

# Lec 09 - Visualization with ggplot2

**Statistical Programming**

**Fall 2021**

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# The Grammar of Graphics

- Visualisation concept created by Leland Wilkinson (1999)
- to define the basic elements of a statistical graphic
- Adapted for R by Hadley Wickham (2009)
- consistent and compact syntax to describe statistical graphics
- highly modular as it breaks up graphs into semantic components
- ggplot2 is not meant as a guide to which graph to use and how to best convey your data (more on that later), but it does have some strong opinions.

# Terminology

A statistical graphic is a...

- mapping of **data**
- which may be **statistically transformed** (summarized, log-transformed, etc.)
- to **aesthetic attributes** (color, size, xy-position, etc.)
- using **geometric objects** (points, lines, bars, etc.)
- and mapped onto a specific **facet** and **coordinate system**

# Anatomy of a ggplot call

```
ggplot(  
  data = [dataframe],  
  mapping = aes(  
    x = [var x], y = [var y],  
    color = [var color],  
    shape = [var shape],  
    ...  
  )  
) +  
  geom_[some geom]([  
    mapping = aes(  
      color = [var geom color],  
      ...  
    )  
  ) +  
  ... # other geometries  
  scale_[some axis]_[some scale]() +  
  facet_[some facet]([formula]) +  
  ... # other options
```

# Data - Palmer Penguins

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



```
library(palmerpenguins)  
penguins
```

```
## # A tibble: 344 × 8  
##   species   island   bill_length_mm   bill_depth_mm flipper_length_mm  
##   <fct>     <fct>           <dbl>            <dbl>                <int>  
## 1 Adelie    Torgersen      39.1             18.7                 181  
## 2 Adelie    Torgersen      39.5             17.4                 186  
## 3 Adelie    Torgersen      40.3              18                  195  
## 4 Adelie    Torgersen       NA               NA                  NA  
## 5 Adelie    Torgersen      36.7             19.3                 193  
## 6 Adelie    Torgersen      39.3             20.6                 190  
## 7 Adelie    Torgersen      38.9             17.8                 181  
## 8 Adelie    Torgersen      39.2             19.6                 195  
## 9 Adelie    Torgersen      34.1             18.1                 193  
## 10 Adelie   Torgersen      42                20.2                 190  
## # ... with 334 more rows, and 3 more variables: body_mass_g <int>,  
## #   sex <fct>, year <int>
```

# A basic ggplot

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

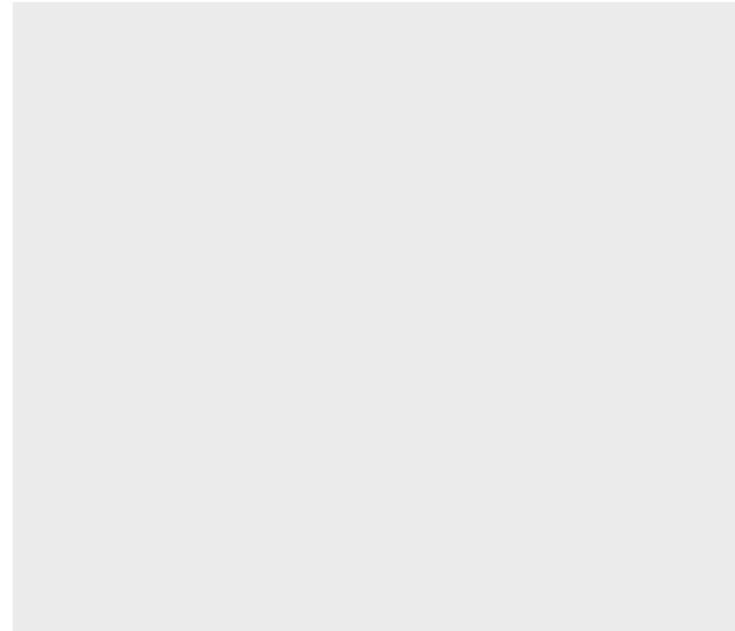
## Warning: Removed 2 rows containing missing valu



