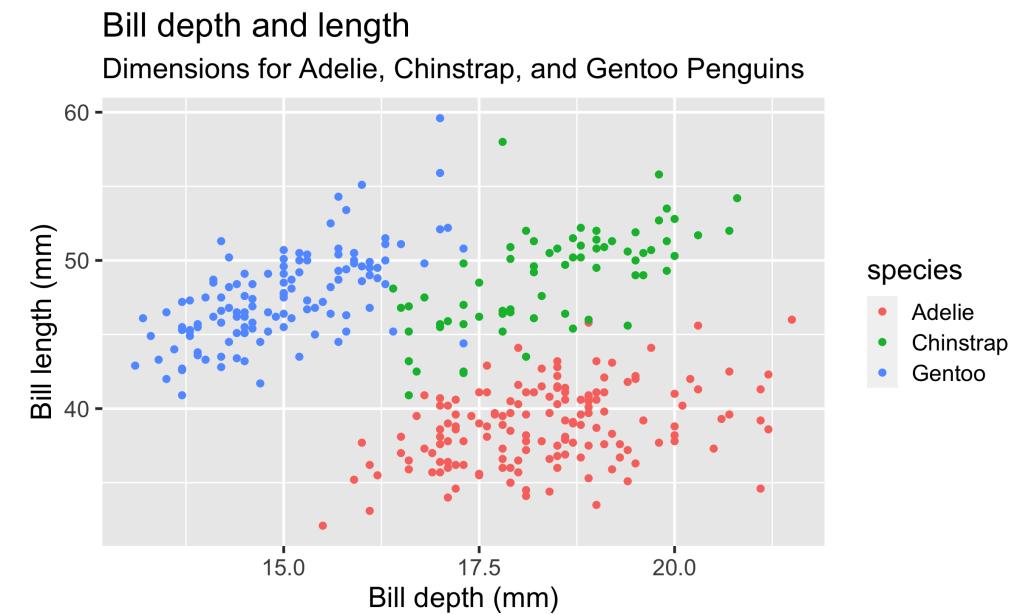
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. Title the plot "Bill depth and length", **add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins"**

```
ggplot(data = penguins,  
       mapping = aes(x = bill_depth_mm,  
                      y = bill_length_mm,  
                      color = species)) +  
  geom_point() +  
  labs(title = "Bill depth and length",  
       subtitle = "Dimensions for Adelie,"
```



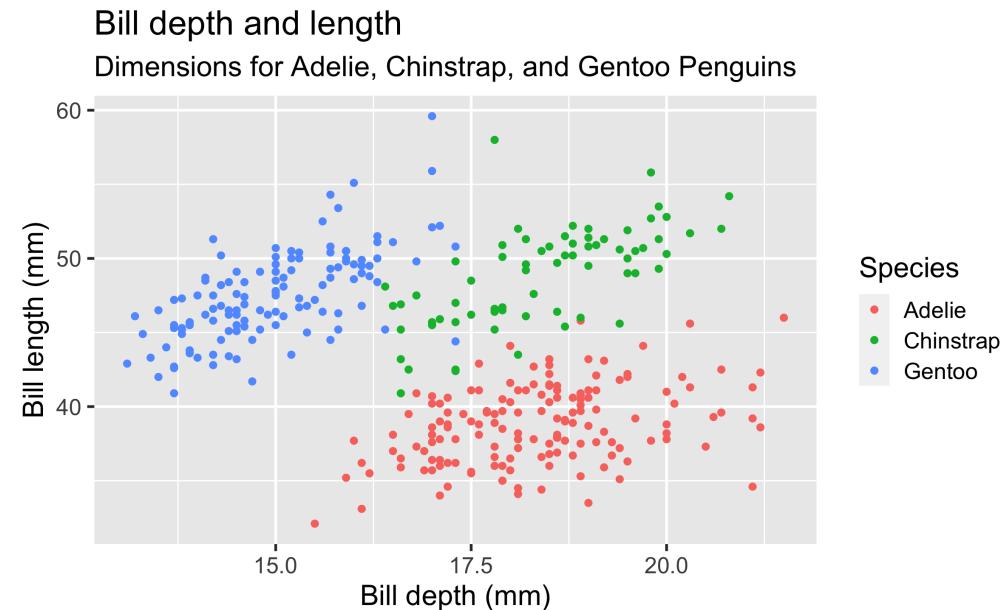
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins", **label the x and y axes as "Bill depth (mm)" and "Bill length (mm)", respectively**

```
ggplot(data = penguins,  
       mapping = aes(x = bill_depth_mm,  
                      y = bill_length_mm,  
                      color = species)) +  
  geom_point() +  
  labs(title = "Bill depth and length",  
       subtitle = "Dimensions for Adelie,  
       x = "Bill depth (mm)", y = "Bill le
```



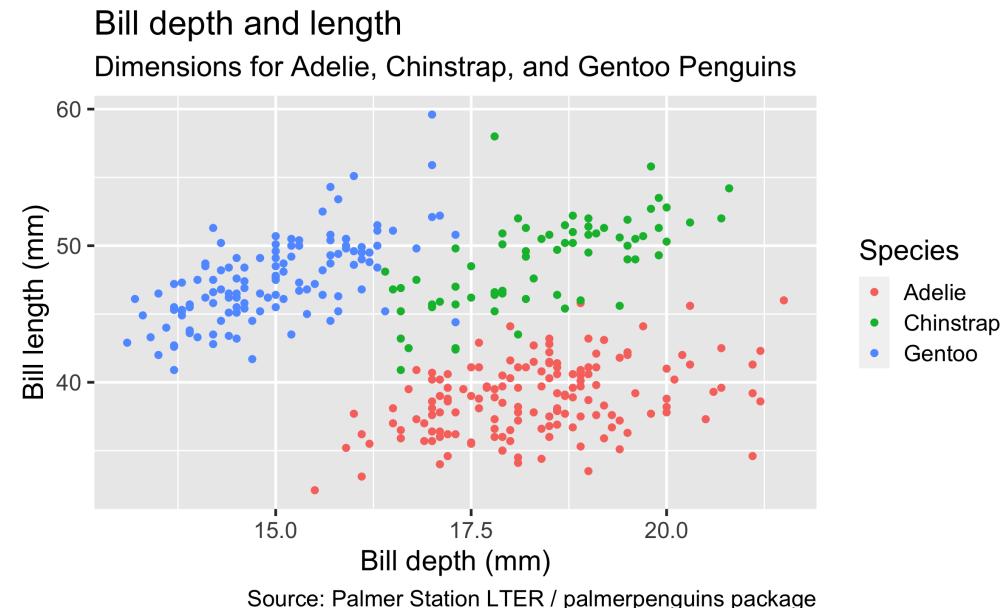
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins", label the x and y axes as "Bill depth (mm)" and "Bill length (mm)", respectively, **label the legend "Species"**

```
ggplot(data = penguins,  
       mapping = aes(x = bill_depth_mm,  
                      y = bill_length_mm,  
                      color = species)) +  
  geom_point() +  
  labs(title = "Bill depth and length",  
       subtitle = "Dimensions for Adelie,  
       x = "Bill depth (mm)", y = "Bill le  
       color = "Species")
```



