Lec 09 - Visualization with ggplot2

Statistical Programming

Fall 2021

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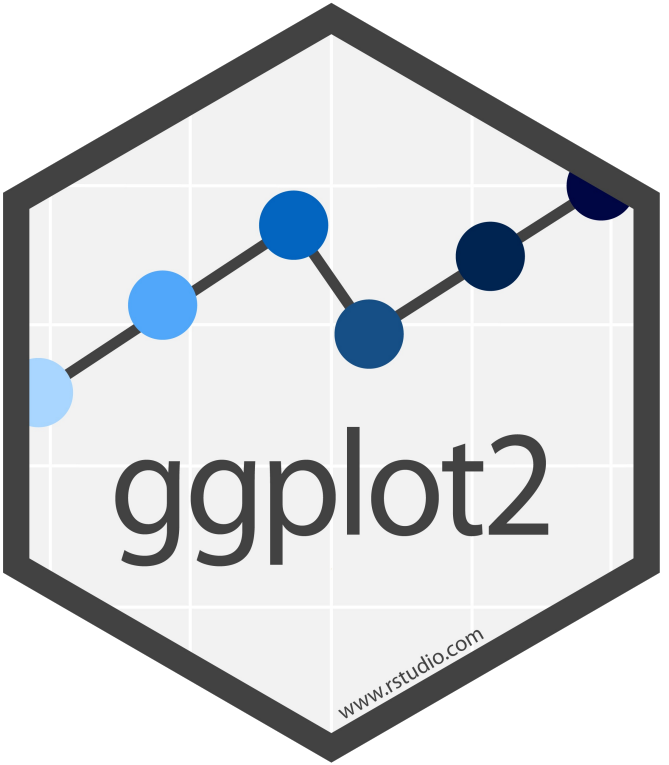

ggplot2
www.rstudio.com

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...

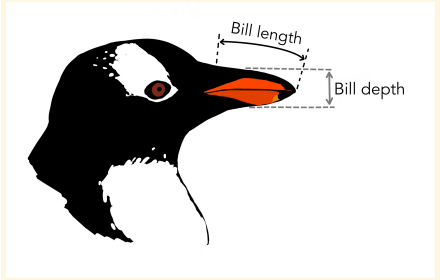
- mapping of **data**
- which may be **statistically transformed** (summarized, log-transformed, etc.)
- to **aesthetic attributes** (color, size, xy-position, etc.)
- using **geometric objects** (points, lines, bars, etc.)
- and mapped onto a specific **facet** and **coordinate system**

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.



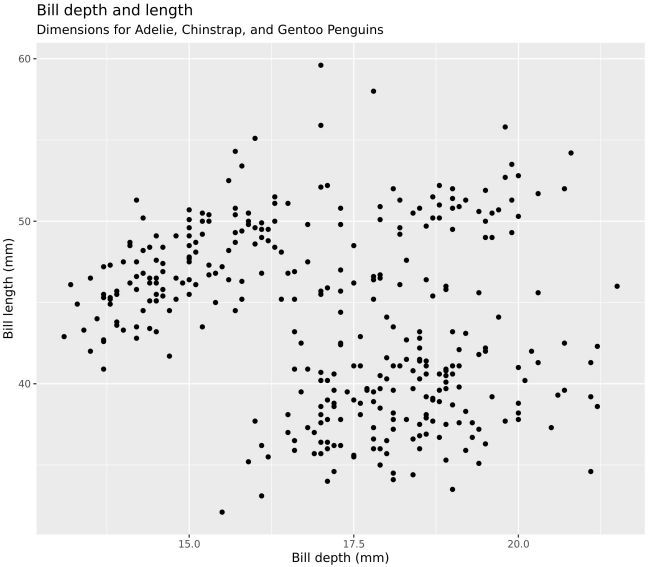

```
library(palmerpenguins)
penguins
```

```
## # 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
```



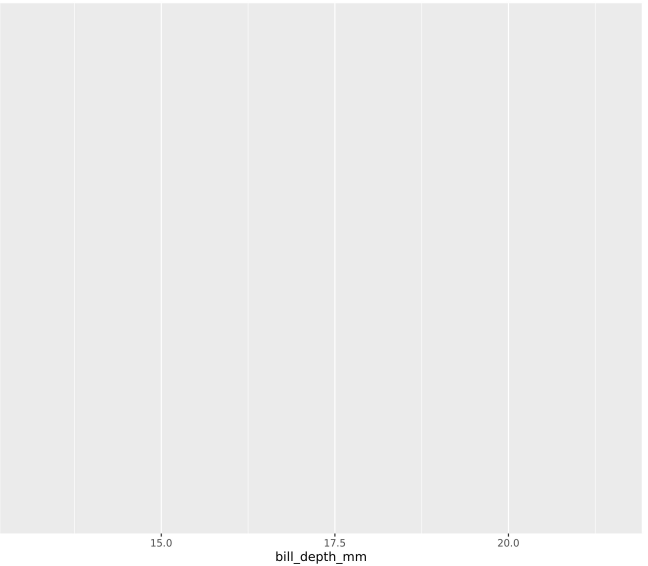
Text <-> Plot

> **Start with the `penguins` data frame**

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

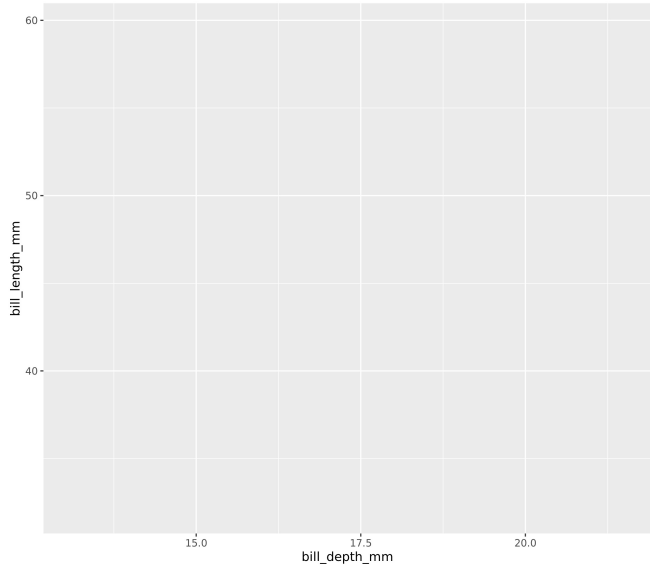
> Start with the `penguins` data frame, **map bill depth to the x-axis**

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



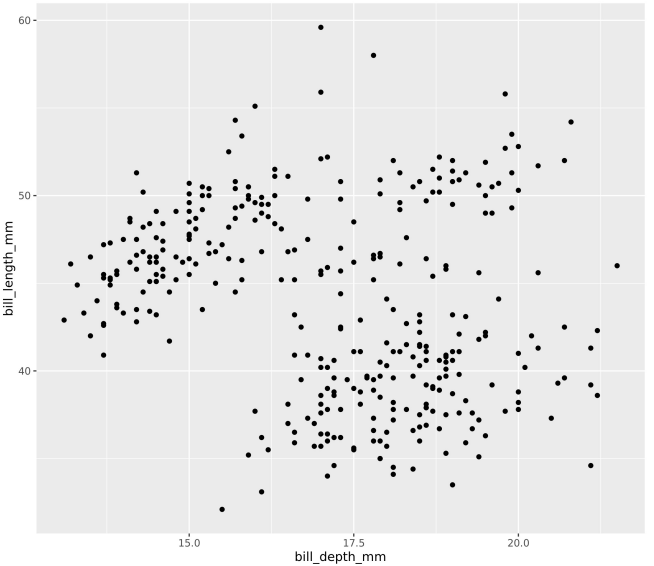
> Start with the `penguins` data frame, map bill depth to the x-axis **and map bill length to the y-axis.**

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



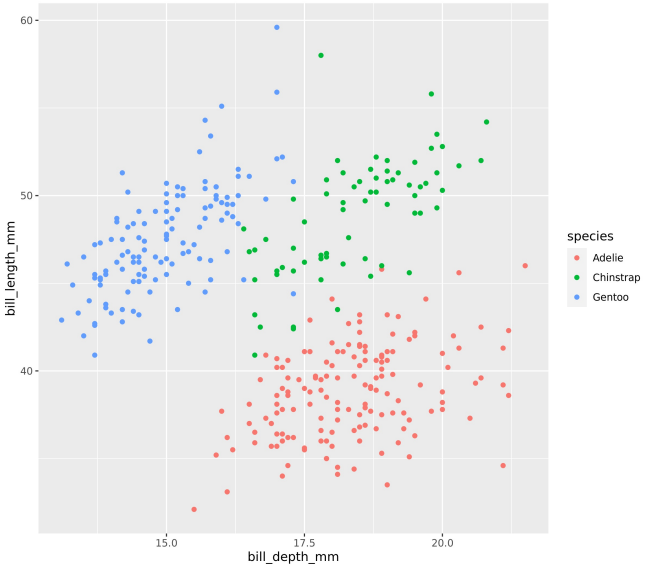
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. **Represent each observation with a point**

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



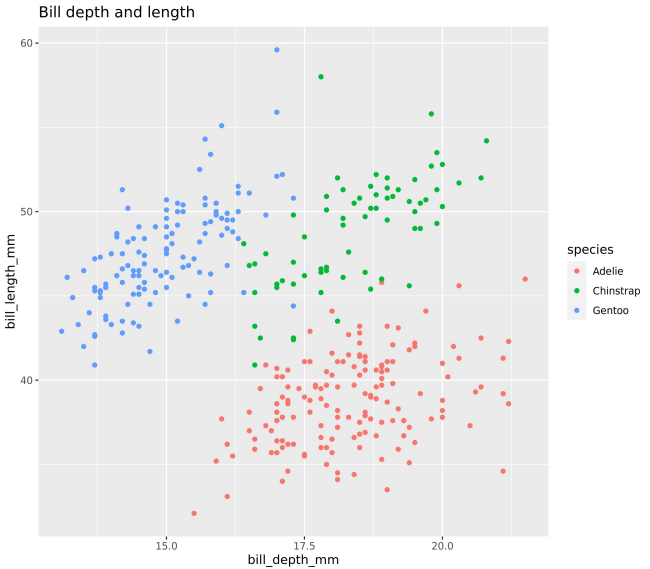
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point **and map species to the color of each point.**

