

Visualising data with ggplot2

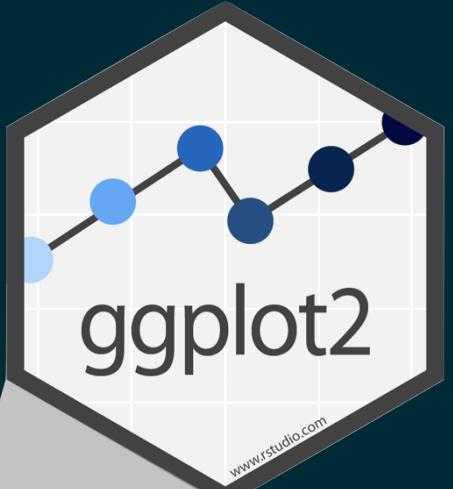
Data Science in a Box
datasciencebox.org



ggplot2 ❤️ 🐧



ggplot2 ∈ tidyverse

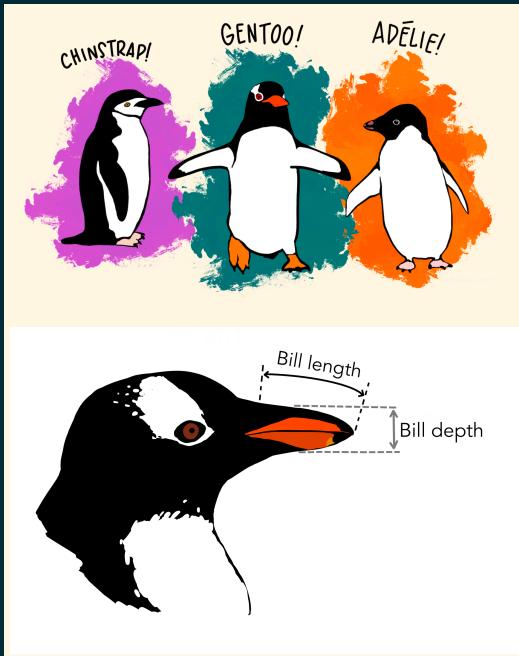


- **ggplot2** is tidyverse's data visualization package
- Structure of the code for plots can be summarized as

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

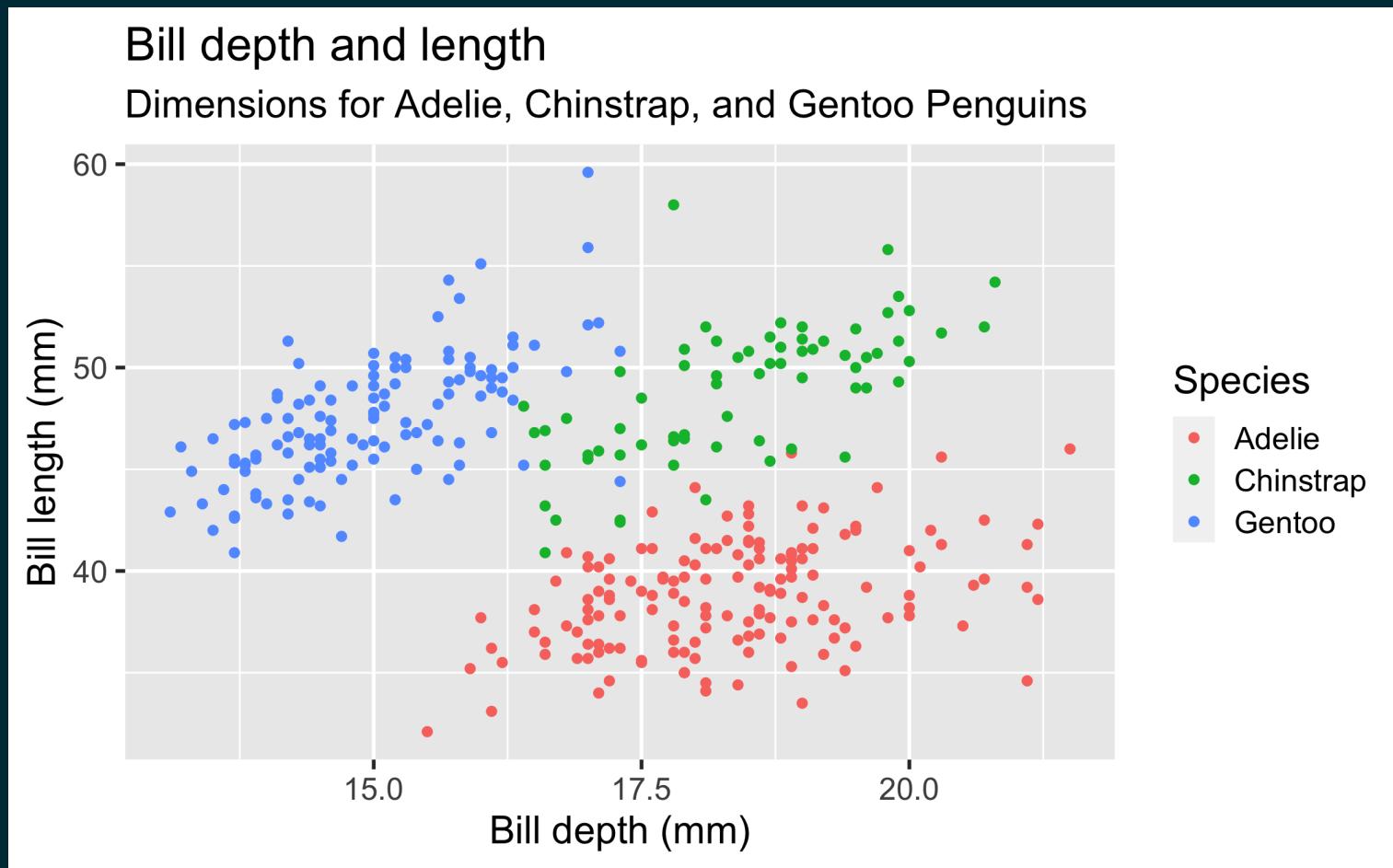
Data: Palmer Penguins

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
```



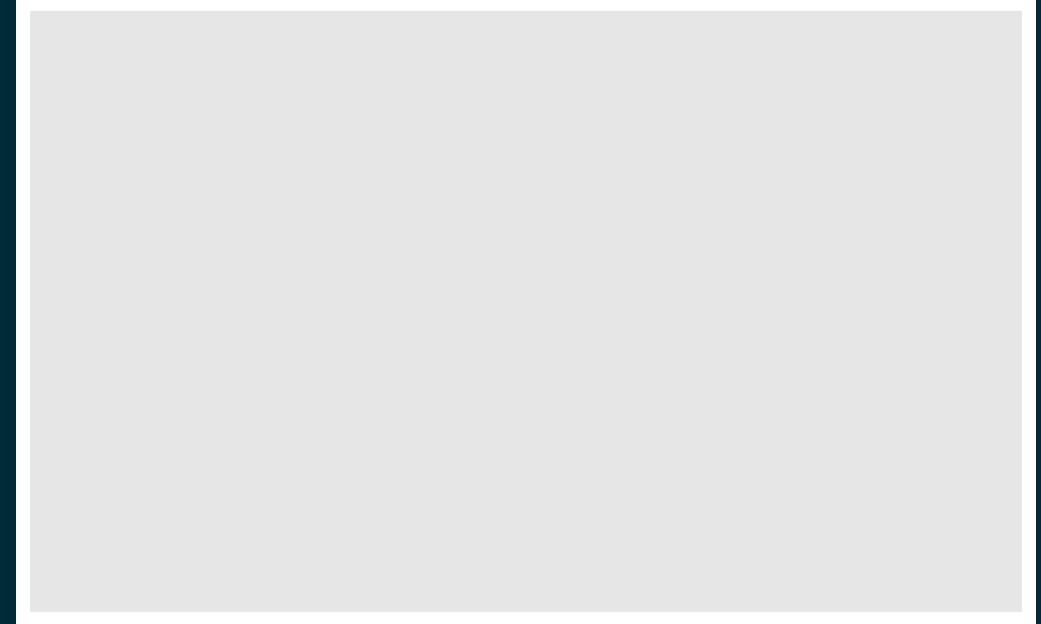
```
ggplot(data = penguins,
       mapping = aes(x = bill_depth_mm, y = bill_length_mm,
                      colour = species)) +
  geom_point() +
  labs(title = "Bill depth and length",
       subtitle = "Dimensions for Adelie, Chinstrap, and Gentoo Penguins",
       x = "Bill depth (mm)", y = "Bill length (mm)",
       colour = "Species")  
  