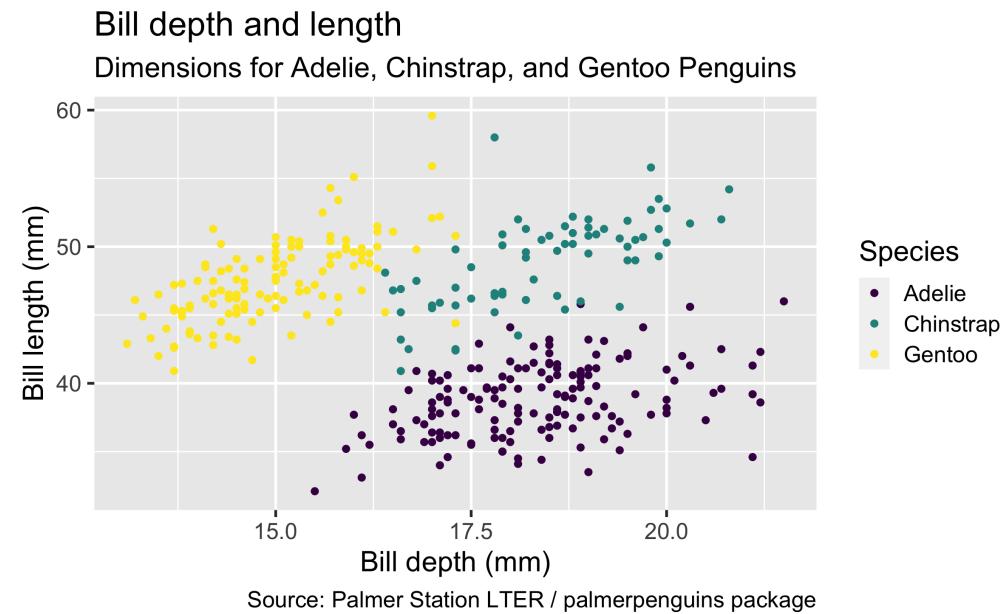
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins", label the x and y axes as "Bill depth (mm)" and "Bill length (mm)", respectively, label the legend "Species", **and add a caption for the data source.**

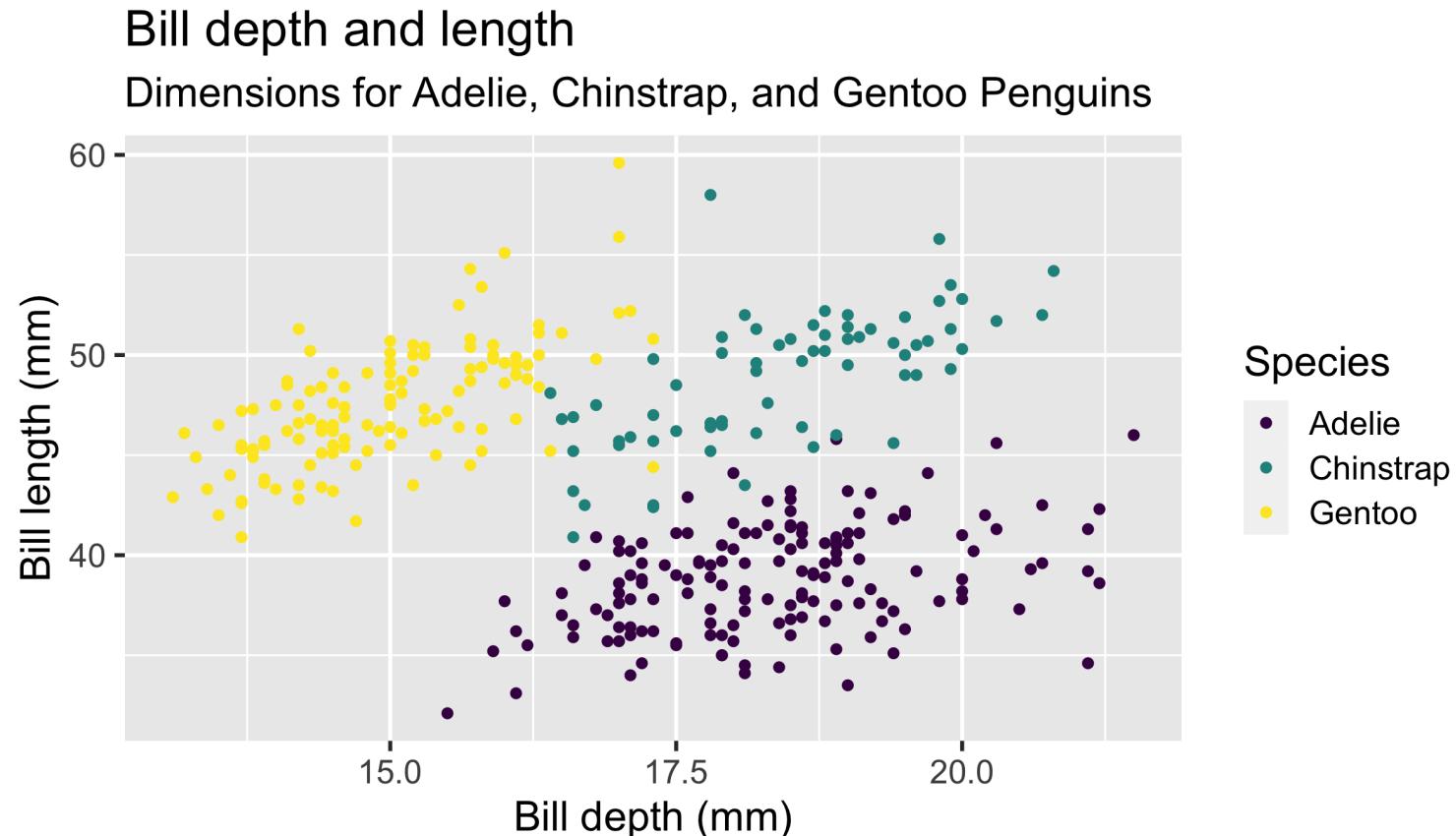
```
ggplot(data = penguins,  
       mapping = aes(x = bill_depth_mm,  
                      y = bill_length_mm,  
                      color = species)) +  
  geom_point() +  
  labs(title = "Bill depth and length",  
       subtitle = "Dimensions for Adelie,  
                  x = "Bill depth (mm)", y = "Bill length (mm)",  
       color = "Species",  
       caption = "Source: Palmer Station LTER / palmerpenguins package")
```



Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins", label the x and y axes as "Bill depth (mm)" and "Bill length (mm)", respectively, label the legend "Species", and add a caption for the data source. **Finally, use a discrete color scale that is designed to be perceived by viewers with common forms of color blindness.**

```
ggplot(data = penguins,  
       mapping = aes(x = bill_depth_mm,  
                      y = bill_length_mm,  
                      color = species)) +  
  geom_point() +  
  labs(title = "Bill depth and length",  
       subtitle = "Dimensions for Adelie,  
x = "Bill depth (mm)", y = "Bill le  
color = "Species",  
       caption = "Source: Palmer Station L  
scale_color_viridis_d()
```





Argument names

You can omit the names of first two arguments when building plots with `ggplot()`.

```
ggplot(data = penguins,  
       mapping = aes(x = bill_depth_mm,  
                      y = bill_length_mm,  
                      color = species)) +  
  geom_point() +  
  scale_color_viridis_d()
```

```
ggplot(penguins,  
       aes(x = bill_depth_mm,  
                      y = bill_length_mm,  
                      color = species)) +  
  geom_point() +  
  scale_color_viridis_d()
```