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



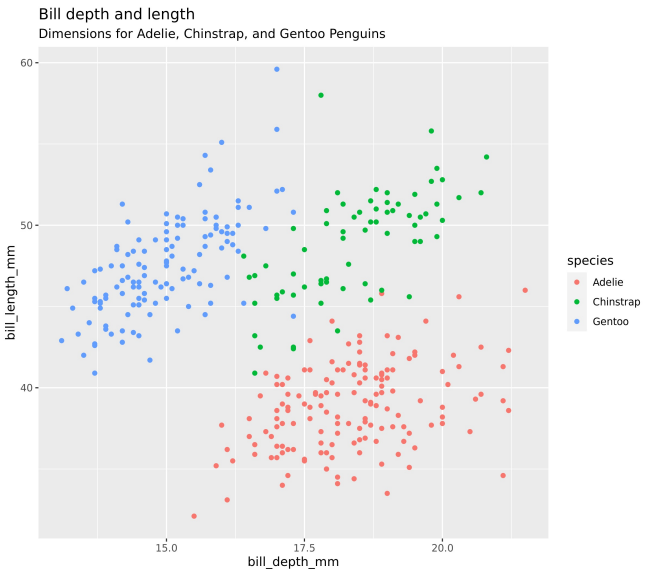
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. **Title the plot "Bill depth and length"**

```
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")
```



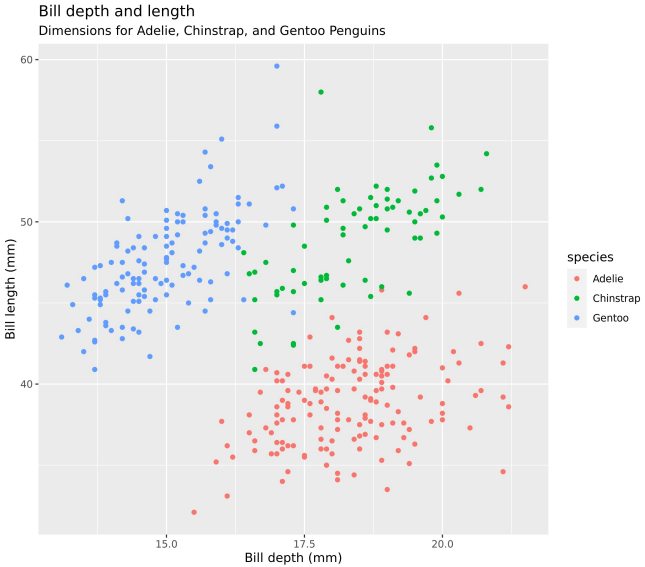
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. Title the plot "Bill depth and length", **add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins"**

```
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")
  )
```



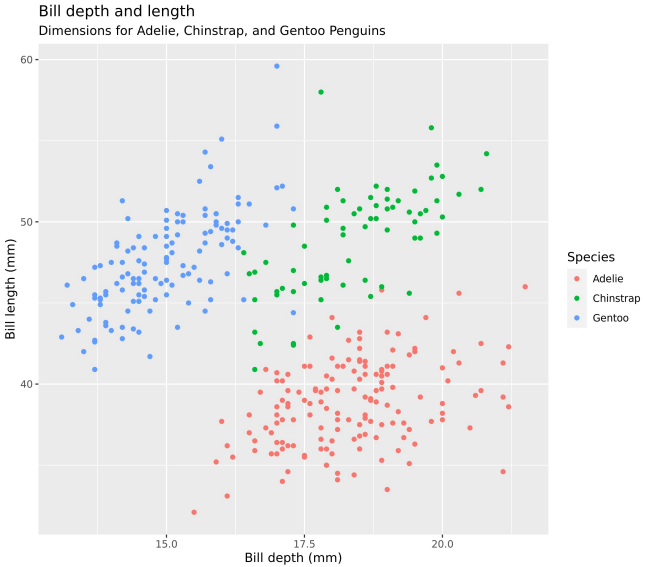
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins",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



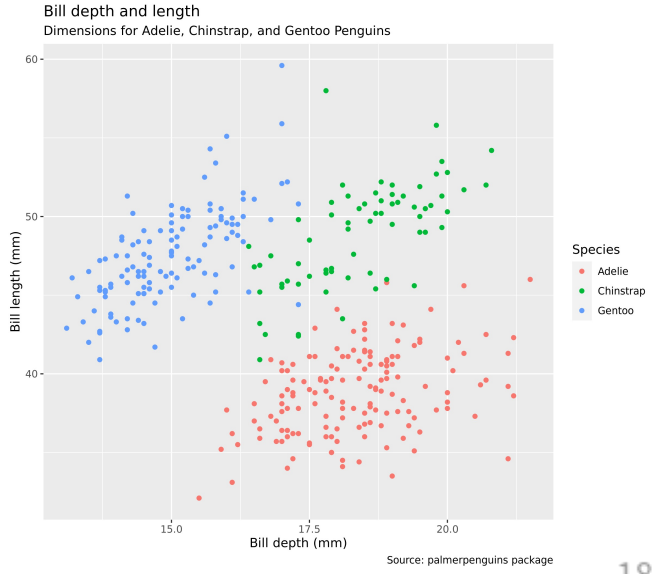
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins",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



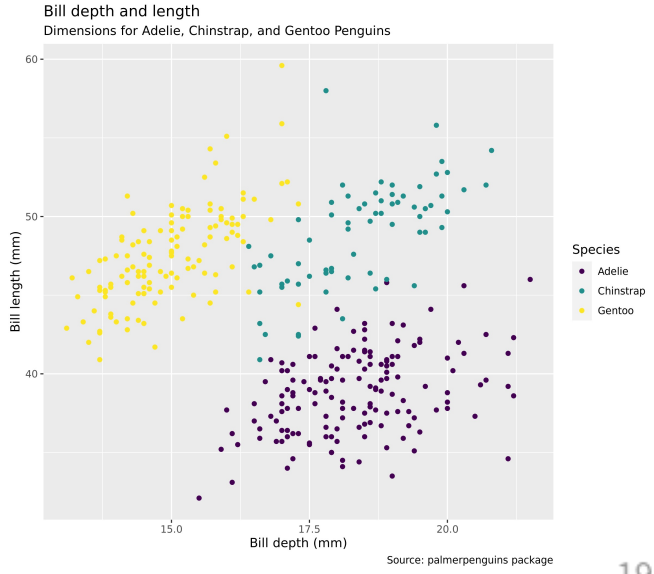
> Start with the `penguins` data frame, map bill depth to the x-axis and map bill length to the y-axis. Represent each observation with a point and map species to the color of each point. Title the plot "Bill depth and length", add the subtitle "Dimensions for Adelie, Chinstrap, and Gentoo Penguins",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

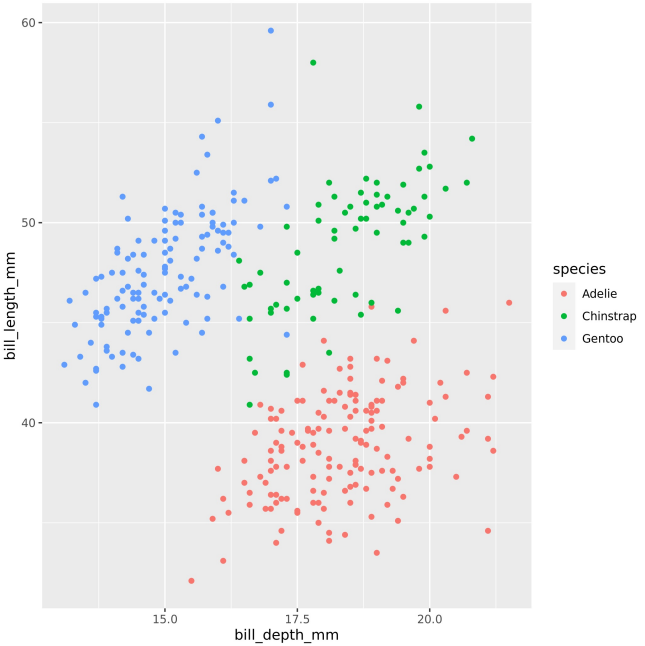
- `color`
- `shape`
- `size`
- `alpha` (transparency)

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

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

color

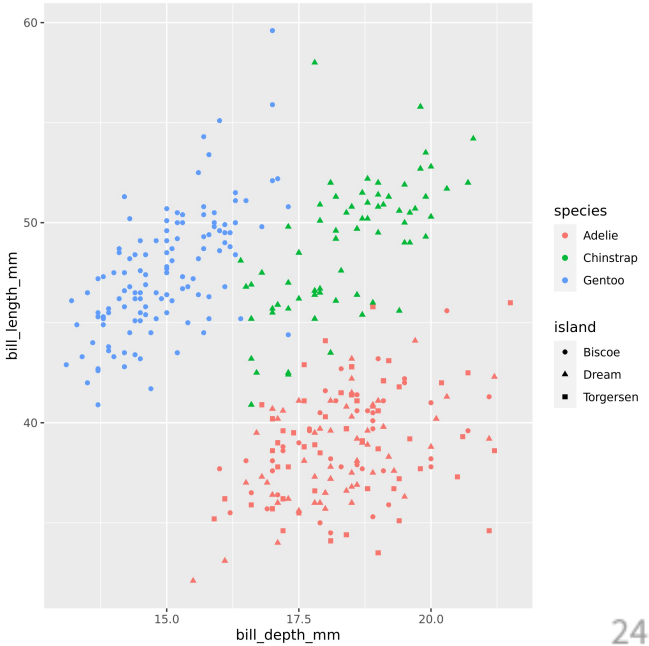
```
ggplot(
  penguins,
  aes(
    x = bill_depth_mm,
    y = bill_length_mm
  )
) +
  geom_point(
    aes(color = species)
  )
```



