Visualising data with ggplot2

Data Science in a Box

datasciencebox.org

ggplot2 ❤️ 🐧

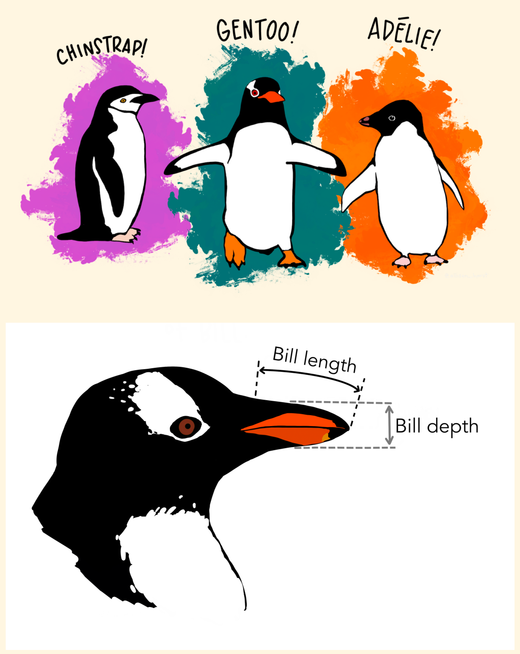
ggplot2 ∈ tidyverse

- **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

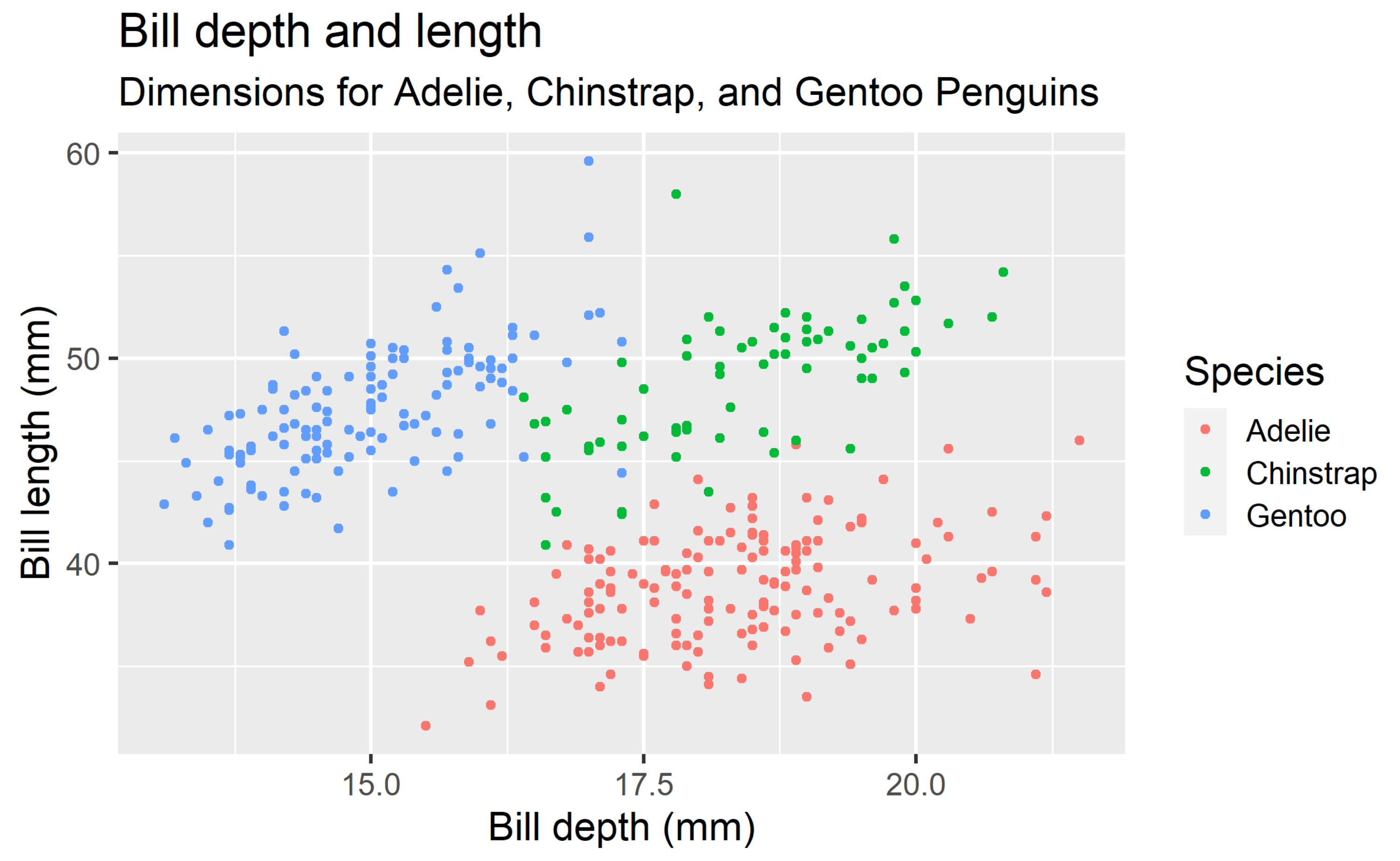
Measurements for penguin species, island in Palmer Archipelago, size (flipper length, body mass, bill dimensions), and sex.



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

```
## Rows: 344
## Columns: 8
## $ species           <fct> Adelie, Adelie, Adelie, Adelie, Adeli~
## $ 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~
```

Plot Code


Bill depth and length
Dimensions for Adelie, Chinstrap, and Gentoo Penguins
60
50
40
Bill length (mm)
15.0
17.5
20.0
Bill depth (mm)
Species
Adelie
Chinstrap
Gentoo