Aesthetics

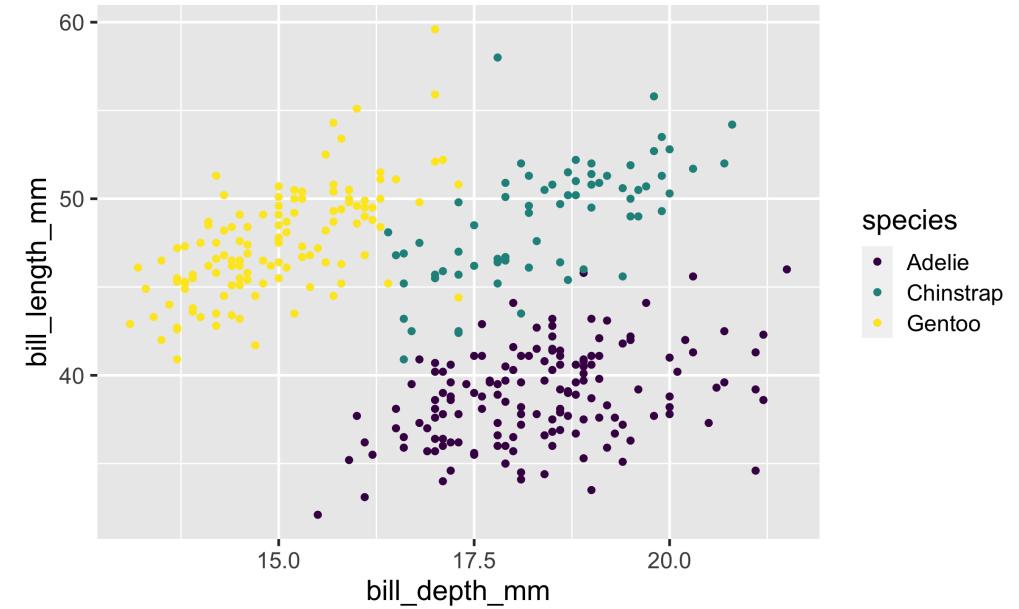
Aesthetics options

Commonly used characteristics of plotting characters that can be **mapped to a specific variable** in the data are

- color
- shape
- size
- alpha (transparency)

Color

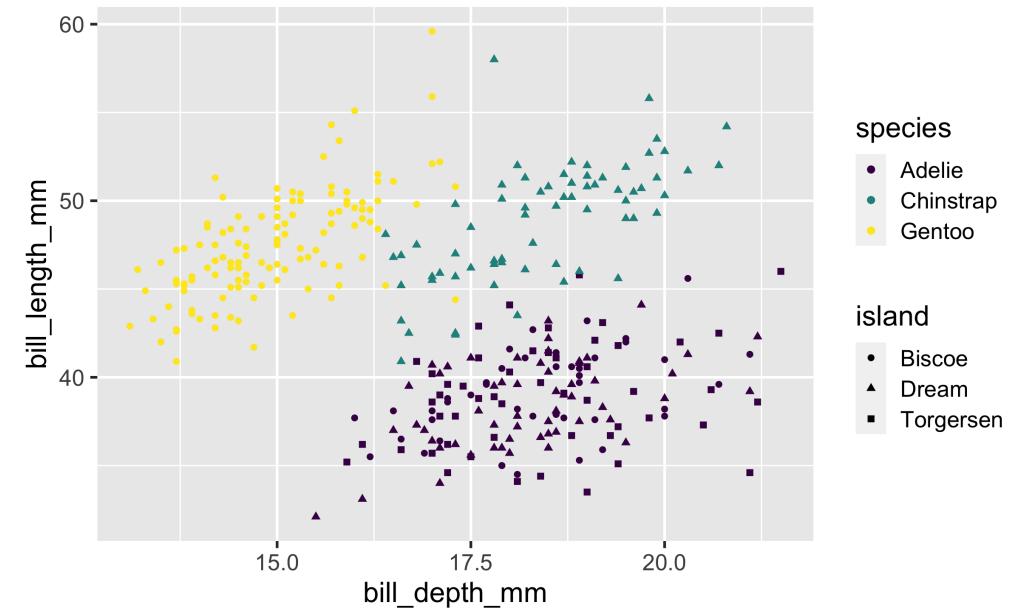
```
ggplot(penguins,  
       aes(x = bill_depth_mm,  
            y = bill_length_mm,  
            color = species)) +  
  geom_point() +  
  scale_color_viridis_d()
```



Shape

Mapped to a different variable than color

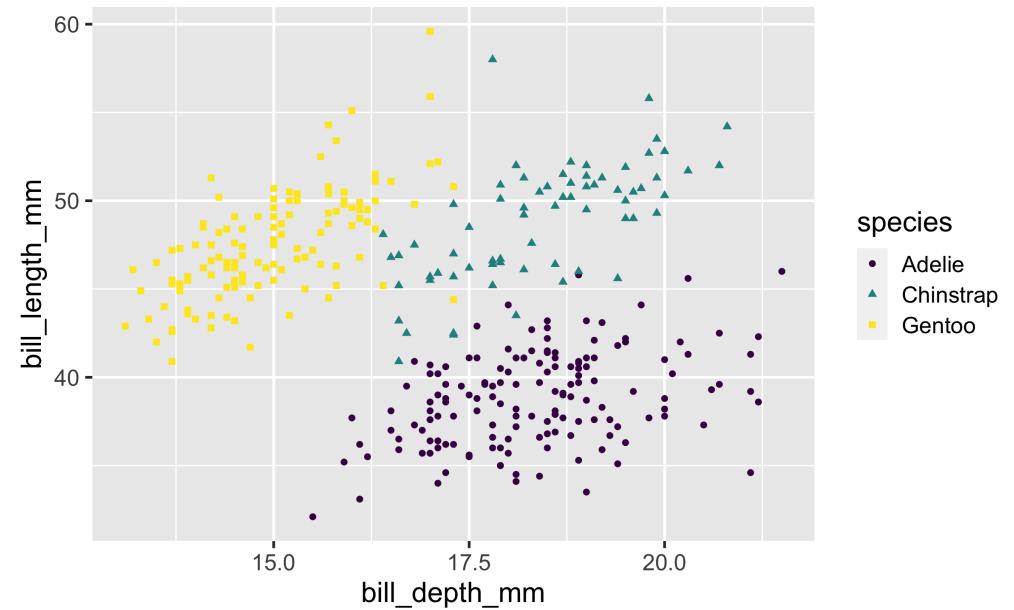
```
ggplot(penguins,  
       aes(x = bill_depth_mm,  
            y = bill_length_mm,  
            color = species,  
            shape = island)) +  
  geom_point() +  
  scale_color_viridis_d()
```



Shape

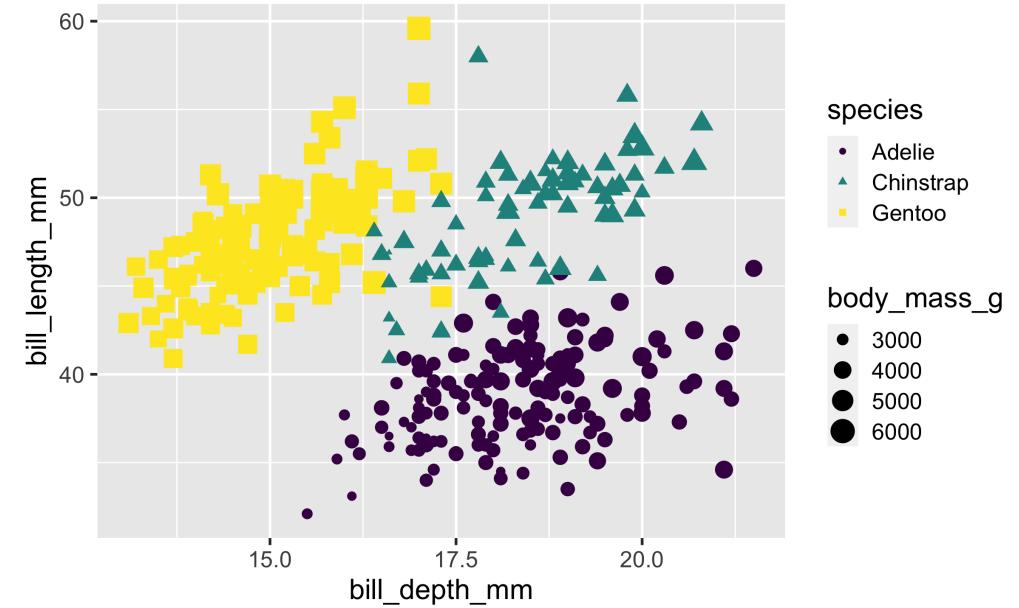
Mapped to same variable as color

```
ggplot(penguins,  
       aes(x = bill_depth_mm,  
            y = bill_length_mm,  
            color = species,  
            shape = species)) +  
  geom_point() +  
  scale_color_viridis_d()
```