Shape

Mapped to a different variable than `color`

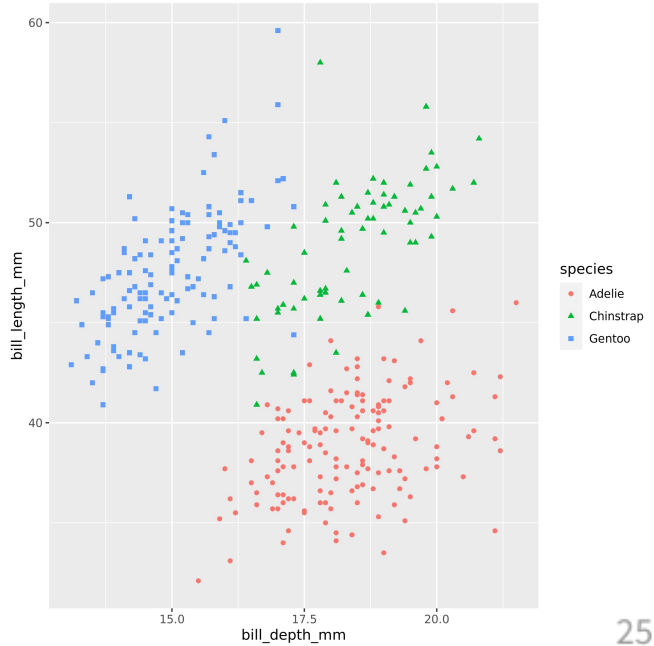
```
ggplot(
  penguins,
  aes(
    x = bill_depth_mm,
    y = bill_length_mm
  )
) +
  geom_point(
    aes(
      color = species,
      shape = island
    )
  )
```



Shape

Mapped to same variable as `color`

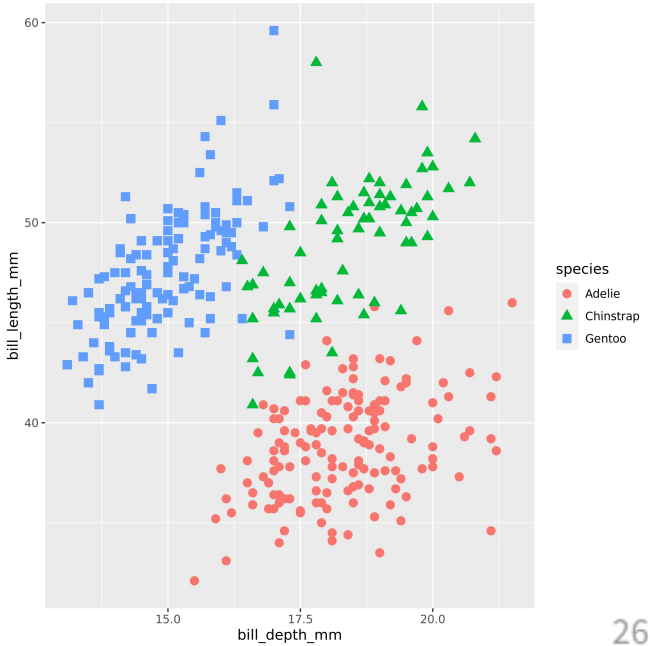
```
ggplot(
  penguins,
  aes(
    x = bill_depth_mm,
    y = bill_length_mm
  )
) +
  geom_point(
    aes(
      color = species,
      shape = species
    )
  )
```



Size

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

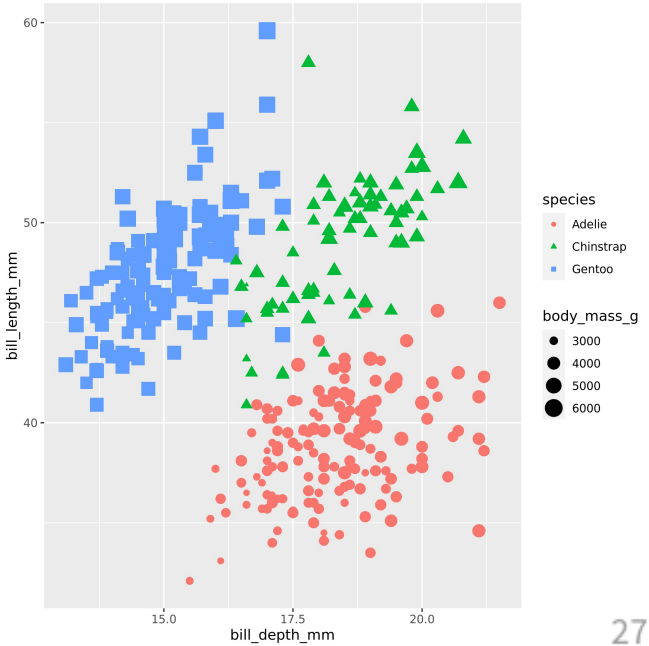
```
ggplot(
  penguins,
  aes(
    x = bill_depth_mm,
    y = bill_length_mm
  )
) +
  geom_point(
    aes(
      color = species,
      shape = species
    ),
    size = 3
  )
```