## Warning: Removed 2 rows containing missing values (geom_point).
```

Coding out loud



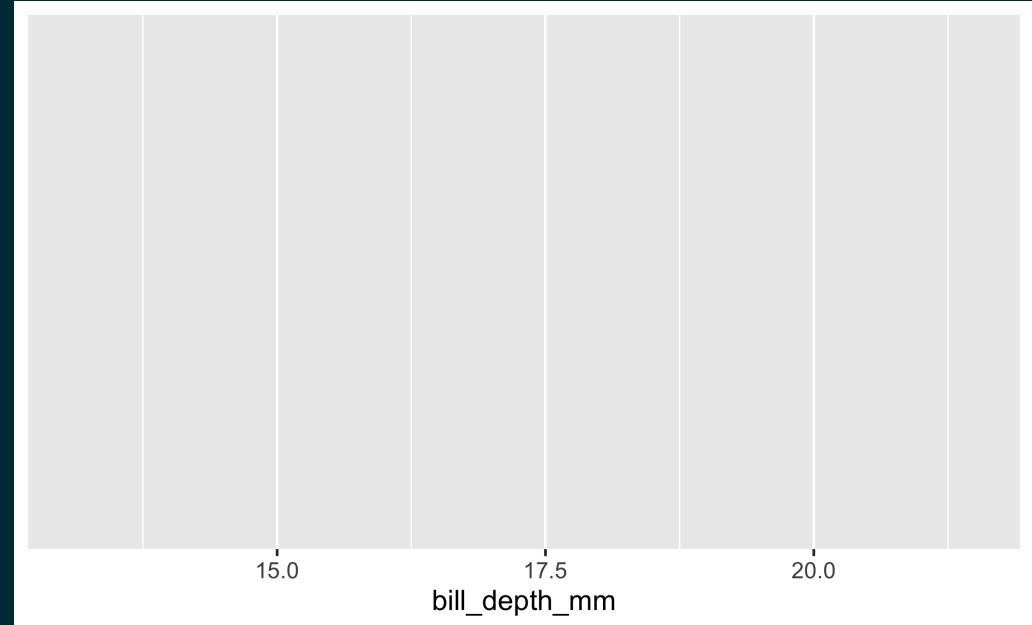
| Start with the penguins data frame

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



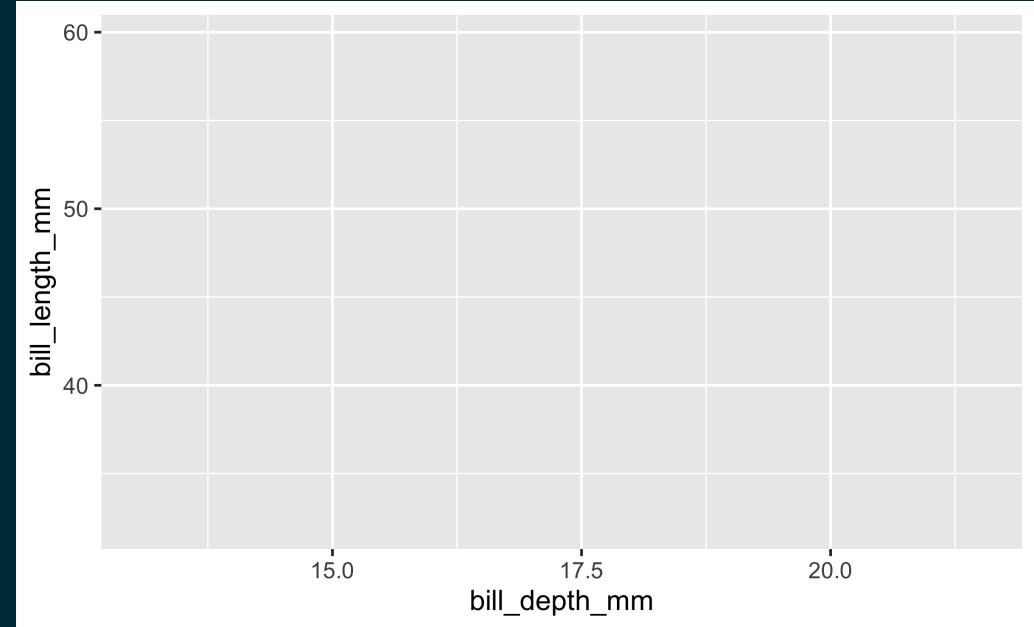
| Start with the penguins data frame, **map bill depth to the x-axis**

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



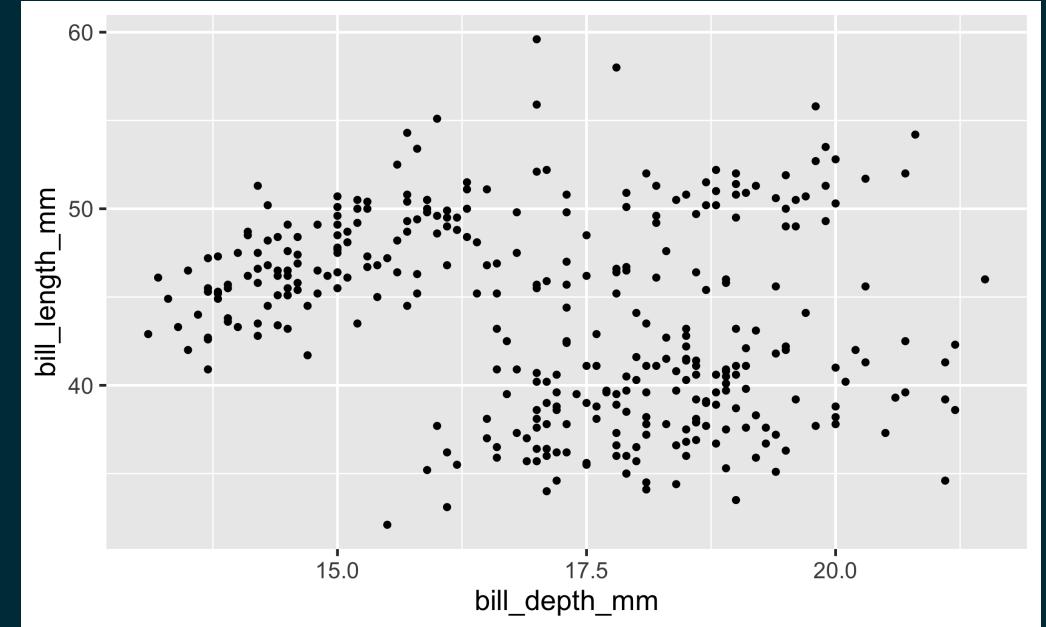
Start with the penguins data frame, map bill depth to the x-axis **and map bill length to the y-axis.**

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



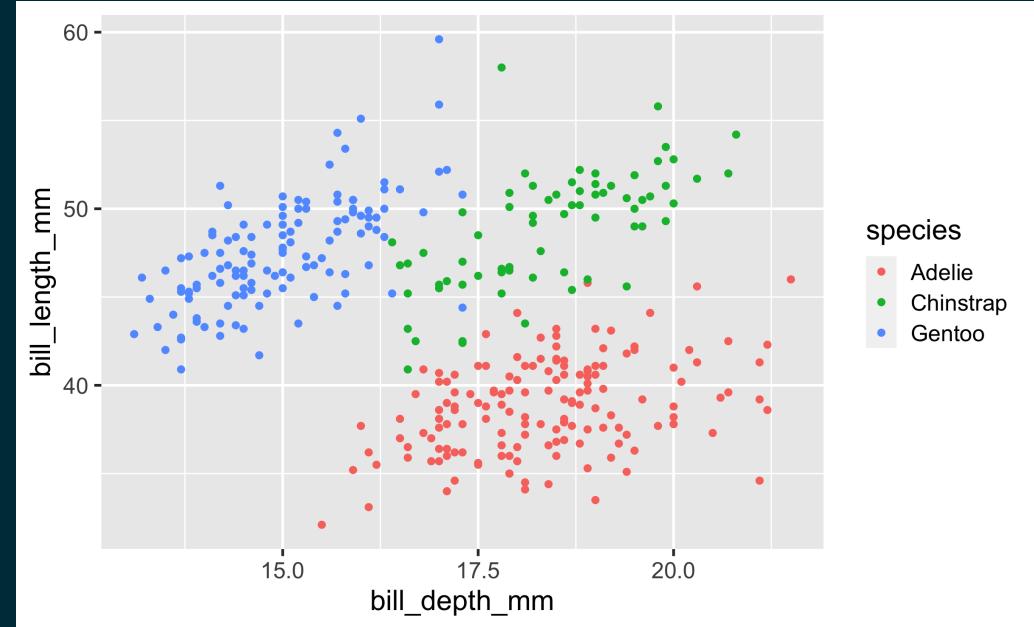
Start with the penguins data frame, map bill depth to the x-axis and map bill length to the y-axis.
Represent each observation with a point

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



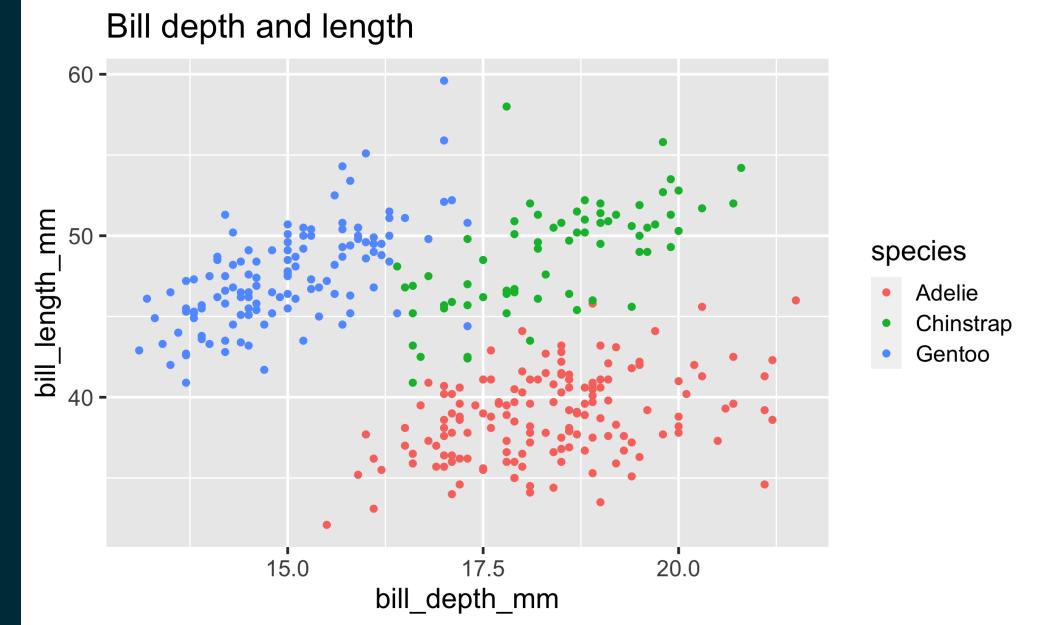
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point **and map species to the colour of each point.**