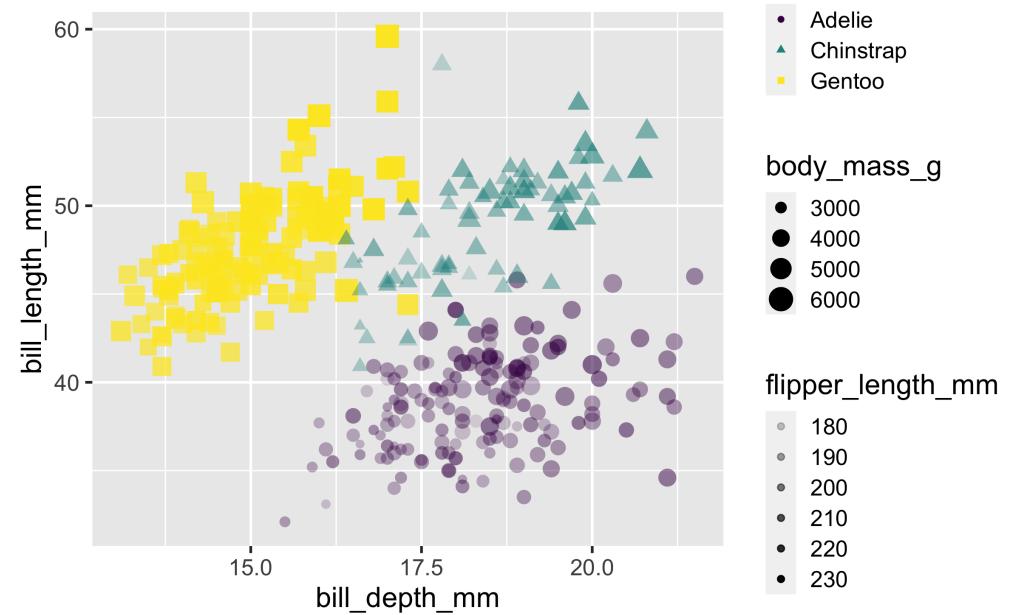
Size

```
ggplot(penguins,  
       aes(x = bill_depth_mm,  
            y = bill_length_mm,  
            color = species,  
            shape = species,  
            size = body_mass_g)) +  
  geom_point() +  
  scale_color_viridis_d()
```



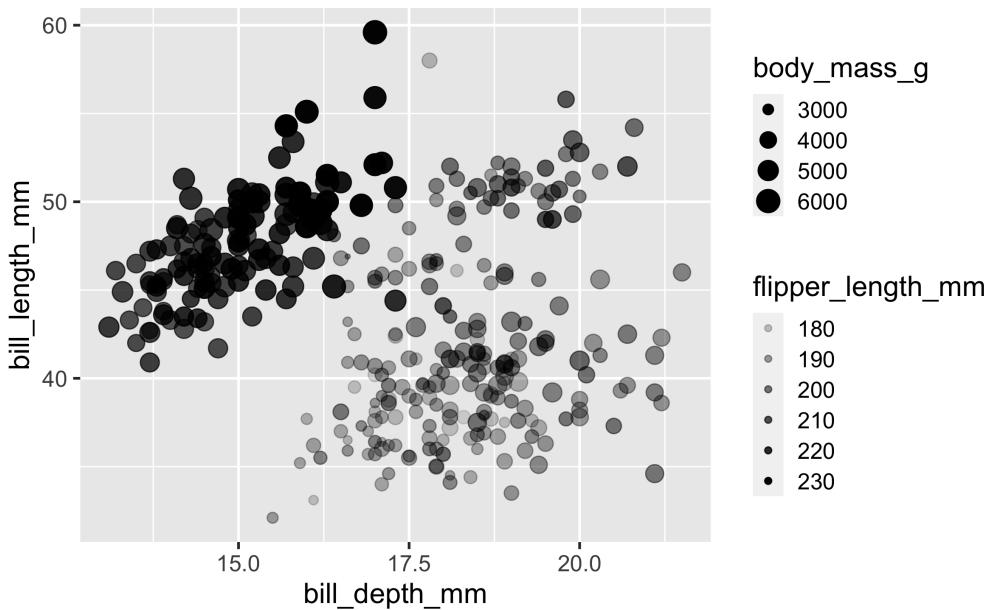
Alpha

```
ggplot(penguins,
       aes(x = bill_depth_mm,
           y = bill_length_mm,
           color = species,
           shape = species,
           size = body_mass_g,
           alpha = flipper_length_mm)) +
  geom_point() +
  scale_color_viridis_d()
```



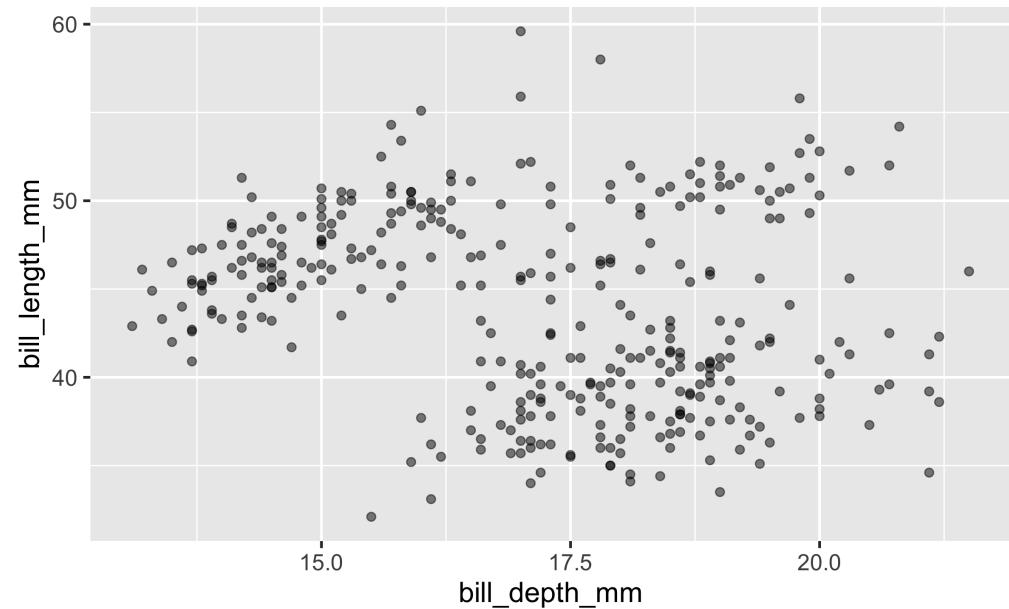
Mapping

```
ggplot(penguins,  
       aes(x = bill_depth_mm,  
            y = bill_length_mm,  
            size = body_mass_g,  
            alpha = flipper_length_mm)) +  
  geom_point()
```