Size

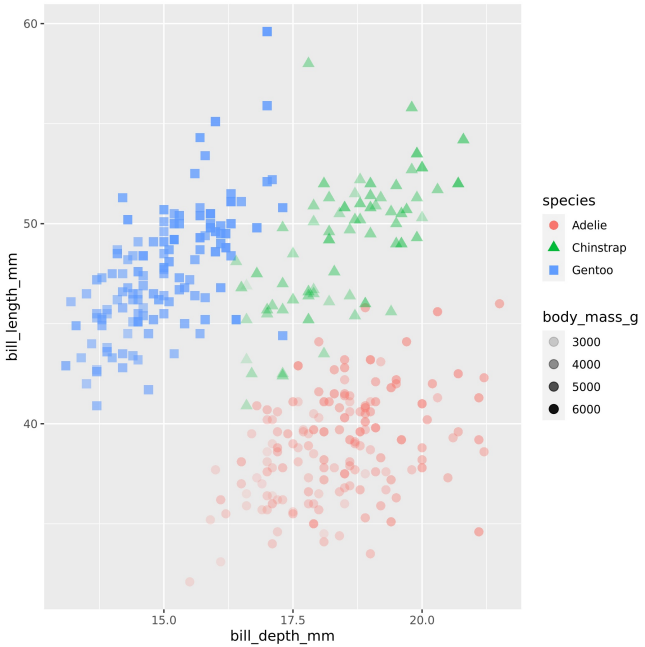
Mapped to a variable

```
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.

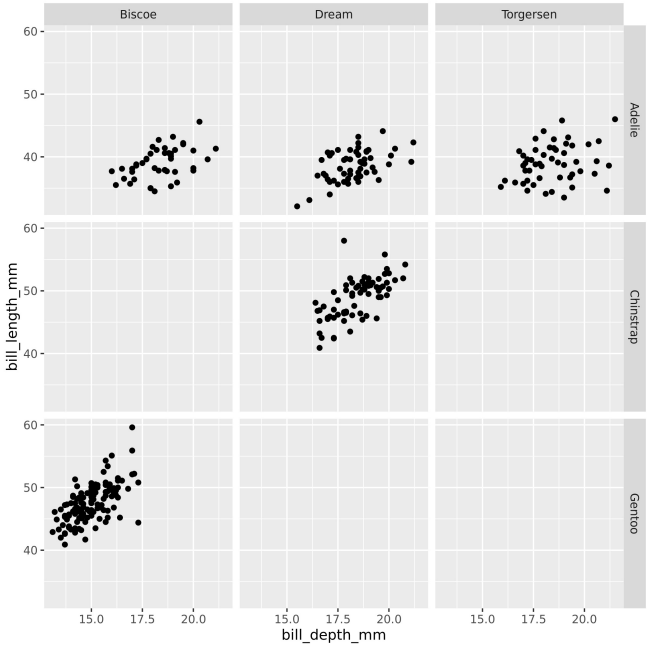
Faceting

Faceting

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

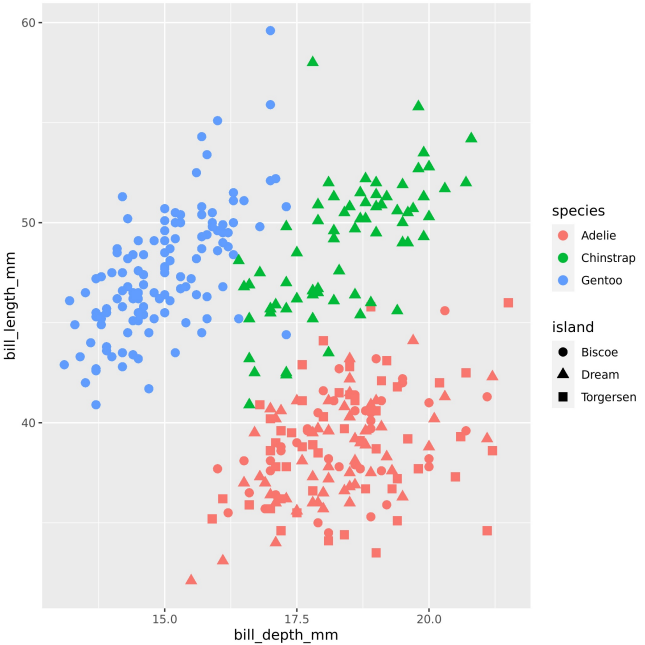
facet_grid

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



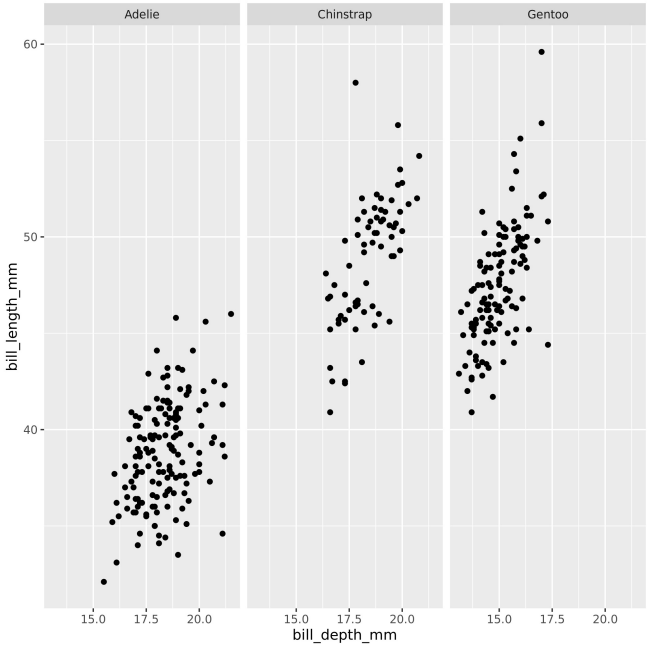
Compare with ...

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



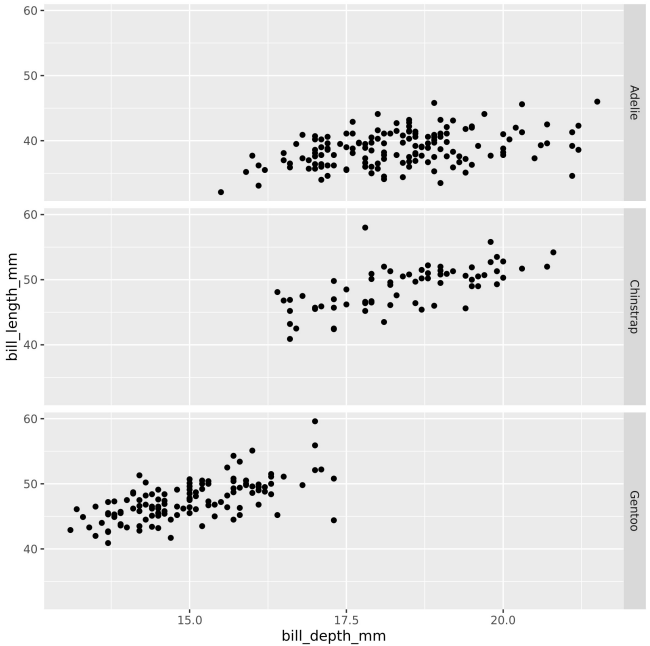
facet_grid (cols)

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



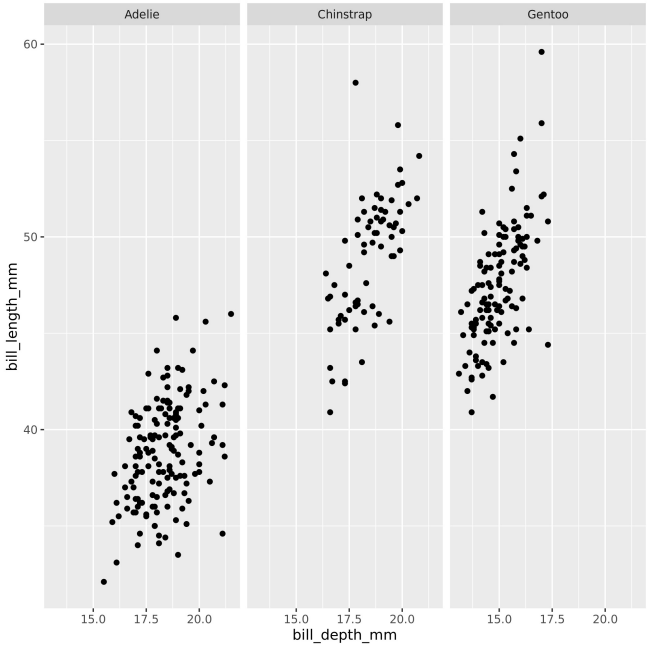
facet_grid (rows)

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



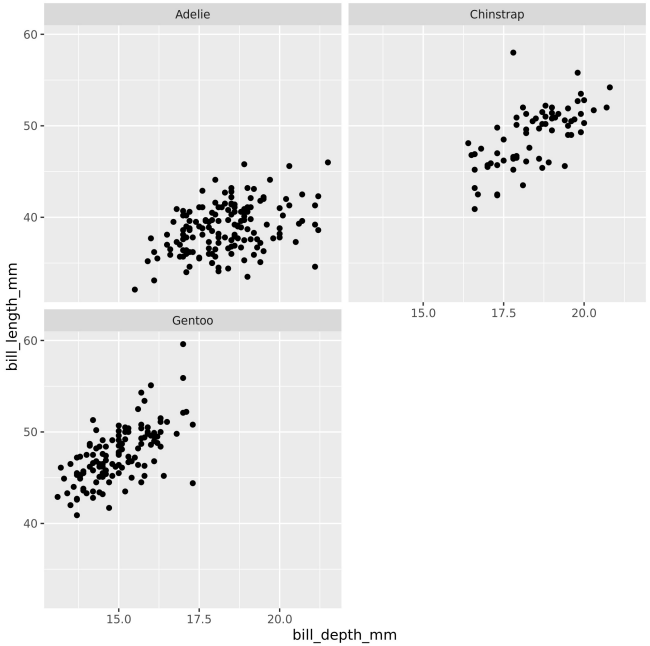
facet_wrap

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



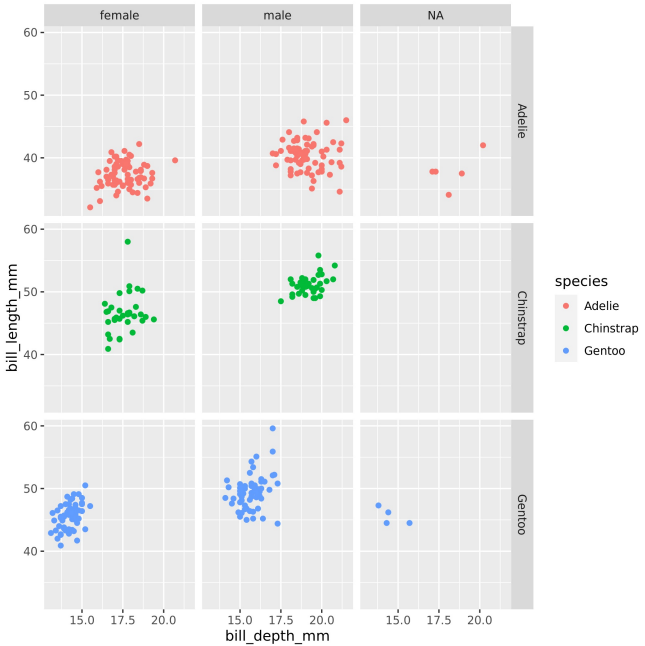
facet_wrap

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



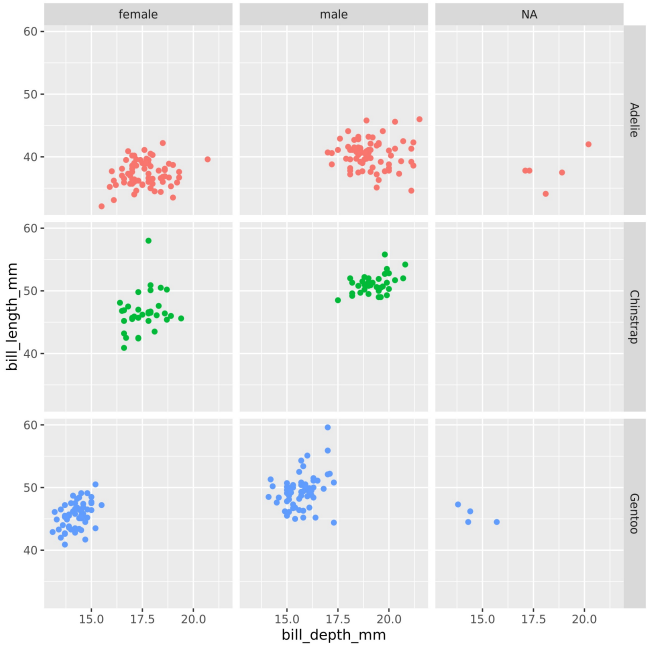
Faceting and color