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



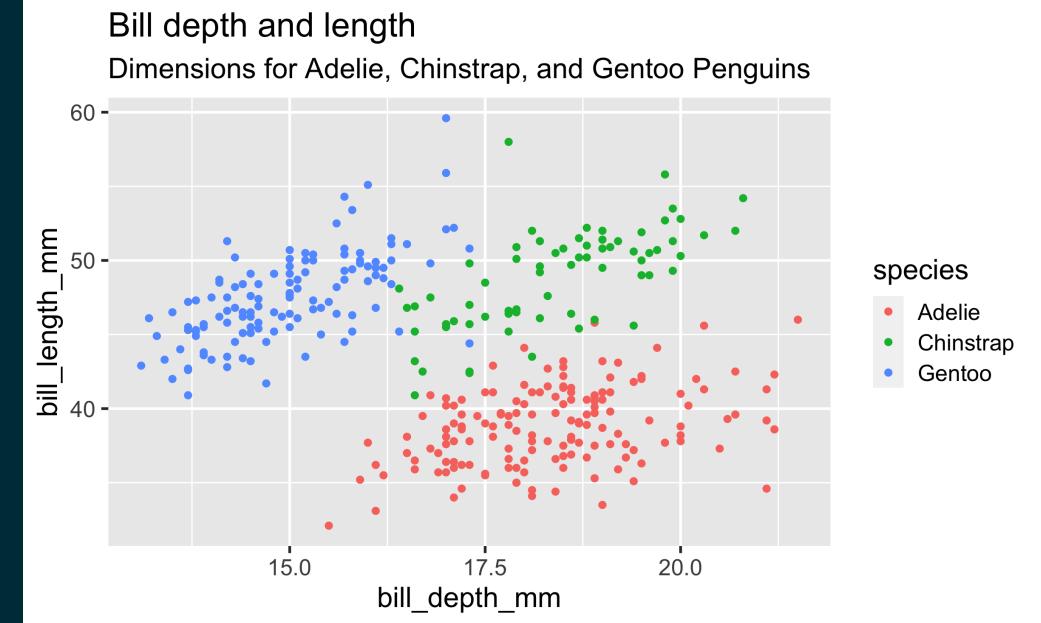
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the colour of each point. **Title the plot "Bill depth and length"**

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



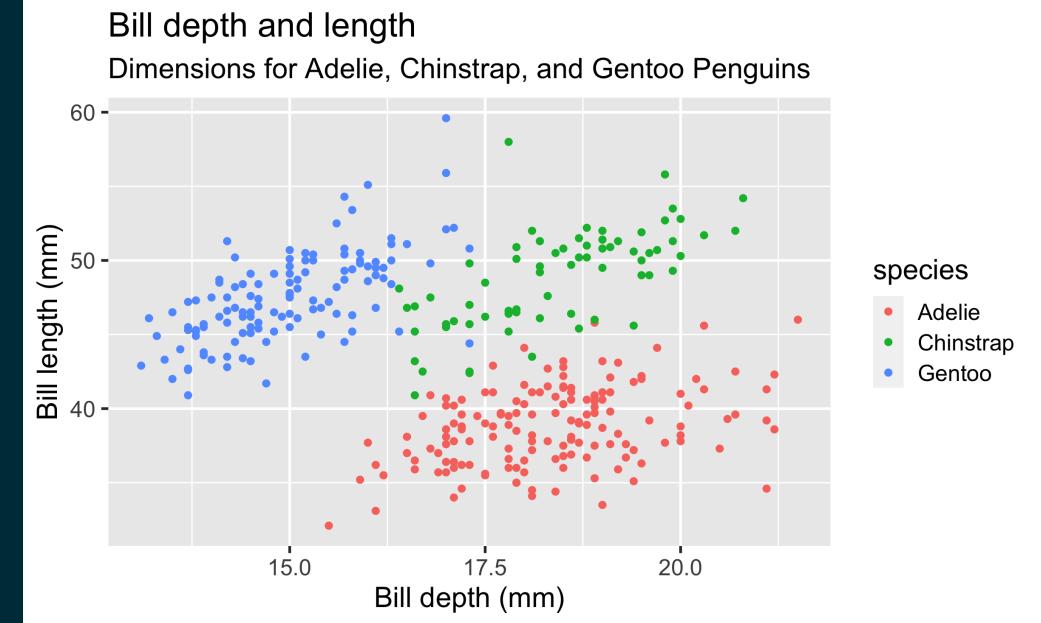
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the colour of each point. Title the plot "Bill depth and length", **add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins"**

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



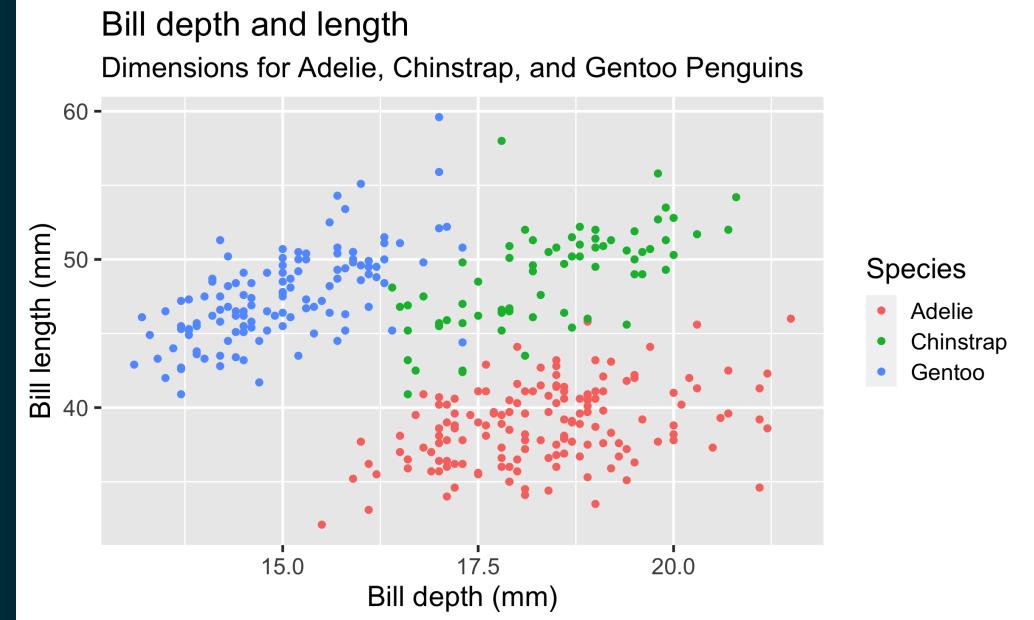
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the colour of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins", **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,  
                      colour = species)) +  
  geom_point() +  
  labs(title = "Bill depth and length",  
       subtitle = "Dimensions for Adelie,  
       x = "Bill depth (mm)", y = "Bill le
```