Plot Code

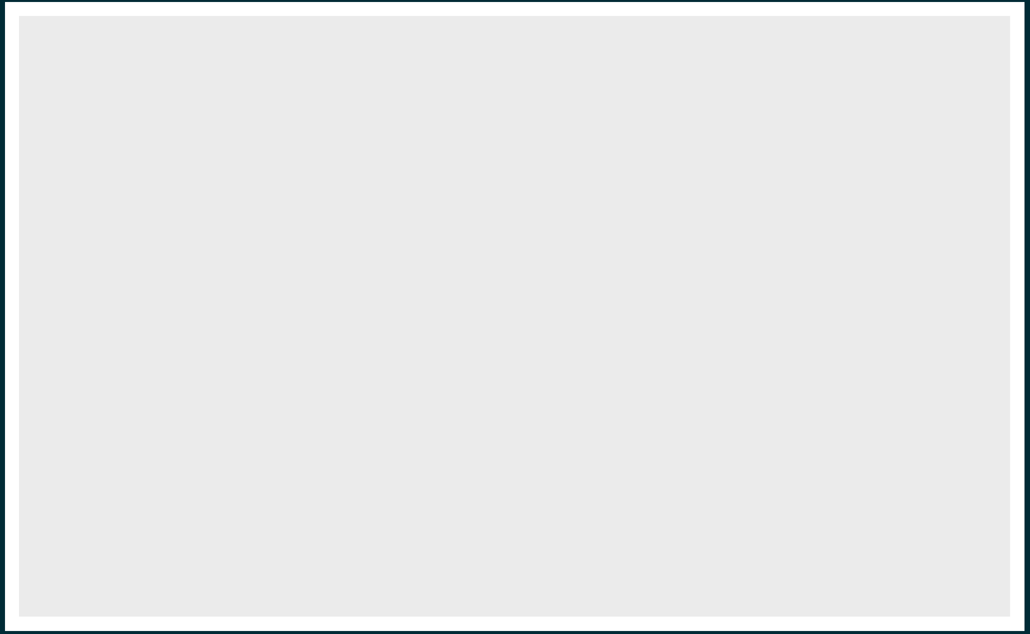
```r
ggplot(data = penguins,
       mapping = aes(x = bill_depth_mm, y = bill_length_mm,
                     colour = species)) +
  geom_point() +
  labs(title = "Bill depth and length",
       subtitle = "Dimensions for Adelie, Chinstrap, and Gentoo Penguins",
       x = "Bill depth (mm)", y = "Bill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

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

Coding out loud

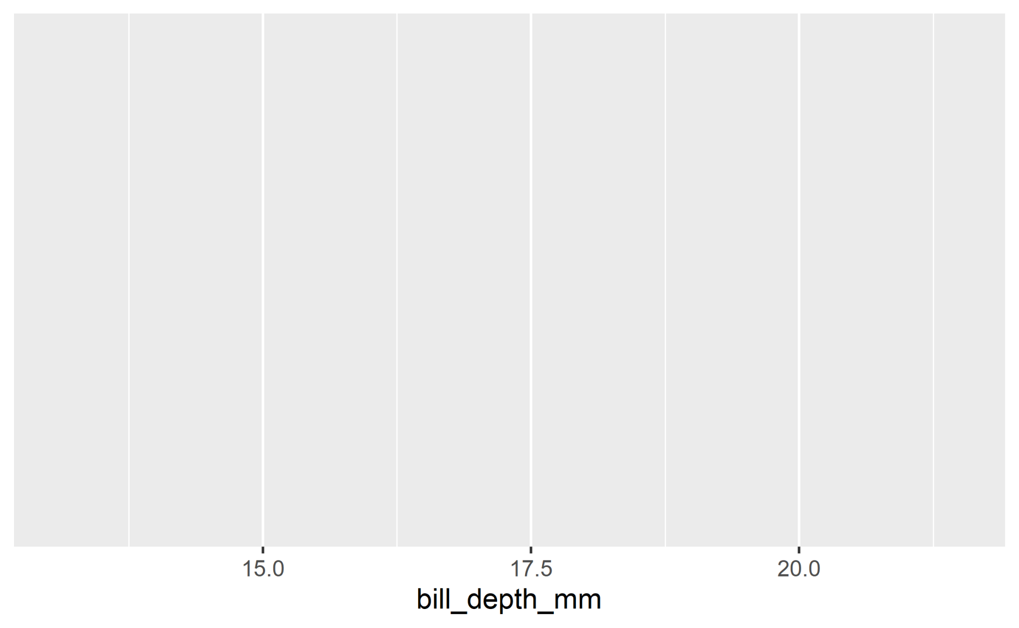
Start with the `penguins` data frame

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



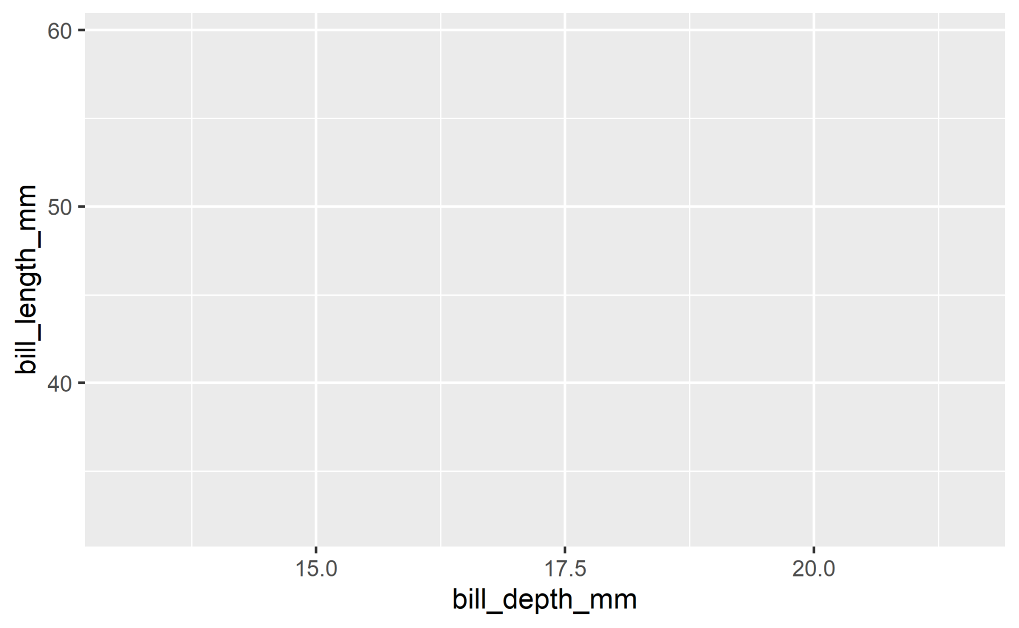
> Start with the `penguins` data frame, **map bill depth to the x-axis**

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



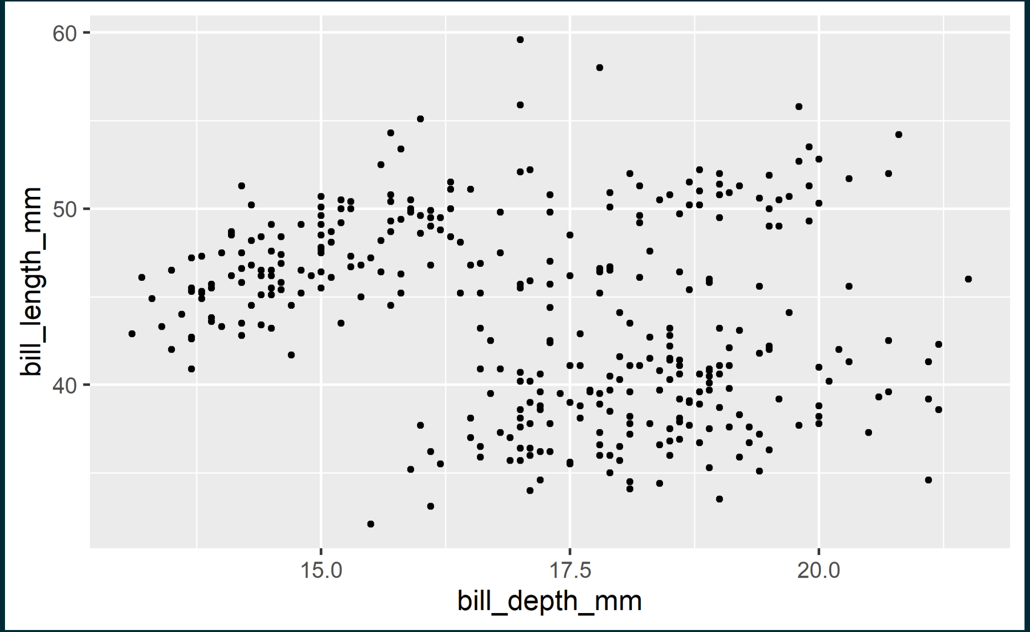
> Start with the `penguins` data frame, map bill depth to the x-axis **and map bill length to the y-axis.**

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



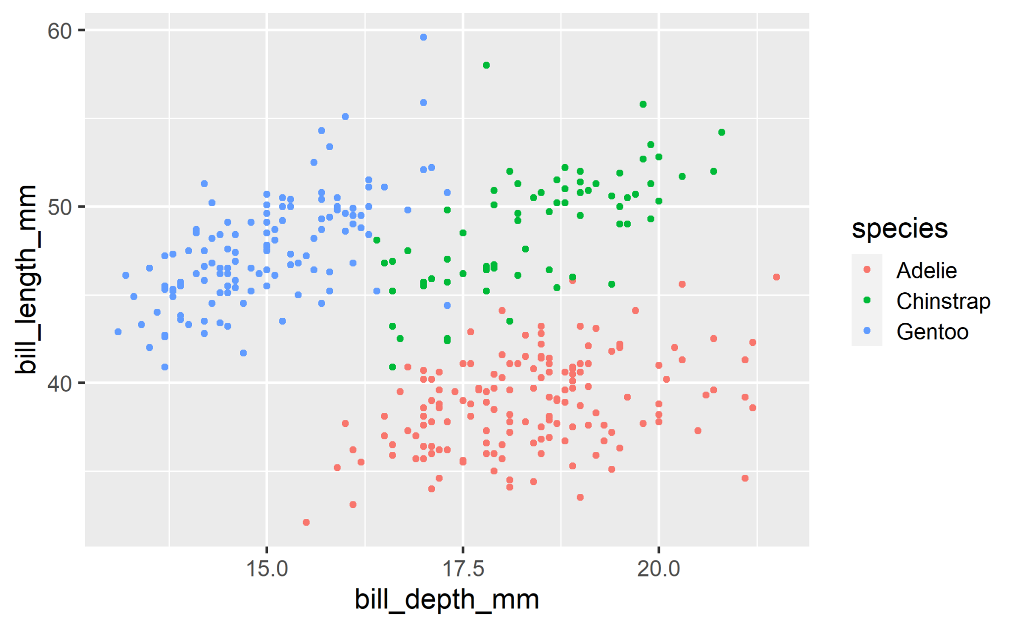
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis.
> **Represent each observation with a point**

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



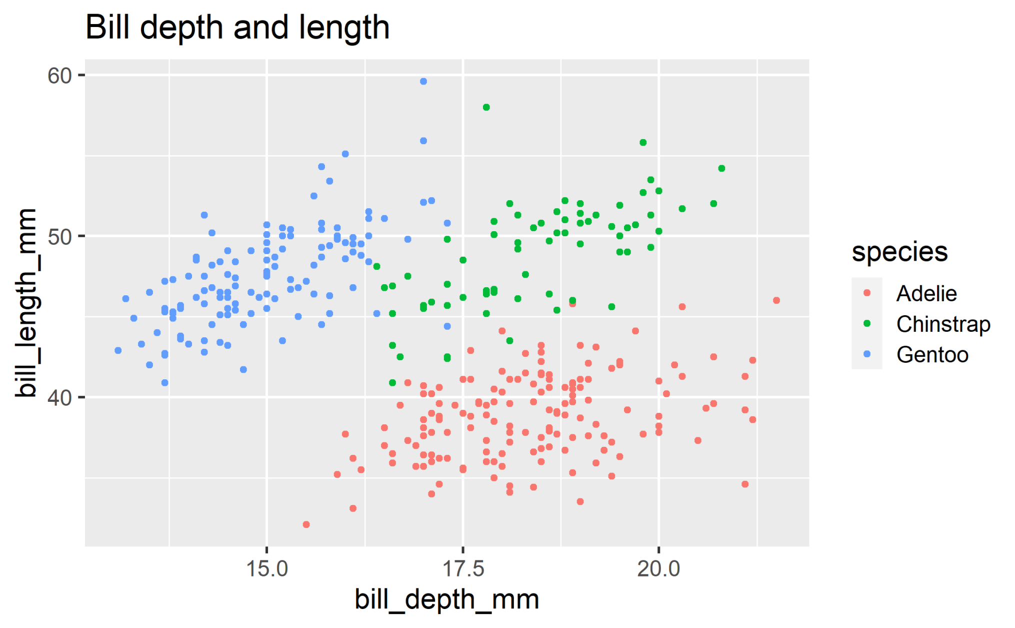
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point **and map species to the colour of each point.**

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

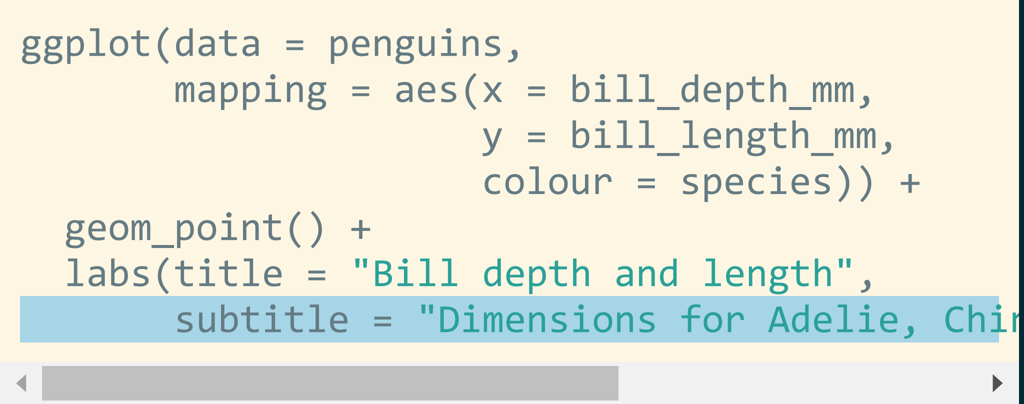


> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the colour of each point. **Title the plot "Bill depth and length"**

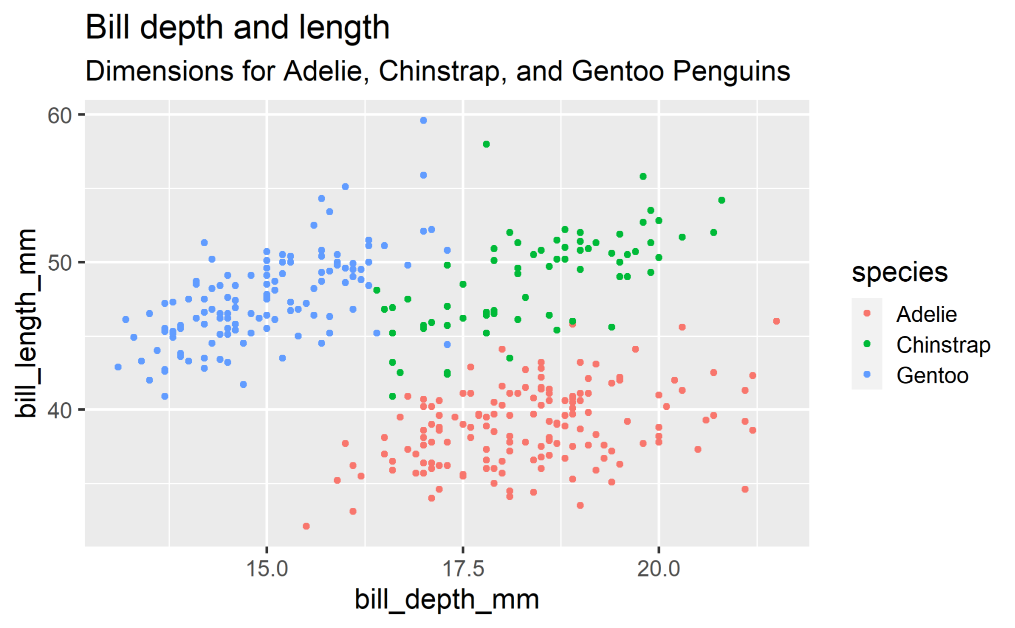
```r
ggplot(data = penguins,
       mapping = aes(x = bill_depth_mm,
                     y = bill_length_mm,
                     colour = species)) +
  geom_point() +