# **Text <-> Plot**

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)  
)
```



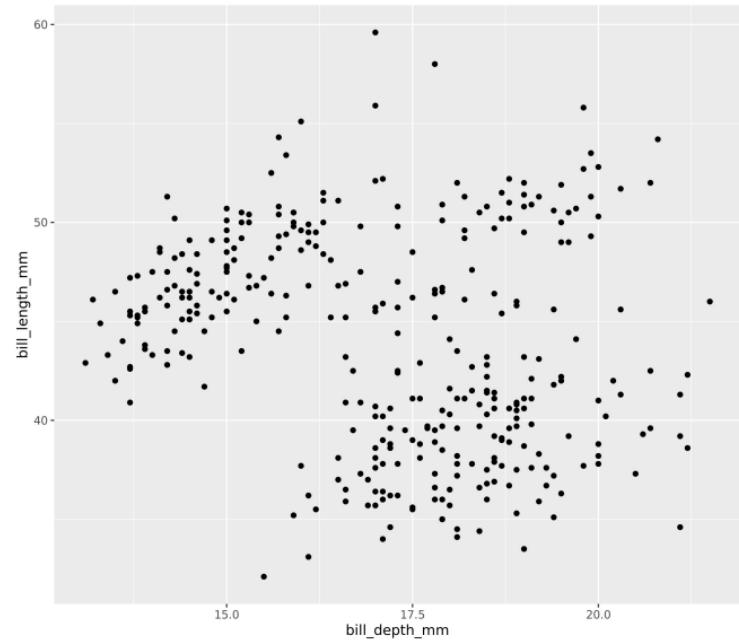
Start with the `penguins` data frame, map bill depth to the x-axis **and map bill length to the y-axis.**

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



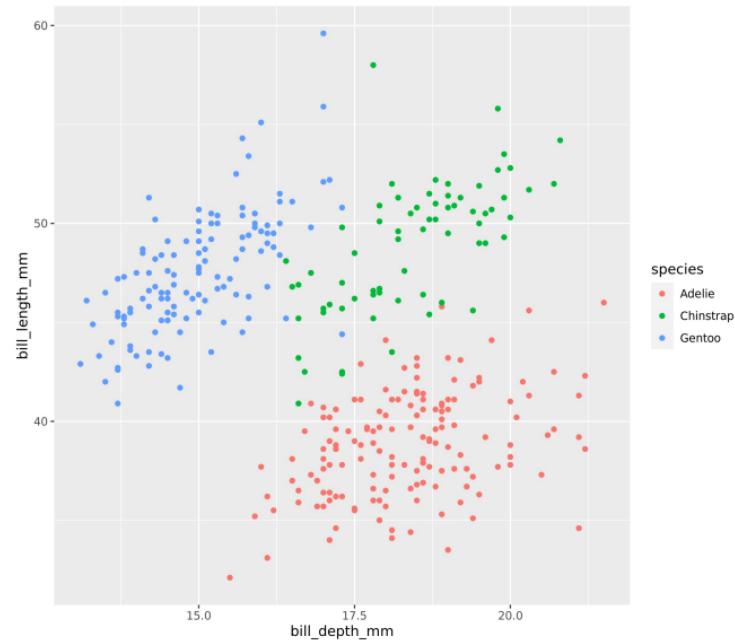
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. **Represent each observation with a point**

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



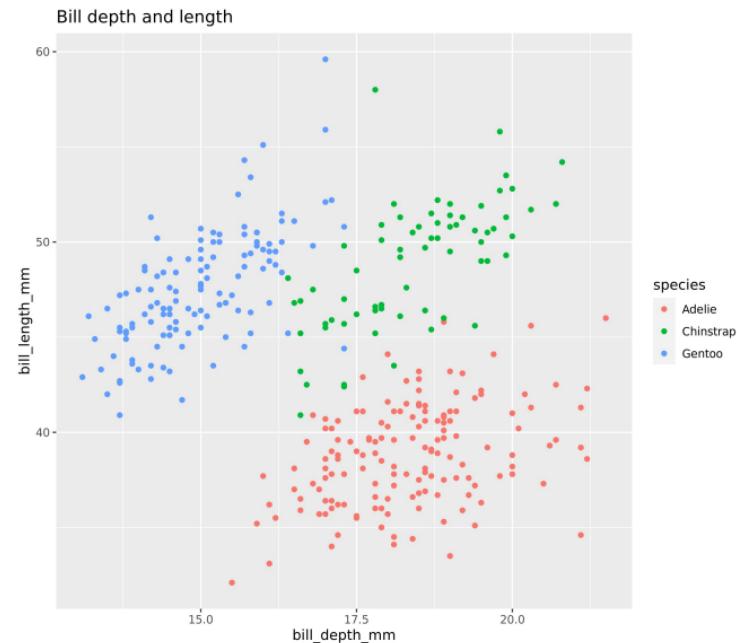
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point **and map species to the color of each point.**

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



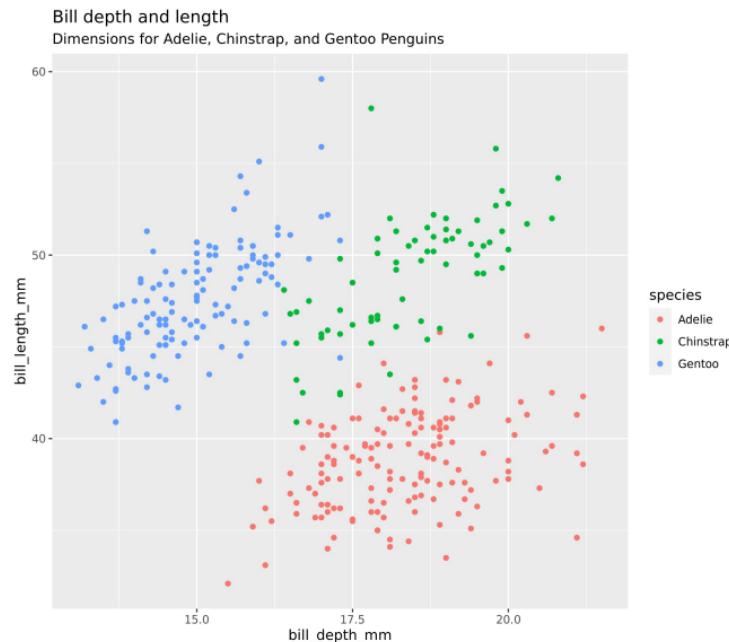
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. **Title the plot "Bill depth and length"**

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



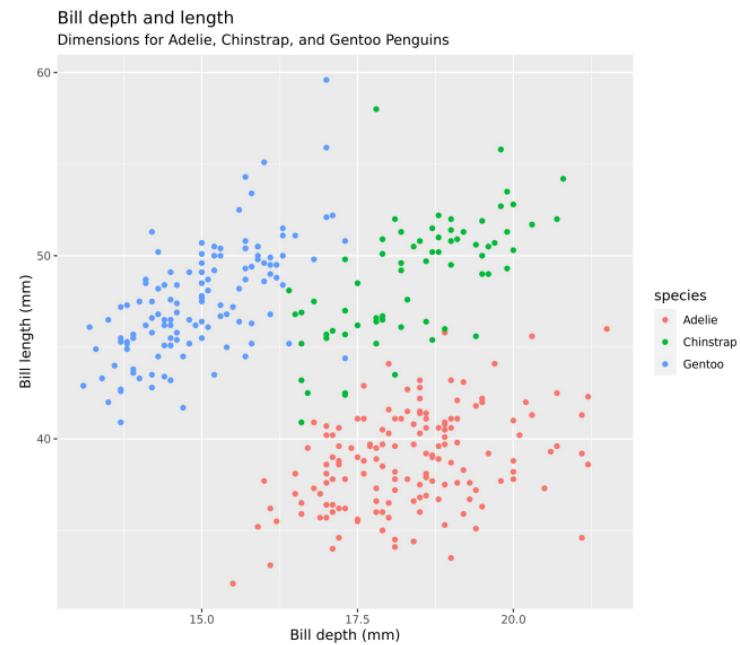
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. Title the plot "Bill depth and length", **add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins"**

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



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  
  )  
) +  
  geom_point(  
    mapping = aes(color = species)  
  ) +  
  labs(  
    title = "Bill depth and length",  
    subtitle = paste("Dimensions for Adelie,",  
      "Chinstrap, and Gentoo",  
      "Penguins"),  
    x = "Bill depth (mm)",  
    y = "Bill length (mm)"  
)
```