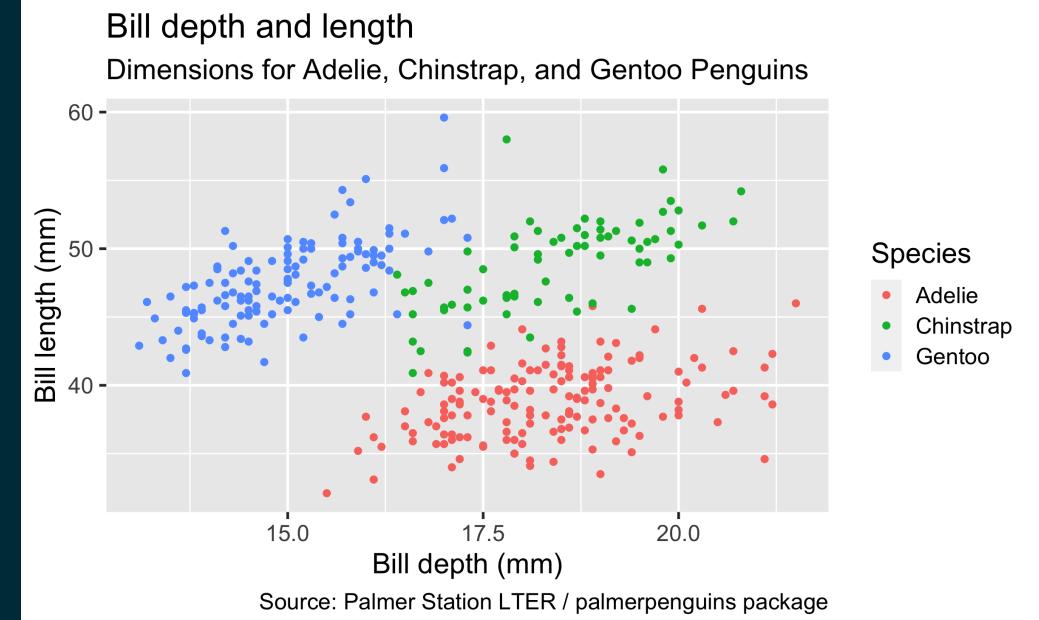
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the colour of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins", 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,  
                      colour = species)) +  
  geom_point() +  
  labs(title = "Bill depth and length",  
       subtitle = "Dimensions for Adelie,  
       x = "Bill depth (mm)", y = "Bill le  
       colour = "Species")
```



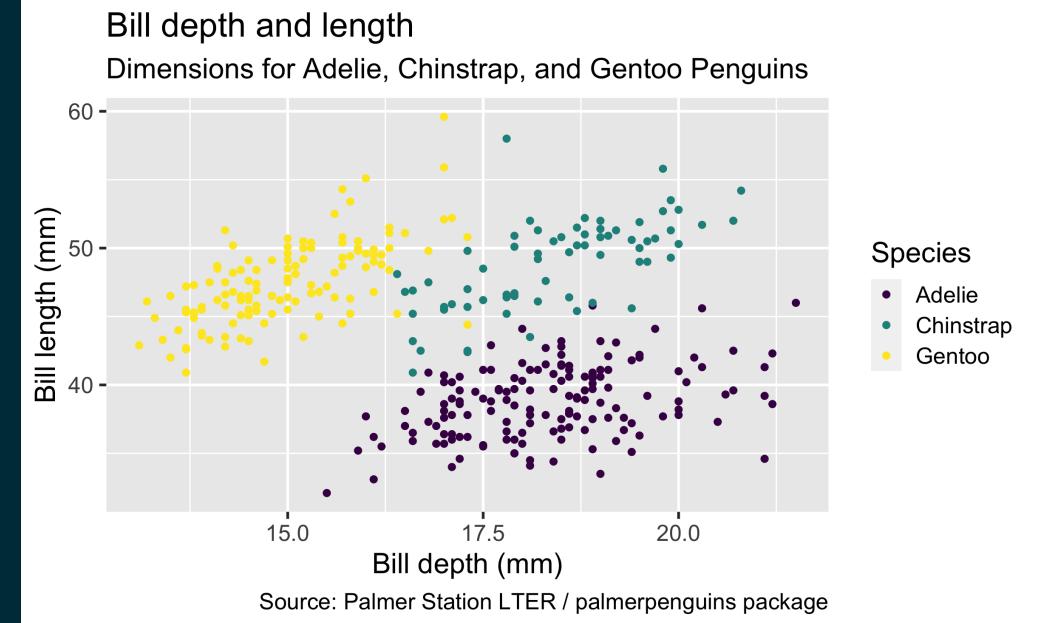
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the colour of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins",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

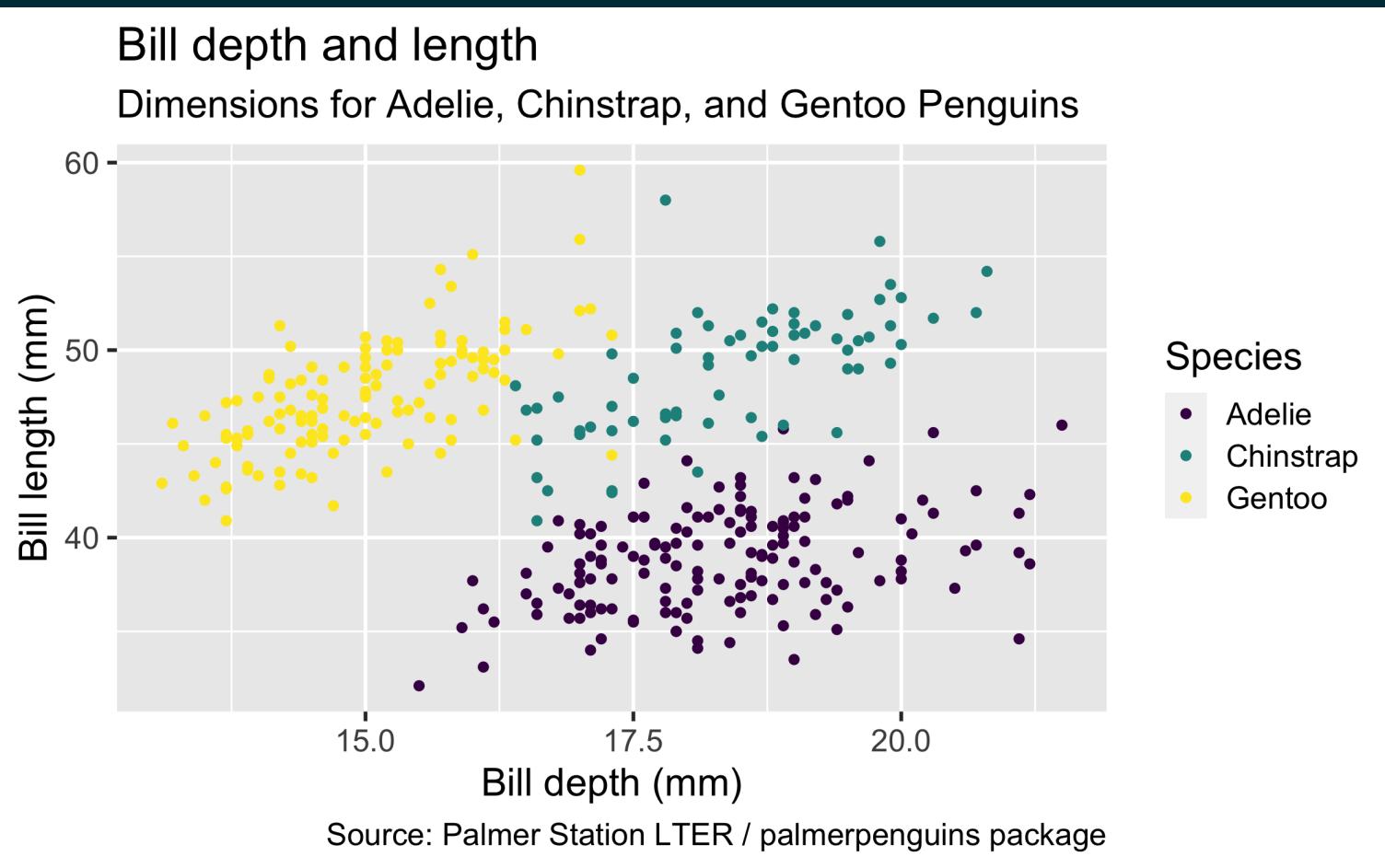
```
ggplot(data = penguins,  
       mapping = aes(x = bill_depth_mm,  
                      y = bill_length_mm,  
                      colour = species)) +  
  geom_point() +  
  labs(title = "Bill depth and length",  
       subtitle = "Dimensions for Adelie,  
                  Chinstrap, and Gentoo  
                  Penguins",  
       x = "Bill depth (mm)", y = "Bill length (mm)",  
       colour = "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 colour 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 colour scale that is designed to be perceived by viewers with common forms of colour blindness.**