  labs(title = "Bill depth and length")
```



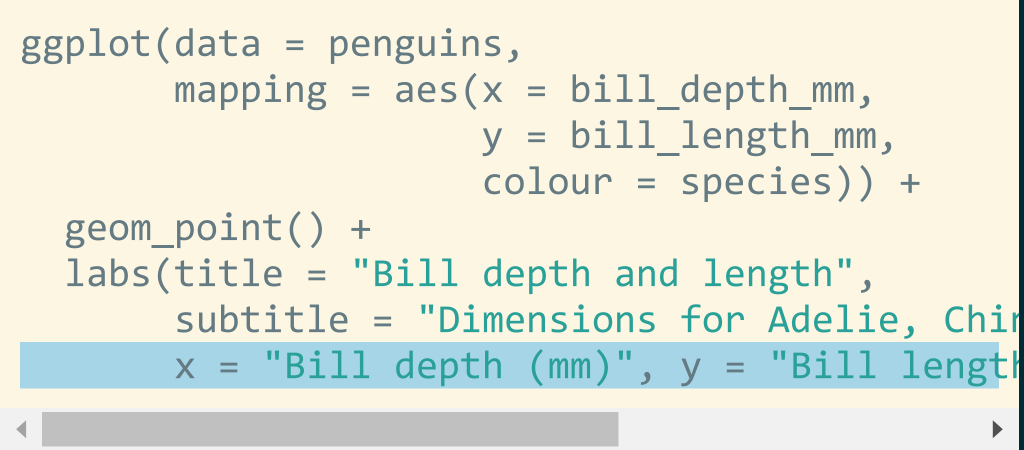
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the colour of each point. Title the plot "Bill depth and length", **add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins"**



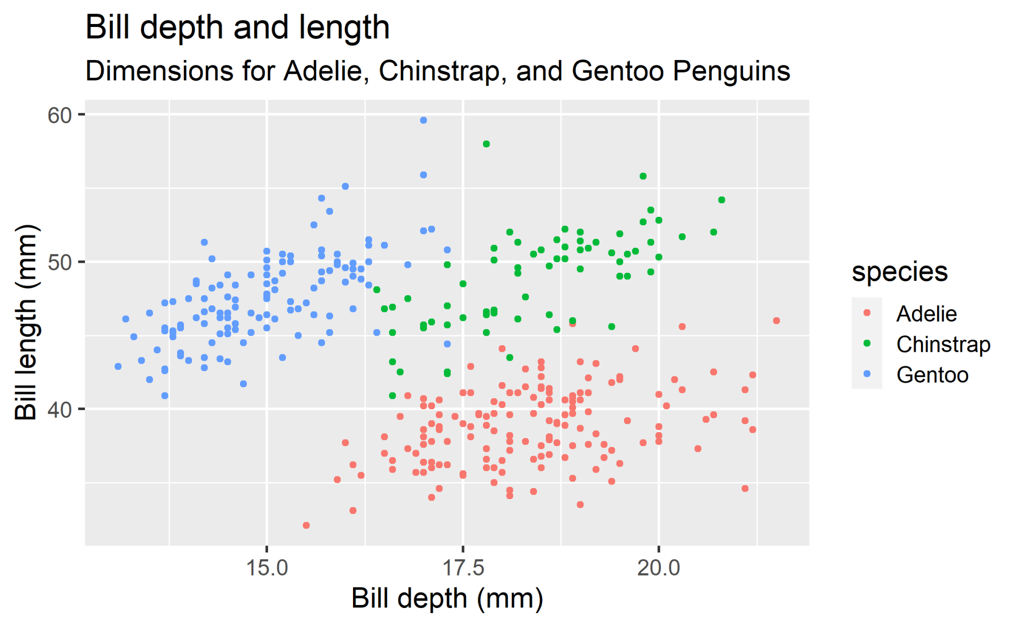
```
ggplot(data = penguins,
       mapping = aes(x = bill_depth_mm,
                     y = bill_length_mm,
                     colour = species)) +
  geom_point() +
  labs(title = "Bill depth and length",
       subtitle = "Dimensions for Adelie, Chi
```



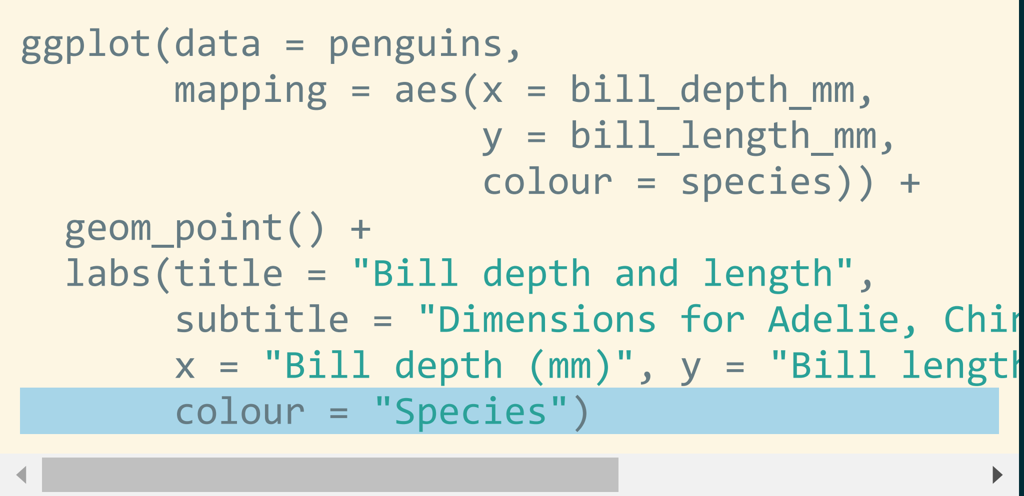
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the colour of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins",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



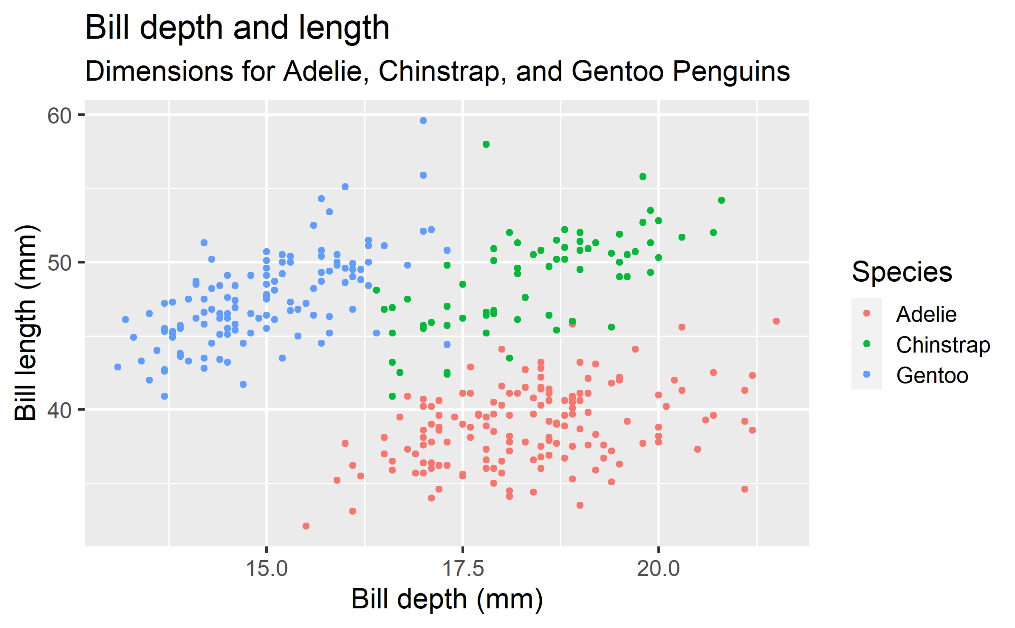
```
ggplot(data = penguins,
       mapping = aes(x = bill_depth_mm,
                     y = bill_length_mm,
                     colour = species)) +
  geom_point() +
  labs(title = "Bill depth and length",
       subtitle = "Dimensions for Adelie, Chi
       x = "Bill depth (mm)", y = "Bill lengt
```



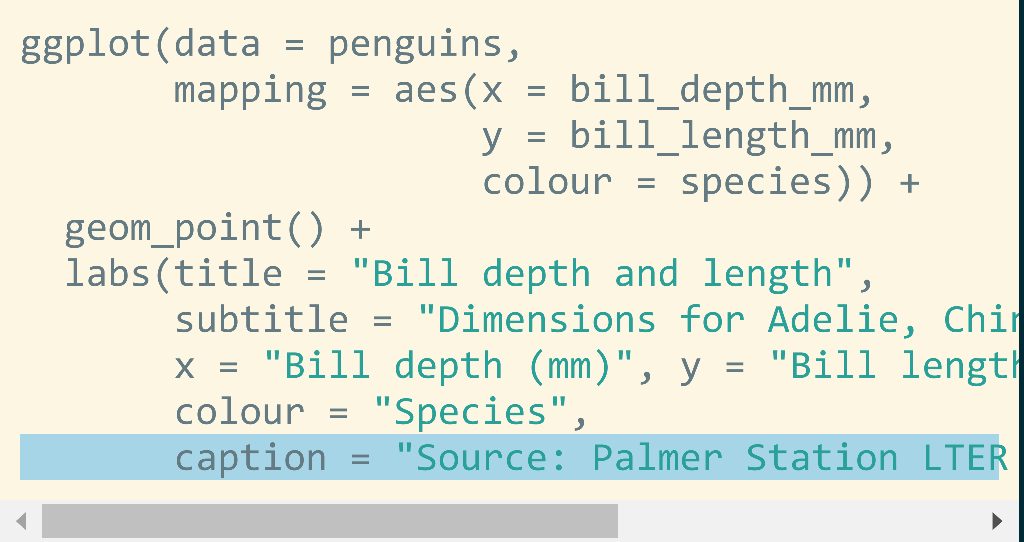
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the colour of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins",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



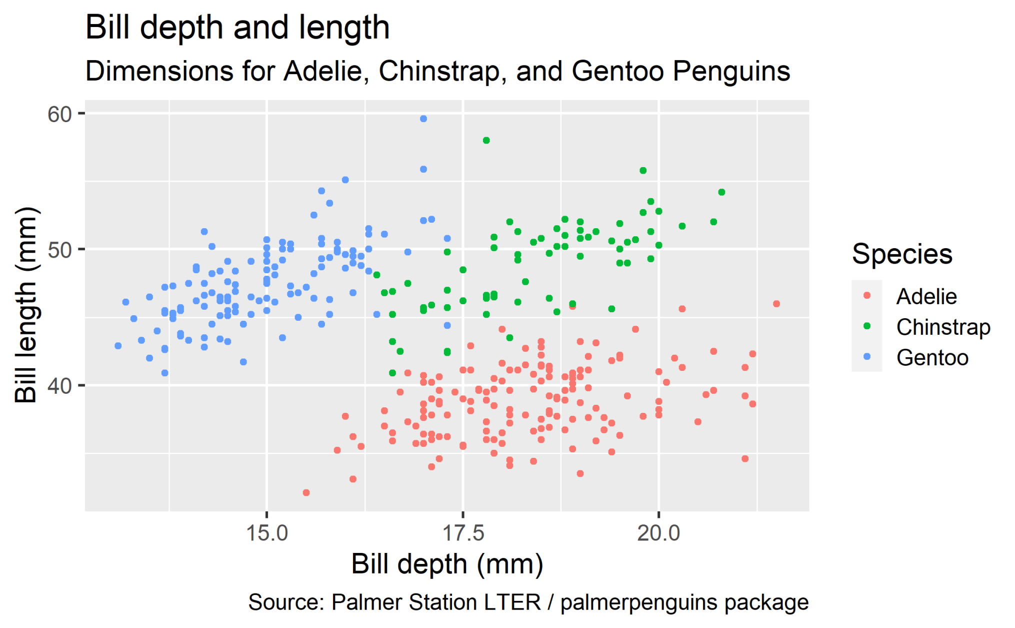
```
ggplot(data = penguins,
       mapping = aes(x = bill_depth_mm,
                     y = bill_length_mm,
                     colour = species)) +
  geom_point() +
  labs(title = "Bill depth and length",
       subtitle = "Dimensions for Adelie, Chi
       x = "Bill depth (mm)", y = "Bill lengt
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