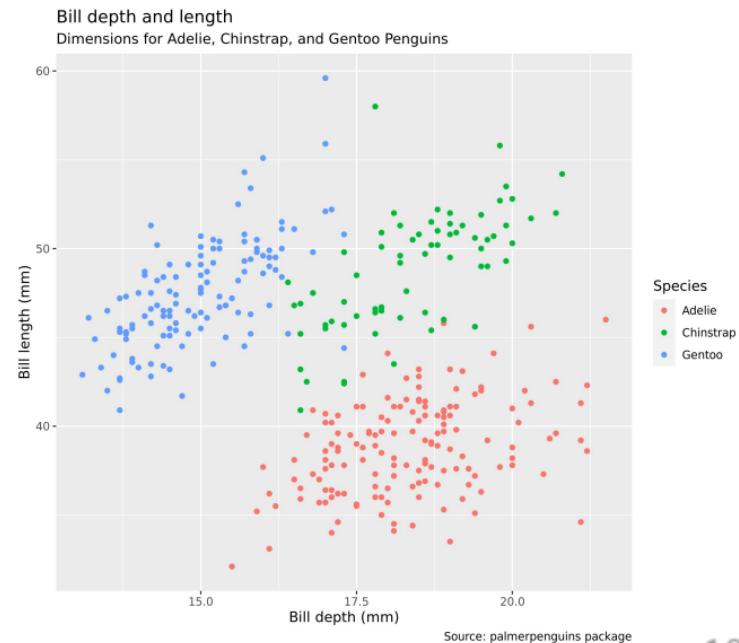
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins", label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



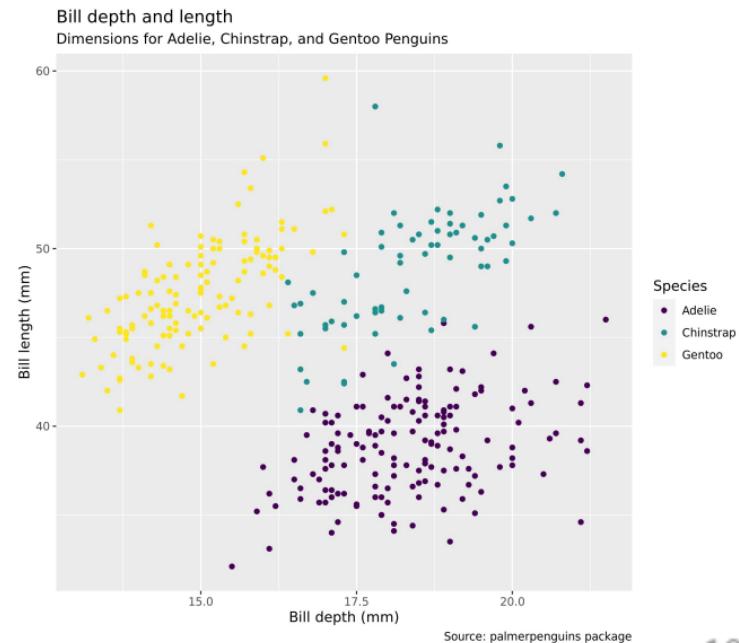
Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins", label 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  
)  
) +  
  geom_point(  
    mapping = aes(color = species)  
) +  
  labs(  
    title = "Bill depth and length",  
    subtitle = paste("Dimensions for Adelie,",  
                    "Chinstrap, and Gentoo",  
                    "Penguins"),  
    x = "Bill depth (mm)",  
    y = "Bill length (mm)",  
    color = "Species",  
    caption = "Source: 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 the viridis color palette for all points.**

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



# Argument names

Often we 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  
  )  
) +  
  geom_point(  
    mapping = aes(color = species)  
  ) +  
  scale_color_viridis_d()
```

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

**Note** that `ggplot` and `geom_*` swap the order of the `data` and `mapping` arguments.

# Aesthetics

# Aesthetics options

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

- color
- shape
- size
- alpha (transparency)

Different geometries have different aesthetics that can be used - see the ggplot2 geoms help files for listings.

- Aesthetics given in `ggplot` apply to all `geoms`.
- Aesthetics for a specific `geom` can be overridden with the `geom_*`'s aesthetics.

# color

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



# Shape

Mapped to a different variable than color

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



# Shape

Mapped to same variable as color

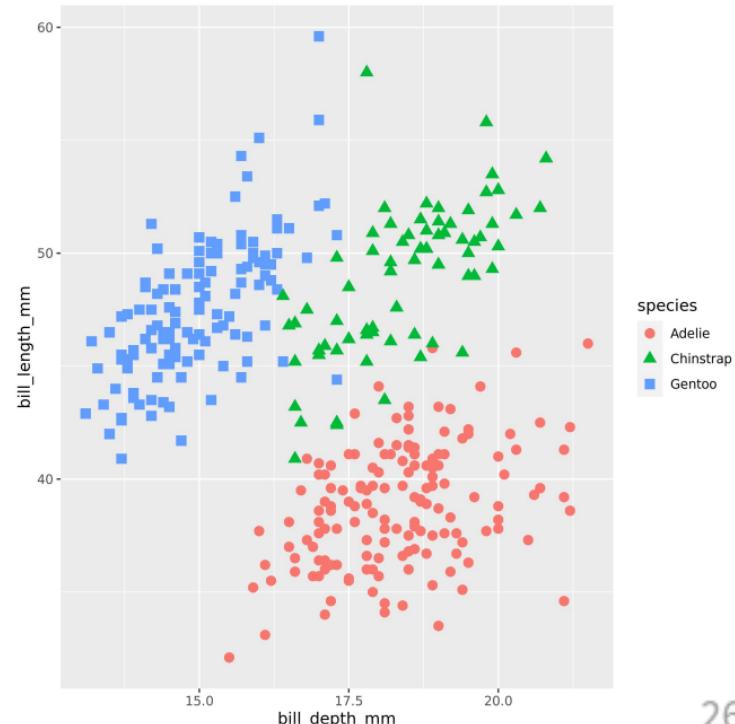
```
ggplot(  
  penguins,  
  aes(  
    x = bill_depth_mm,  
    y = bill_length_mm  
  )  
) +  
  geom_point(  
    aes(  
      color = species,  
      shape = species  
    )  
)
```



# Size

Using a fixed value (note this value is outside of the `aes` call)

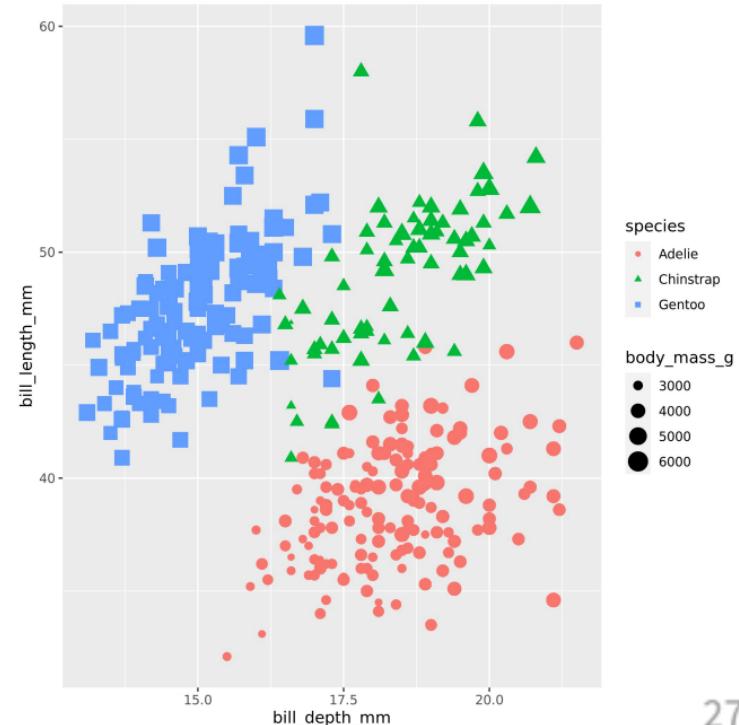
```
ggplot(  
  penguins,  
  aes(  
    x = bill_depth_mm,  
    y = bill_length_mm  
  )  
) +  
  geom_point(  
    aes(  
      color = species,  
      shape = species  
    ),  
    size = 3  
  )
```



# Size

Mapped to a variable

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



# Alpha