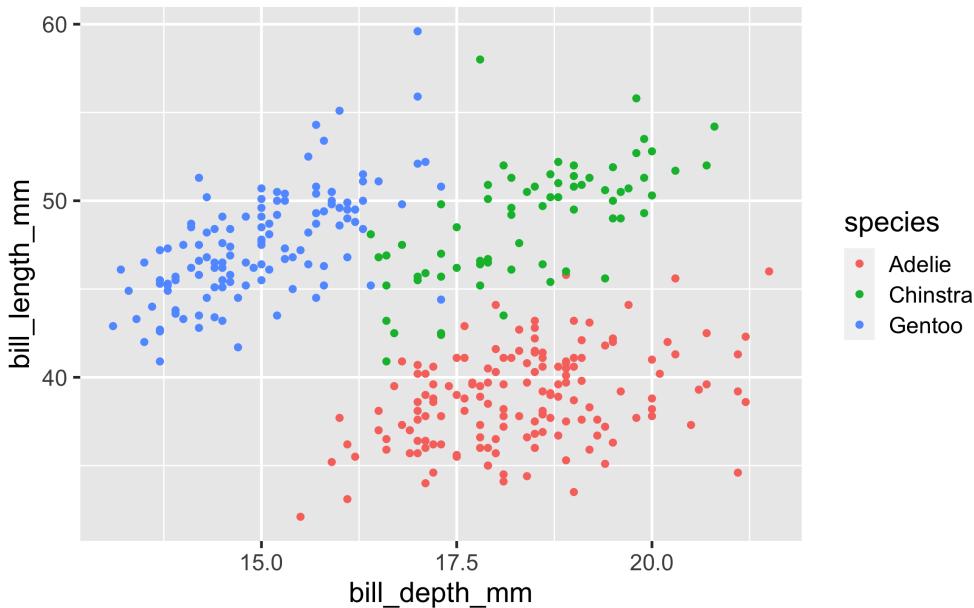
Setting

```
ggplot(penguins,  
       aes(x = bill_depth_mm,  
            y = bill_length_mm)) +  
  geom_point(size = 2, alpha = 0.5)
```



Mapping

```
ggplot(penguins,  
       aes(x = bill_depth_mm,  
            y = bill_length_mm,  
            color = species)) +  
  geom_point()
```



Setting

```
ggplot(penguins,  
       aes(x = bill_depth_mm,  
            y = bill_length_mm)) +  
  geom_point(color = penguins$species)
```

```
## Error: Unknown colour name: Adelie
```

Mapping vs. setting

- **Mapping:** Determine the size, alpha, etc. of points based on the values of a variable in the data
 - goes into `aes()`
 - ggplot computes the actual value using its *scales*
- **Setting:** Determine the size, alpha, etc. of points **not** based on the values of a variable in the data
 - goes into `geom_*`
 - this was `geom_point()` in the previous example, but we'll learn about other geoms soon!
 - ggplot uses the value you give it directly (sets the color to "Adelie")

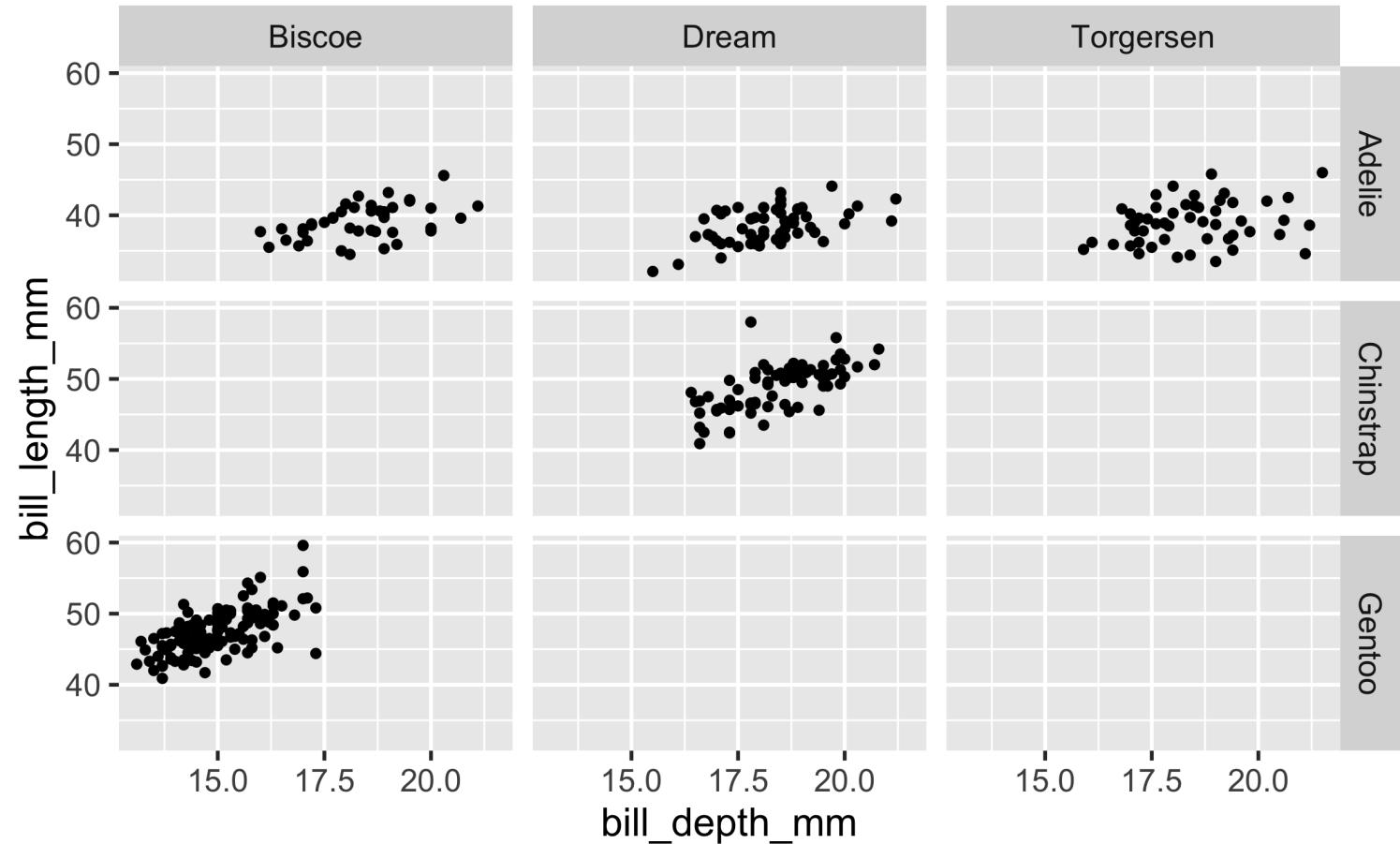
Faceting

Faceting

- Smaller plots that display different subsets of the data
- Useful for exploring conditional relationships and large data