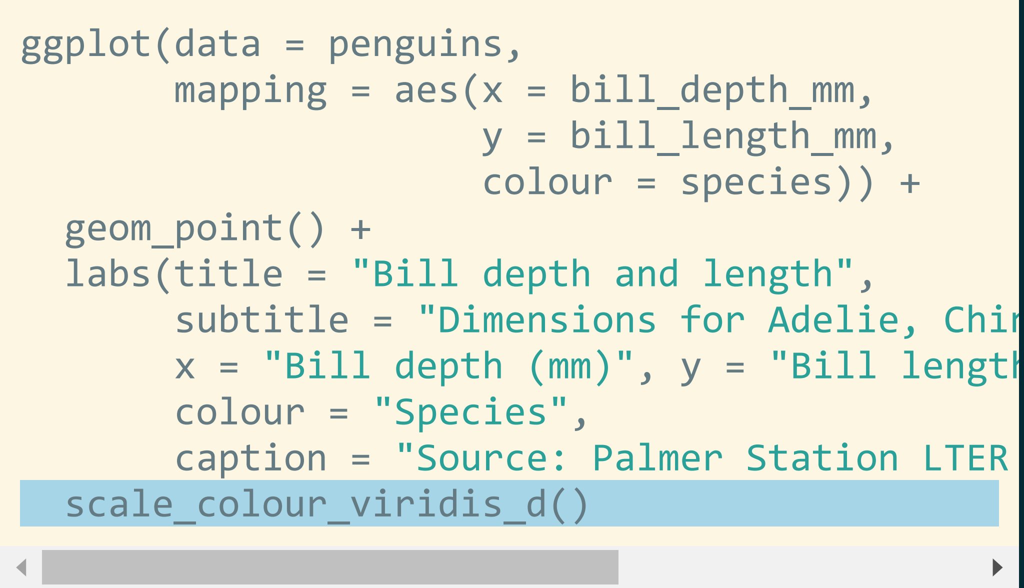


Bill depth and length

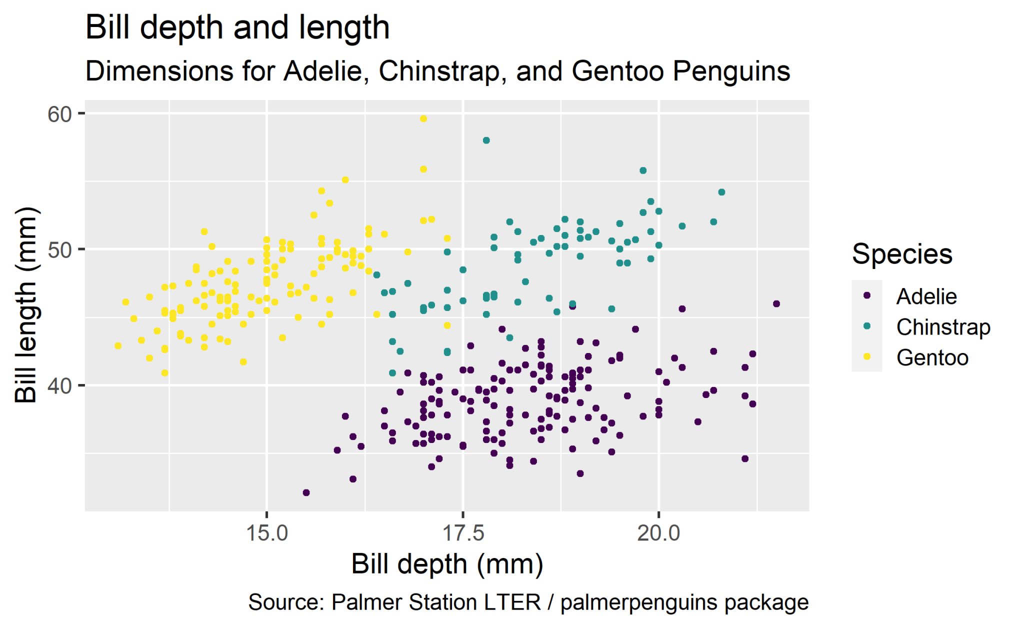
Dimensions for Adelie, Chinstrap, and Gentoo Penguins

Source: Palmer Station LTER / palmerpenguins package

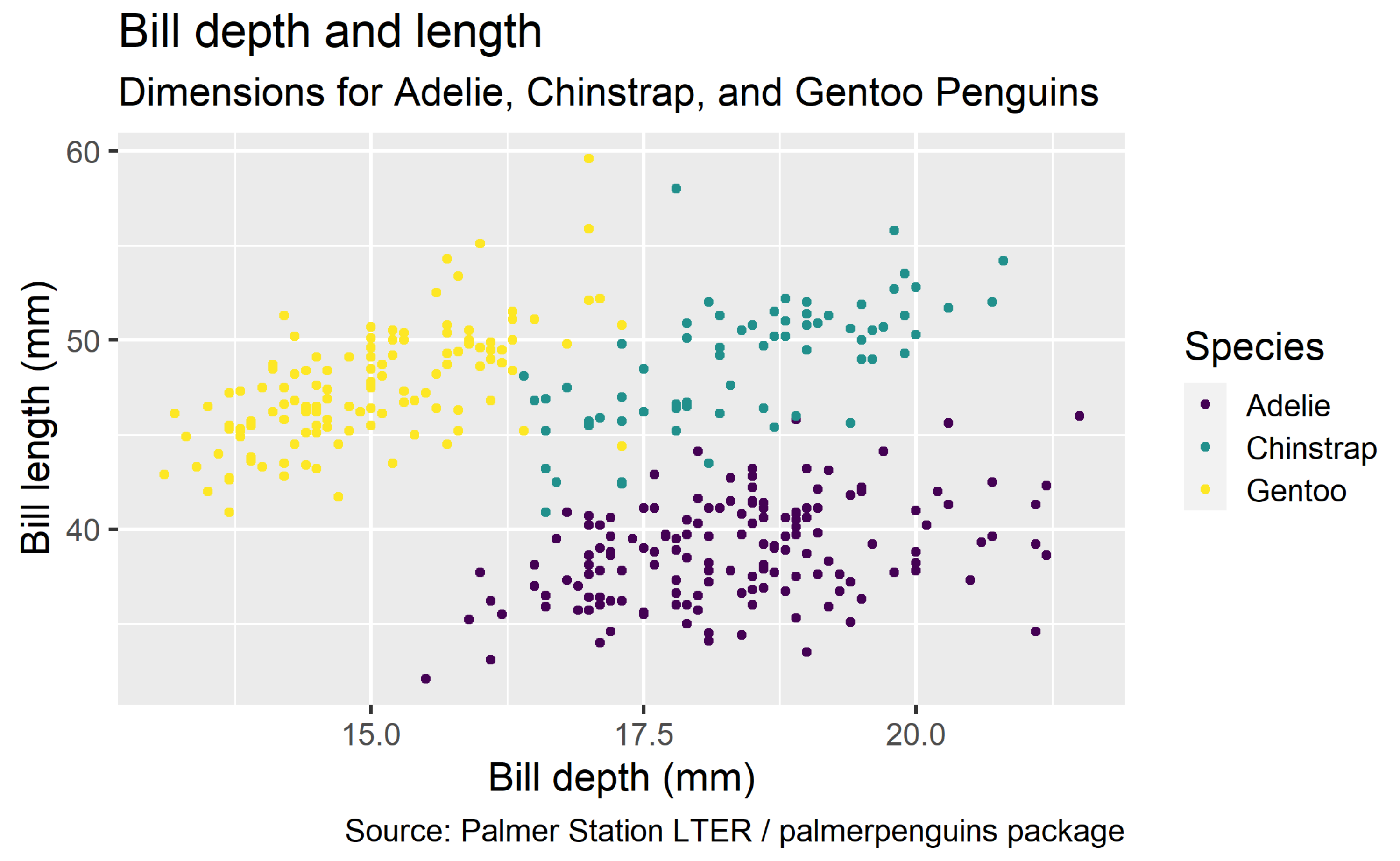
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the colour of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins", 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, Chi
       x = "Bill depth (mm)", y = "Bill lengt
       colour = "Species",
       caption = "Source: Palmer Station LTER
  scale_colour_viridis_d()
```



Plot Code Narrative



Plot Code Narrative