```
ggplot(  
  penguins,  
  aes(  
    x = bill_depth_mm,  
    y = bill_length_mm  
)  
) +  
  geom_point(  
    aes(  
      color = species,  
      shape = species,  
      alpha = body_mass_g  
,  
      size = 3  
)
```



# Mapping vs settings

- **Mapping:** Determine an aesthetic (the size, alpha, etc.) of a geom based on the values of a variable in the data
- goes into `aes()` as an argument which is then an argument of `ggplot2` or `geom_*`.
- **Setting:** Determine an aesthetic (the size, alpha, etc.) of a geom **not** based on the values of a variable in the data
- goes directly into `geom_*` as an argument.

# Faceting

# Faceting

- Smaller plots that display different subsets of the data
- Useful for exploring conditional relationships and large data
- Sometimes referred to as "small multiples"

# facet\_grid

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



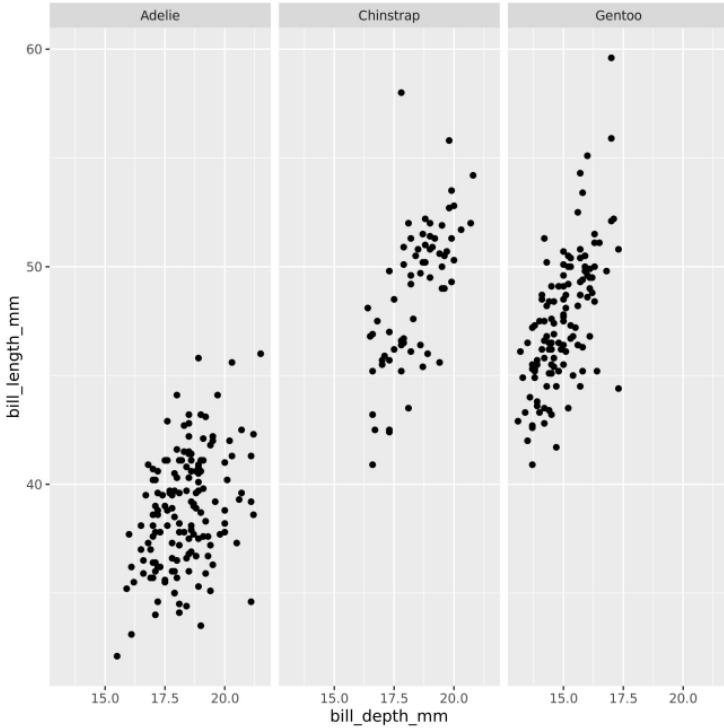
# Compare with ...

```
ggplot(  
  penguins,  
  aes(  
    x = bill_depth_mm,  
    y = bill_length_mm  
  )  
) +  
  geom_point(  
    aes(  
      color = species,  
      shape = island  
    ),  
    size = 3  
)
```



# facet\_grid (cols)

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



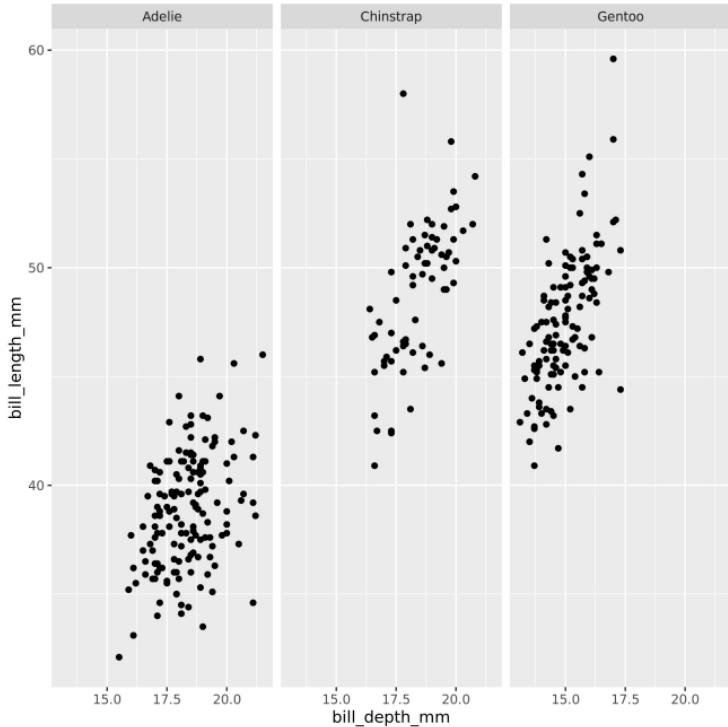
# facet\_grid (rows)

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



# facet\_wrap

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



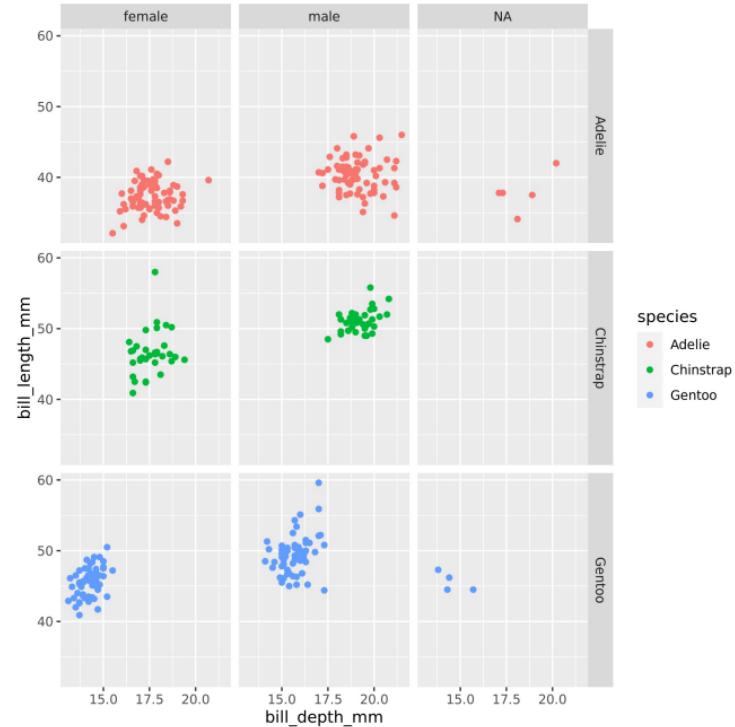
# facet\_wrap

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



# Faceting and color

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



# Hiding redundancy

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



# A brief plot Tour of ggplot2

# Histograms