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





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

## Warning: Removed 2 rows containing missing values (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 colour 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 colour scale that is designed to be perceived by viewers with common forms of colour blindness.

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,  
                      colour = species)) +  
  geom_point() +  
  scale_colour_viridis_d()
```

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



Aesthetics



datasciencebox.org

Aesthetics options

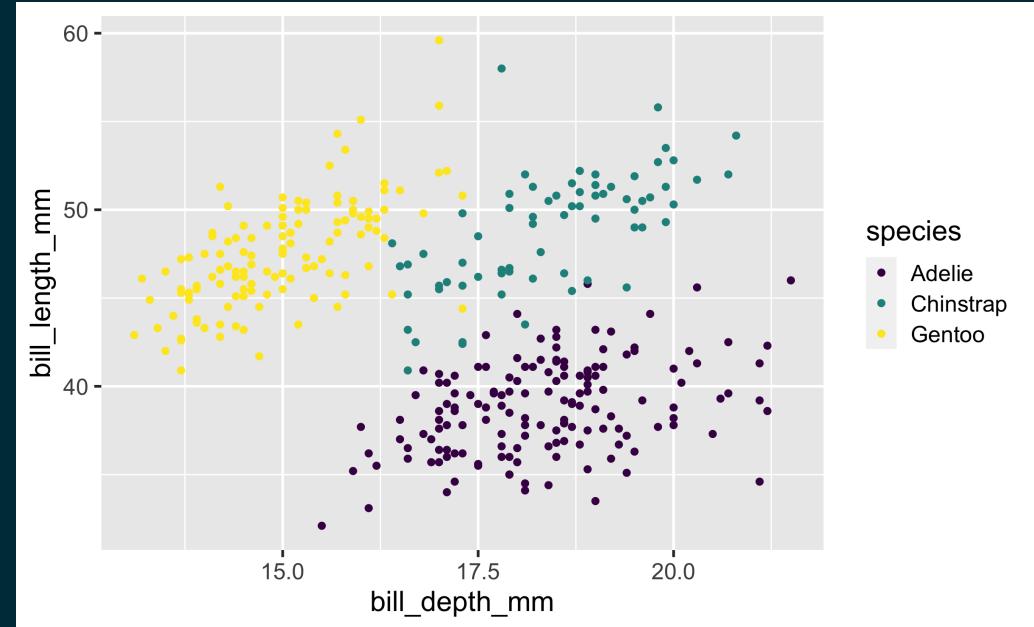
Commonly used characteristics of plotting characters that can be **mapped to a specific variable** in the data are

- colour
- shape
- size
- alpha (transparency)



Colour

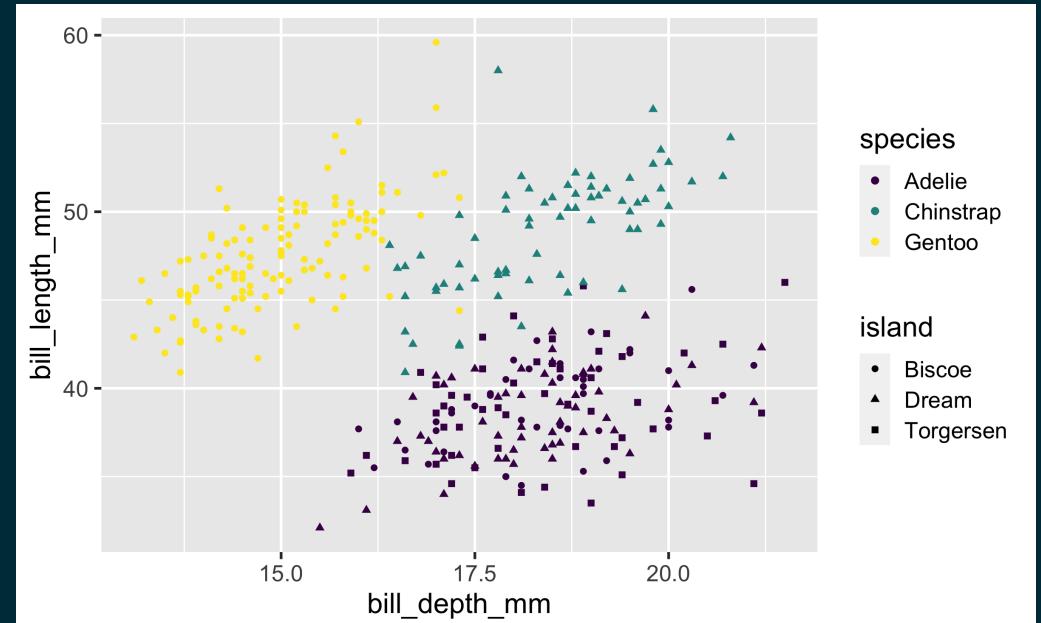