```
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)
```

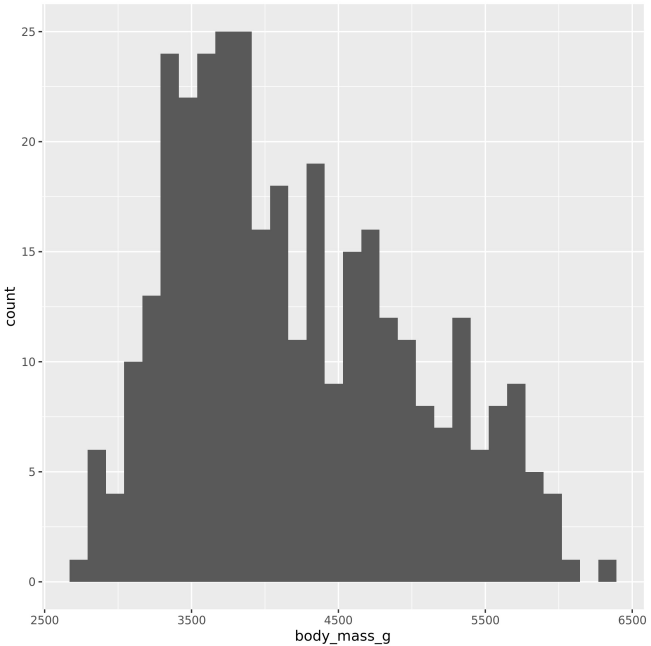


A brief plot Tour of ggplot2

Histograms

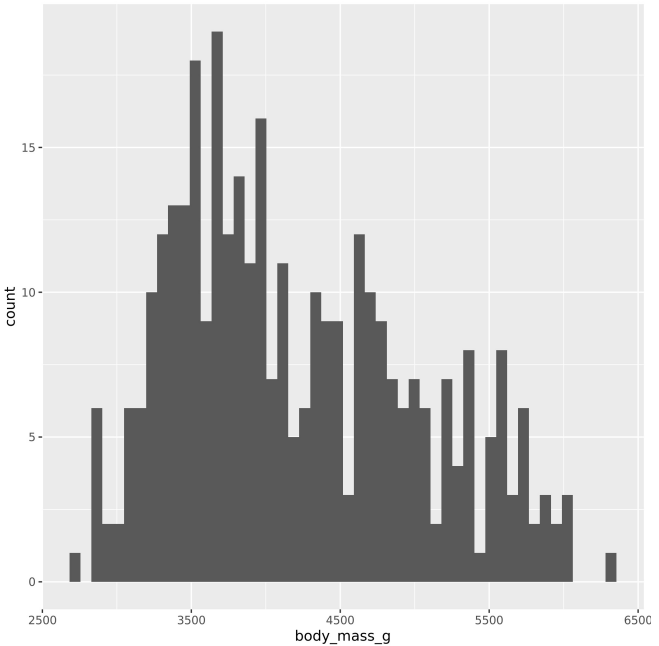
```
ggplot(
  penguins,
  aes(
    x = body_mass_g,
  )
) +
  geom_histogram()
```

```
## `stat_bin()` using `bins = 30`. Pick better val
## `binwidth`.
```



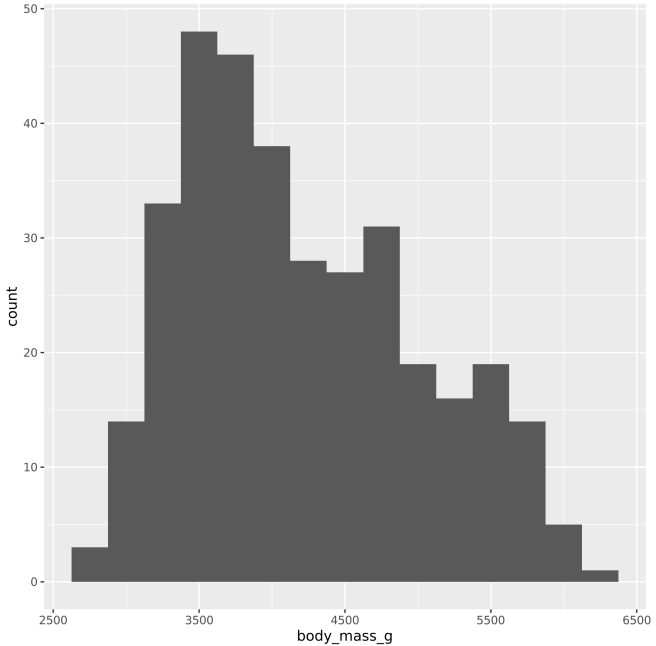
Histograms - bins

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



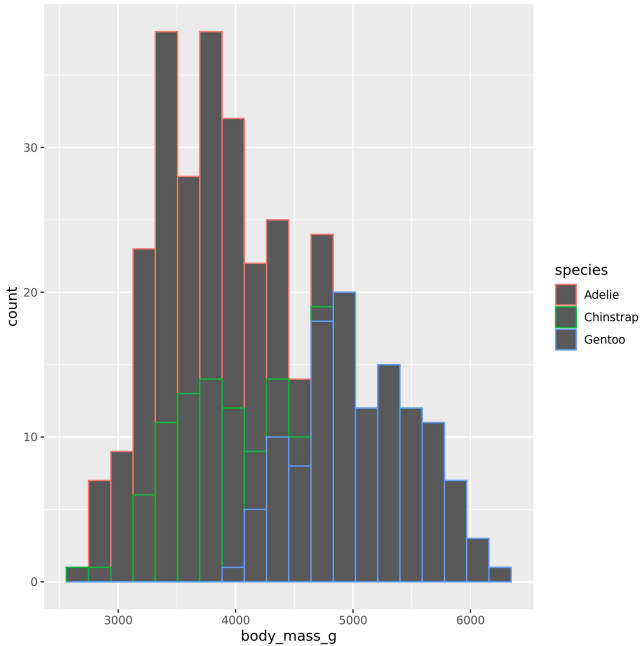
Histograms - binwidth

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



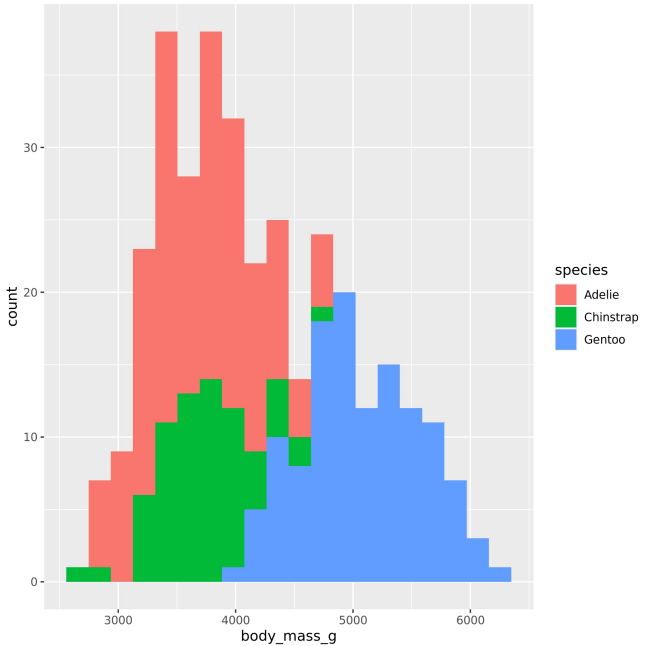
Histograms - color

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



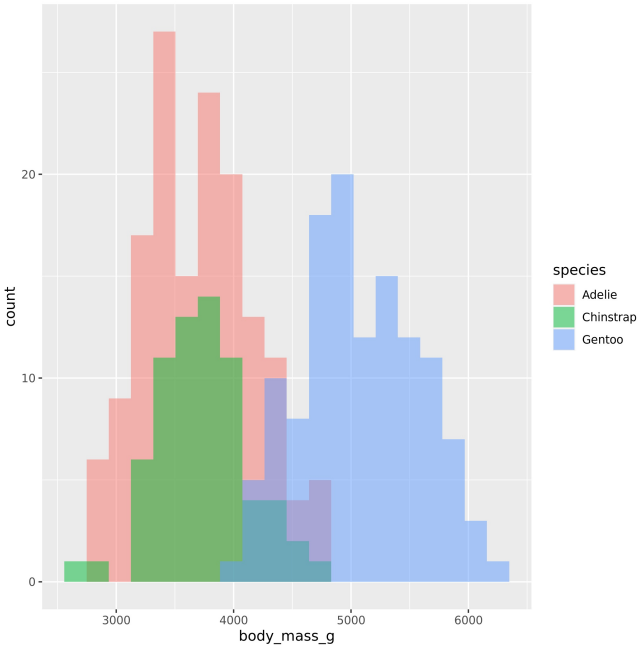
Histograms - fill

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