```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g,  
  )) +  
  geom_histogram()  
  
## `stat_bin()` using `bins = 30`. Pick better val  
## `binwidth`.
```



# Histograms - bins

```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g,  
  )) +  
  geom_histogram(bins = 50)
```



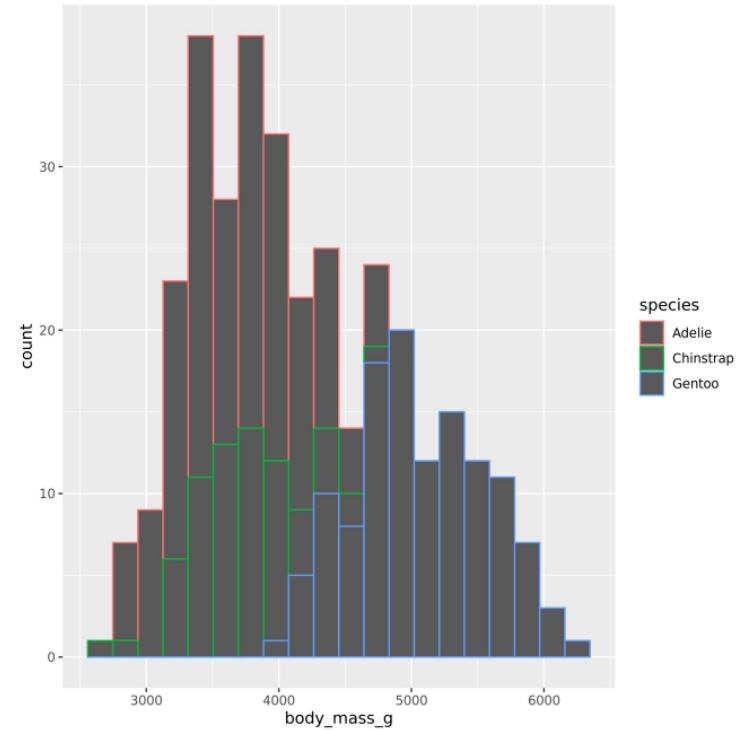
# Histograms - binwidth

```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g,  
  )) +  
  geom_histogram(binwidth = 250)
```



# Histograms - color

```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g,  
    color = species  
  )  
) +  
  geom_histogram(bins = 20)
```



# Histograms - fill

```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g,  
    fill = species  
  )  
) +  
  geom_histogram(bins = 20)
```



# Histograms - position

```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g,  
    fill = species  
  )  
) +  
  geom_histogram(  
    bins = 20,  
    position = "identity",  
    alpha = 0.5  
)
```



# Histograms - facets

```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g,  
    fill = species  
  )  
) +  
  geom_histogram(bins = 20) +  
  facet_grid(species ~ .) +  
  guides(fill = FALSE)
```



# Density plot

```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g  
  )  
) +  
  geom_density()
```



# Density plot - fill

```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g,  
    fill = species  
  )  
) +  
  geom_density(alpha = 0.25)
```



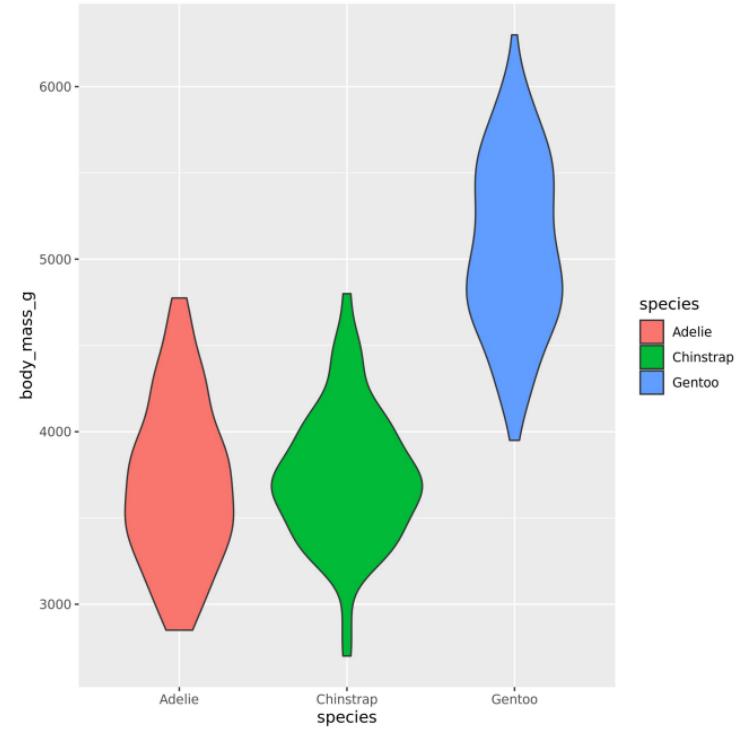
# Density plot - adjust

```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g,  
    fill = species  
  )  
) +  
  geom_density(  
    adjust = 0.5,  
    alpha = 0.25  
  )
```



# Violin plot