Plot

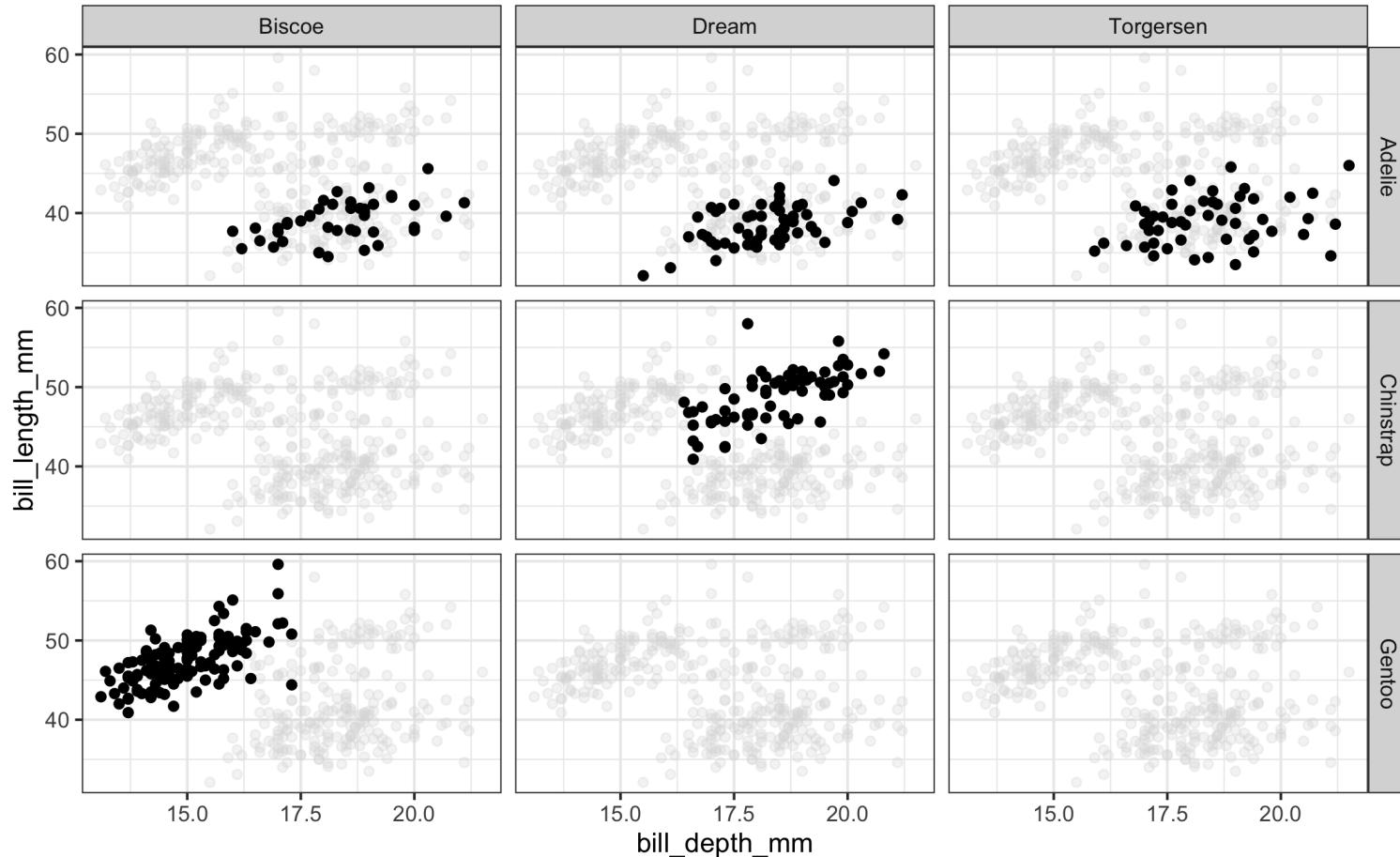
Code



Aside: complete data in background

Plot

Code

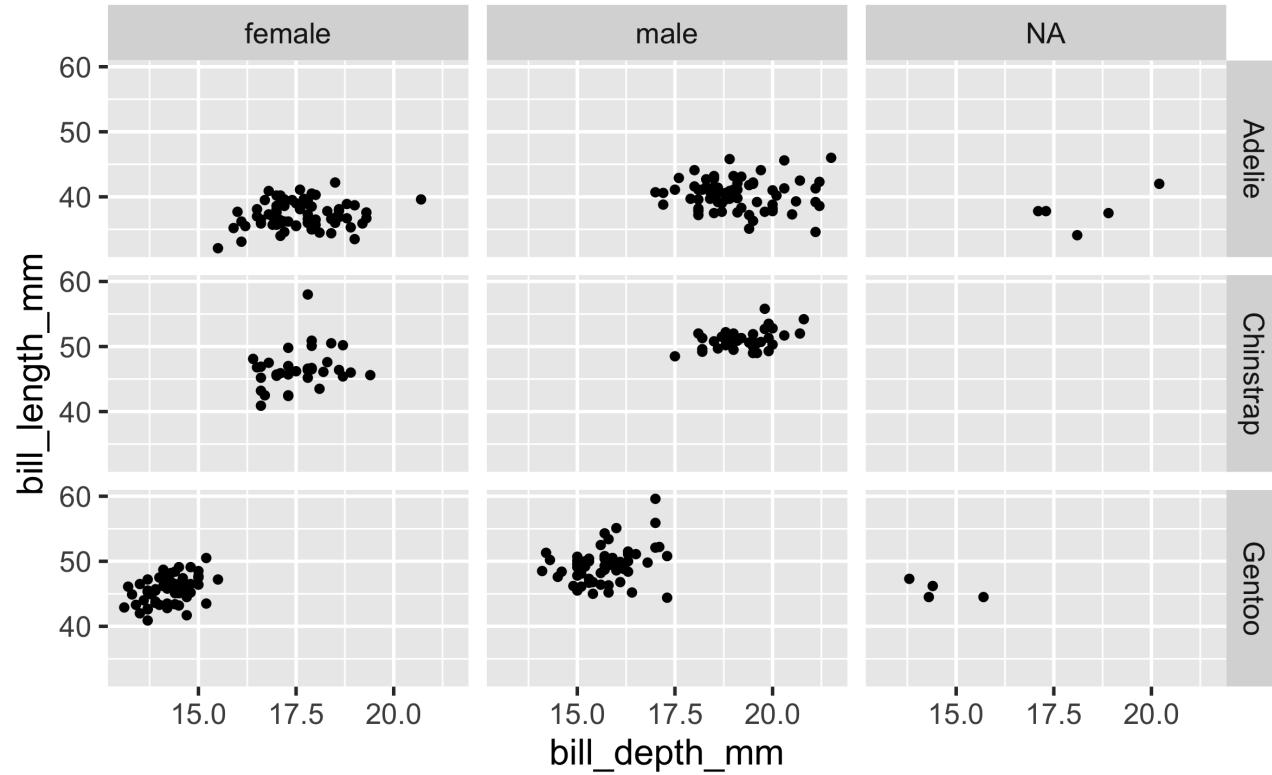


Various ways to facet

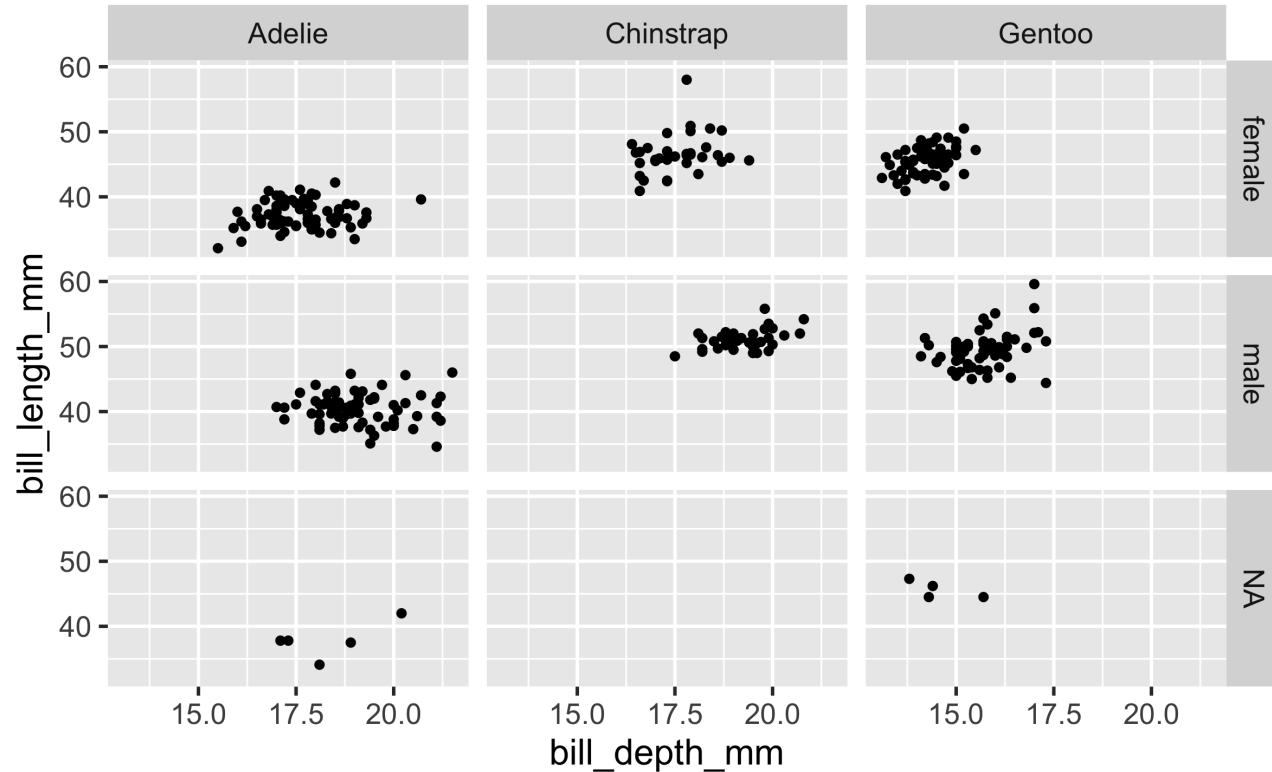
In the next few slides describe what each plot displays. Think about how the code relates to the output.