```
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).
```

Plot Code **Narrative**

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

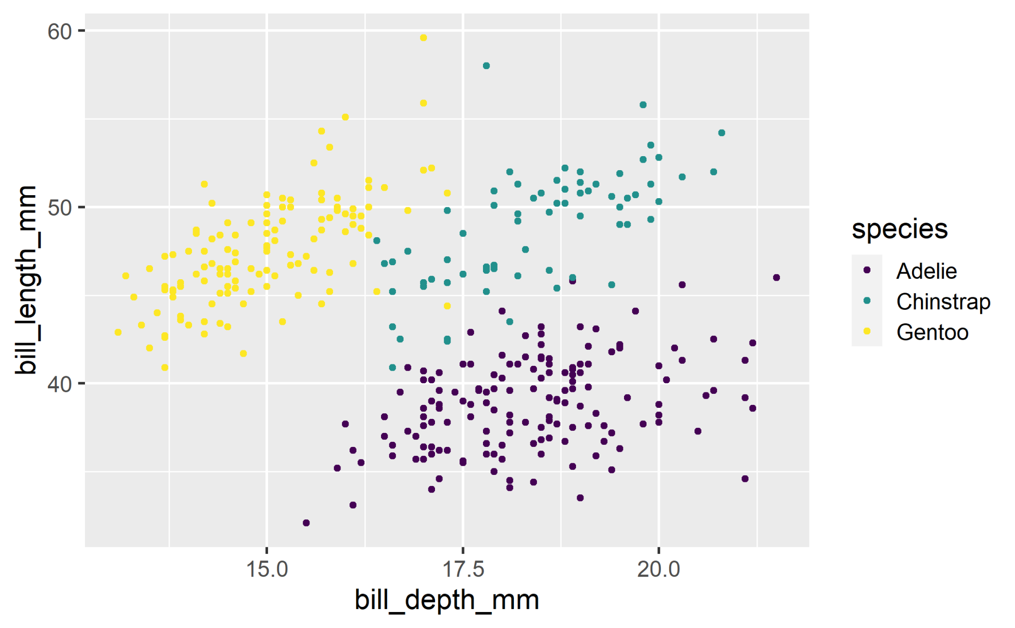
Aesthetics options

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

- `colour`
- `shape`
- `size`
- `alpha` (transparency)

Colour

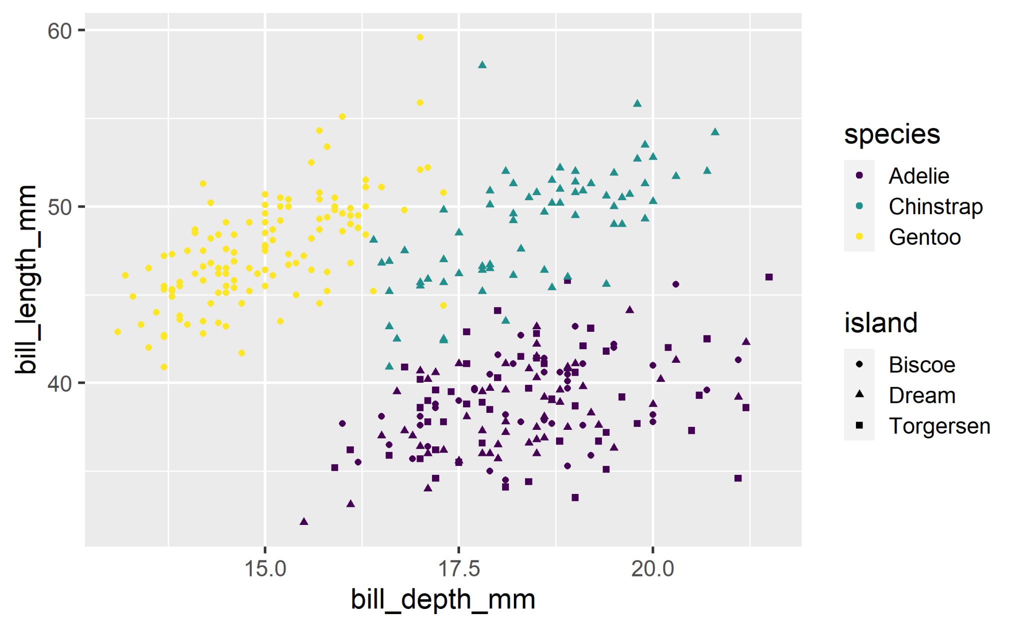
```r
ggplot(penguins,
       aes(x = bill_depth_mm,
           y = bill_length_mm,
           colour = species)) +
  geom_point() +
  scale_colour_viridis_d()
```



Shape

Mapped to a different variable than `colour`

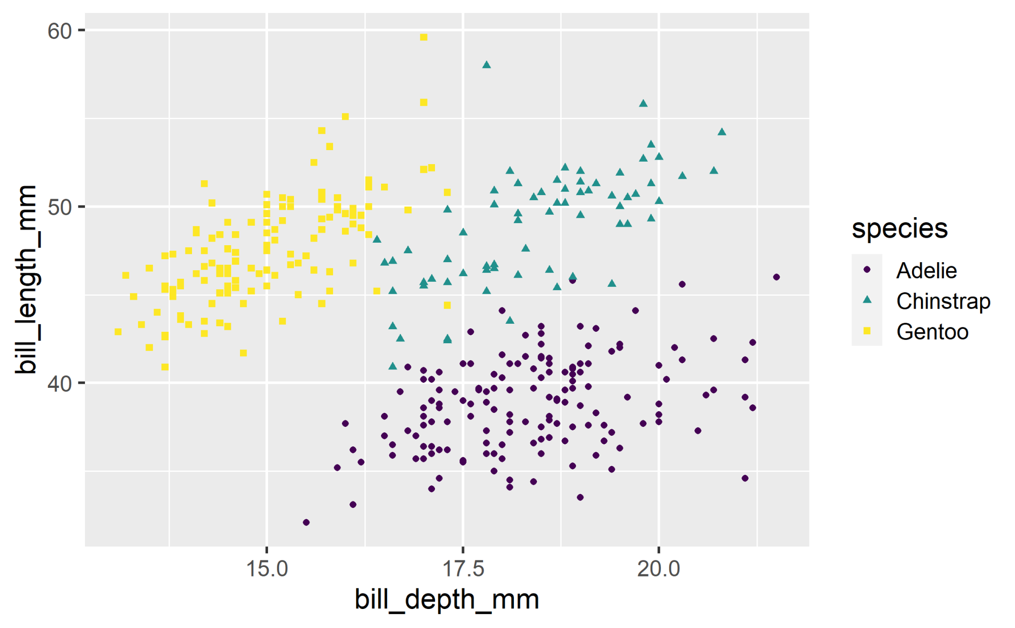
```
ggplot(penguins,
       aes(x = bill_depth_mm,
           y = bill_length_mm,
           colour = species,
           shape = island)) +
  geom_point() +
  scale_colour_viridis_d()
```



Shape

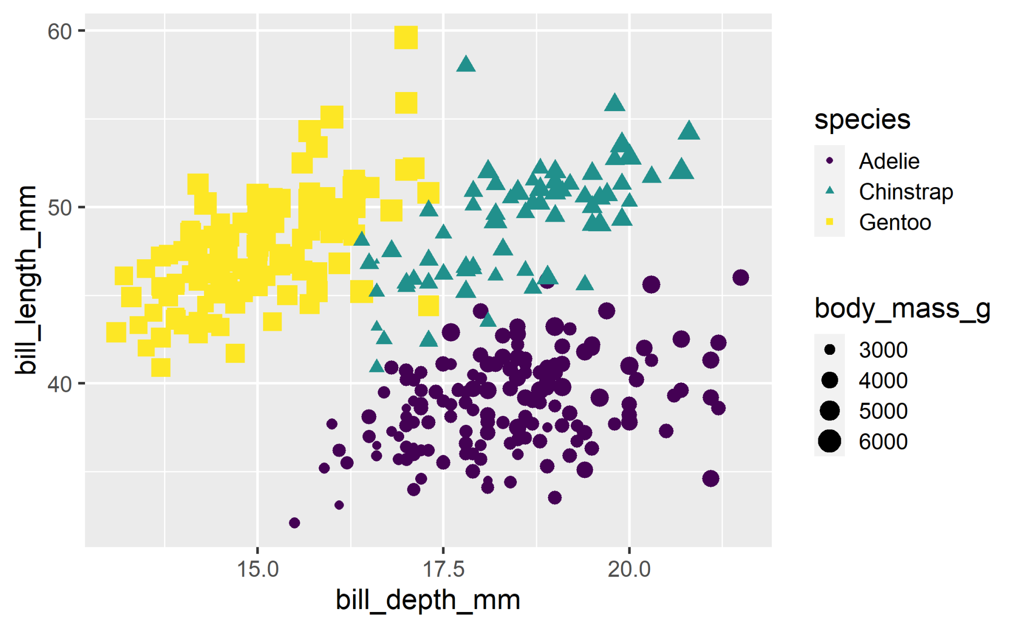
Mapped to same variable as `colour`

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



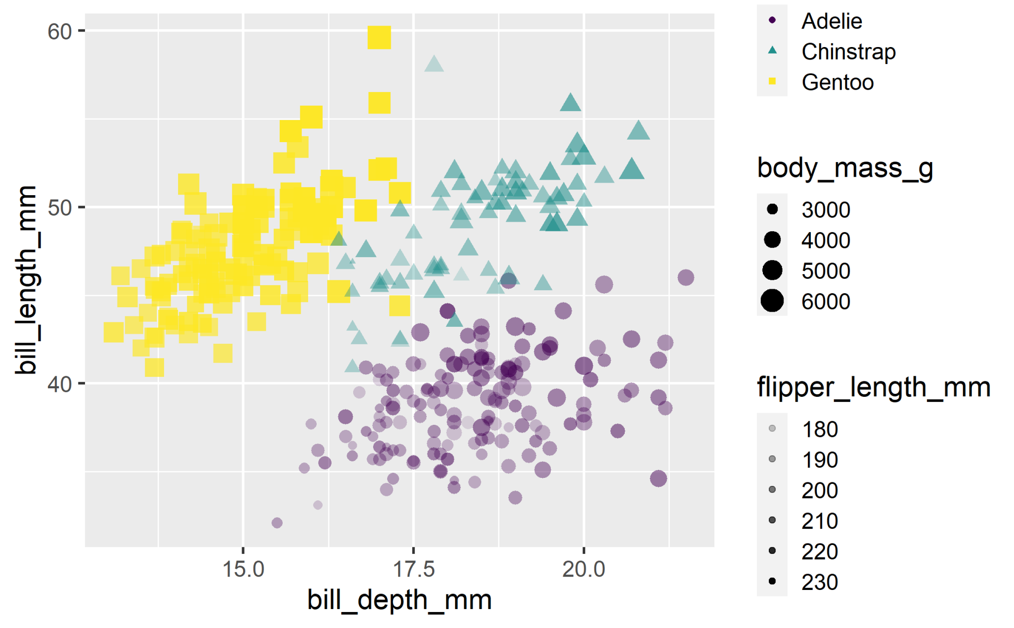
Size