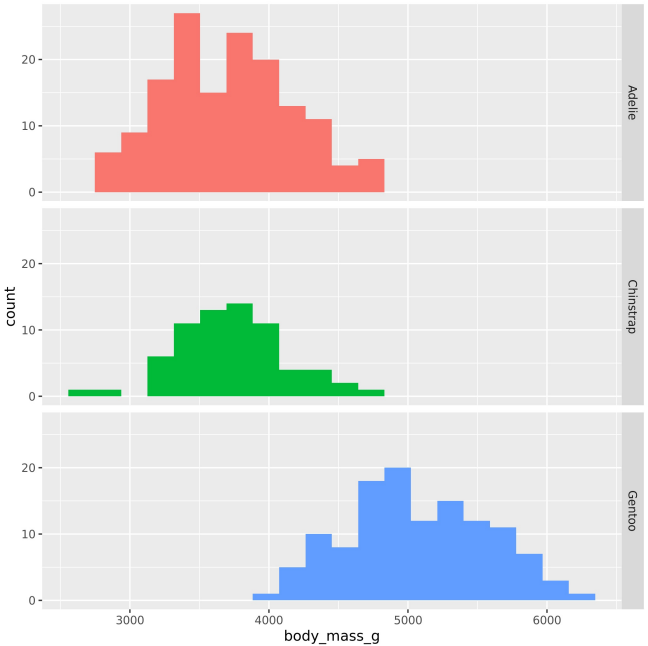
Histograms - position

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



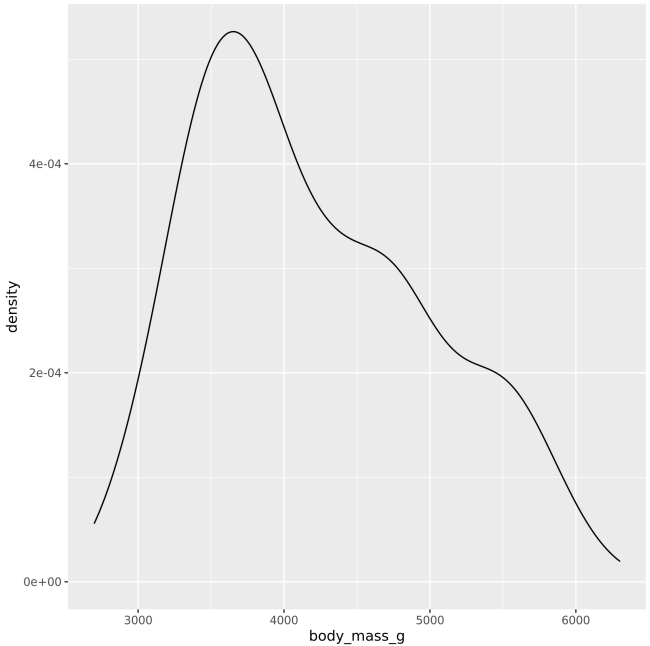
Histograms - facets

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



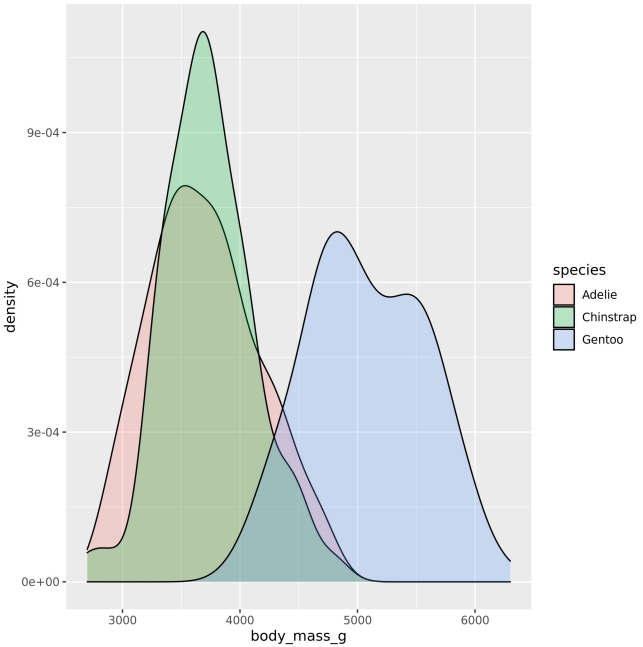
Density plot

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



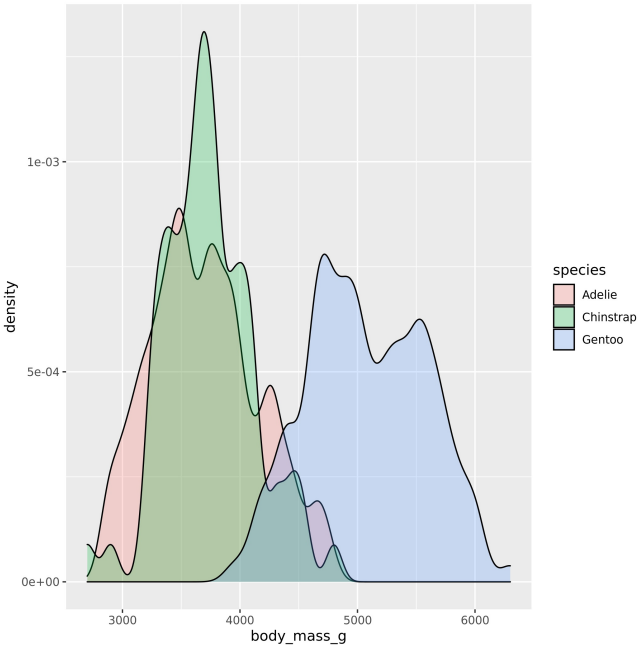
Density plot - fill

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



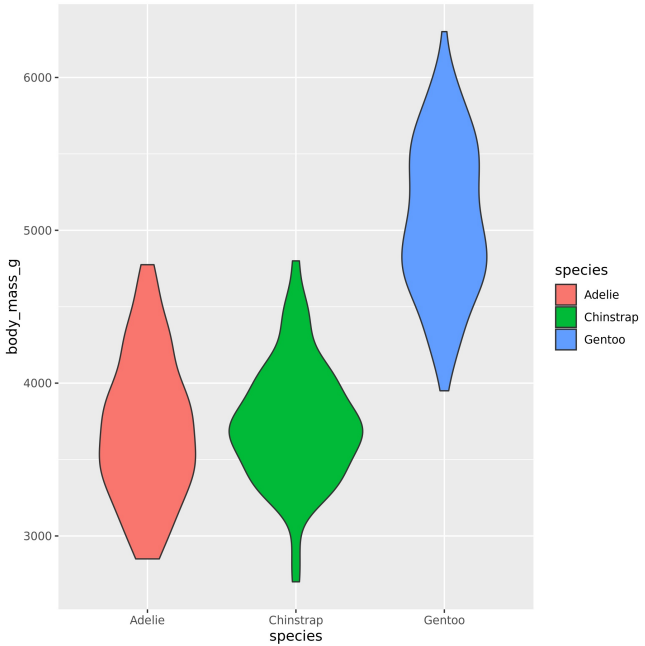
Density plot - adjust

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



Violin plot

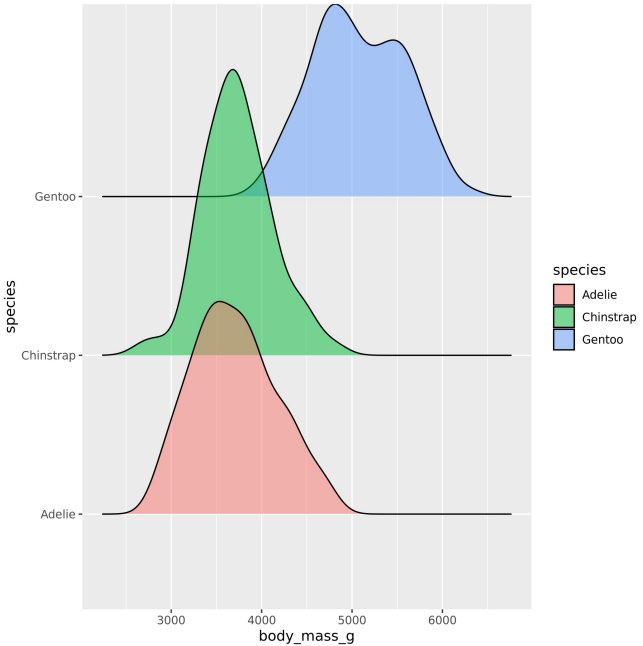
```
ggplot(
  penguins,
  aes(
    x = species,
    y = body_mass_g,
    fill = species
  )
) +
  geom_violin()
```



Ridge plot