```
ggplot(  
  penguins,  
  aes(  
    x = species,  
    y = body_mass_g,  
    fill = species  
  )  
) +  
  geom_violin()
```



# Ridge plot

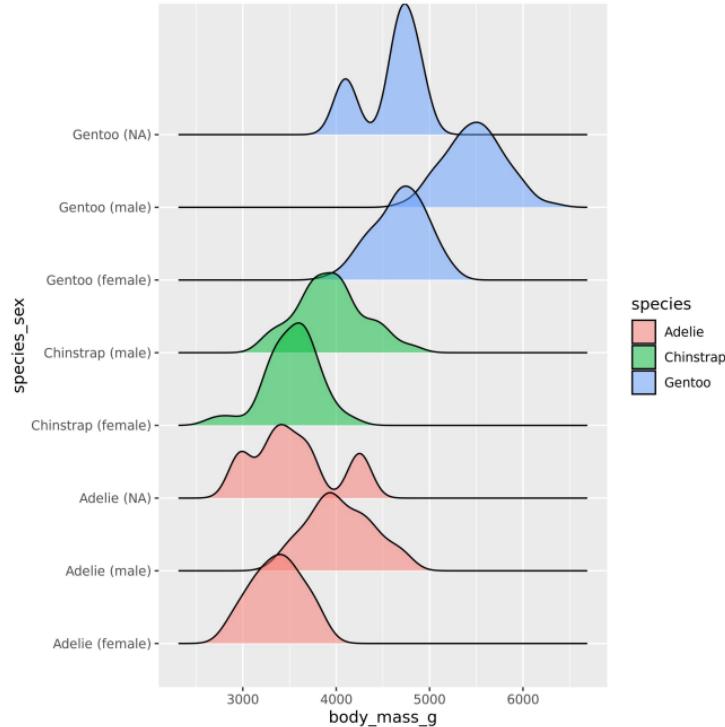
```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g,  
    y = species,  
    fill = species  
  )  
) +  
  ggridges::geom_density_ridges(alpha = 0.5)  
  
## Picking joint bandwidth of 153
```



# Ridge plot - more categories + dplyr

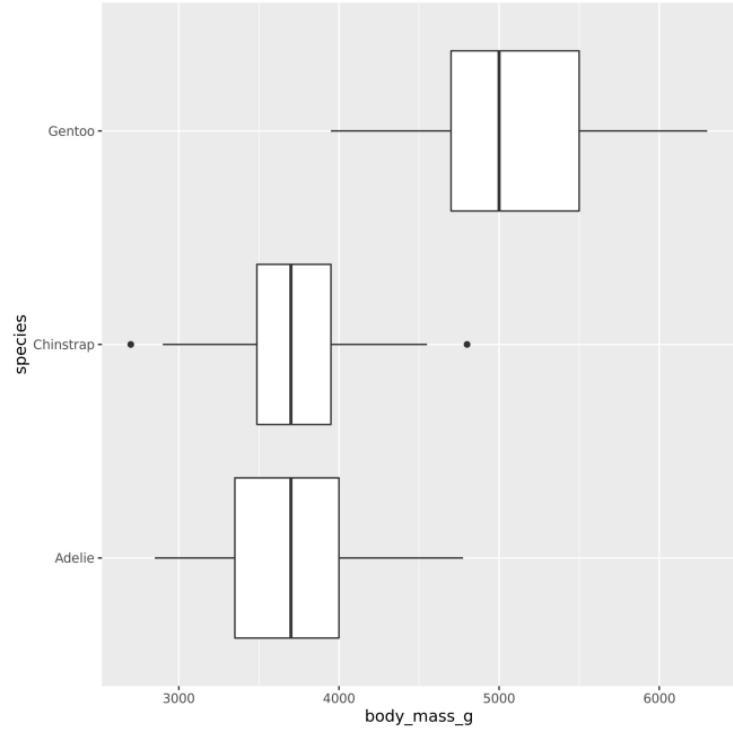
```
penguins %>%  
  mutate(  
    species_sex = paste0(species, " (", sex, ")")  
  ) %>%  
  ggplot(  
    aes(  
      x = body_mass_g,  
      y = species_sex,  
      fill = species  
    )  
  ) +  
  ggridges::geom_density_ridges(alpha = 0.5)
```

```
## Picking joint bandwidth of 127
```



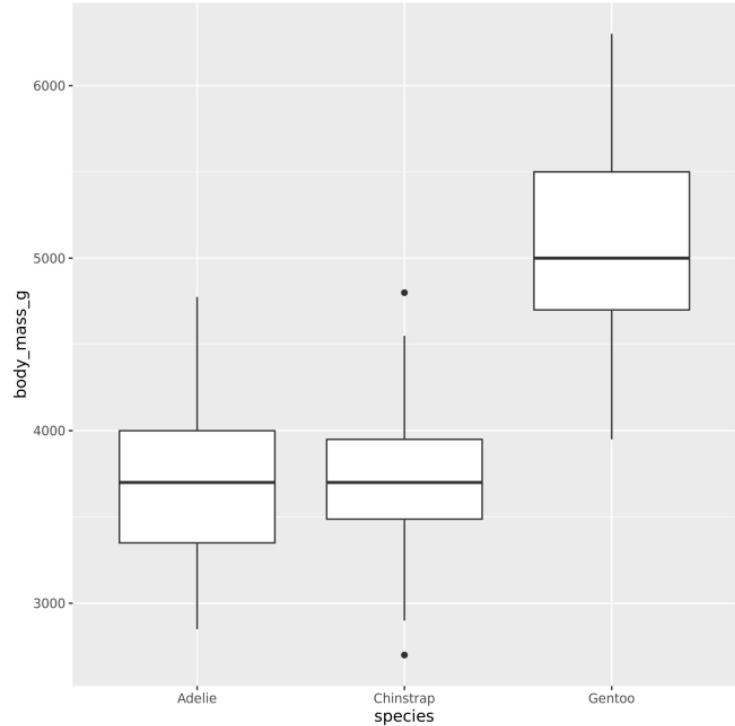
# Box plot