```
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()
```



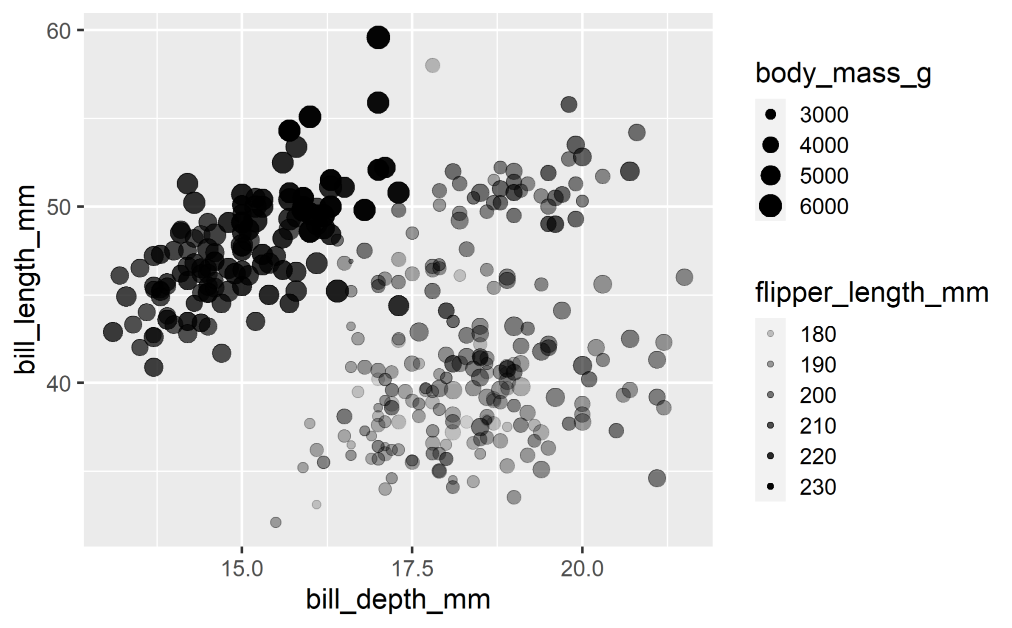
Alpha