```
ggplot(
  penguins,
  aes(
    x = body_mass_g,
    y = species,
    fill = species
  )
) +
  ggridges::geom_density_ridges(alpha = 0.5)
```

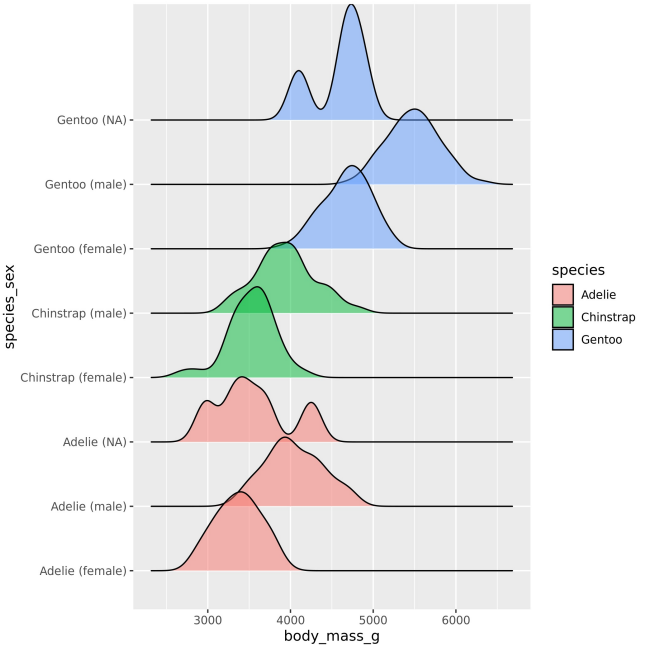
```
## Picking joint bandwidth of 153
```



Ridge plot - more categories + dplyr

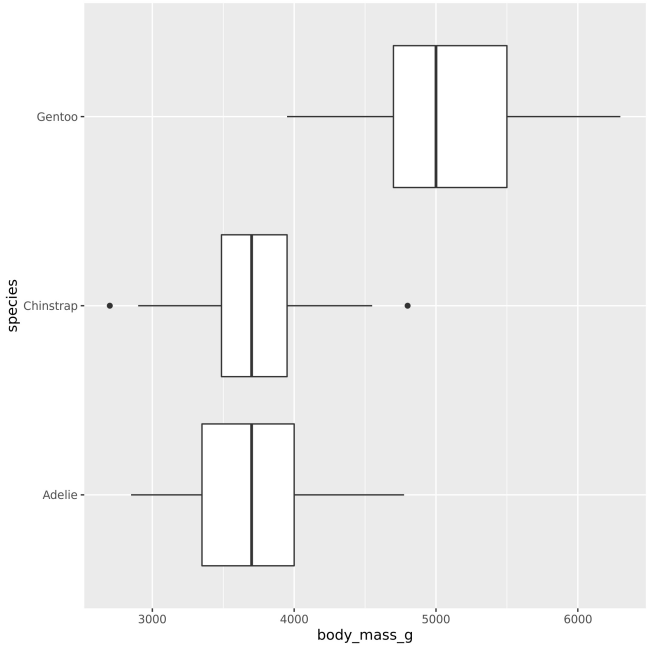
```
penguins %>%
  mutate(
    species_sex = paste0(species, " (", sex, ")")
  ) %>%
  ggplot(
    aes(
      x = body_mass_g,
      y = species_sex,
      fill = species
    )
  ) +
  ggridges::geom_density_ridges(alpha = 0.5)
```

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



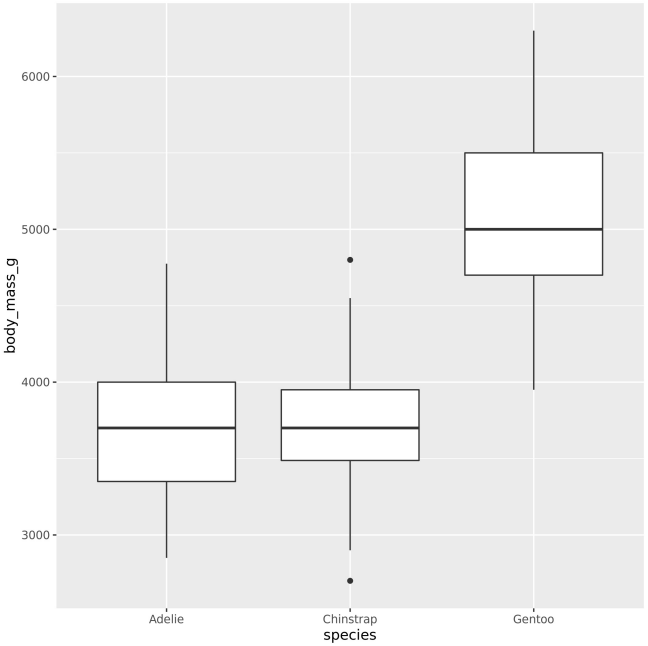
Box plot

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



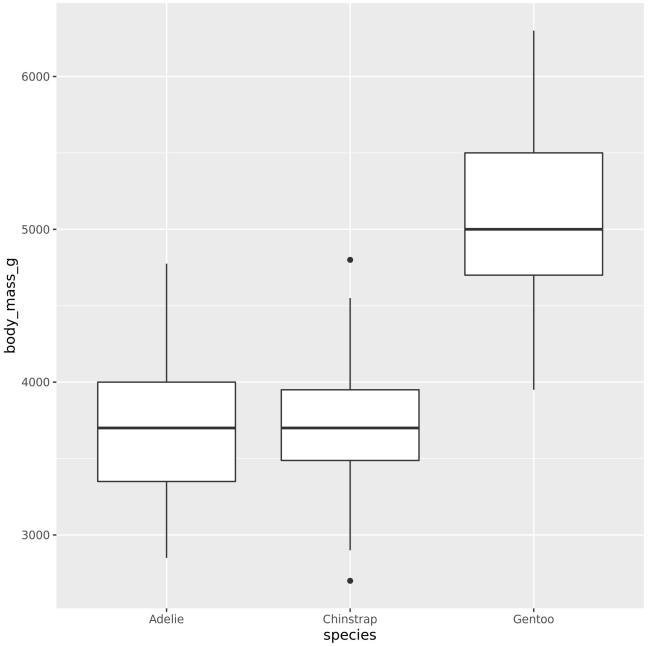
Box plot - coord_flip

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



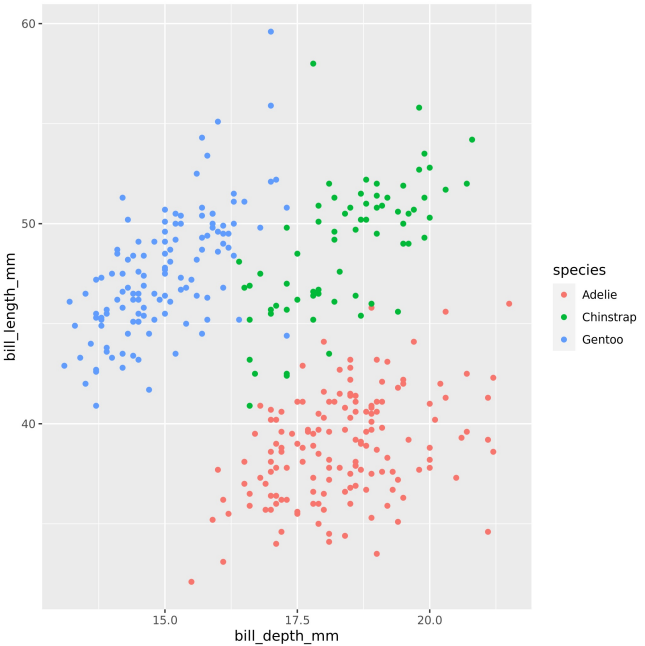
Box plot - swap coords

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



Scatter plot

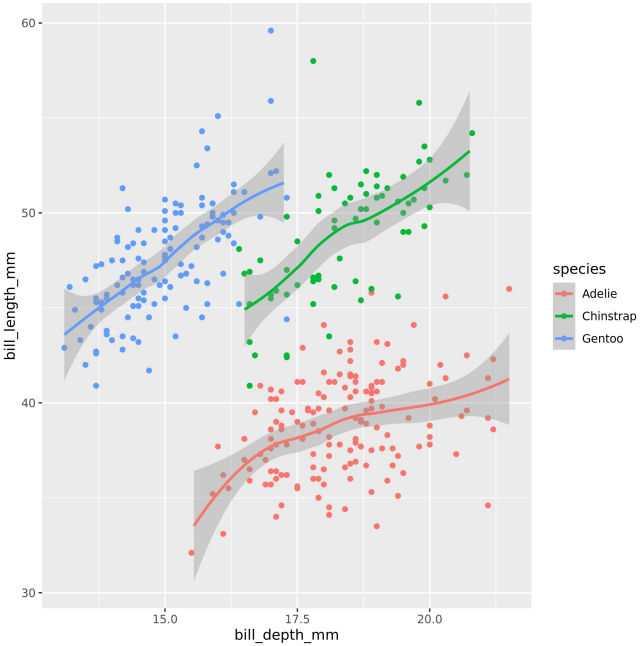
```
ggplot(
  penguins,
  aes(
    x = bill_depth_mm,
    y = bill_length_mm,
    color = species
  )
) +
  geom_point()
```



Scatter plot - geom_smooth

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

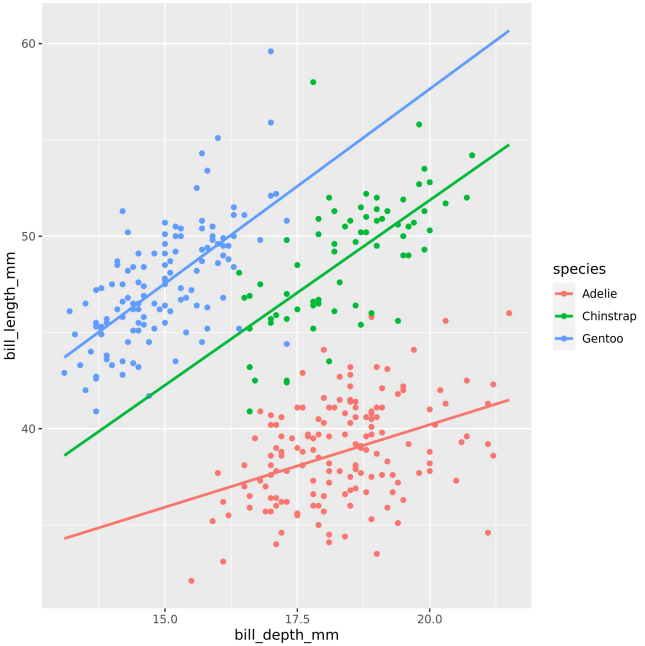
```
## `geom_smooth()` using method = 'loess' and form
```



Scatter plot - geom_smooth w/ lm

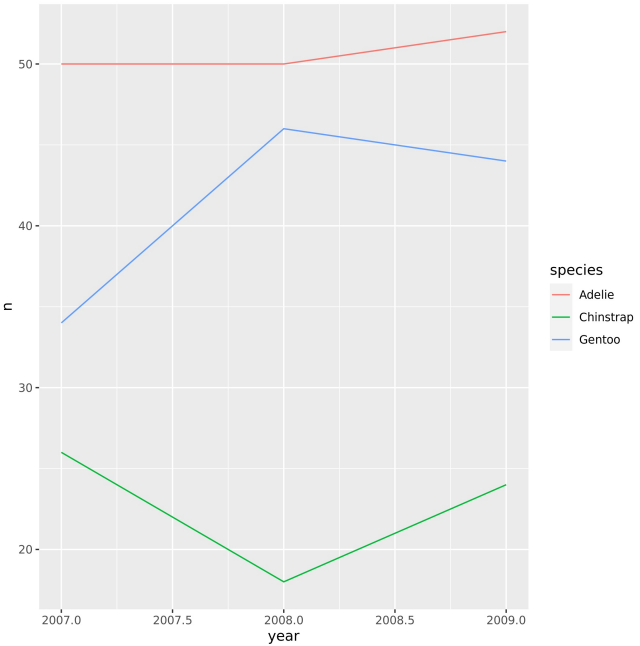
```
ggplot(
  penguins,
  aes(
    x = bill_depth_mm,
    y = bill_length_mm,
    color = species
  )
) +
  geom_point() +
  geom_smooth(
    method = "lm",
    se = FALSE,
    fullrange = TRUE
  )
```