```
ggplot(penguins,  
       aes(x = bill_depth_mm,  
            y = bill_length_mm,  
            colour = species)) +  
  geom_point() +  
  scale_colour_viridis_d()
```



Shape

Mapped to a different variable than colour

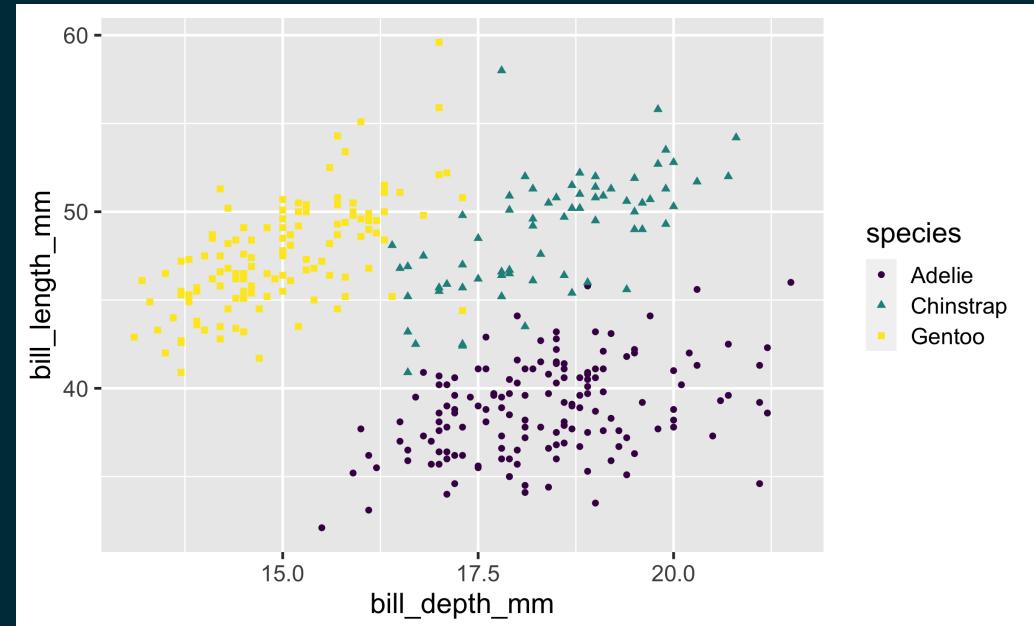
```
ggplot(penguins,  
       aes(x = bill_depth_mm,  
            y = bill_length_mm,  
            colour = species,  
            shape = island)) +  
  geom_point() +  
  scale_colour_viridis_d()
```



Shape

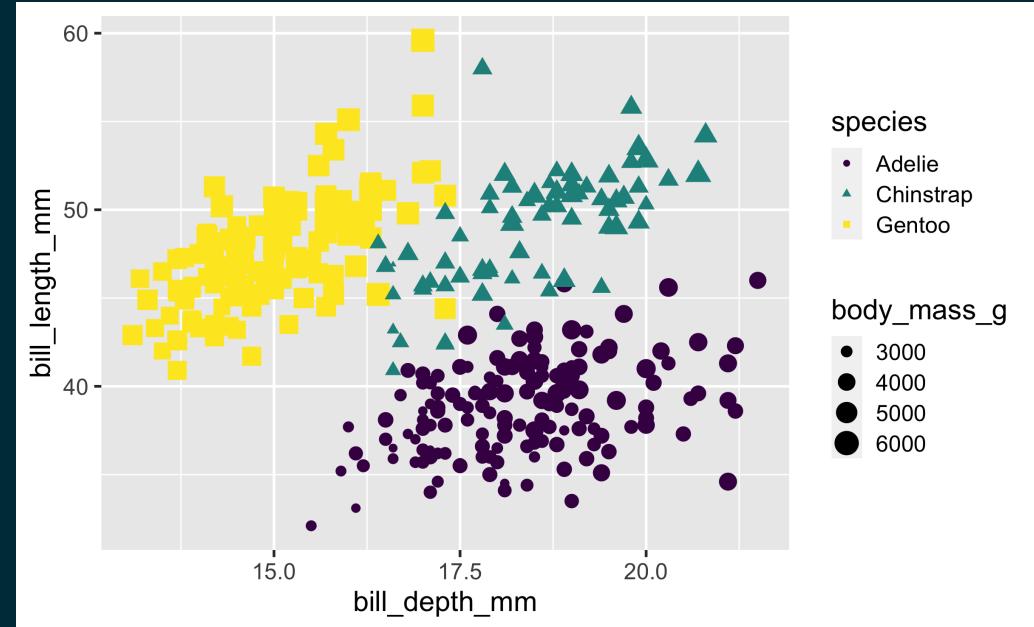
Mapped to same variable as colour

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



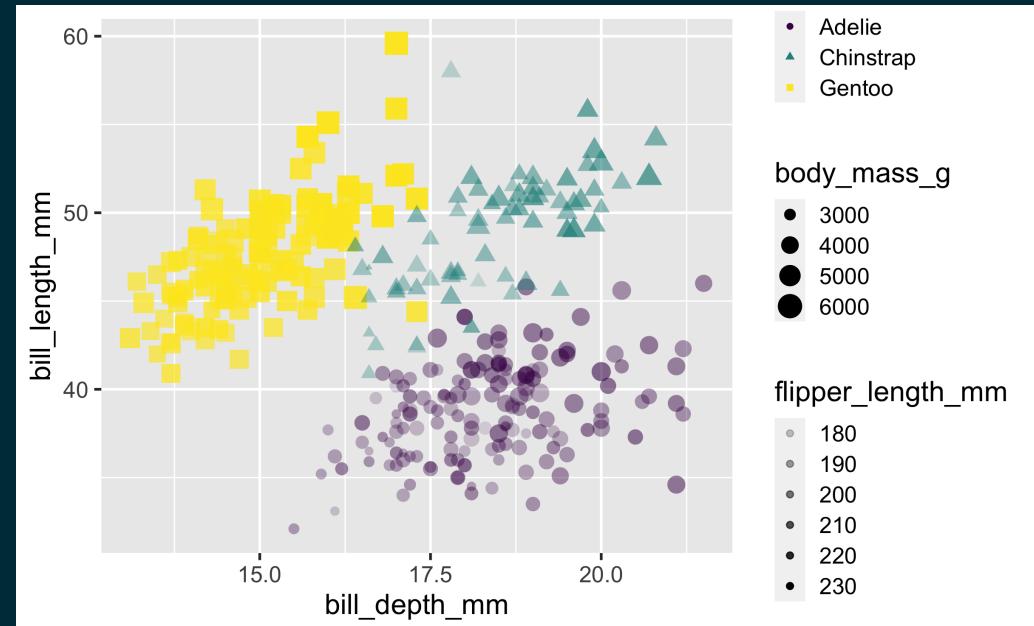
Size

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



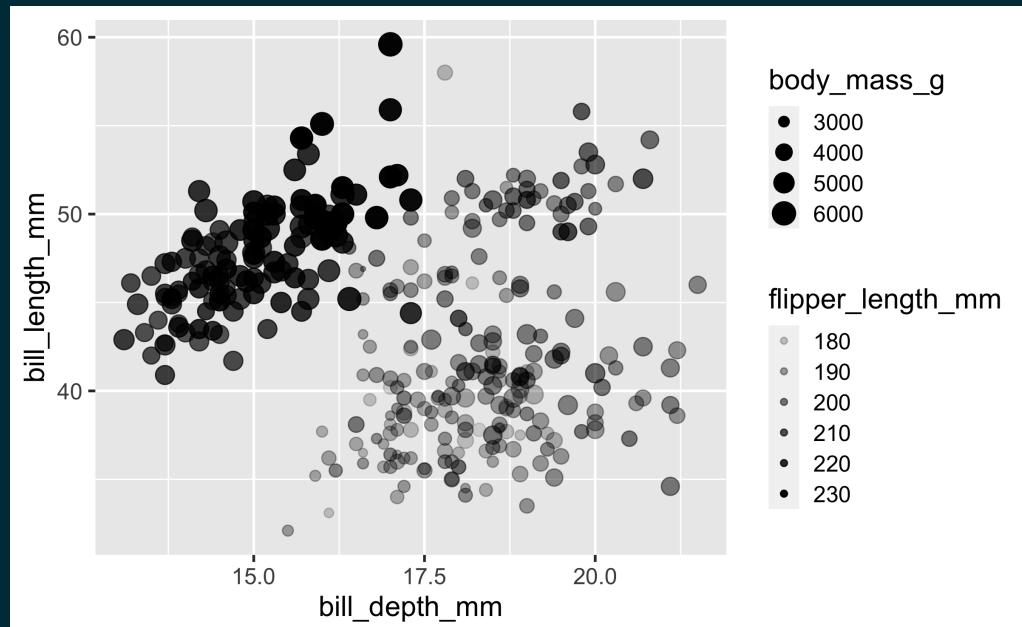
Alpha

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



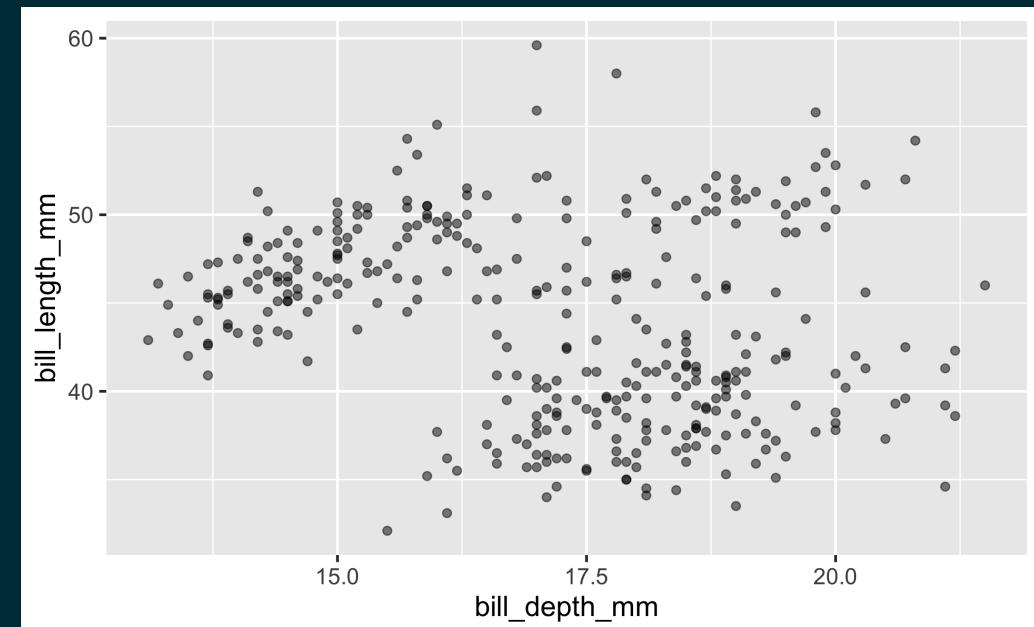
Mapping