```
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()
```



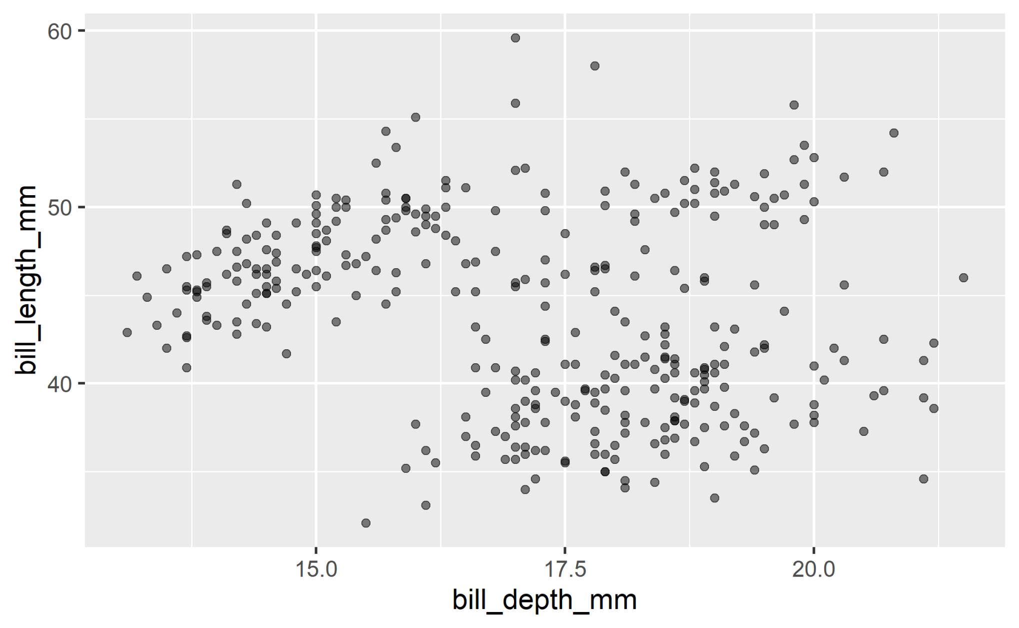
Mapping

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



Setting

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



Mapping vs. setting

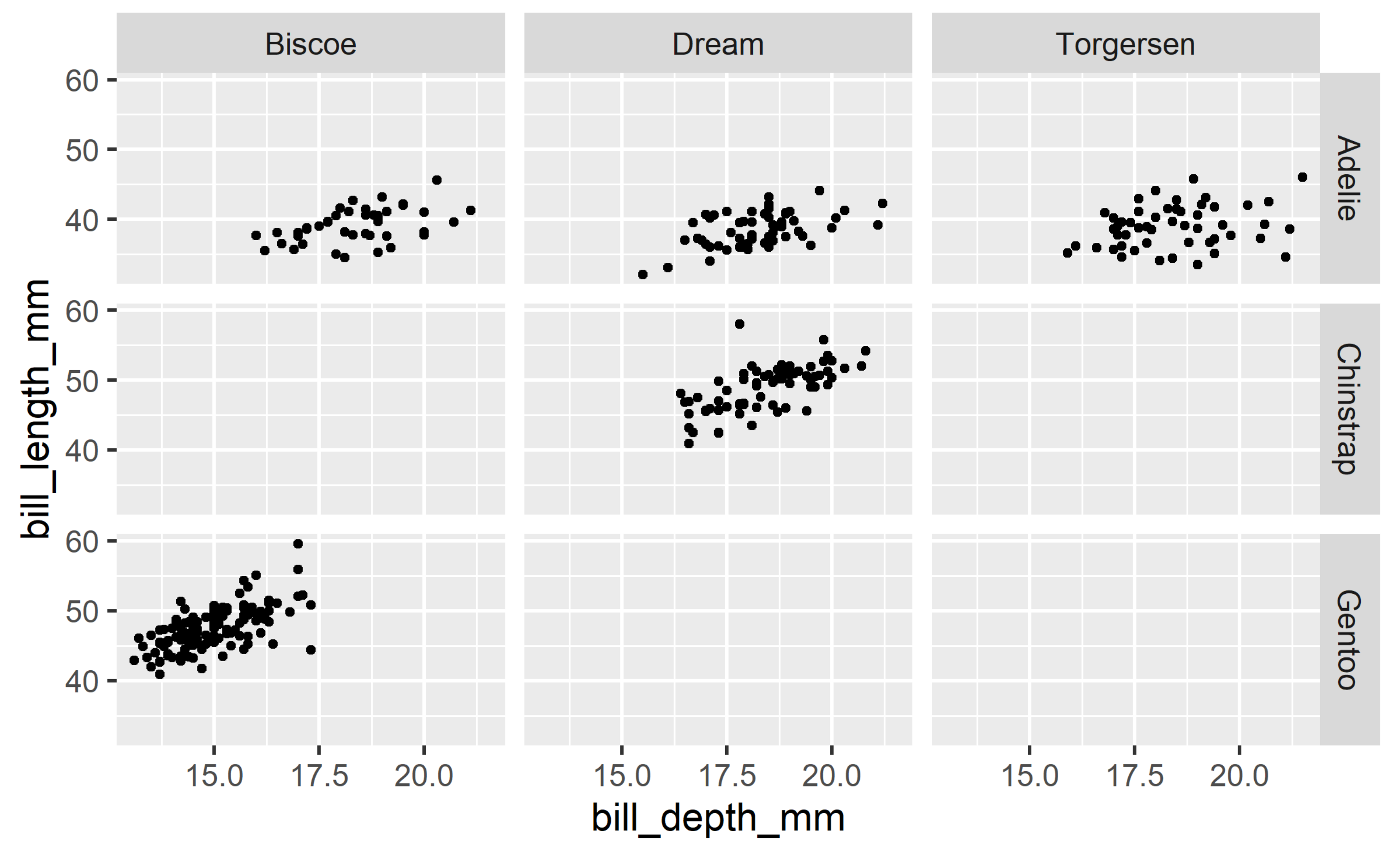
- **Mapping:** Determine the size, alpha, etc. of points based on the values of a variable in the data
  - goes into `aes()`
- **Setting:** Determine the size, alpha, etc. of points **not** based on the values of a variable in the data
  - goes into `geom_*()` (this was `geom_point()` in the previous example, but we'll learn about other geoms soon!)

Faceting

Faceting

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

Plot Code


Biscoe
Dream
Torgersen
Adelie
Chinstrap
Gentoo
bill_length_mm
60
50
40
60
50
40
60
50
40
15.0
17.5
20.0
15.0
17.5
20.0
15.0
17.5
20.0
bill_depth_mm

Plot Code

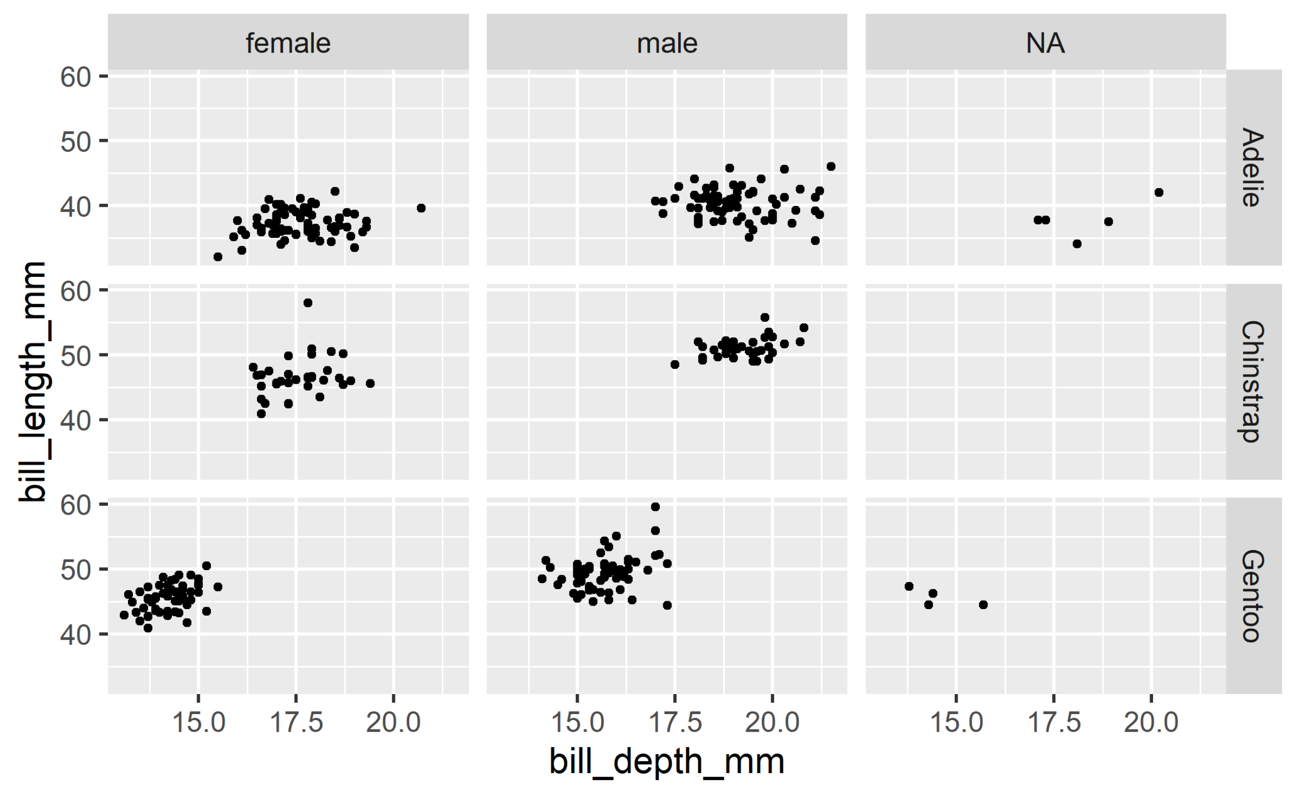
```r
ggplot(penguins, aes(x = bill_depth_mm, y = bill_length_mm)) +
  geom_point() +
  facet_grid(species ~ island)
```

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

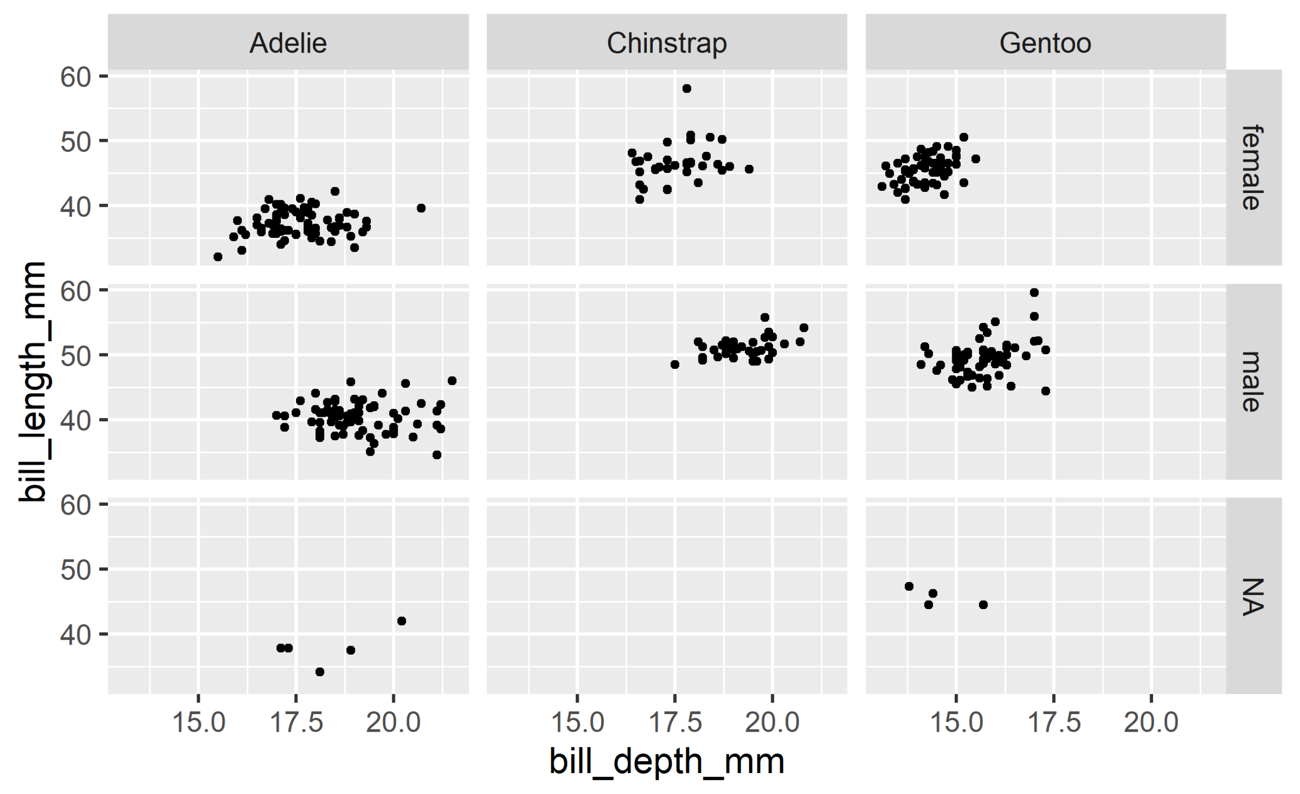
Various ways to facet

> 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!

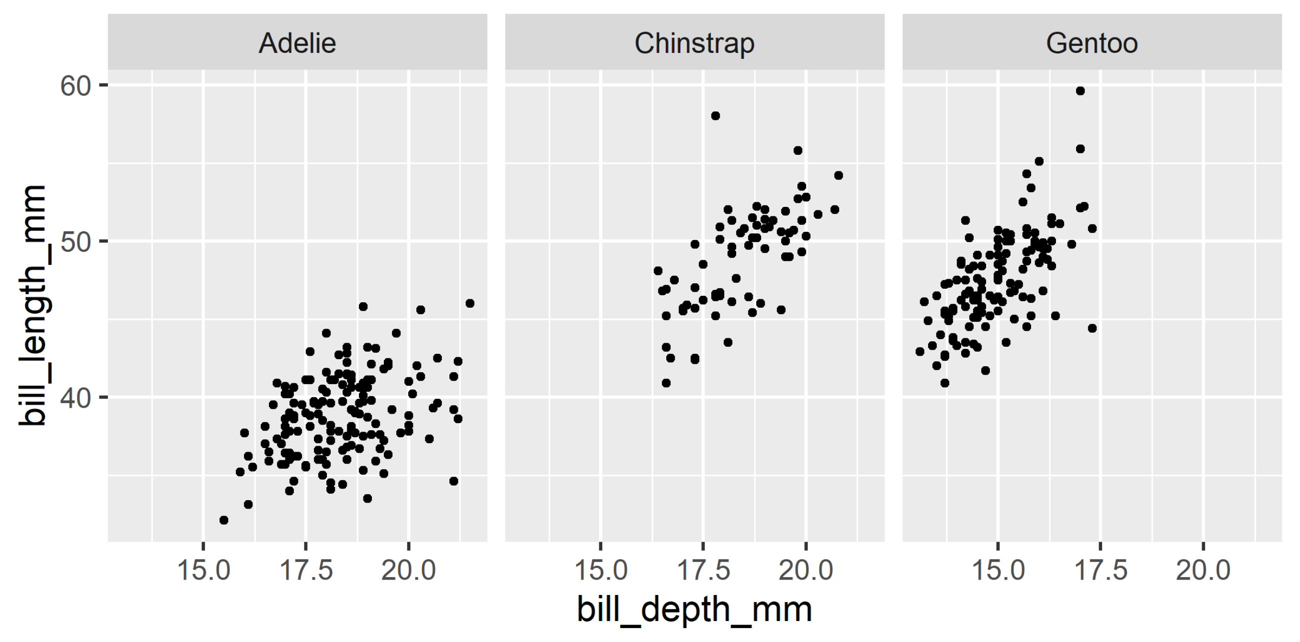
```
ggplot(penguins, aes(x = bill_depth_mm, y = bill_length_mm)) +
  geom_point() +
  facet_grid(species ~ sex)
```



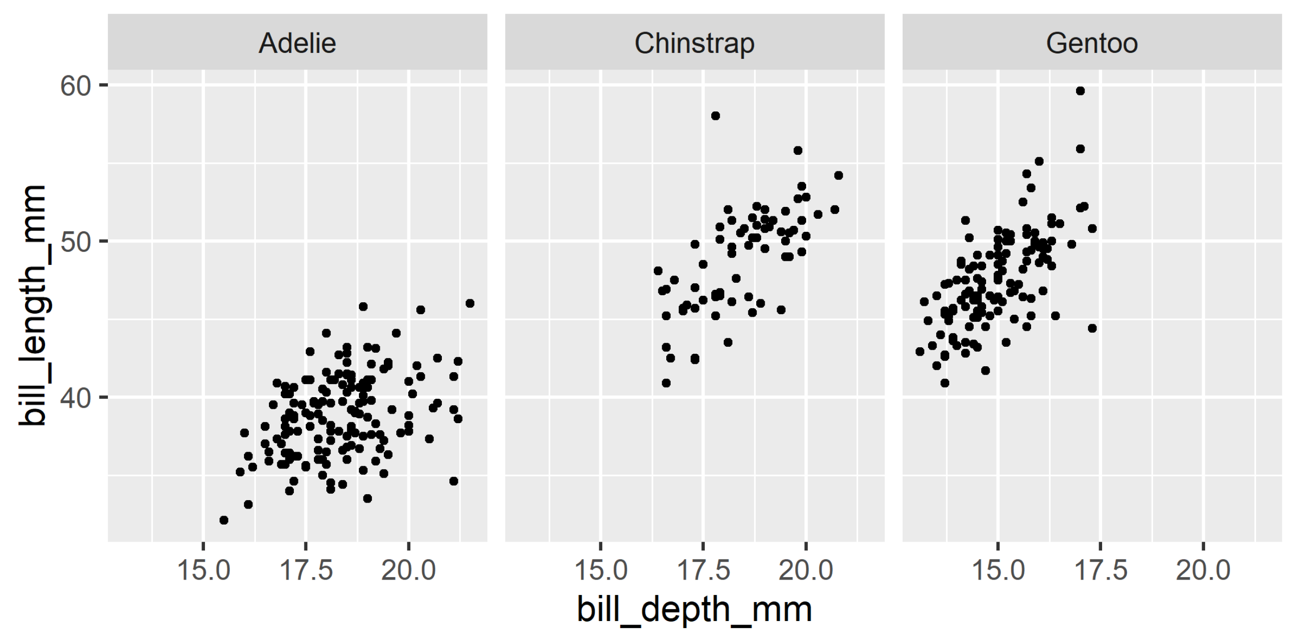
```r
ggplot(penguins, aes(x = bill_depth_mm, y = bill_length_mm)) +
  geom_point() +
  facet_grid(sex ~ species)
```



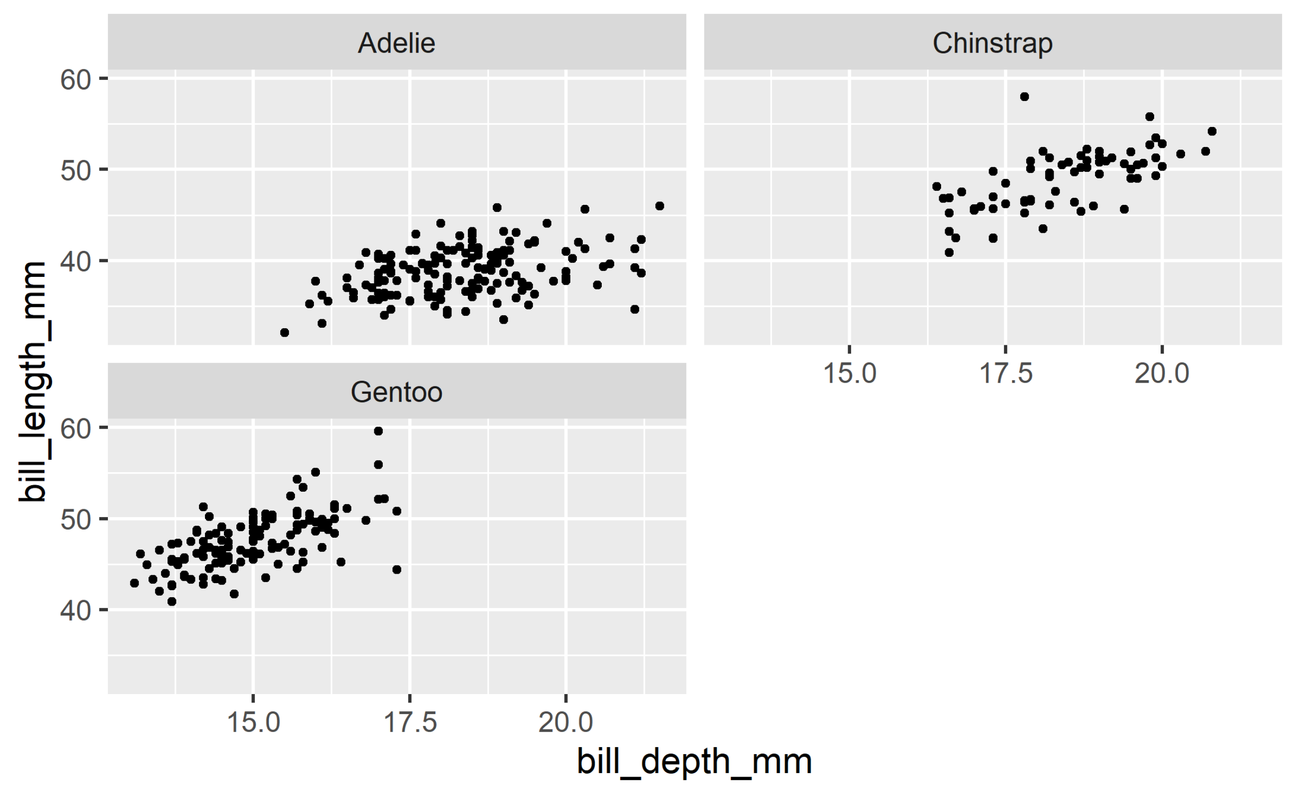
```r
ggplot(penguins, aes(x = bill_depth_mm, y = bill_length_mm)) +
  geom_point() +
  facet_wrap(~ species)
```