```
## `geom_smooth()` using formula 'y ~ x'
```



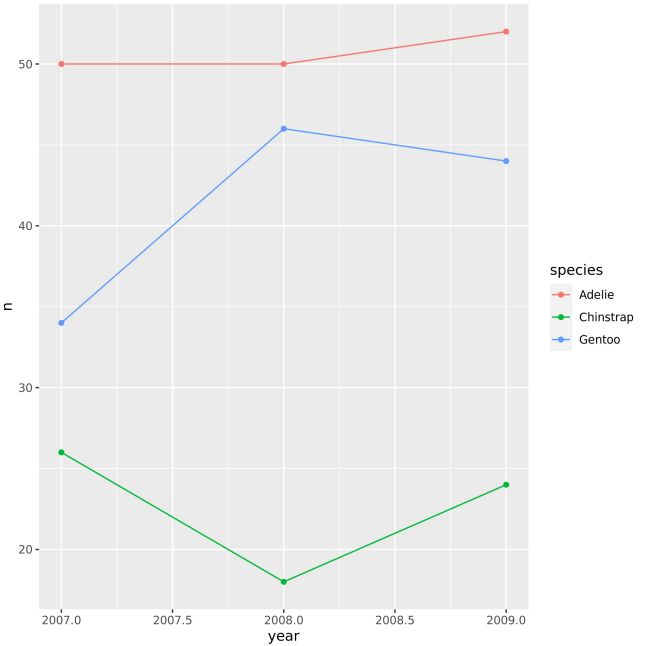
Line plot

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



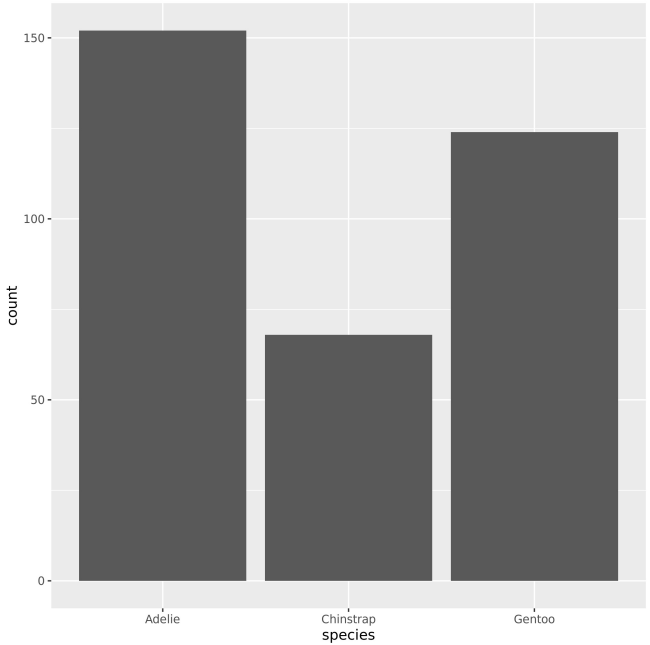
Line plot - with points

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



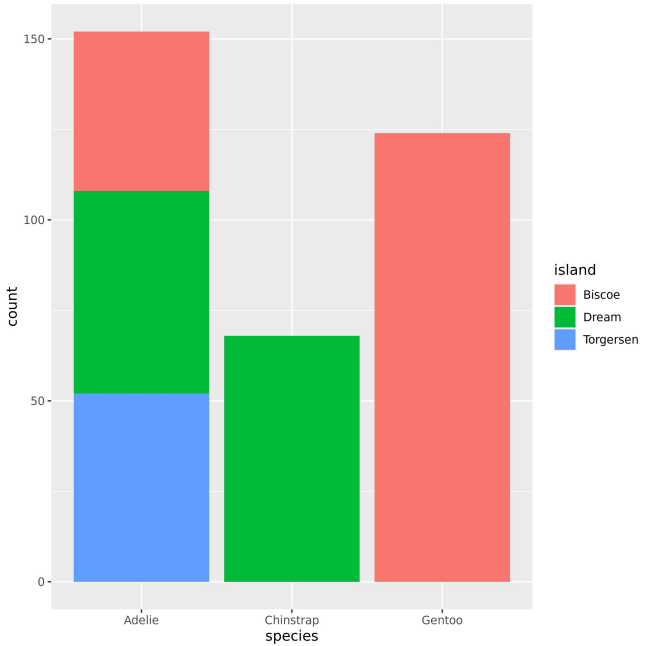
Bar plot

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



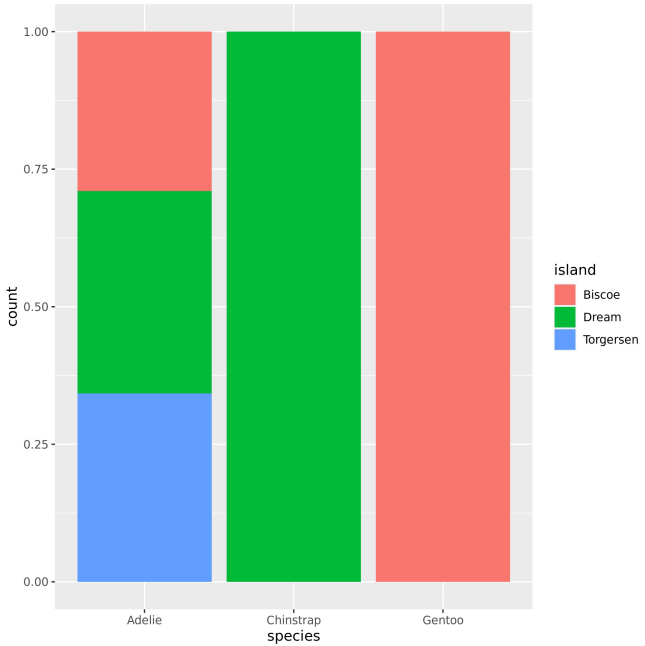
Stacked bar plot

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



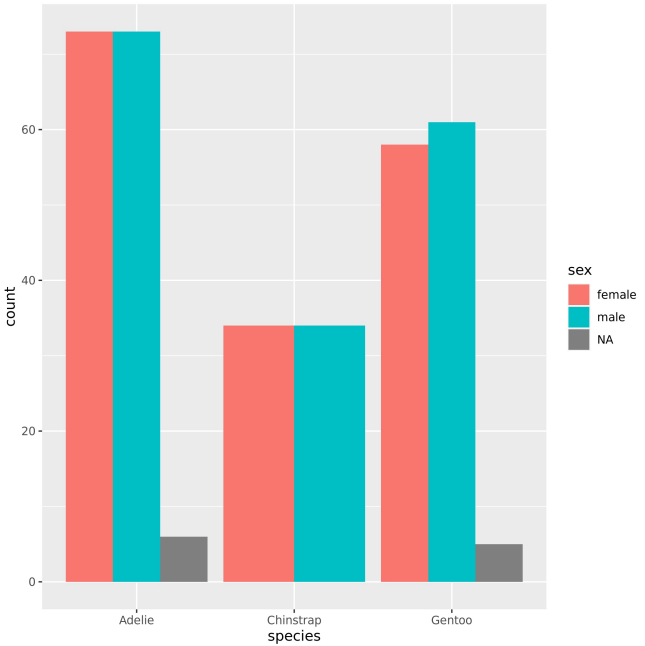
Stacked relative frequency bar plot

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



Dodged bar plot

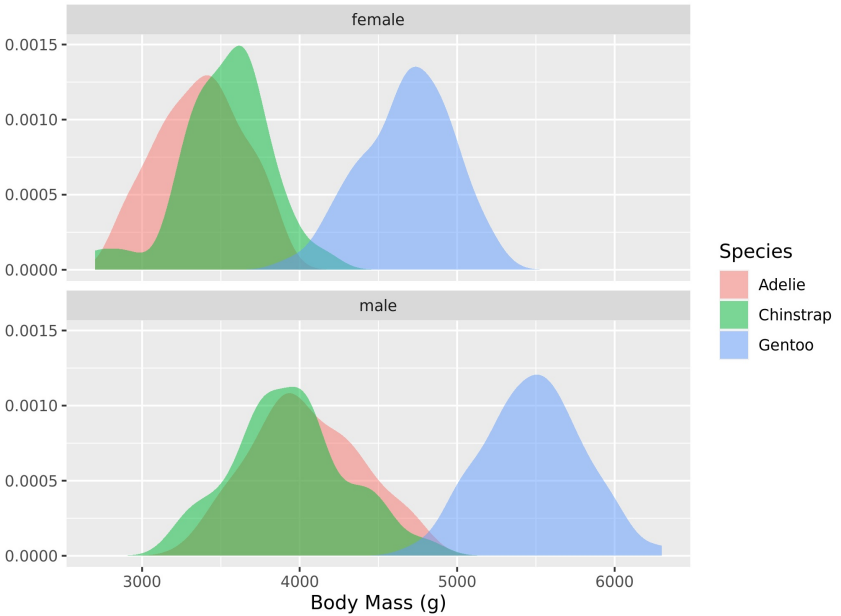
```
ggplot(
  penguins,
  aes(
    x = species,
    fill = sex
  )
) +
  geom_bar(position = "dodge")
```



Exercises

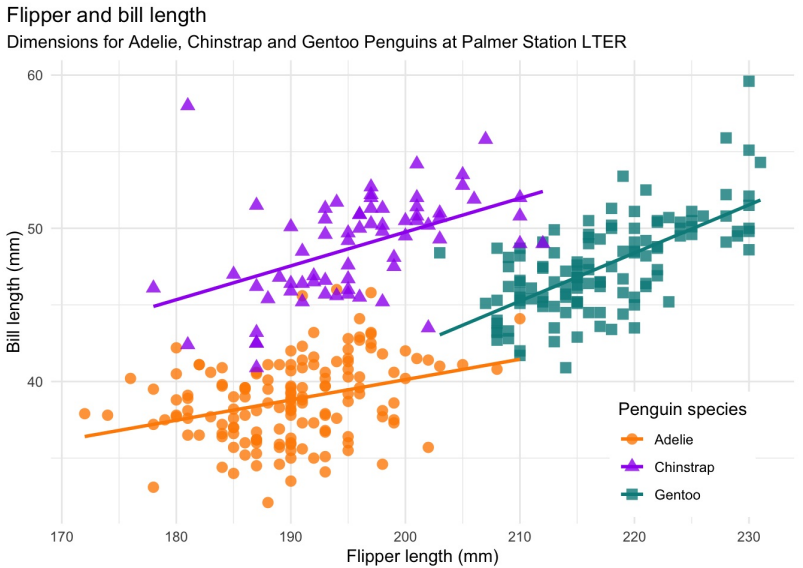
Exercise 1

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 `palmerpenguin` package readme in ggplot2.



`palmerpenguins` pkgdown site