```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g,  
    y = species  
  )  
) +  
  geom_boxplot()
```



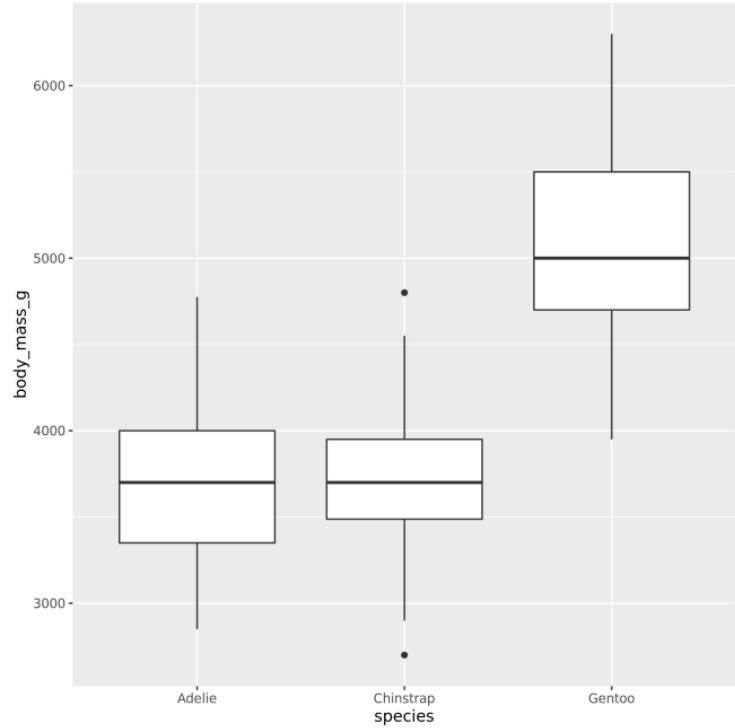
# Box plot - coord\_flip

```
ggplot(  
  penguins,  
  aes(  
    x = body_mass_g,  
    y = species  
  )  
) +  
  geom_boxplot() +  
  coord_flip()
```



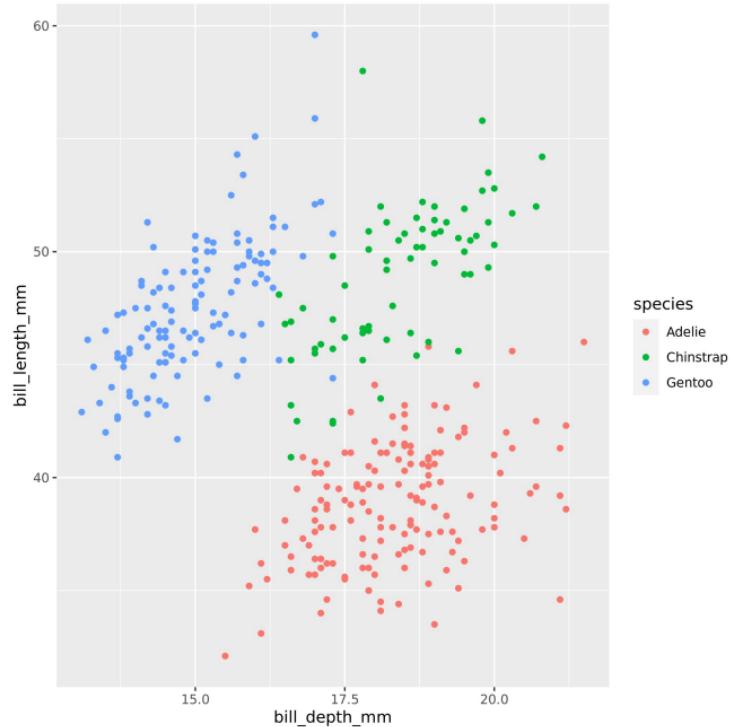
# Box plot - swap coords

```
ggplot(  
  penguins,  
  aes(  
    x = species,  
    y = body_mass_g  
  )  
) +  
  geom_boxplot()
```



# Scatter plot

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



# Scatter plot - geom\_smooth

```
ggplot(  
  penguins,  
  aes(  
    x = bill_depth_mm,  
    y = bill_length_mm,  
    color = species  
)  
) +  
  geom_point() +  
  geom_smooth(  
    fullrange = TRUE  
)  
  
## `geom_smooth()` using method = 'loess' and form
```



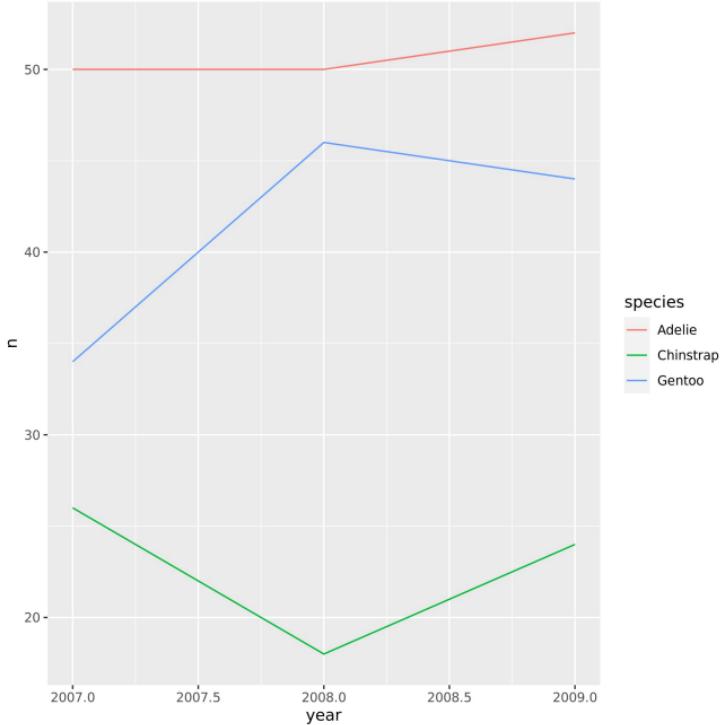
# Scatter plot - geom\_smooth w/ lm

```
ggplot(  
  penguins,  
  aes(  
    x = bill_depth_mm,  
    y = bill_length_mm,  
    color = species  
)  
  ) +  
  geom_point() +  
  geom_smooth(  
    method = "lm",  
    se = FALSE,  
    fullrange = TRUE  
)  
  