```
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)
```

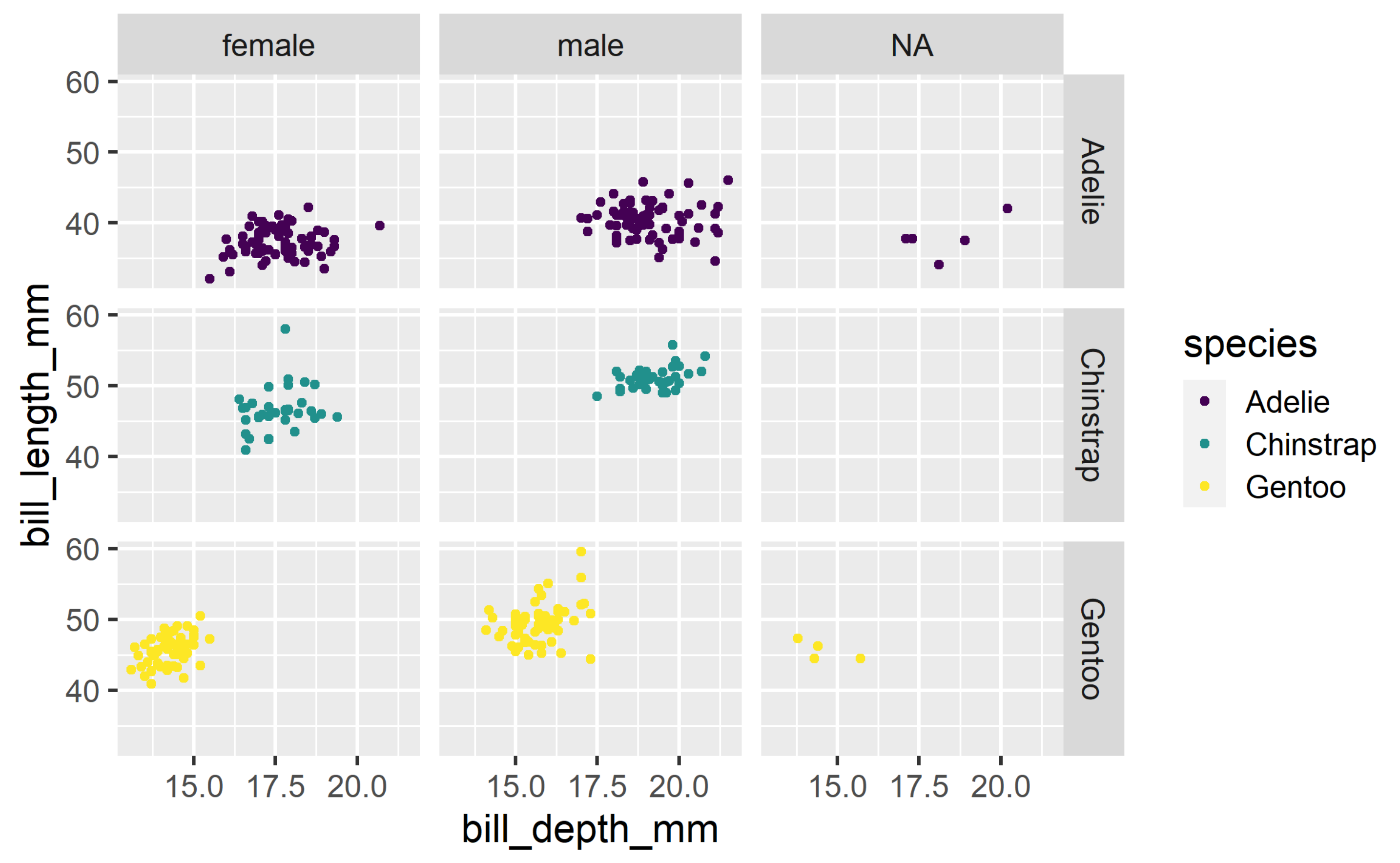


Faceting summary

- `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 = "none")
```