Note: The plots in the next few slides do not have proper titles, axis labels, etc. because we want you to figure out what's happening in the plots. But you should always label your plots!

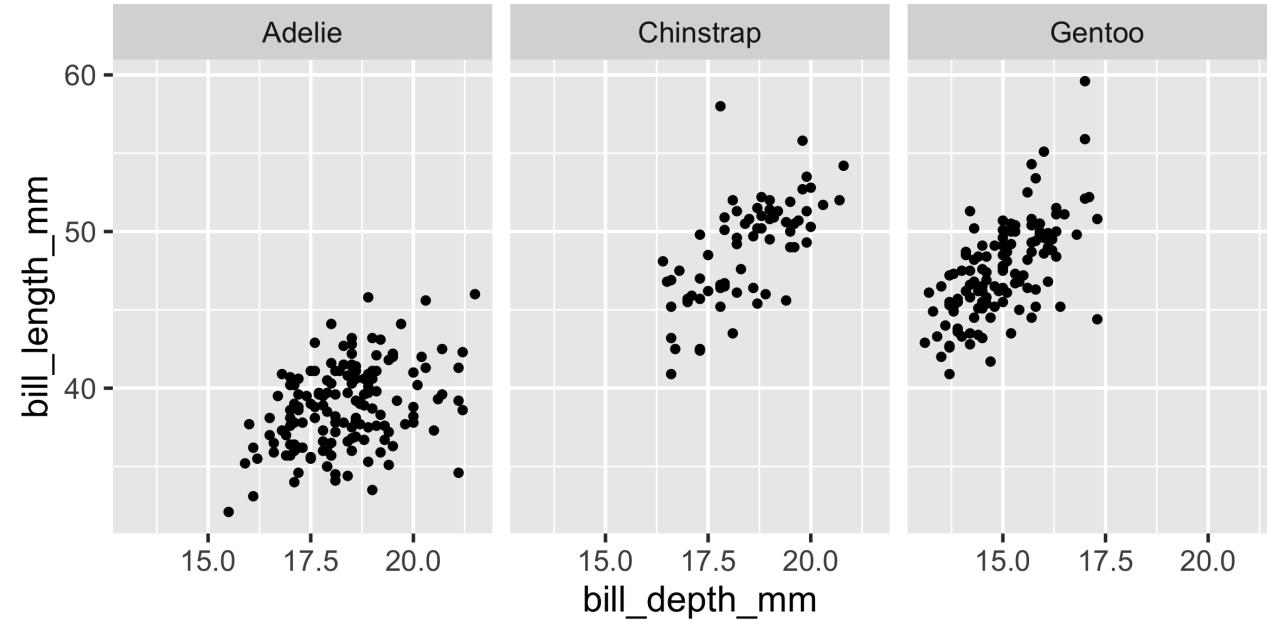
```
ggplot(penguins, aes(x = bill_depth_mm, y = bill_length_mm)) +  
  geom_point() +  
  facet_grid(rows = vars(species),  
             cols = vars(sex))
```



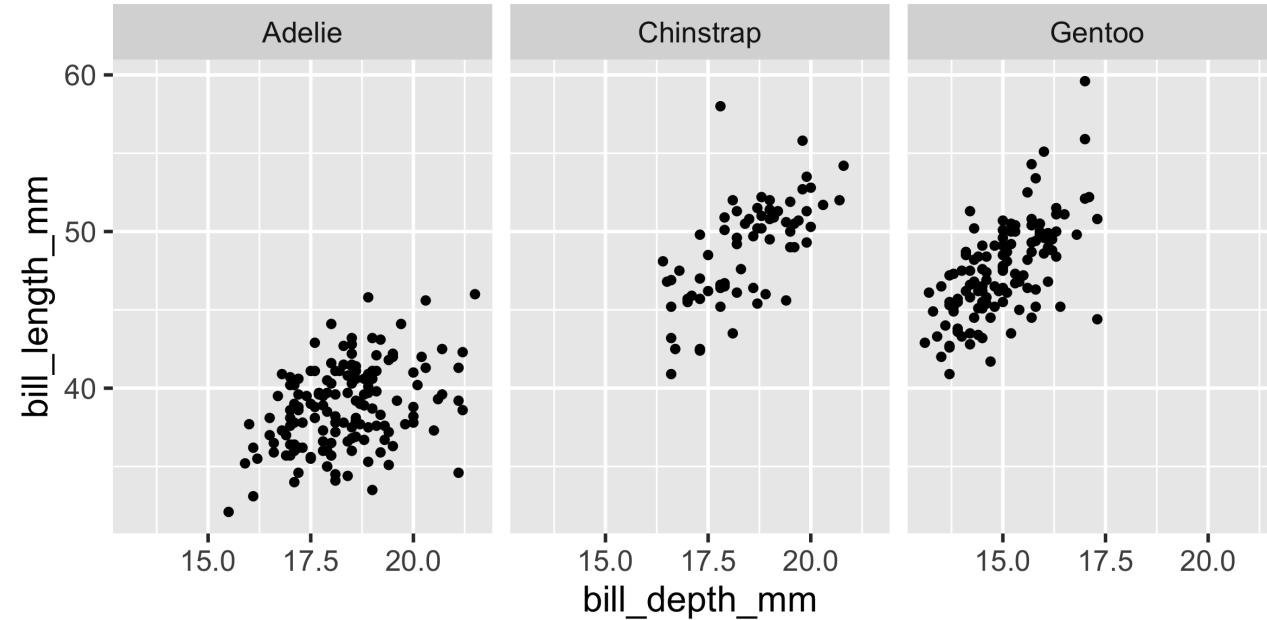
```
ggplot(penguins, aes(x = bill_depth_mm, y = bill_length_mm)) +  
  geom_point() +  
  facet_grid(rows = vars(sex),  
             cols = vars(species))
```