## `geom_smooth()` using formula 'y ~ x'
```



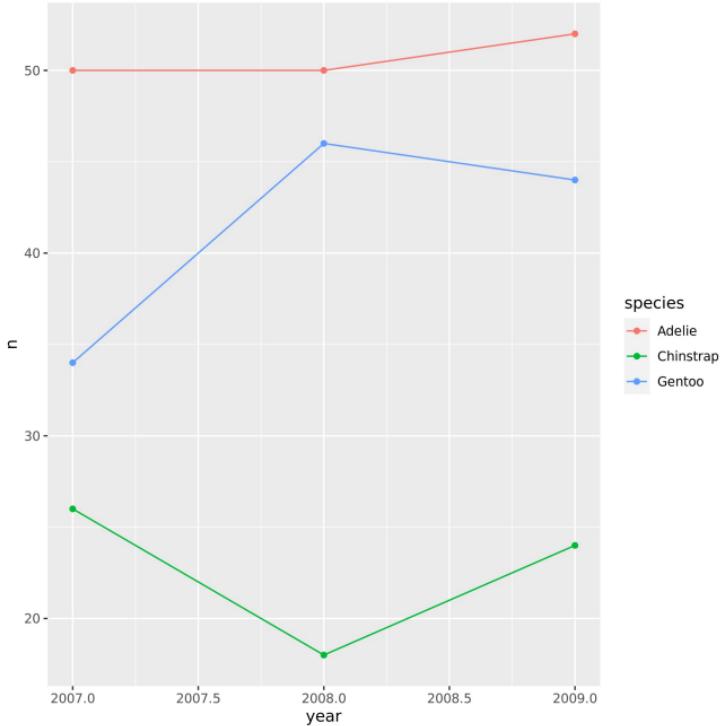
# Line plot

```
penguins %>%
  count(species, year) %>%
  ggplot(
    aes(
      x = year,
      y = n,
      color = species,
      group = species
    )
  ) +
  geom_line()
```



# Line plot - with points

```
penguins %>%
  count(species, year) %>%
  ggplot(
    aes(
      x = year,
      y = n,
      color = species,
      group = species
    )
  ) +
  geom_line() +
  geom_point()
```



# Bar plot

```
ggplot(  
  penguins,  
  aes(  
    x = species  
  )  
) +  
  geom_bar()
```



# Stacked bar plot

```
ggplot(  
  penguins,  
  aes(  
    x = species,  
    fill = island  
  )  
) +  
  geom_bar()
```



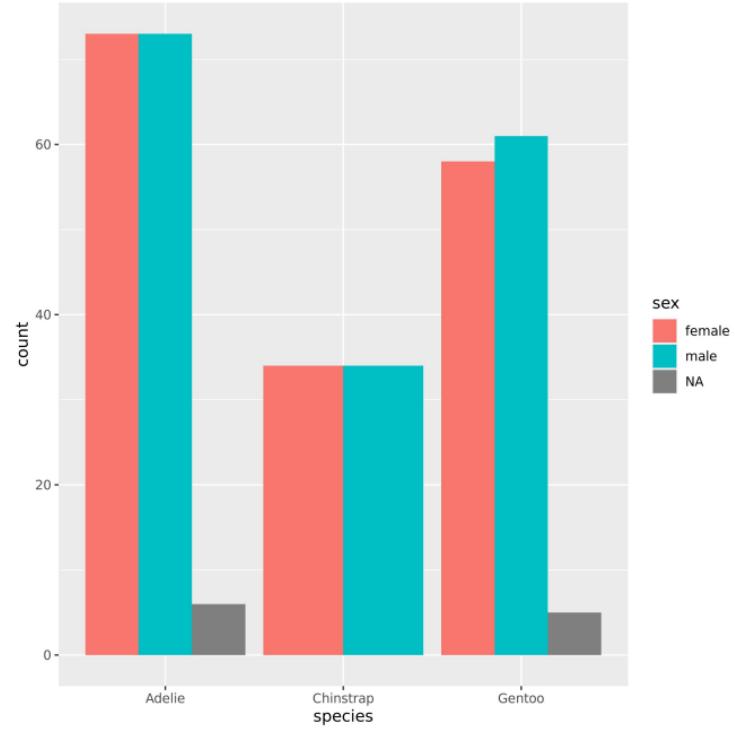
# Stacked relative frequency bar plot

```
ggplot(  
  penguins,  
  aes(  
    x = species,  
    fill = island  
  )  
) +  
  geom_bar(position = "fill")
```



# Dodged bar plot

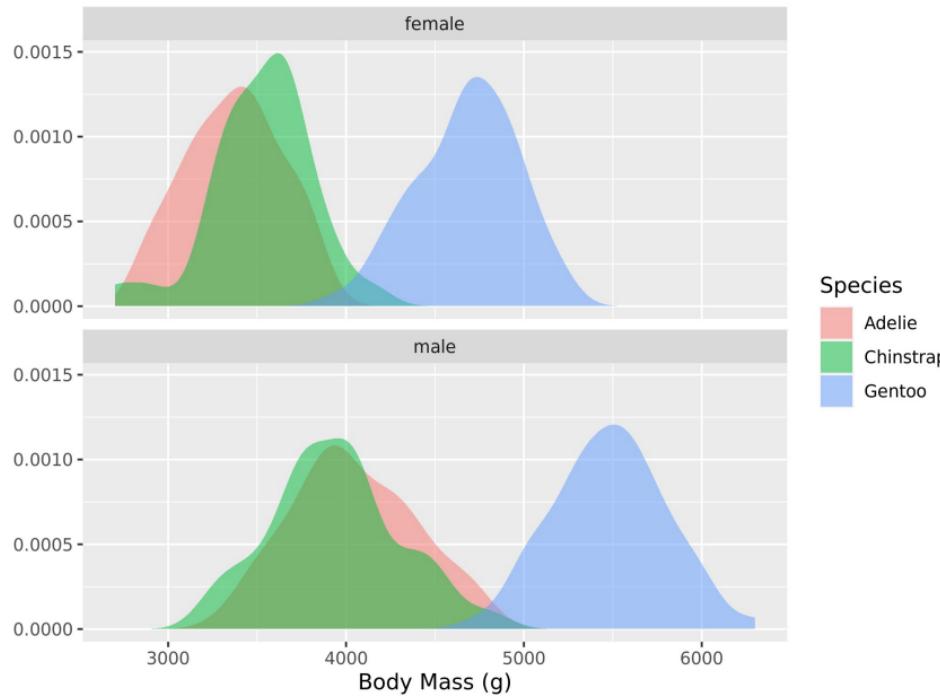
```
ggplot(  
  penguins,  
  aes(  
    x = species,  
    fill = sex  
  )  
) +  
  geom_bar(position = "dodge")
```



# Exercises

# Exercise 1

Recreate, as faithfully as possible, the following plot using ggplot2 and the penguins data.



# Exercise 2

Recreate, as faithfully as possible, the following plot from the `palmerpenguins` package readme in `ggplot2`.