```
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 vs. setting

- **Mapping:** Determine the size, alpha, etc. of points based on the values of a variable in the data
 - goes into `aes()`
- **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!)



Faceting



datasciencebox.org

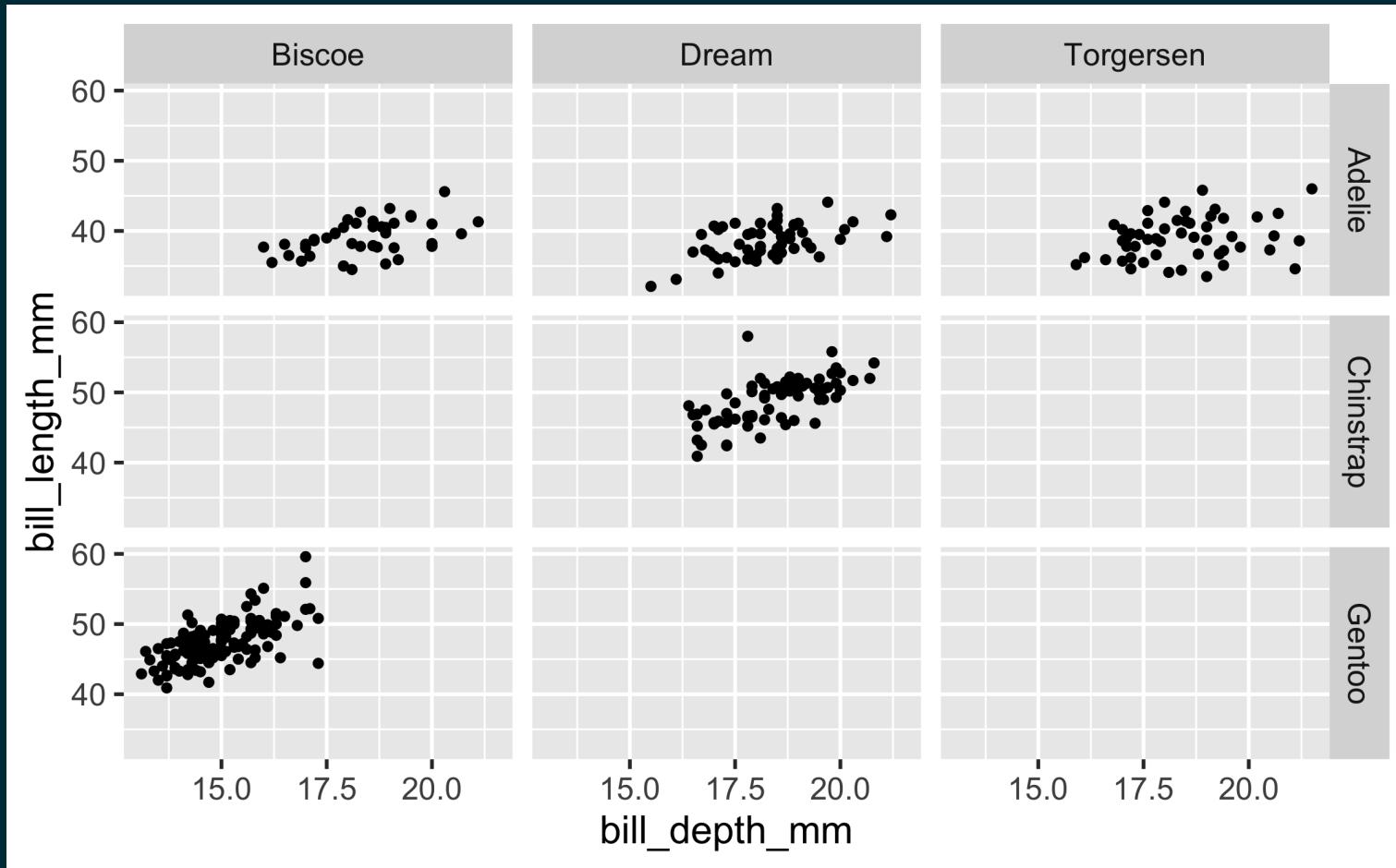
Faceting

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



Plot

Code



Plot

Code

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

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



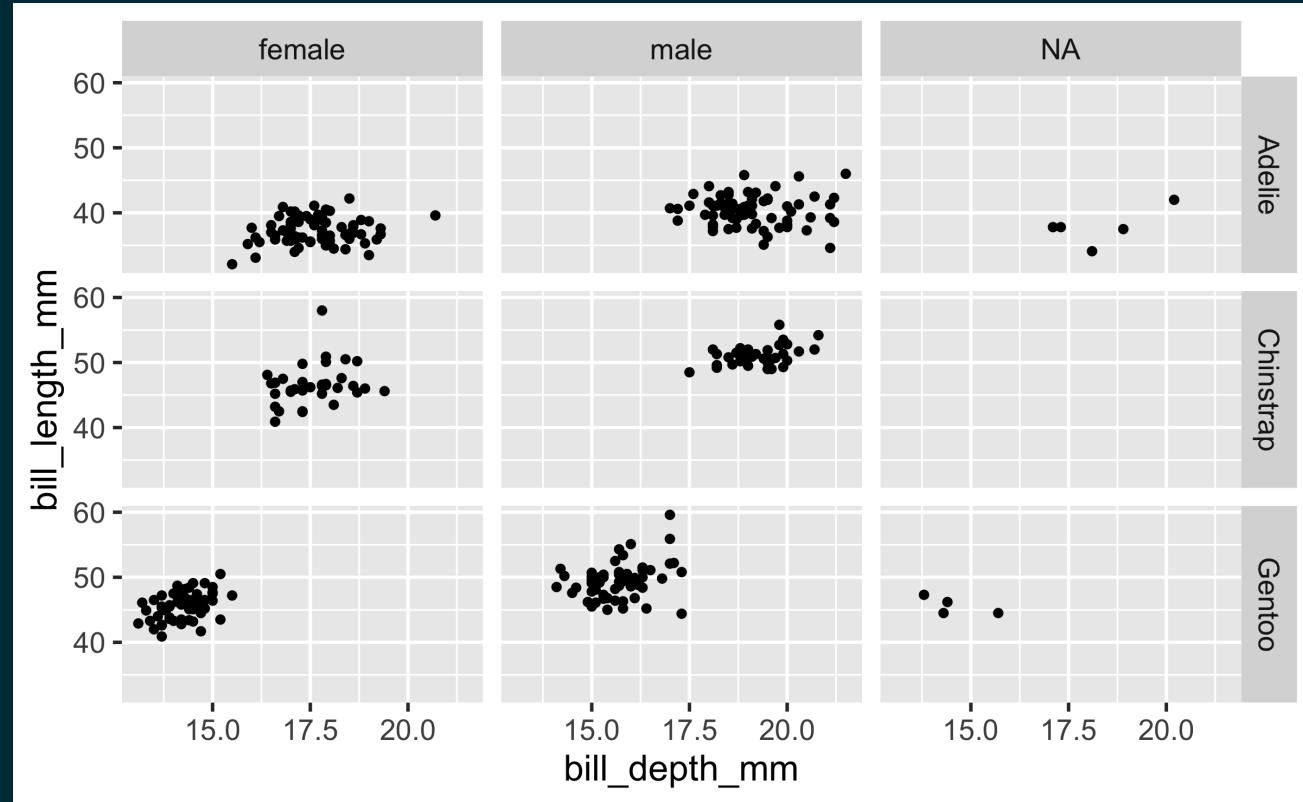
Various ways to facet

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

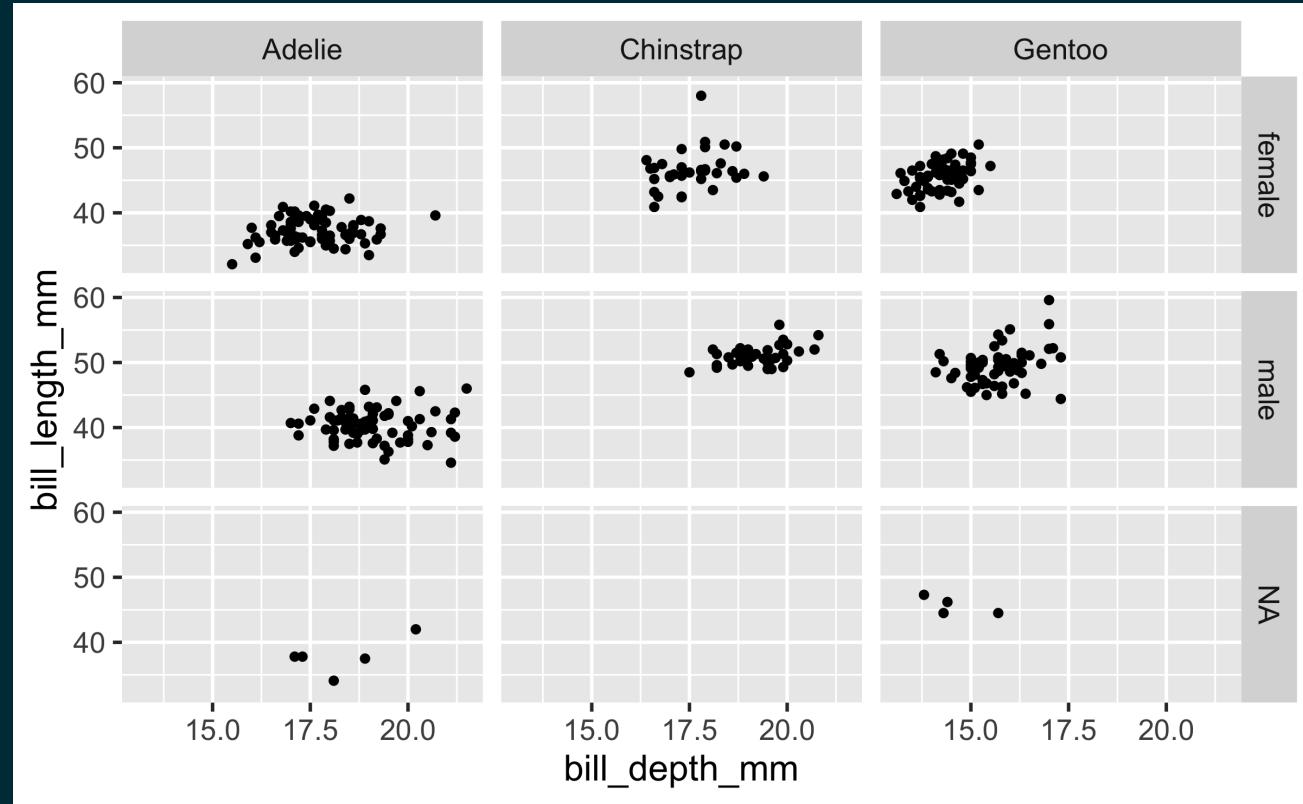
Note: The plots in the next few slides do not have proper titles, axis labels, etc. because we want you to figure out what's happening in the plots. But you should always label your plots!



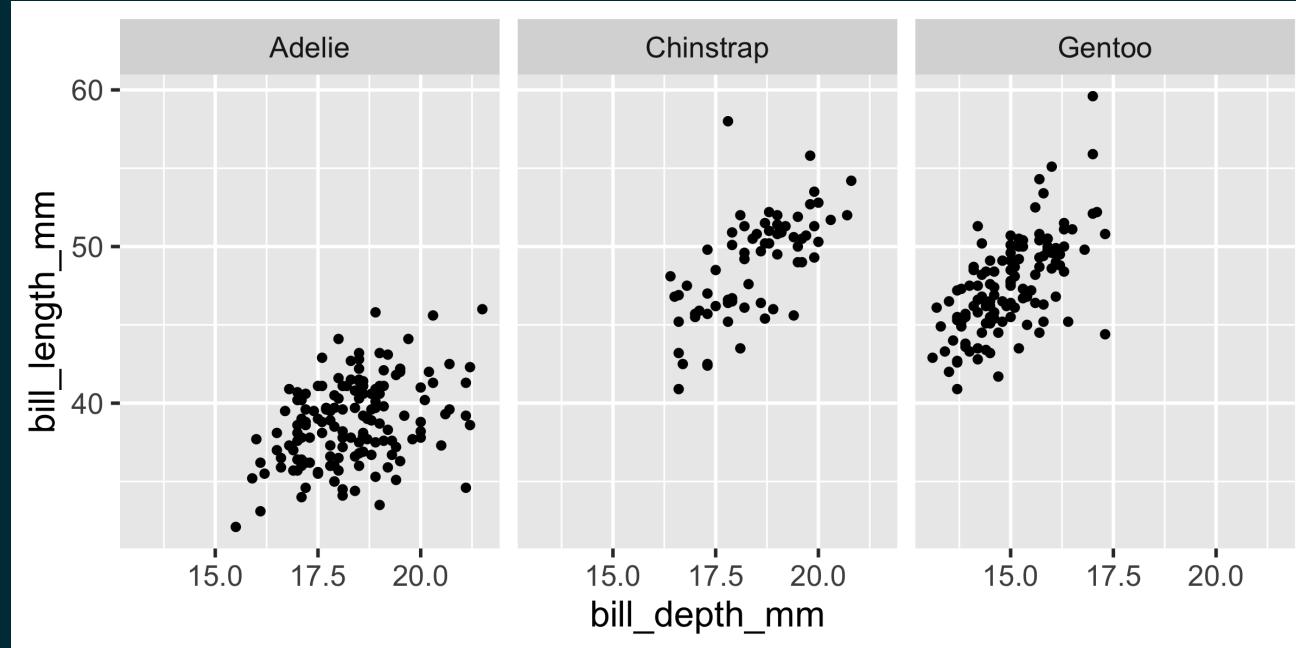
```
ggplot(penguins, aes(x = bill_depth_mm, y = bill_length_mm)) +  
  geom_point() +  
  facet_grid(species ~ sex)
```