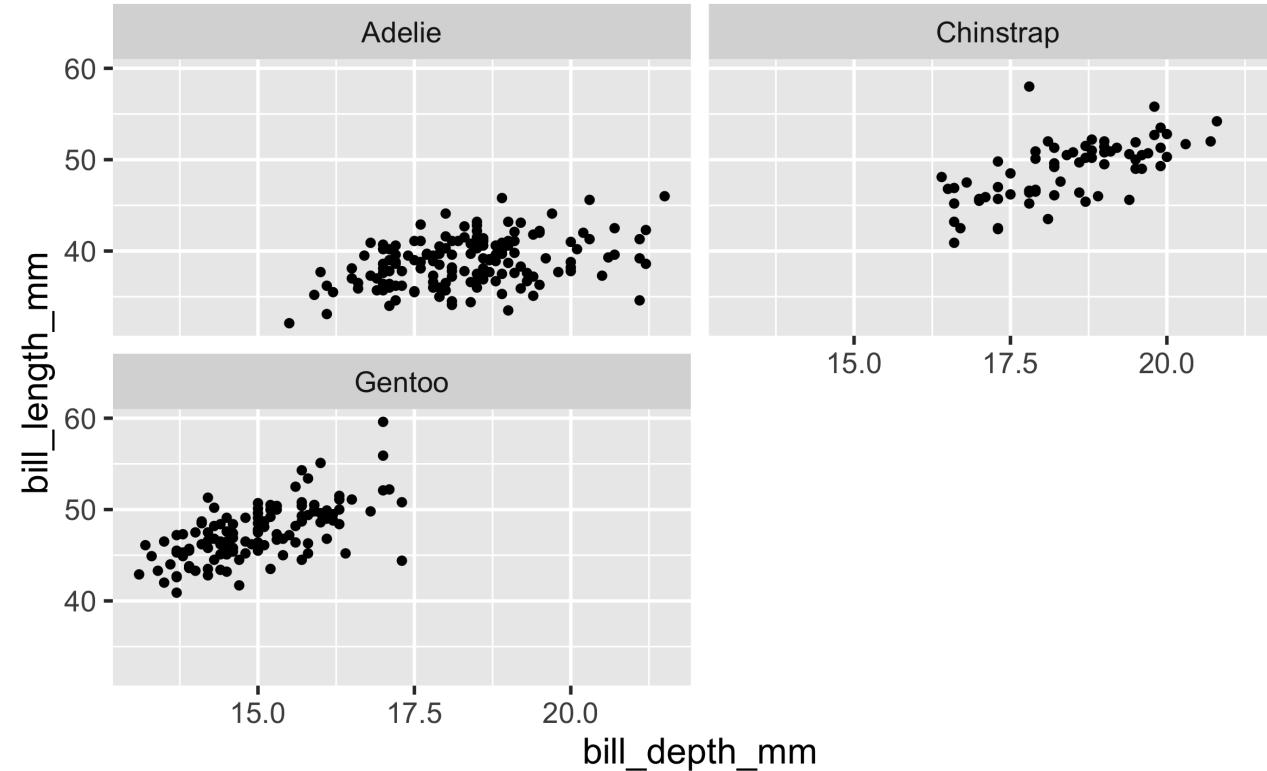
```
ggplot(penguins, aes(x = bill_depth_mm, y = bill_length_mm)) +  
  geom_point() +  
  facet_wrap(vars(species))
```



```
ggplot(penguins, aes(x = bill_depth_mm, y = bill_length_mm)) +  
  geom_point() +  
  facet_grid(cols = vars(species))
```



```
ggplot(penguins, aes(x = bill_depth_mm, y = bill_length_mm)) +  
  geom_point() +  
  facet_wrap(vars(species), ncol = 2)
```

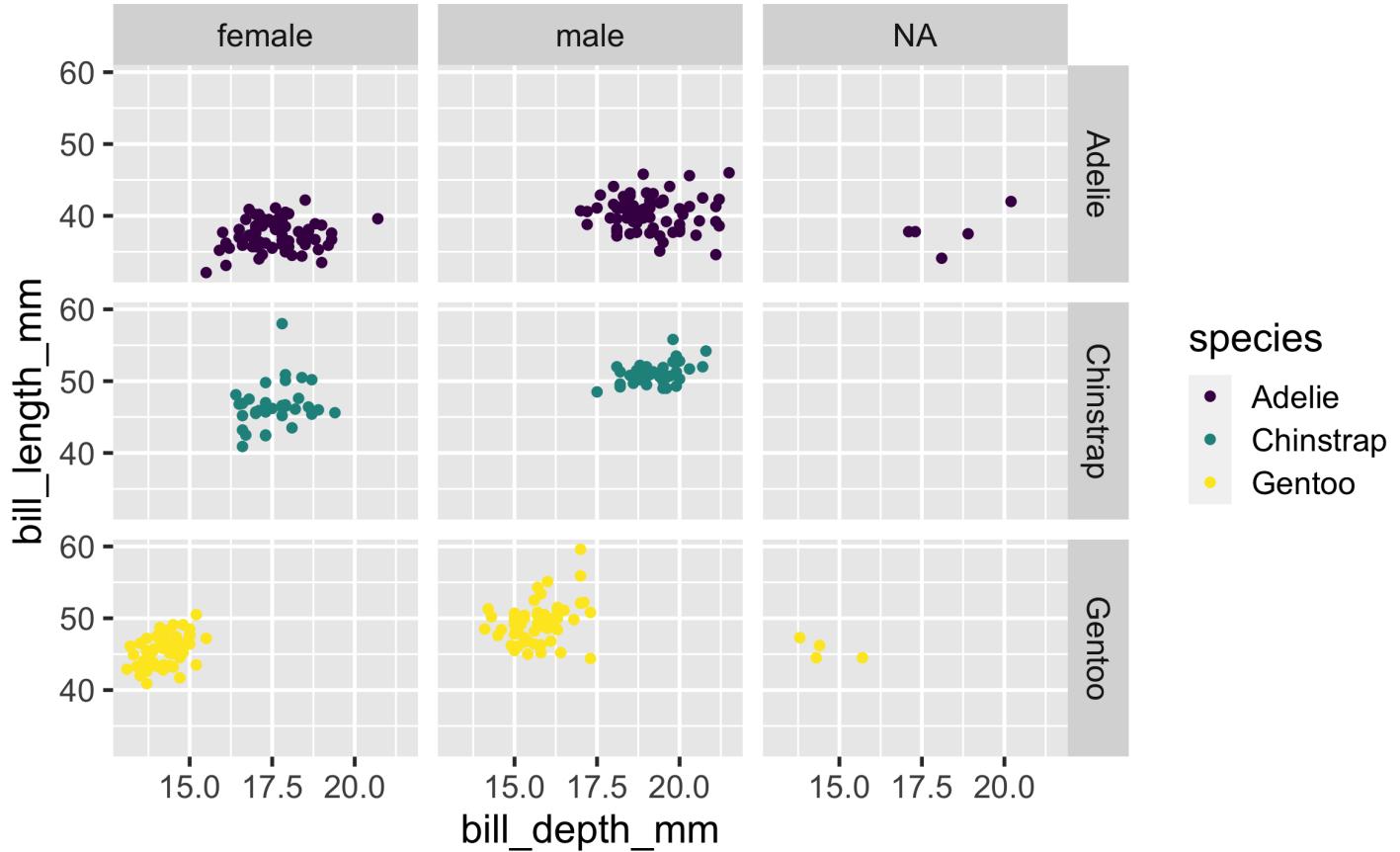


Faceting summary

- `facet_grid()`:
 - 2d grid
- `facet_wrap()`: 1d ribbon wrapped according to number of rows and columns specified or available plotting area
- "quote" variable names using `vars()`

Facet and color

```
ggplot(  
  penguins,  
  aes(x = bill_depth_mm,  
      y = bill_length_mm,  
      color = species)) +  
  geom_point() +  
  facet_grid(rows = vars(si  
scale_color_viridis_d()
```



Face and color, no legend

```
ggplot(  
  penguins,  
  aes(x = bill_depth_mm,  
      y = bill_length_mm,  
      color = species)) +  
  geom_point() +  
  facet_grid(rows = vars(sex),  
             scales = "free_y") +  
  scale_color_viridis_d()  
  guides(color = FALSE)
```