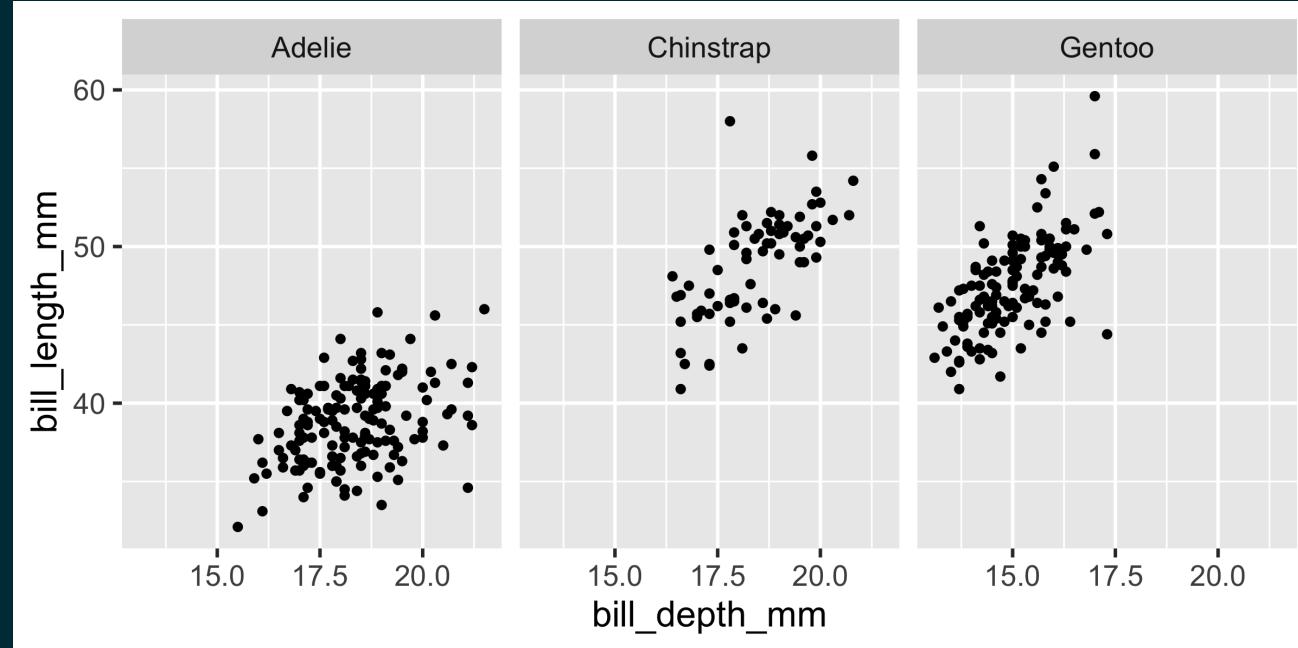
```
ggplot(penguins, aes(x = bill_depth_mm, y = bill_length_mm)) +  
  geom_point() +  
  facet_grid(sex ~ species)
```



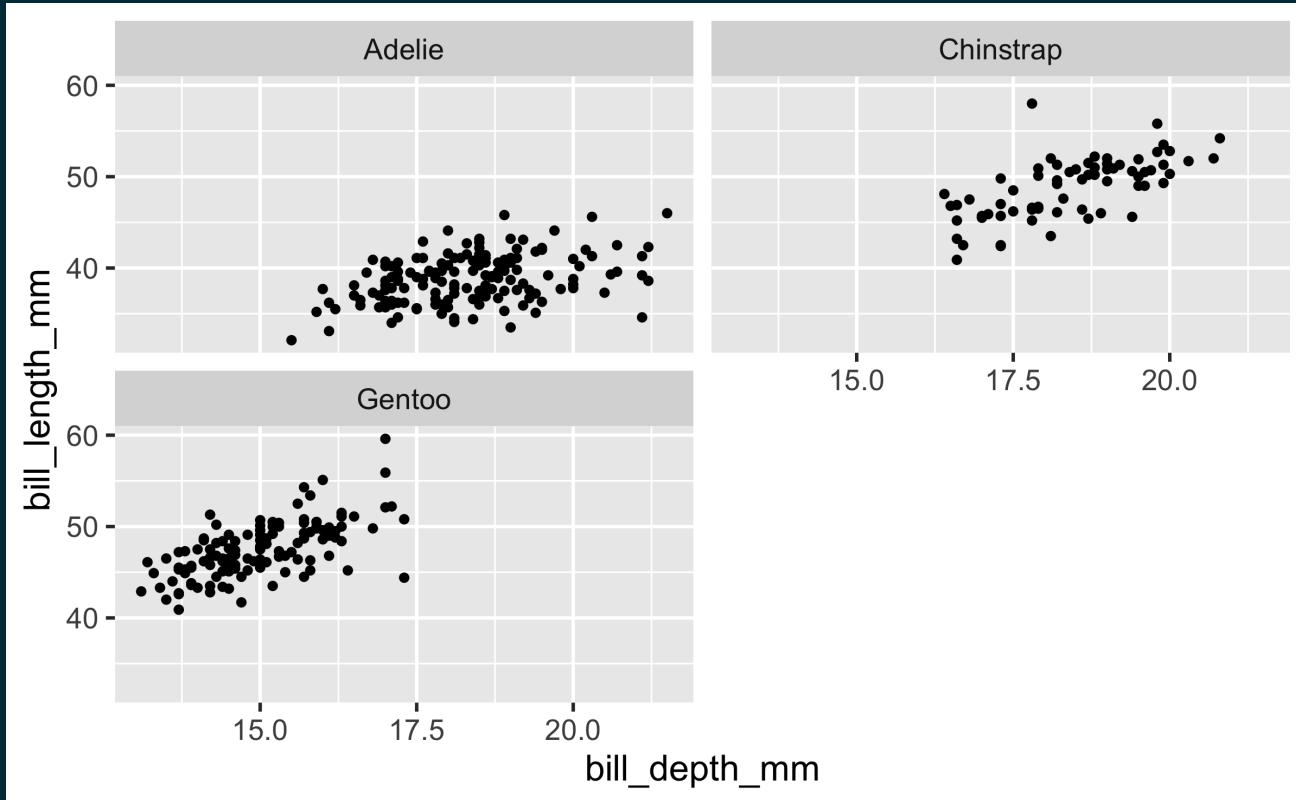
```
ggplot(penguins, aes(x = bill_depth_mm, y = bill_length_mm)) +  
  geom_point() +  
  facet_wrap(~ species)
```



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



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



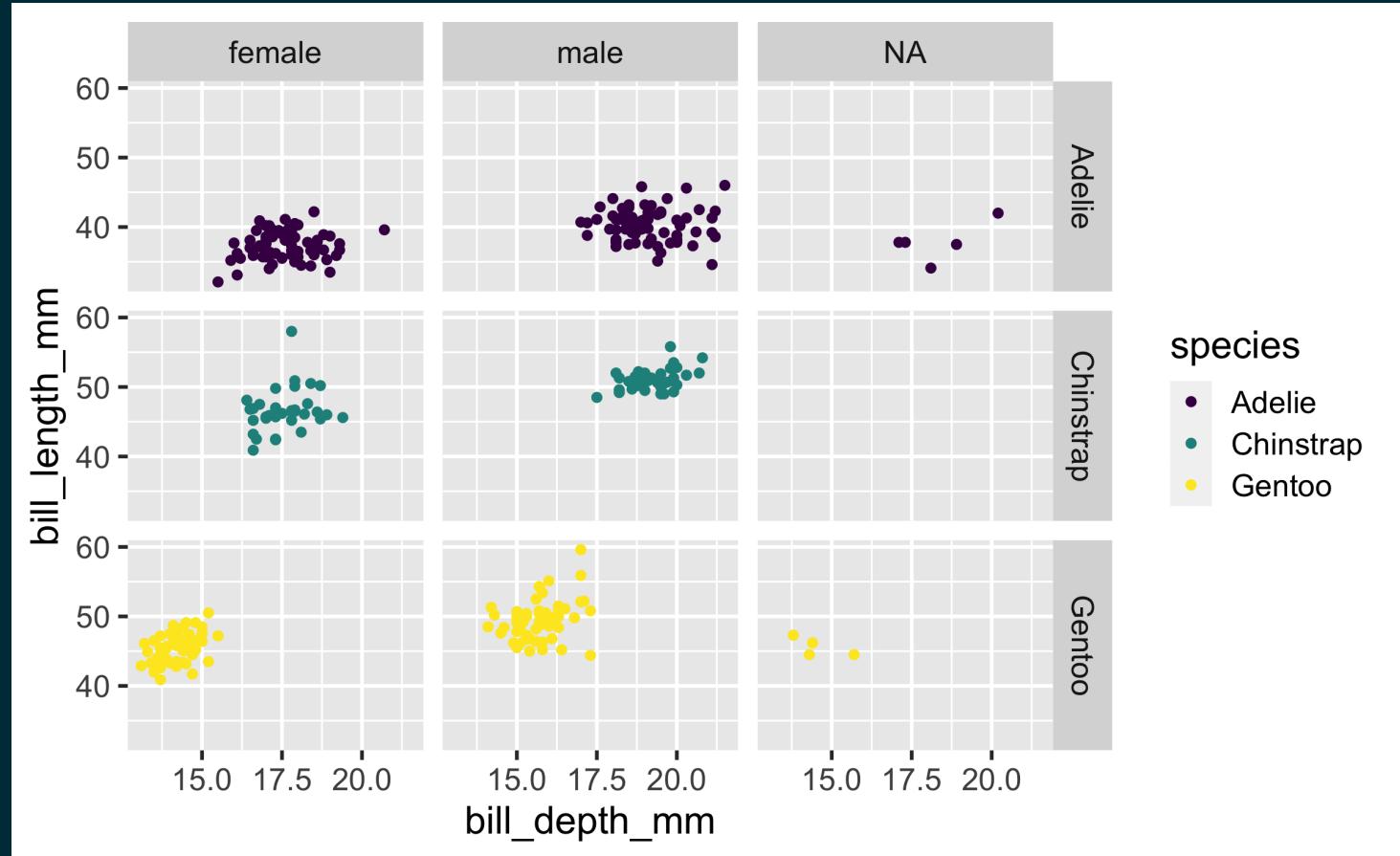
Faceting summary

- `facet_grid()`:
 - 2d grid
 - `rows ~ cols`
 - use `.` for no split
- `facet_wrap()`: 1d ribbon wrapped according to number of rows and columns specified or available plotting area



Facet and color

```
ggplot(  
  penguins,  
  aes(x = bill_depth_mm,  
      y = bill_length_mm,  
      color = species)) +  
  geom_point() +  
  facet_grid(species ~ sex)  
  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(species ~ sex)  
  scale_color_viridis_d()  
  guides(color = FALSE)
```

